

Body Mass Index Associated with Genome-Wide Methylation in Breast Tissue. *Breast Cancer Research and Treatment*. Hair BY, Xu Z, Kirk E, Harlid S, Sandhu R, Robinson WR, Wu MC, Olshan AF, Conway K, Taylor JA, Troester MA. Corresponding author affiliation: University of North Carolina at Chapel Hill. Corresponding author email: bhair@email.unc.edu

Supplemental Table 4. BMI-Associated Methylation Sites Correlated* with Gene Expression in the Normal Breast Study

Probe	CHR	MAPINFO	Gene	CPG Location**	Regression Coefficient	Regression p-value	Regression q-value	Correlation Coefficient
cg13674705	1	184829177	FAM129A	Other	-101.276974	8.33E-07	0.014051189	0.344148312
cg01440934	1	47051752	MKNK1	Other	-94.2767073	1.61E-06	0.01753765	-0.335594144
cg00407944	9	139424152	NOTCH1	N_Shore	-53.8192238	3.38E-06	0.01753765	-0.318637313
cg11967765	7	2774195	GNA12	N_Shore	-57.0537378	3.51E-06	0.01753765	-0.315805216
cg11967765	7	2774195	GNA12	N_Shore	-57.0537378	3.51E-06	0.01753765	-0.304079827
cg03458695	10	78163703	C10orf11	Other	-87.0132836	3.52E-06	0.01753765	-0.42568575
cg13071208	8	145686887	CYHR1	N_Shore	44.69189078	4.44E-06	0.017953013	-0.313453792
cg08202836	3	196373751	NRROS	Other	-37.8588563	4.57E-06	0.017953013	-0.321379438
cg10499974	3	46244099	CCR1	Other	-59.4992213	4.57E-06	0.017953013	-0.509214704
cg24527008	5	177870233	COL23A1	Other	-52.5998842	4.73E-06	0.017953013	0.336076261
cg27571769	4	185704063	ACSL1	Other	-42.3024057	5.07E-06	0.018431368	-0.30987341
cg25346117	1	116923256	ATP1A1	Other	-95.435554	5.35E-06	0.018431368	0.364885922
cg18418051	5	32734970	NPR3	Other	-57.9046566	6.96E-06	0.019667893	-0.347727421
cg18418051	5	32734970	NPR3	Other	-57.9046566	6.96E-06	0.019667893	-0.344993546
cg10145584	11	117860269	IL10RA	S_Shelf	-75.4771634	7.00E-06	0.019667893	-0.3182674
cg17207512	6	11382553	NEDD9	Other	-54.5438913	9.27E-06	0.020329339	-0.342631971
cg16250868	7	3710628	SDK1	Other	-23.0014561	9.88E-06	0.020530477	-0.321875136
cg03886558	12	57869490	ARHGAP9	Island	48.72049739	0.0000121	0.021227324	0.412887365
cg00471696	2	173955214	ZAK	Other	46.52696998	0.0000127	0.021227324	0.312485925
cg07113653	6	13428657	GFOD1	Other	-47.9442335	0.0000133	0.02128061	-0.357707397
cg11297046	19	49657000	HRC	S_Shore	-57.8059166	0.0000151	0.022120253	-0.363250195
cg20049422	15	26044289	ATP10A	Other	-41.9534232	0.0000154	0.02222974	-0.511643919
cg13549277	12	6659520	IFFO1	S_Shore	-57.0321044	0.0000173	0.023421457	-0.402985469
cg16903174	2	9468351	ASAP2	Other	-44.572783	0.0000177	0.023726249	-0.377155948
cg10058766	1	12186079	TNFRSF8	Other	-38.620051	0.0000178	0.023726249	-0.313556651
cg23854567	12	120694893	PXN	Other	43.28749085	0.0000179	0.023780737	0.362143519

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cg13674705	1	184829177	FAM129A	Other	-101.276974	8.33E-07	0.014051189	0.344148312
cg15757292	11	119994008	TRIM29	Other	-61.9120724	0.000018	0.02384259	0.314865953
cg24413778	13	110977981	COL4A2	Other	-45.8082533	0.0000215	0.02494369	-0.347805947
cg02933639	4	8207325	SH3TC1	Other	-60.3490474	0.0000303	0.027884148	-0.397432534
cg06787669	7	45018789	MYO1G	Other	-49.7575419	0.000032	0.028284147	-0.484234196
cg14669515	1	9386821	SPSB1	Other	47.05358741	0.0000329	0.028423821	0.526071625
cg14669515	1	9386821	SPSB1	Other	47.05358741	0.0000329	0.028423821	0.37237836
cg04217515	21	46325853	ITGB2	S_Shore	-50.8259327	0.0000338	0.028646773	-0.402658542
cg01457077	2	239228573	TRAF3IP1	N_Shore	80.9412732	0.0000339	0.028646773	0.316682326
cg06385449	11	63974123	FERMT3	N_Shore	-64.538606	0.0000343	0.028686554	-0.330149066
cg10271819	7	139426030	HIPK2	Other	-51.7229897	0.0000358	0.028686554	-0.337330308
cg06942450	20	57583520	CTSZ	S_Shore	-78.8698746	0.0000383	0.029141948	-0.347182691
cg04516672	10	126411663	FAM53B	Other	-28.8922973	0.0000399	0.029317869	-0.301108942
cg17184477	15	67360705	SMAD3	S_Shore	51.26763455	0.0000422	0.029413144	0.309560487
cg13795831	20	57582706	CTSZ	S_Shore	-45.3974555	0.0000429	0.029413144	-0.420406302
cg21271945	1	2080081	PRKCZ	N_Shelf	-39.4927655	0.0000431	0.029413144	0.432941869
cg00539174	20	57583434	CTSZ	S_Shore	-66.2131124	0.0000486	0.029863233	-0.392719359
cg01721313	3	169751609	GPR160	N_Shelf	-86.6887198	0.0000492	0.029863233	0.3195447
cg11433866	12	115126908	TBX3	S_Shore	-67.2161668	0.0000494	0.029863233	0.463476999
cg20306863	1	3593812	TP73	Other	-63.1574357	0.0000501	0.029863233	-0.31711067
cg20682563	5	133460874	TCF7	Other	36.85168441	0.0000506	0.029863233	-0.412707244
cg18315380	7	1095666	GPR146	N_Shore	-42.5972866	0.0000537	0.030379861	-0.452534009
cg06579738	11	111165311	C11orf93	N_Shelf	28.51727134	0.0000563	0.030715591	-0.355951033
cg17013990	1	161091682	NIT1	S_Shelf	-51.6580163	0.0000564	0.030715591	0.35937513
cg10163050	X	153637650	DNASE1L1	N_Shelf	-71.771804	0.0000566	0.030715591	-0.303283861
cg02794695	8	134072611	SLA	Other	-56.4211034	0.000058	0.03071835	-0.304140433
cg09676376	12	54779077	ZNF385A	Other	-68.9131942	0.0000596	0.030864952	-0.364534874
cg00520380	22	31643997	LIMK2	Other	64.92136629	0.0000608	0.031167938	-0.397712157
cg01578632	16	69958298	WWP2	Other	27.27033285	0.0000614	0.03116932	-0.300824996
cg07103201	17	20171047	SPECC1	Other	-29.2620128	0.0000632	0.031251895	-0.43441431
cg07103201	17	20171047	SPECC1	Other	-29.2620128	0.0000632	0.031251895	0.372381964

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cg13674705	1	184829177	FAM129A	Other	-101.276974	8.33E-07	0.014051189	0.344148312
cg18576206	22	44392384	PARVB	Island	-44.8674889	0.0000655	0.031438207	-0.406940429
cg11589536	3	46250518	CCR1	Other	-73.5453451	0.0000671	0.031449516	-0.508539897
cg03514239	1	153329781	S100A9	Other	-82.3085371	0.0000699	0.031600501	-0.372705885
cg00620452	3	32147645	GPD1L	N_Shore	54.03599609	0.0000705	0.031679513	-0.306121011
cg02671382	1	120457856	NOTCH2	Other	56.32861277	0.0000725	0.031945154	0.315673262
cg23682913	1	2080710	PRKCZ	N_Shore	-57.1478494	0.0000725	0.031945154	0.544192206
cg13279083	4	110128090	COL25A1	Other	42.08120393	0.0000739	0.032293853	0.374526886
cg03342032	13	94725495	GPC6	Other	26.89400088	0.0000761	0.032516439	0.353542051
cg03857553	22	29976613	NIPSNAP1	N_Shore	25.23257142	0.0000762	0.032516439	-0.368926472
cg26938118	18	56059556	NEDD4L	Other	53.84284933	0.000077	0.032516439	-0.380406978
cg22609908	12	858759	WNK1	N_Shelf	-27.7460806	0.0000812	0.032902116	-0.368977827
cg26371957	12	739280	NINJ2	Other	-18.0394608	0.0000824	0.033059549	-0.328590991
cg18809126	3	11623526	VGLL4	Other	36.87658165	0.0000844	0.033392811	-0.346109734
cg23013850	2	225266304	FAM124B	Other	-33.5574251	0.0000858	0.033542161	-0.308753012
cg13826666	9	136600241	SARDH	Other	-52.6148075	0.0000863	0.033542161	0.353481609
cg11300147	12	7596703	CD163L1	S_Shelf	-25.3911477	0.0000921	0.034018006	-0.437121539
cg12080566	2	75798232	EVA1A	Other	68.67582074	0.0000938	0.034274745	-0.302090897
cg08354401	5	177824353	COL23A1	S_Shore	48.88484681	0.0000969	0.034660739	-0.348502701
cg26863600	19	2616921	GNG7	S_Shelf	-25.1013393	0.0000972	0.034660739	0.435841136
cg07431973	14	52142383	FRMD6	Other	30.2567186	0.0000978	0.034759923	-0.364099383
cg03277819	12	772529	NINJ2	Other	25.96065939	0.000107866	0.035661028	0.395542267
cg16129800	11	2920414	SLC22A18	N_Shelf	-55.7550841	0.0001109	0.036015728	0.346017553
cg20271057	3	16974160	PLCL2	Other	-56.8921052	0.000111493	0.0360725	-0.301263064
cg23787937	12	29303160	FAR2	S_Shore	-48.9595654	0.000112136	0.036082857	-0.473436885
cg08160072	2	40009501	THUMPD2	S_Shelf	-43.90711	0.000112339	0.036106863	0.408024474
cg17869960	6	12718530	PHACTR1	Other	21.89379142	0.000114825	0.036110687	0.41872729
cg07984358	10	24704829	KIAA1217	Other	37.20186931	0.000116757	0.036331314	-0.321807981
cg10783294	12	679668	NINJ2	S_Shore	49.23197696	0.000116792	0.036331314	0.376135202
cg06663317	16	56641101	MT2A	N_Shore	47.59135917	0.000118872	0.036521611	0.400773275
cg00353571	19	49238653	RASIP1	Island	52.98746852	0.000121987	0.0368364	0.360947364

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cg13674705	1	184829177	FAM129A	Other	-101.276974	8.33E-07	0.014051189	0.344148312
cg21870662	17	2241570	SGSM2	S_Shore	92.81487158	0.000122217	0.0368364	-0.306204981
cg13071185	11	860134	TSPAN4	S_Shore	27.3888583	0.000123014	0.0368364	0.402397481
cg13728131	11	19799633	NAV2	S_Shore	56.7727934	0.000127593	0.0368364	-0.456007137
cg13728131	11	19799633	NAV2	S_Shore	56.7727934	0.000127593	0.0368364	-0.412670856
cg15674813	2	238608549	LRRFIP1	Other	-51.6178547	0.000127987	0.0368364	-0.360082037
cg21031128	8	21771278	DOK2	S_Shore	-47.8311475	0.000128531	0.0368364	-0.308963706
cg02771464	22	19108494	DGCR2	N_Shore	33.01485719	0.000130617	0.037093957	-0.345167622
cg14944269	14	65439602	RAB15	S_Shore	45.4477371	0.000130799	0.037093957	-0.323550176
cg04615460	12	115125098	TBX3	Island	-36.9950629	0.000130925	0.037093957	0.532759986
cg03690812	12	111875483	SH2B3	Other	-80.9646839	0.000131803	0.037093957	-0.340613464
cg21785723	1	6551782	PLEKHG5	S_Shore	-62.2850588	0.000133743	0.037199839	-0.412077907
cg19771173	1	204296545	PLEKHA6	Other	-41.537495	0.000135638	0.037337498	0.453304896
cg13695585	6	30853014	DDR1	S_Shore	34.11463886	0.000135995	0.037337498	-0.506674916
cg20454518	12	133135463	FBRSL1	Island	-45.0909608	0.000137775	0.037480601	0.315715296
cg06332304	10	126782397	CTBP2	Other	33.61985743	0.000137973	0.037480601	-0.328613011
cg01458495	3	48310544	ZNF589	Other	25.68879712	0.000140862	0.037642484	-0.332030208
cg22337438	19	54327437	NLRP12	Other	-45.8446941	0.000142759	0.037801273	-0.600892577
cg09358422	1	1023247	C1orf159	Island	26.32197965	0.000143905	0.037801273	-0.377406289
cg06959773	7	76033795	SRCRB4D	S_Shelf	-62.6525356	0.000148019	0.037801822	-0.426606464
cg22867608	10	64573356	EGR2	Island	27.20529237	0.000148031	0.037801822	-0.302760868
cg10129493	19	51728586	CD33	Other	-66.1939403	0.000148549	0.037892307	-0.454814434
cg25752703	3	128710390	KIAA1257	N_Shelf	-42.904647	0.00014936	0.037995577	0.39104489
cg04483936	15	57668247	CGNL1	N_Shore	-55.3512029	0.000150078	0.03804522	0.381106858
cg25141611	13	113422162	ATP11A	S_Shore	-57.5637982	0.000151396	0.038167284	-0.358623779
cg00136547	6	56507796	DST	Other	22.70377225	0.000151729	0.038182774	-0.31488223
cg23497683	2	100759159	AFF3	Other	-35.3116602	0.000154367	0.03839667	0.336310258
cg24523322	1	1023281	C1orf159	Island	24.48992738	0.000156178	0.03857589	-0.389513114
cg05584759	12	57869421	ARHGAP9	Island	47.12909213	0.000157359	0.03863862	0.352100837
cg13101705	1	183248593	NMNAT2	Other	-37.2948053	0.000161959	0.039034245	-0.32800228
cg04541607	22	27013978	CRYBB1	Other	-51.7261521	0.000165761	0.039349767	-0.315188641

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cg13674705	1	184829177	FAM129A	Other	-101.276974	8.33E-07	0.014051189	0.344148312
cg02865595	1	36771714	SH3D21	N_Shore	23.56649089	0.000167116	0.039349767	-0.391840387
cg16438525	3	52517742	NISCH	N_Shelf	25.87624162	0.000174475	0.039728888	-0.311014759
cg12004641	2	218750749	TNS1	Other	-45.5716139	0.000177045	0.039728888	-0.32490151
cg19015961	10	90712748	ACTA2	Other	49.69787477	0.000181152	0.040065433	-0.308968822
cg13666041	14	69442697	ACTN1	N_Shore	19.67549811	0.000181923	0.040065433	-0.30566671
cg15726700	3	196370254	NRROS	S_Shelf	-47.5221336	0.000185678	0.040214346	-0.389652702
cg20149168	1	68512807	DIRAS3	Island	-68.6520196	0.000185867	0.040214346	0.354889542
cg23715045	11	124621944	VSIG2	Other	40.8902228	0.000190062	0.040401171	-0.49879915
cg14590912	9	135905092	GTF3C5	N_Shore	41.89504678	0.000190566	0.040411945	-0.378846204
cg15545878	11	111782607	CRYAB	Other	38.34746071	0.000195419	0.040529458	0.345356116
cg02334109	15	26044050	ATP10A	Other	-44.2909677	0.000198236	0.040596074	-0.559265682
cg05143345	14	23447408	AJUBA	N_Shelf	33.43803925	0.000201082	0.040649634	-0.438962101
cg01844235	22	23487969	RAB36	Island	53.00313692	0.00020186	0.040707018	-0.48760018
cg03335246	4	4860431	MSX1	N_Shore	-41.4246815	0.000205441	0.040923827	-0.345216013
cg14285050	1	40778294	COL9A2	N_Shelf	-59.2546573	0.000209697	0.041366798	0.45629124
cg11700584	14	50088544	MGAT2	S_Shore	71.46860032	0.000211868	0.041495656	0.326736824
cg12414070	12	117627133	FBXO21	N_Shore	45.74758956	0.000212644	0.041495656	-0.380604214
cg10413136	4	8207119	SH3TC1	Other	-45.4466599	0.000213143	0.041495656	-0.409968149
cg14413904	10	62423377	ANK3	Other	-40.58738	0.000213282	0.041495656	0.455511551
cg12532266	5	132201652	UQCRQ	N_Shore	26.24170338	0.000223944	0.041792459	0.501260835
cg24553170	1	49243472	BEND5	S_Shore	32.26771441	0.00022656	0.04192076	-0.366214232
cg08120210	15	66682733	MAP2K1	S_Shelf	-18.8777589	0.000227227	0.04192352	-0.322665801
cg02424715	14	75893680	JDP2	N_Shore	-46.4620499	0.000227526	0.04192352	-0.411776939
cg01226614	13	44947593	SERP2	Island	39.37580587	0.000231528	0.042184712	-0.36217921
cg01123186	17	36514710	SOCS7	Other	29.70050653	0.000234658	0.042357582	-0.418065699
cg00728848	6	13483832	GFOD1	N_Shelf	-34.2444635	0.000236635	0.042426476	-0.386585081
cg08651590	2	65543410	SPRED2	S_Shelf	26.70280266	0.000241108	0.042673154	-0.316094083
cg21188037	7	45018658	MYO1G	Other	-50.4949968	0.000245002	0.042992623	-0.507324595
cg12974599	22	46770195	CELSR1	N_Shore	-25.7029749	0.000246673	0.043048176	0.386562052
cg14365457	9	124029877	GSN	Other	-68.4497531	0.000246726	0.043048176	-0.323392213

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cg26083045	3	8560168	LMCD1	Other	-77.7309928	0.000247773	0.043048176	-0.444697397
cg26933869	1	19218007	ALDH4A1	Other	-59.2558425	0.00024995	0.043083921	-0.516520927
cg26933869	1	19218007	ALDH4A1	Other	-59.2558425	0.00024995	0.043083921	-0.459426608
cg09920804	8	42053994	PLAT	Other	45.46278887	0.000250576	0.043083921	-0.422539134
cg16846069	12	6462681	SCNN1A	Other	-43.5003455	0.000250896	0.043083921	0.313417647
cg03730946	19	6475456	DENND1C	Island	45.65329342	0.000257585	0.043519747	0.37883714
cg20425130	3	183273245	KLHL6	Other	-26.576149	0.000257622	0.043519747	-0.36592199
cg20425130	3	183273245	KLHL6	Other	-26.576149	0.000257622	0.043519747	-0.361648324
cg00387090	1	201615401	NAV1	N_Shore	-27.0543047	0.000261118	0.043579434	-0.397127586
cg03473377	10	33568029	NRP1	Other	-59.6711245	0.000262025	0.043604477	-0.453264625
cg03473377	10	33568029	NRP1	Other	-59.6711245	0.000262025	0.043604477	-0.427517762
cg09447621	11	134254646	B3GAT1	S_Shore	-37.3016478	0.000265009	0.043817951	0.478038627
cg02059317	16	89024511	CBFA2T3	Other	-55.759888	0.000267026	0.043904453	-0.327447346
cg02845870	11	85524670	SYTL2	S_Shelf	-72.9289365	0.000267867	0.043904453	0.456527537
cg18498263	14	91034963	TTC7B	Other	21.86304525	0.000269697	0.043904453	0.393104161
cg26633373	19	54377836	MYADM	S_Shore	-34.8225532	0.000271335	0.043904453	-0.34154398
cg02807984	11	722258	EPS8L2	S_Shore	-35.2471368	0.000272666	0.043969779	0.335844553
cg23033749	7	116610238	ST7	Other	-62.4233266	0.000274658	0.044138811	-0.306497594
cg21110337	12	113671028	TPCN1	Other	-32.053929	0.00027529	0.044164494	0.310634408
cg14685146	17	42088751	TMEM101	N_Shelf	22.75253322	0.000277225	0.044202722	-0.444144181
cg00580562	10	21789124	C10orf114	Island	-19.846809	0.000278316	0.044293414	-0.312606377
cg07175797	16	50317656	ADCY7	Other	-50.5983335	0.000280312	0.044340074	-0.447325765
cg00255726	8	21769114	DOK2	N_Shore	-61.7149725	0.000280871	0.044364972	-0.350482999
cg08578641	9	34457440	FAM219A	Island	30.97381911	0.000280963	0.044364972	0.363311362
cg12484113	1	27898757	AHDC1	N_Shelf	44.4891951	0.000284043	0.044365371	-0.463177154
cg17244340	6	36973448	FGD2	Other	-35.1373115	0.000287362	0.044413839	-0.404303846
cg13509421	12	110476821	ANKRD13A	Other	28.79556146	0.000287888	0.044413839	-0.327460896
cg18113826	6	31583942	AIF1	N_Shelf	-59.3534699	0.000288027	0.044413839	-0.392083723
cg04332442	22	46770063	CELSR1	N_Shore	-24.5412114	0.000294517	0.044790573	0.468566115
cg22908922	14	105855008	PACS2	S_Shelf	-59.0401959	0.000297173	0.044797334	-0.325413806

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Probe	CHR	MAPINFO	Gene	CPG Location**	Regression Coefficient	Regression p-value	Regression q-value	Correlation Coefficient
cg13674705	1	184829177	FAM129A	Other	-101.276974	8.33E-07	0.014051189	0.344148312
cg25623459	11	1861344	TNNI2	Other	-34.3510194	0.000301797	0.044797334	0.3198241
cg04822621	5	169724656	LCP2	Other	-23.0850569	0.000302276	0.044797334	-0.487521781
cg17297216	15	99194474	IGF1R	Island	63.96682134	0.000302822	0.044797334	-0.37548385
cg19011001	14	93539613	ITPK1	Other	-40.9950513	0.000303778	0.044861768	-0.428826621
cg24566261	6	30854164	DDR1	S_Shore	50.51346402	0.000310482	0.045232832	-0.490689865
cg21579294	13	113997499	GRTP1	Other	-53.6846378	0.000312917	0.045347389	0.355569358
cg05266786	10	49742271	ARHGAP22	Other	26.80664352	0.000313605	0.045404854	0.347676947
cg22935317	14	23447078	AJUBA	N_Shelf	33.70054854	0.000315236	0.045473327	-0.44345081
cg01595717	9	140586201	EHMT1	N_Shore	-31.8748602	0.000321068	0.045764723	0.395075851
cg01595717	9	140586201	EHMT1	N_Shore	-31.8748602	0.000321068	0.045764723	0.347164826
cg08343834	17	15168658	PMP22	S_Shelf	22.71280141	0.00032503	0.045991101	0.381852344
cg21957813	11	44638520	CD82	Other	43.77805284	0.000332202	0.046066512	-0.416224612
cg09990481	10	90712684	ACTA2	Other	46.02028079	0.000336096	0.046089905	-0.338312191
cg17674726	2	231743193	ITM2C	Other	-57.7073664	0.000336874	0.046089905	0.422665806
cg13578303	19	49838698	CD37	N_Shelf	-53.4177968	0.000346141	0.046494819	-0.305529781
cg02395812	14	105955879	C14orf80	N_Shore	43.94719053	0.000346267	0.046494819	0.37569943
cg15155441	11	57005981	APLNR	Other	-83.2017034	0.000348933	0.046670987	-0.345783219
cg12871285	17	76713379	CYTH1	Other	25.99114121	0.000357634	0.046935802	0.308699939
cg16277944	5	169068404	DOCK2	S_Shelf	27.19535217	0.00036366	0.047220961	0.319624464
cg02434051	19	54848878	LILRA4	Other	38.05598988	0.000367561	0.047313904	0.30377886
cg19272266	8	38125865	PPAPDC1B	N_Shore	32.55549522	0.000368499	0.047313904	-0.590225747
cg24947456	12	57441432	MYO1A	Other	-48.4262511	0.000373489	0.047469296	-0.366172642
cg26583078	4	186877778	SORBS2	Other	25.77714715	0.00037406	0.047492184	-0.330979876
cg04812726	5	171875049	SH3PXD2B	Other	45.57905142	0.000374653	0.047524476	-0.302709456
cg17460386	1	207095668	FAIM3	Other	-36.0211424	0.000376046	0.047584461	-0.447397337
cg17243643	12	56114269	RDH5	S_Shelf	22.85456507	0.000377505	0.04758944	0.369228722
cg18069290	12	58013539	SLC26A10	Island	-38.7349464	0.000378611	0.047630324	0.304079652
cg19256813	12	117627286	FBXO21	N_Shore	33.98857689	0.000378713	0.047630324	-0.498548526
cg25550753	2	47205281	TTC7A	Other	-41.9544369	0.000382027	0.04781135	-0.359555494
cg14260643	7	99277394	CYP3A5	Other	28.67260883	0.000392184	0.048352538	0.401393968

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Probe	CHR	MAPINFO	Gene	CPG Location**	Regression Coefficient	Regression p-value	Regression q-value	Correlation Coefficient
cg13674705	1	184829177	FAM129A	Other	-101.276974	8.33E-07	0.014051189	0.344148312
cg03333377	11	93277841	SMCO4	S_Shore	-18.992271	0.000392554	0.048352538	0.355220597
cg26536240	16	89509760	ANKRD11	Other	26.32058099	0.000393198	0.048389356	-0.333613705
cg15049549	3	48732213	IP6K2	Other	24.13211405	0.000394456	0.048437262	-0.369533072
cg09472600	1	183537770	NCF2	Other	-15.934396	0.00039757	0.048586364	-0.401385973
cg19747945	6	42946146	PEX6	N_Shore	30.97356268	0.000399011	0.048626895	-0.31947469
cg03779374	3	114343825	ZBTB20	Other	-32.0131299	0.000399342	0.048629208	-0.319000832
cg17311022	3	119379792	POPDC2	Other	30.24198373	0.00040184	0.048684173	-0.318644251
cg25076039	5	169128937	DOCK2	Other	32.47079968	0.000409267	0.049010636	0.342291786
cg07702311	11	128646953	FLI1	Other	29.10081038	0.000411434	0.049010636	0.335095053
cg00861207	4	8098270	ABLIM2	N_Shore	-67.9355783	0.000413213	0.049010636	-0.329687739
cg14729344	10	121129753	GRK5	Other	-31.8234917	0.00041733	0.049204549	-0.319868128
cg11077392	11	19719446	NAV2	Other	47.67942451	0.000417939	0.049204549	-0.455455315
cg11077392	11	19719446	NAV2	Other	47.67942451	0.000417939	0.049204549	-0.403889524
cg02804819	19	49238364	RASIP1	N_Shore	40.24802635	0.000418264	0.049204549	0.356273436
cg14671926	6	169930772	WDR27	Other	43.0718287	0.000422072	0.049312859	-0.361748066
cg18750833	2	71358451	MPHOSPH1	S_Shore	24.87698932	0.000422575	0.049312859	-0.369024573
cg16671238	13	20987145	CRYL1	N_Shore	-61.584221	0.000424484	0.049312859	-0.406870748
cg14654385	11	63973006	FERMT3	N_Shore	-66.9777126	0.000424759	0.049312859	-0.300483562
cg03732056	8	21771059	DOK2	S_Shore	-21.5810307	0.000425148	0.049312859	-0.312533604
cg06015525	12	57872123	ARHGAP9	S_Shore	-51.0618954	0.000425587	0.049312859	-0.332450734
cg25064052	4	166216151	KLHL2	Other	-32.3624436	0.000428276	0.049388542	0.353712167
cg00748218	11	19372553	NAV2	Other	43.33571902	0.000431943	0.049388542	-0.441738426
cg00748218	11	19372553	NAV2	Other	43.33571902	0.000431943	0.049388542	-0.406439334
cg11953913	5	139562873	CYSTM1	Other	-42.8271889	0.000433007	0.049388542	-0.403685101
cg14647287	4	6927183	TBC1D14	S_Shore	-56.3108666	0.000433656	0.049388542	0.304101461
cg12193327	2	31454631	EHD3	N_Shelf	-37.2843386	0.00043541	0.049396091	0.340952071
cg26959945	7	20233217	MACC1	Other	-17.8885435	0.000437529	0.049396091	0.325614657
cg07187855	6	30854161	DDR1	S_Shore	43.86416343	0.000438847	0.049396091	-0.440350371
cg04388657	9	127623377	RPL35	N_Shore	24.01906625	0.000452059	0.049788704	-0.443657926
cg17753974	1	201622519	NAV1	S_Shelf	-35.2481808	0.000453778	0.049788704	-0.347566735

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cg13674705	1	184829177	FAM129A	Other	-101.276974	8.33E-07	0.014051189	0.344148312
cg08133755	11	19792080	NAV2	Other	31.33865693	0.000457378	0.049877914	-0.451077657
cg08133755	11	19792080	NAV2	Other	31.33865693	0.000457378	0.049877914	-0.451077657

*A correlation coefficient of ≤ -0.30 or ≥ 0.30 was the cut-off for determining which CpG sites were correlated with gene expression

**N_Shore = North shore; N_Shelf = North shelf; S_Shore = South shore; S_Shelf = South shelf; Other = Not in or near a CpG Island

Note: the 226 unique CpG methylation sites linked to 238 gene expression probes