Supplementary Table 3. Alteration of DNA methylation state of the brain of female offspring prenatally exposed to TiO_2-NP.

The relative DNA methylation was calculated by dividing Cy5 signal by Cy3 signal obtained from CpG island microarray and then compared between Sham and TiO_2-NP groups.

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P29455874	chr14:22804989-22805033	NM_145459:3813	Zfp503	INSIDE	6.806	12.105	640.93	7758.46	82.389	599.62	49402.73
A_68_P31350850	chr17:74695143-74695187	NM_133771:-961	Memo1	PROMOTER	5.241	2.878	450.72	1297.15	15.083	368.81	5562.66
A_68_P26795688	chr9:105033875-105033919	NM_029385:239	Nudt16	INSIDE	4.477	3.082	440.46	1357.41	13.798	418.55	5775.31
A_68_P25228678	chr7:80521046-80521090	NM_177740:663	Rgma	INSIDE	4.245	0.556	663.33	368.98	2.361	644.67	1522.29
A_68_P23644448	chr5:43626040-43626084	NR_028417:531	Gm7854	INSIDE	4.107	0.491	627.14	307.93	2.017	723.63	1459.38
A_68_P25574929	chr7:146132486-146132530	NM_028708:76	Jakmip3	INSIDE	4.012	0.451	881.02	397.57	1.810	713.30	1291.35
A_68_P33007146	chr9_random:49897-49941	NR_015516:-3490	4930526I15Rik	PROMOTER	3.692	6.288	3418.87	21499.06	23.215	2298.35	53355.95
A_68_P20231213	chr1:53353942-53353986	NM_145517:26	Ormdl1	INSIDE	3.543	1.826	419.01	764.99	6.468	388.28	2511.27
A_68_P32533200	chrX:90534061-90534105	NM_007492:2098	Arx	INSIDE	3.504	13.814	6300.76	87041.16	48.399	3229.51	156305.70
A_68_P26171007	chr8:114465131-114465175	NM_026693:535	Gabarapl2	INSIDE	3.497	27.141	3597.79	97649.33	94.902	1892.10	179564.50
A_68_P26164572	chr8:113262808-113262852	NM_198625:17447	Mtss1l	INSIDE	3.486	7.191	2535.96	18235.83	25.068	1841.30	46157.41
A_68_P24513815	chr6:65728982-65729026	NM_027547:49	Prdm5	INSIDE	3.419	8.570	852.11	7302.43	29.302	723.73	21206.73
A_68_P26164573	chr8:113262875-113262919	NM_198625:17513	Mtss1l	INSIDE	3.405	4.778	3372.57	16114.77	16.269	2472.91	40232.99
A_68_P25724843	chr8:26127513-26127557	NM_007404:-140	Adam9	DIVERGENT_PROMOTER	3.403	7.316	1524.90	11155.47	24.892	1145.63	28517.06
A_68_P25845477	chr8:49195740-49195784	NM_001161515:396	Dctd	INSIDE	3.295	10.942	2629.12	28768.68	36.052	1918.64	69170.72
A_68_P21084949	chr2:27330700-27330744	NM_023336:196	Brd3	INSIDE	3.270	18.917	430.60	8145.76	61.868	299.91	18554.51
A_68_P27693341	chr11:33101001-33101045	NM_019916:2566	Tlx3	INSIDE	3.266	11.424	11521.46	131618.90	37.311	7480.28	279095.00
A_68_P26812299	chr9:107888278-107888322	NM_026597:-53	6230427J02Rik	PROMOTER	3.211	41.034	2065.67	84762.66	131.746	820.78	108134.90
A_68_P31167789	chr17:37334385-37334429	NM_001011518:505	Olfr94	INSIDE	3.185	0.553	612.40	338.39	1.760	485.62	854.62
A_68_P29619050	chr14:56262458-56262502	NM_028780:163	Tm9sf1	INSIDE	3.144	21.737	4434.65	96395.99	68.347	2167.49	148140.80
A_68_P24638868	chr6:91361534-91361578	NM_009527:-193	Wnt7a	PROMOTER	3.112	4.262	1684.23	7177.50	13.263	1343.70	17822.06
A_68_P23203724	chr4:109649844-109649888	NM_172296:-763	Dmrta2	PROMOTER	3.082	29.984	17420.38	522325.10	92.404	8951.32	827137.40
A_68_P27980117	chr11:84693941-84693985	NM_001077636:-175	Pigw	PROMOTER	3.046	8.934	7846.91	70105.60	27.217	4810.06	130915.60
A_68_P27928203	chr11:75608556-75608600	NM_007873:981	Doc2b	INSIDE	3.043	7.601	425.29	3232.70	23.131	319.99	7401.59
A_68_P29060390	chr13:56397734-56397778	NM_019568:156	Cxcl14	INSIDE	3.036	3.480	3675.66	12793.06	10.568	2602.92	27507.92
A_68_P28222996	chr12:8506600-8506644	NM_007483:169	Rhob	INSIDE	3.027	29.504	8519.70	251363.70	89.305	4297.86	383821.30
A_68_P32778409	chrX:156576281-156576325	NM_008810:-34	Pdha1	PROMOTER	3.016	7.865	716.04	5631.76	23.720	359.32	8523.27
A_68_P31155038	chr17:34784397-34784441	NM_017406:294	Atf6b	INSIDE	2.986	23.608	887.30	20947.48	70.495	609.26	42949.85
A_68_P32536642	chrX:91168388-91168432	ENSMUST00000117999:-1109		DIVERGENT_PROMOTER	2.977	7.201	1376.55	9912.26	21.433	728.70	15618.38
A_68_P29450509	chr14:21871923-21871967	NM_134079:90	Adk	INSIDE	2.951	1.754	1736.13	3045.36	5.176	1477.41	7646.82
A_68_P30374043	chr15:80542551-80542595	NM_144812:830	Tnrc6b	INSIDE	2.901	10.575	3462.10	36612.34	30.679	2420.22	74249.83
A_68_P32464342	chrX:70961468-70961512	NM_012060:24	Bcap31	INSIDE	2.898	3.555	4575.87	16269.43	10.304	2149.12	22144.39
A_68_P30137691	chr15:36213148-36213192	NM_013923:-268	Rnf19a	PROMOTER	2.895	7.973	1368.64	10911.67	23.081	795.84	18368.76
A_68_P25703829	chr8:19535136-19535180	ENSMUST00000118143:-745		PROMOTER	2.887	8.233	5523.50	45473.70	23.771	3532.43	83970.59
A_68_P24568080	chr6:77929479-77929523	NM_001109764:161	Ctnna2	INSIDE	2.885	5.838	2978.31	17387.62	16.841	1751.66	29498.86
A_68_P22028773	chr3:30407847-30407891	NM_021442:541	Mecom	INSIDE	2.882	13.646	2919.90	39844.77	39.327	2080.76	81830.92
A_68_P21888635	chr2:177853739-177853783	NM_001177789:81	Phactr3	INSIDE	2.868	25.028	2515.99	62971.06	71.771	1619.79	116252.80
A_68_P32351252	chrX:42143188-42143232	NM_001190718:128	Dcaf12l1	INSIDE	2.865	7.296	3767.38	27487.72	20.901	2077.17	43415.76
A_68_P25571662	chr7:145589207-145589251	NM_183289:185	Tcerg1l	INSIDE	2.863	9.562	4573.94	43735.11	27.371	2937.71	80409.07
A_68_P28155403	chr11:115664957-115665001	NM_080643:9928	Caskin2	INSIDE	2.858	7.044	4618.06	32531.25	20.130	3180.69	64028.48
A_68_P28059604	chr11:98821830-98821874	NM_001176528:68	Rara	INSIDE	2.846	9.755	2977.11	29040.29	27.760	2211.13	61381.64
A_68_P23324350	chr4:134260533-134260577	NM_207237:-349	Man1c1	PROMOTER	2.820	6.404	6070.41	38876.71	18.062	3941.66	71192.51
A_68_P33007145	chr9_random:49764-49808	NR_015516:-3622	4930526I15Rik	PROMOTER	2.796	13.504	11845.74	159960.60	37.756	6253.91	236121.30
A_68_P28307263	chr12:28027320-28027364	NM_009234:241	Sox11	INSIDE	2.795	16.492	4774.96	78748.73	46.092	3149.38	145159.90
A_68_P25196205	chr7:74994369-74994413			Unknown	2.771	7.120	6927.70	49326.62	19.730	5073.07	100093.90
A_68_P26344891	chr9:20780545-20780589	NM_010333:671	S1pr2	INSIDE	2.748	1.576	1964.61	3095.35	4.330	1484.57	6427.85
A_68_P22199719	chr3:65196469-65196513	NM_026155:-15	Ssr3	PROMOTER	2.746	17.796	15091.40	268560.50	48.865	7125.09	348164.30

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27129526	chr10:50312500-50312544	NM_001146089:48	Ascc3	INSIDE	2.737	7.551	1717.70	12970.13	20.665	1310.39	27079.84
A_68_P22531299	chr3:130975017-130975061	NM_008212:-83	Hadh	PROMOTER	2.737	10.628	15469.42	164409.20	29.089	9081.46	264171.40
A_68_P23567791	chr5:29805138-29805182	NM_019944:-150	Mnx1	PROMOTER	2.737	4.281	2107.37	9020.61	11.717	1689.85	19799.24
A_68_P20412166	chr1:88338644-88338688	AK089549:7401		DOWNSTREAM	2.737	6.103	1274.33	7777.15	16.703	910.84	15214.20
A_68_P21582988	chr2:121632726-121632770	NM_172673:45	Frmd5	INSIDE	2.734	8.279	6123.14	50694.51	22.637	3823.30	86547.30
A_68_P26167383	chr8:113783057-113783101	NM_009149:24	Glg1	INSIDE	2.733	6.404	3079.88	19722.76	17.500	1937.32	33903.41
A_68_P24686653	chr6:99472198-99472242	ENSMUST00000155466:144571		INSIDE	2.730	8.343	2538.43	21179.35	22.775	1588.22	36171.95
A_68_P21969040	chr3:17955766-17955810	NM_021560:1464	Bhlhe22	INSIDE	2.727	11.831	7289.10	86236.40	32.261	4657.85	150267.20
A_68_P24973879	chr7:13551564-13551609	NM_178732:374	Zfp324	INSIDE	2.727	10.119	12804.14	129564.20	27.590	6837.10	188638.10
A_68_P20457532	chr1:95700895-95700939	NM_025454:375	Ing5	INSIDE	2.724	6.716	2820.91	18944.70	18.295	1637.99	29967.65
A_68_P20184680	chr1:42755426-42755470	NM_008900:1458	Pou3f3	INSIDE	2.714	6.638	5306.77	35227.30	18.016	3602.30	64898.50
A_68_P26878663	chr9:120486371-120486416	NM_025974:5760	Rpl14	DOWNSTREAM	2.712	1.510	1244.63	1879.28	4.095	974.70	3991.69
A_68_P25992690	chr8:81636588-81636632	NM_178267:84275	Zfp827	INSIDE	2.710	18.337	18328.51	336097.60	49.688	10239.56	508780.30
A_68_P31472616	chr18:6241499-6241543	NM_008448:2	Kif5b	INSIDE	2.705	13.405	1618.85	21700.12	36.255	1036.17	37566.28
A_68_P26466435	chr9:44041858-44041902	NM_007619:249	Cbl	INSIDE	2.703	8.729	4609.01	40229.81	23.595	3069.96	72435.80
A_68_P20644107	chr1:138036961-138037006	NM_001039472:9006	Kif21b	INSIDE	2.698	10.540	4945.35	52121.62	28.439	3189.20	90698.85
A_68_P24092948	chr5:130731326-130731370	NM_023248:-16	Sbds	DIVERGENT_PROMOTER	2.697	2.449	2368.30	5800.12	6.606	1776.61	11735.43
A_68_P20094994	chr1:24685459-24685503	NM_026719:98	Lmbrd1	INSIDE	2.688	20.375	4317.54	87970.49	54.775	2990.87	163823.90
A_68_P31126969	chr17:29401134-29401178	NM_026845:-240	Ppil1	DIVERGENT_PROMOTER	2.682	11.142	1321.08	14720.04	29.885	882.61	26376.44
A_68_P29329250	chr13:112279384-112279428	NM_001122963:843	Gpbp1	INSIDE	2.680	12.969	18361.71	238134.20	34.760	9847.22	342287.80
A_68_P32365466	chrX:45947510-45947554	NM_153532:-2222	Zfp280c	PROMOTER	2.676	5.021	1811.17	9094.51	13.439	945.31	12704.10
A_68_P32099204	chr19:38129403-38129447	NM_028293:-90	Cep55	PROMOTER	2.661	14.261	12747.94	181792.80	37.952	7793.33	295773.50
A_68_P21426271	chr2:91895625-91895669	ENSMUST00000123840:3880		INSIDE	2.658	8.286	5247.23	43479.63	22.024	3647.86	80341.66
A_68_P22278904	chr3:82162070-82162114	NM_001081230:99	Mtap9	INSIDE	2.656	15.147	1784.01	27022.45	40.232	980.84	39461.13
A_68_P26529572	chr9:54997117-54997161	NM_180600:-37	Ube2q2	PROMOTER	2.656	11.264	2664.79	30016.69	29.913	1875.82	56110.90
A_68_P20417972	chr1:89371861-89371906	NM_028473:5045	3110079O15Rik	INSIDE	2.652	18.741	968.94	18158.52	49.706	756.70	37611.98
A_68_P25032017	chr7:31319995-31320040	NM_178252:11	Arhgap33	INSIDE	2.650	5.817	30484.87	177343.10	15.418	21467.82	330995.40
A_68_P32396713	chrX:53862851-53862895	NM_172780:-139	Slc9a6	PROMOTER	2.649	5.416	1489.93	8069.17	14.349	796.83	11433.70
A_68_P31322348	A_68_P31322348			Unknown	2.647	7.240	1352.79	9794.43	19.167	1045.04	20030.55
A_68_P24922453	chr6:145289480-145289524			Unknown	2.645	0.564	817.78	461.17	1.492	706.91	1054.43
A_68_P20412593	chr1:88422665-88422709	NM_008972:-624	Ptma	PROMOTER	2.644	5.930	4838.46	28693.15	15.677	3042.74	47701.42
A_68_P27476522	chr10:116018238-116018282	NM_001037846:307	Cnot2	INSIDE	2.636	8.518	13218.99	112595.80	22.456	8717.08	195749.60
A_68_P25516578	chr7:136735619-136735663	NM_172255:264	Wdr11	INSIDE	2.632	0.212	1316.65	279.76	0.559	1149.78	642.91
A_68_P28103521	chr11:106649919-106649963	NM_007840:-132	Ddx5	DIVERGENT_PROMOTER	2.625	6.666	17960.68	119723.90	17.499	11517.85	201546.70
A_68_P21490977	chr2:104656727-104656771	NM_001123327:105	Qser1	INSIDE	2.622	8.015	3488.35	27959.02	21.018	2688.77	56512.11
A_68_P29856568	chr14:102128930-102128974	NM_201529:-192	Lmo7	PROMOTER	2.621	10.226	4507.02	46087.56	26.806	2966.50	79519.01
A_68_P32796350	chrX:160514136-160514180	NM_009173:-177	Siah1b	PROMOTER	2.621	3.643	1852.28	6747.79	9.547	1061.03	10129.19
A_68_P28099478	chr11:105946211-105946255	NM_011947:17	Map3k3	INSIDE	2.617	6.441	23400.69	150731.30	16.857	15983.49	269440.70
A_68_P23146552	chr4:99602526-99602570	NM_028132:493	Pgm2	INSIDE	2.610	5.642	12527.75	70679.57	14.726	8253.81	121548.50
A_68_P21076600	chr2:25996203-25996247	ENSMUST00000133808:-183		PROMOTER	2.610	5.557	1035.44	5754.15	14.505	736.72	10685.75
A_68_P28041915	chr11:95866931-95866976	NM_009951:305	Igf2bp1	INSIDE	2.608	8.882	6026.23	53526.77	23.168	4126.34	95599.91
A_68_P31144961	chr17:32458430-32458474	NM_017476:29070	Akap8l	INSIDE	2.604	5.486	2734.95	15003.88	14.287	1952.87	27900.76
A_68_P26845381	chr9:114473232-114473276	NM_001042503:233	Trim71	INSIDE	2.604	6.462	664.84	4295.91	16.825	520.90	8764.06
A_68_P23297033	chr4:129190774-129190818	NM_010807:-28	Marcksl1	PROMOTER	2.602	5.773	10432.74	60230.91	15.025	7036.61	105722.20
A_68_P28771927	chr12:118392576-118392621	NR_033538:-2856	Gm10421	PROMOTER	2.599	4.131	733.51	3030.00	10.736	537.89	5774.98
A_68_P23763011	chr5:67009509-67009553	NM_009686:380	Apbb2	INSIDE	2.598	8.757	907.55	7947.11	22.748	649.96	14785.56
A_68_P26342514	chr9:20264309-20264353	NM_011753:274	Zfp26	INSIDE	2.597	5.833	12946.13	75517.71	15.147	9104.24	137900.20
A_68_P28053223	chr11:97744951-97744995	NM_001081435:496	Fbxo47	INSIDE	2.589	10.903	9736.38	106154.20	28.224	4882.70	137808.30
A_68_P30590967	chr16:21205377-21205421	NM_010143:531	Ephb3	INSIDE	2.587	10.916	1196.74	13063.33	28.244	837.42	23652.29
A_68_P20240462	chr1:55188131-55188175	NM_025283:64	Mobkl3	INSIDE	2.583	1.455	1093.20	1591.01	3.759	1044.28	3925.12
A_68_P27594327	chr11:11937393-11937437	NM_001177629:-9440	Grb10	PROMOTER	2.580	7.830	15526.51	121565.50	20.197	11291.17	228048.70

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26864195	chr9:117949694-117949738	NM_001048146:100	Azi2	INSIDE	2.577	9.490	2913.48	27648.78	24.453	2021.37	49428.26
A_68_P31458875	chr18:3507840-3507884	NM_026505:-92	Bambi	PROMOTER	2.575	17.069	2820.94	48149.43	43.952	1883.09	82765.38
A_68_P20432927	chr1:91819381-91819425	NM_010262:8349	Gbx2	DOWNSTREAM	2.570	8.925	4387.88	39160.32	22.935	2276.94	52221.25
A_68_P20170470	chr1:40323556-40323600	NM_001123382:148	Il1r1	INSIDE	2.563	9.463	1749.87	16559.53	24.254	1125.93	27308.32
A_68_P27840810	chr11:59919914-59919958	NM_009021:1422	Rai1	INSIDE	2.563	8.736	3024.48	26422.84	22.390	2287.83	51223.82
A_68_P31866219	chr18:80894683-80894727	NM_001164111:10208	Nfatc1	INSIDE	2.561	3.778	1960.18	7405.43	9.674	1497.88	14490.19
A_68_P24423934	chr6:47544675-47544719	NM_001146689:333	Ezh2	INSIDE	2.559	4.342	3868.12	16795.29	11.113	2711.43	30131.82
A_68_P21556049	chr2:116946411-116946455	NM_033524:-753	Spred1	PROMOTER	2.559	7.004	7406.18	51873.25	17.920	5638.84	101048.30
A_68_P21836350	chr2:167423298-167423342	NM_023230:34185	Ube2v1	DOWNSTREAM	2.559	1.736	6057.44	10517.36	4.443	3948.40	17542.62
A_68_P32453217	chrX:68617827-68617871	NM_016985:-86	Mtmr1	PROMOTER	2.555	3.098	2572.42	7970.05	7.916	1433.82	11349.50
A_68_P33007166	A_68_P33007166			Unknown	2.552	11.771	2314.31	27242.83	30.035	1471.56	44198.88
A_68_P24764862	chr6:114232614-114232658	NM_178703:8	Slc6a1	INSIDE	2.549	17.190	6602.31	113494.20	43.825	3404.89	149218.90
A_68_P24052414	chr5:123270992-123271036	NM_001042491:334	Anapc5	INSIDE	2.546	24.473	4557.84	111543.90	62.308	2482.58	154683.20
A_68_P30567429	chr16:15887235-15887279	NM_007679:-122	Cebpd	PROMOTER	2.546	13.072	7367.64	96311.68	33.284	5181.40	172455.10
A_68_P25736450	chr8:28196606-28196651	NM_054044:316	Gpr124	INSIDE	2.545	10.594	3452.96	36580.26	26.957	2485.27	66994.82
A_68_P27358653	chr10:93774633-93774677	ENSMUST00000147869:-39		PROMOTER	2.542	4.982	10801.78	53819.71	12.664	7829.95	99155.27
A_68_P32576281	chrX:101395430-101395474	NM_001077354:1004	C77370	INSIDE	2.536	5.175	658.04	3405.35	13.124	385.33	5057.16
A_68_P25094516	chr7:52949587-52949631	NM_001033356:9825	Ntn5	INSIDE	2.535	6.663	3395.28	22623.71	16.894	2411.55	40740.20
A_68_P23272336	chr4:124804630-124804674	NM_153159:473	Zc3h12a	INSIDE	2.534	8.868	9988.09	88569.59	22.468	6409.08	143996.90
A_68_P22973925	chr4:63678841-63678885	NM_011607:29187	Tnc	INSIDE	2.532	7.689	1740.85	13385.58	19.465	1214.65	23643.61
A_68_P20416757	chr1:89160862-89160906	NM_028889:-54	Efhd1	PROMOTER	2.531	6.089	109823.20	668703.40	15.413	67870.99	1046093.00
A_68_P31151615	chr17:34168722-34168766	NM_001205214:-12	Rxrb	DIVERGENT_PROMOTER	2.525	2.326	584.39	1359.19	5.873	474.20	2785.18
A_68_P32717145	chrX:140752482-140752526	NM_026247:-4	Alg13	PROMOTER	2.523	6.564	4083.98	26807.27	16.561	2514.84	41647.48
A_68_P32684276	chrX:133653076-133653120	NM_007957:1767	Esx1	INSIDE	2.514	6.193	1542.14	9549.78	15.565	819.74	12759.33
A_68_P31220008	chr17:49071618-49071662	NM_027452:-266	Lrfn2	PROMOTER	2.514	5.727	9111.94	52180.14	14.397	5782.67	83254.10
A_68_P27050627	chr10:32609677-32609721	NM_001013411:23	Nkain2	INSIDE	2.512	7.636	4966.00	37922.42	19.182	3697.67	70929.86
A_68_P24141205	chr5:140865282-140865326	NM_172277:-103	Snx8	PROMOTER	2.512	5.782	13712.53	79285.45	14.522	8932.21	129716.30
A_68_P25522110	chr7:137662756-137662800	NM_001136054:266	Ate1	INSIDE	2.507	2.149	975.56	2096.60	5.388	765.52	4124.45
A_68_P31542491	chr18:21160534-21160578	NM_019706:715	Rnf138	INSIDE	2.507	6.232	7347.22	45784.44	15.622	4984.46	77866.60
A_68_P26469100	chr9:44516622-44516666	NM_153537:26633	Phldb1	INSIDE	2.502	21.012	5164.24	108511.90	52.574	2894.18	152159.80
A_68_P21587981	chr2:122591010-122591054	NM_001162503:-62	Sqrdl	PROMOTER	2.501	7.553	2476.02	18700.67	18.891	1784.22	33705.88
A_68_P27265507	chr10:76495860-76495904	NM_031196:-74	Slc19a1	PROMOTER	2.499	9.071	5096.34	46231.10	22.666	3101.46	70297.76
A_68_P27138494	chr10:52410512-52410556	NM_178675:228	Slc35f1	INSIDE	2.495	3.924	618.16	2425.63	9.792	614.22	6014.29
A_68_P25031610	chr7:31242110-31242154	NM_172898:402	Kirrel2	INSIDE	2.494	15.068	2274.51	34272.62	37.583	1235.22	46423.38
A_68_P26541141	chr9:57109407-57109451	NM_028820:978	1700017B05Rik	INSIDE	2.493	5.134	2336.99	11998.43	12.798	1913.17	24484.04
A_68_P22310075	chr3:87600813-87600858	NM_011832:-37	Insrr	DIVERGENT_PROMOTER	2.490	5.861	4961.28	29078.26	14.593	3144.29	45884.25
A_68_P26465911	chr9:43943262-43943306	NM_023061:544	Mcam	INSIDE	2.490	3.450	1701.35	5869.09	8.589	1308.16	11235.64
A_68_P29624689	chr14:57396463-57396507	NM_025682:669	Pspc1	INSIDE	2.487	5.474	4853.09	26567.70	13.612	3701.11	50381.05
A_68_P28332409	chr12:32319733-32319777	NM_001164090:-231	Bcap29	PROMOTER	2.486	9.592	2652.51	25441.57	23.849	1708.35	40742.33
A_68_P30656969	chr16:33251415-33251459	NM_080557:-105	Snx4	PROMOTER	2.486	10.407	3440.30	35804.83	25.873	2337.93	60489.97
A_68_P32553143	chrX:96238297-96238345	NM_199018:401	Stard8	INSIDE	2.484	6.859	445.03	3052.42	17.039	246.79	4205.01
A_68_P29218716	chr13:91599885-91599929	NM_024186:-795	Ssbp2	PROMOTER	2.476	16.971	563.62	9565.23	42.025	488.52	20530.01
A_68_P29338034	chr13:113777821-113777865	NM_001081062:-167	Ccno	PROMOTER	2.475	3.687	601.99	2219.36	9.124	484.42	4420.08
A_68_P24449884	chr6:52266647-52266691	NR_038163:-1842	5730457N03Rik	PROMOTER	2.474	11.257	8241.17	92768.87	27.844	5150.16	143401.90
A_68_P29643100	chr14:60795943-60795987	ENSMUST00000140924:412		INSIDE	2.473	5.834	4663.00	27202.57	14.424	3814.13	55015.58
A_68_P23397281	chr4:148275240-148275284	NM_027195:96762	Casz1	INSIDE	2.472	7.602	17403.01	132294.10	18.791	11859.44	222849.10
A_68_P29237600	chr13:95653897-95653941	NM_011021:8337	Otp	DOWNSTREAM	2.471	2.116	4449.75	9414.95	5.227	3177.96	16612.19
A_68_P31003040	chr17:3084893-3084937	NR_003519:-731	Pisd-ps2	PROMOTER	2.471	9.924	20698.53	205421.40	24.520	13630.62	334218.10
A_68_P30784285	chr16:57122018-57122062	NM_138599:214	Tomm70a	INSIDE	2.470	9.905	4797.46	47520.59	24.470	3311.14	81023.28
A_68_P21569910	chr2:119303067-119303111	NM_026574:277	Ino80	INSIDE	2.468	6.138	4882.70	29972.16	15.151	3573.68	54146.25
A_68_P20765302	chr1:162125324-162125368	NM_025474:-44	Mrps14	PROMOTER	2.468	10.418	5914.69	61622.12	25.708	3725.32	95770.00

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26292118	chr9:8544562-8544606	NM_013838:443	Trpc6	INSIDE	2.466	3.342	924.53	3089.86	8.241	744.87	6138.87
A_68_P26742258	chr9:95412445-95412489	NM_001114977:-51	2610101N10Rik	PROMOTER	2.465	9.638	28756.99	277163.20	23.754	16578.52	393802.70
A_68_P30350128	chr15:76540931-76540975	NM_058214:37	Recql4	INSIDE	2.464	4.532	3611.54	16368.01	11.166	2597.51	29002.98
A_68_P26164568	chr8:113262460-113262504	NM_198625:17099	Mtss1l	INSIDE	2.463	10.638	6103.81	64933.75	26.205	4061.40	106430.50
A_68_P28605007	chr12:86940319-86940363	NM_030887:-25	Jdp2	PROMOTER	2.462	7.922	7190.55	56964.74	19.503	5194.50	101306.80
A_68_P32471622	chrX:72661675-72661719	NM_010839:186	Mtcp1	INSIDE	2.460	3.523	1439.66	5072.36	8.668	783.74	6793.80
A_68_P31618899	chr18:35721824-35721868	NM_010771:35	Matr3	INSIDE	2.459	1.495	1916.90	2865.17	3.676	1857.74	6829.22
A_68_P31934224	chr19:6364358-6364402	NM_001110791:691	Sf1	INSIDE	2.459	12.680	1791.20	22713.16	31.175	1325.53	41323.44
A_68_P22408449	chr3:107563183-107563227	NM_001113529:183	Csf1	INSIDE	2.457	11.554	10695.95	123580.20	28.391	6189.87	175737.30
A_68_P32817209	chrX:165111905-165111949	NM_010832:-92	Msl3	PROMOTER	2.457	2.364	835.90	1976.12	5.809	516.85	3002.34
A_68_P32287119	chrX:19637488-19637532	NM_021715:815	Chst7	INSIDE	2.452	3.851	2163.89	8333.81	9.443	1159.22	10946.07
A_68_P32385147	chrX:50341550-50341594	NM_013556:318	Hprt	INSIDE	2.451	3.348	1957.19	6553.16	8.208	1013.19	8316.29
A_68_P30575400	chr16:17734120-17734164			Unknown	2.447	6.556	12299.05	80630.62	16.041	9298.61	149159.30
A_68_P22888054	chr4:46318111-46318155	ENSMUST00000123933:38171		INSIDE	2.447	4.268	1176.07	5019.52	10.445	855.56	8936.54
A_68_P27688946	chr11:32355594-32355638	NM_173784:245	Ubtd2	INSIDE	2.445	5.514	5760.64	31763.89	13.479	4170.34	56213.19
A_68_P21762364	chr2:154617306-154617350	NM_001139511:483	Raly	INSIDE	2.443	9.092	3562.21	32388.11	22.209	2473.01	54924.23
A_68_P27293831	chr10:82275065-82275109	NR_038042:219	1700028I16Rik	INSIDE	2.437	6.388	11619.79	74232.92	15.569	8124.71	126492.50
A_68_P22921606	chr4:53172577-53172621	NM_013454:169	Abca1	INSIDE	2.437	2.829	163.57	462.78	6.896	94.45	651.32
A_68_P27315977	chr10:86241971-86242015	NM_175331:243	Nt5dc3	INSIDE	2.437	8.680	2362.38	20505.09	21.157	1771.77	37484.74
A_68_P23418024	chr4:151700327-151700371	NM_009079:362	Rpl22	INSIDE	2.437	4.492	1567.13	7039.64	10.946	1298.21	14210.70
A_68_P31427919	A_68_P31427919			Unknown	2.436	9.712	763.42	7414.61	23.661	575.48	13616.52
A_68_P27862290	chr11:63734698-63734742	NM_018805:1066	Hs3st3b1	INSIDE	2.430	7.416	3406.97	25266.90	18.019	2541.56	45797.47
A_68_P23222249	chr4:114580688-114580732	NM_008593:793	Foxd2	INSIDE	2.427	6.487	1921.84	12467.91	15.742	1486.86	23406.71
A_68_P28585119	chr12:83270170-83270214	NM_001167983:-810	Sipa1l1	PROMOTER	2.427	9.389	1250.51	11740.61	22.786	826.90	18841.71
A_68_P26085413	chr8:98330883-98330927	NR_015574:175	4930513N10Rik	INSIDE	2.426	7.226	17038.37	123120.90	17.533	11905.60	208738.70
A_68_P25456593	chr7:125259495-125259539	NM_170669:145	Rps15a	INSIDE	2.426	5.742	1683.11	9663.99	13.927	1116.17	15544.89
A_68_P27951947	chr11:79787924-79787968			Unknown	2.425	2.515	1153.67	2901.97	6.099	1034.23	6307.86
A_68_P21890601	chr2:178148869-178148913	NM_001085501:287	Ppp1r3d	INSIDE	2.424	10.660	2909.91	31019.30	25.839	1951.87	50435.31
A_68_P32766765	chrX:153929388-153929432	NM_009214:568	Sms	INSIDE	2.423	5.494	1673.83	9195.71	13.311	1054.97	14042.84
A_68_P32674751	chrX:131543547-131543591	NM_175446:180	Zmat1	INSIDE	2.422	19.742	5109.23	100864.00	47.809	3031.64	144939.50
A_68_P21143643	chr2:37559408-37559452	ENSMUST00000155237:-51		PROMOTER	2.422	21.024	2553.66	53687.95	50.919	1577.89	80345.03
A_68_P27938553	chr11:77421084-77421128	NM_144825:211	Taok1	INSIDE	2.421	10.195	1625.76	16575.32	24.688	1096.06	27059.37
A_68_P21100500	chr2:29821292-29821336	NM_001076554:235	Spna2	INSIDE	2.415	5.503	3190.19	17554.30	13.290	2465.20	32762.30
A_68_P20768477	chr1:162723220-162723264	NM_013862:-173	Rabgap1l	PROMOTER	2.414	12.018	13257.93	159330.70	29.007	7275.12	211026.50
A_68_P28688419	chr12:103150855-103150899	NM_028446:505	Trip11	INSIDE	2.414	4.319	6889.77	29759.31	10.425	5098.42	53151.19
A_68_P23288229	chr4:127665953-127665997	ENSMUST00000144298:687		INSIDE	2.412	4.500	4613.46	20761.36	10.856	3159.82	34303.98
A_68_P29871680	chr14:104872642-104872686	NM_011143:-5448	Pou4f1	PROMOTER	2.411	11.000	6367.29	70042.71	26.520	4744.22	125818.80
A_68_P20239578	chr1:54983378-54983422	NM_001081433:-169	Ankrd44	PROMOTER	2.409	2.608	6346.65	16554.50	6.284	4761.34	29920.98
A_68_P31544271	chr18:21458929-21458973	NM_001033445:-310	Fam59a	PROMOTER	2.408	7.221	15083.00	108913.00	17.386	9309.07	161852.10
A_68_P32260801	chrX:11735963-11736007	NM_001168321:1497	Bcor	INSIDE	2.406	5.141	2235.03	11489.89	12.371	1508.11	18656.45
A_68_P30572936	chr16:17276365-17276409	NM_177473:-6	Tmem191c	PROMOTER	2.406	10.155	1116.24	11334.84	24.427	920.55	22486.71
A_68_P30550104	chr16:11984103-11984147	NM_001174086:-81	Shisa9	PROMOTER	2.405	2.187	9712.97	21244.19	5.261	6807.54	35811.66
A_68_P27282935	A_68_P27282935			Unknown	2.403	14.380	970.24	13952.13	34.556	611.57	21133.49
A_68_P23594805	chr5:34868409-34868453	NM_011893:-2	Sh3bp2	PROMOTER	2.402	20.833	5614.36	116962.20	50.042	3130.32	156648.20
A_68_P32441102	chrX:65932146-65932191	NM_008031:439	Fmr1	INSIDE	2.396	4.896	1079.66	5286.01	11.733	634.73	7447.07
A_68_P24820868	chr6:125444847-125444891	NM_007657:-95	Cd9	PROMOTER	2.390	11.281	9567.66	107930.20	26.957	5477.58	147659.80
A_68_P29455876	chr14:22805255-22805299	NM_145459:3547	Zfp503	INSIDE	2.388	4.903	8384.65	41113.51	11.710	5045.05	59078.81
A_68_P24089922	chr5:130089988-130090034	NM_011846:-78	Mmp17	PROMOTER	2.386	10.764	5163.23	55575.58	25.684	3039.76	78072.02
A_68_P31117105	chr17:27693117-27693161	NM_001025427:-380	Hmga1	PROMOTER	2.385	5.460	803.42	4386.29	13.019	638.81	8316.76
A_68_P22412541	chr3:108218746-108218790	NM_001004177:-356	Celsr2	PROMOTER	2.381	3.887	1745.81	6786.45	9.257	1460.57	13520.87
A_68_P28043617	chr11:96166483-96166527	NM_008268:1679	Hoxb5	INSIDE	2.377	2.543	7392.87	18798.29	6.045	5490.85	33193.03

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28051732	chr11:97489553-97489597	NM_175332:1456	E130012A19Rik	INSIDE	2.375	10.917	6860.96	74899.38	25.922	4341.43	112540.60
A_68_P28069996	chr11:100621272-100621316	NM_001081194:-202	Kcnh4	PROMOTER	2.374	4.449	752.81	3349.60	10.562	555.22	5864.15
A_68_P23278482	chr4:125826960-125827005	NM_172145:1736	Fam176b	INSIDE	2.373	12.234	2471.48	30237.07	29.028	1293.78	37556.21
A_68_P25770033	chr8:34764110-34764154	NM_010344:423	Gsr	INSIDE	2.372	5.357	3869.14	20727.80	12.708	3194.58	40595.16
A_68_P31201770	chr17:45692568-45692612	NM_008690:-74	Nfkbie	DIVERGENT_PROMOTER	2.372	9.998	12623.07	126210.50	23.715	8032.57	190492.00
A_68_P22532055	chr3:131153686-131153730			Unknown	2.371	10.441	2576.84	26904.95	24.751	1612.79	39917.49
A_68_P32760538	chrX:152057229-152057273	NM_001093750:620	Ptchd1	INSIDE	2.370	7.084	3332.40	23607.79	16.787	2229.53	37426.19
A_68_P28936016	chr13:34094703-34094748	NM_009068:-17	Ripk1	DIVERGENT_PROMOTER	2.369	5.834	3745.72	21850.67	13.820	2666.49	36851.95
A_68_P25372610	chr7:108469852-108469896	NM_019990:42	Stard10	INSIDE	2.367	5.981	15543.06	92958.13	14.156	11160.96	157990.00
A_68_P26886028	chr9:121766761-121766805	NM_001112668:-133	Gm9790	PROMOTER	2.363	5.533	4191.24	23188.72	13.072	3175.11	41505.89
A_68_P27781641	chr11:48982982-48983026	NM_172793:17587	Btnl9	INSIDE	2.360	0.624	1571.69	981.26	1.473	1783.94	2628.61
A_68_P24381989	chr6:39155596-39155640	NM_001033430:1154	Jhdm1d	INSIDE	2.359	5.189	5116.70	26550.66	12.238	3987.22	48797.57
A_68_P27536264	chr10:126948850-126948894	NM_001098789:-3122	Ndufa4l2	PROMOTER	2.359	3.890	1188.21	4622.23	9.177	968.88	8890.91
A_68_P21017263	chr2:13495869-13495913	NM_011701:-47	Vim	PROMOTER	2.359	3.510	257.85	905.15	8.280	190.22	1574.90
A_68_P32533286	chrX:90544628-90544672	NM_007492:12666	Arx	DOWNSTREAM	2.358	4.450	2021.28	8993.94	10.492	1357.54	14243.46
A_68_P28567140	chr12:80108151-80108195	NM_178745:92	Tmem229b	INSIDE	2.358	6.724	9582.42	64433.40	15.858	7192.83	114067.00
A_68_P32578106	chrX:101866324-101866368	NM_175358:57	Zdhhc15	INSIDE	2.357	1.895	739.72	1402.08	4.467	457.94	2045.51
A_68_P28149790	chr11:114652964-114653008	NM_028055:4220	Btbd17	INSIDE	2.356	6.334	2909.45	18427.57	14.919	2289.11	34151.24
A_68_P31936825	chr19:7016840-7016884	NM_001177361:78	Gpr137	INSIDE	2.355	1.625	788.65	1281.49	3.826	596.15	2280.83
A_68_P23777458	chr5:69732840-69732884	NM_175519:86	Kctd8	INSIDE	2.354	17.034	6463.80	110101.70	40.098	4087.66	163905.10
A_68_P32268347	chrX:13423633-13423677	NM_009806:13	Cask	INSIDE	2.352	4.775	4033.45	19260.09	11.231	2219.51	24926.78
A_68_P24590984	chr6:82983529-82983573	NM_010070:-85	Dok1	DIVERGENT_PROMOTER	2.352	3.562	1137.34	4051.68	8.379	847.92	7104.88
A_68_P32563826	chrX:98580104-98580148	NM_008124:7451	Gjb1	INSIDE	2.352	3.539	937.42	3317.78	8.324	424.00	3529.44
A_68_P31256333	chr17:56601586-56601630	NM_011218:14295	Ptprs	INSIDE	2.352	1.518	961.67	1459.97	3.570	669.84	2391.35
A_68_P31311926	chr17:67704196-67704240	NM_008984:-419	Ptprm	PROMOTER	2.351	6.912	3804.89	26300.93	16.250	2810.62	45673.54
A_68_P30650943	chr16:32099956-32100000	NM_025892:91	1500031L02Rik	INSIDE	2.348	3.775	7748.81	29255.63	8.866	5745.28	50940.39
A_68_P26827666	chr9:111020550-111020594	NM_001164838:-42	Lrrfip2	PROMOTER	2.347	5.128	3893.76	19967.23	12.037	2948.94	35497.62
A_68_P29032310	chr13:51503858-51503902	NM_010101:-106	S1pr3	PROMOTER	2.347	4.881	1406.71	6866.52	11.458	969.33	11106.33
A_68_P22299774	chr3:85691661-85691705	NM_177130:-242	Glt28d2	PROMOTER	2.345	6.115	2137.83	13071.99	14.340	1643.46	23567.60
A_68_P20741945	chr1:158134987-158135031	NM_177838:148	Fam163a	INSIDE	2.344	0.728	1936.10	1410.28	1.708	1837.68	3138.08
A_68_P21109951	chr2:31428059-31428103	NM_001033389:-164	Fubp3	PROMOTER	2.343	13.413	1326.63	17793.56	31.430	941.46	29589.95
A_68_P27569379	chr11:6505657-6505701	NM_001081652:379	Nacad	INSIDE	2.343	8.268	5339.75	44151.53	19.370	3628.25	70280.29
A_68_P24604715	chr6:85324050-85324094	NM_001003955:556	Rab11fip5	INSIDE	2.343	8.621	4194.89	36164.41	20.197	2530.98	51118.48
A_68_P25505713	chr7:134615484-134615528	NM_145589:379	Prr14	INSIDE	2.340	4.798	2228.95	10694.08	11.228	1578.60	17725.31
A_68_P31112418	chr17:26918319-26918363	NM_172149:317	Bnip1	INSIDE	2.338	3.275	5084.44	16652.05	7.656	3514.57	26906.28
A_68_P32365934	chrX:46048429-46048473	NM_173376:270	Rbmx2	INSIDE	2.338	12.123	3931.16	47655.81	28.346	2266.75	64254.35
A_68_P20556967	chr1:121317480-121317524	NM_008381:1323	Inhbb	INSIDE	2.337	6.799	1585.18	10777.19	15.888	1233.25	19593.83
A_68_P24039940	chr5:121081339-121081383	NM_001195094:2884	Ccdc42b	INSIDE	2.335	2.020	661.34	1335.89	4.717	629.67	2969.92
A_68_P29958338	chr14:122278102-122278146	NM_026861:297	Ubac2	INSIDE	2.334	4.232	2780.86	11768.46	9.877	2012.80	19879.47
A_68_P23244381	chr4:118905195-118905239	NM_001012400:113	AU022252	INSIDE	2.333	2.690	5994.47	16124.96	6.275	4417.41	27719.49
A_68_P21621794	chr2:128690006-128690050	NM_024237:361	Fbln7	INSIDE	2.332	1.496	749.56	1121.25	3.489	627.27	2188.52
A_68_P25645821	chr8:9976314-9976358	NM_176953:-13	Lig4	DIVERGENT_PROMOTER	2.332	7.229	11513.48	83233.88	16.857	7753.00	130696.00
A_68_P28989794	chr13:43460884-43460928	NM_178848:-5178	Sirt5	PROMOTER	2.332	3.269	1508.13	4930.73	7.626	1101.35	8398.55
A_68_P21334154	chr2:73729891-73729935	NM_001025093:773	Atf2	INSIDE	2.330	9.939	23555.36	234127.40	23.161	14168.05	328151.80
A_68_P31373358	chr17:79136029-79136073	NM_011500:-150	Strn	PROMOTER	2.327	2.976	1194.14	3553.45	6.925	955.41	6616.44
A_68_P31428327	chr17:88929344-88929388	NM_028658:-97	Klraq1	PROMOTER	2.326	8.666	2680.12	23227.16	20.154	1767.89	35629.85
A_68_P24004683	chr5:115017800-115017844	NM_001004180:-437	BC057022	PROMOTER	2.324	15.416	3357.74	51764.02	35.833	2417.21	86615.99
A_68_P27564951	chr11:5688365-5688409	NM_001146308:-99	Dbnl	PROMOTER	2.322	6.341	2538.53	16095.66	14.726	1987.15	29262.25
A_68_P23336241	chr4:136391071-136391115	NM_010142:758	Ephb2	INSIDE	2.322	3.395	3359.27	11404.09	7.883	2536.99	19998.83
A_68_P25016756	chr7:28119811-28119855	NM_001113549:-1165	Ltbp4	PROMOTER	2.321	7.348	4064.11	29862.64	17.053	2879.70	49106.29
A_68_P25009065	chr7:26004933-26004977	NM_207677:-76	Dedd2	DIVERGENT_PROMOTER	2.316	2.652	8195.44	21737.08	6.143	5505.81	33821.86

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28530101	chr12:73186989-73187033	NM_001205067:185	Jkamp	INSIDE	2.316	6.814	2167.14	14767.70	15.779	1323.51	20883.40
A_68_P27095209	chr10:42222002-42222046	NM_017472:165	Snx3	INSIDE	2.314	4.285	1119.07	4795.47	9.918	862.62	8555.08
A_68_P32260371	chrX:11668288-11668332	NM_001168321:69171	Bcor	INSIDE	2.313	1.587	1844.59	2926.56	3.669	931.85	3419.40
A_68_P23980413	chr5:110973506-110973550	NM_198306:165	Galnt9	INSIDE	2.313	2.123	903.04	1916.98	4.911	837.52	4113.03
A_68_P22951804	chr4:58566187-58566231	NM_172989:-43	Lpar1	PROMOTER	2.313	12.789	2033.78	26009.86	29.587	1471.32	43531.41
A_68_P28997682	chr13:44829049-44829093	NM_001205043:2431	Jarid2	INSIDE	2.312	8.821	15712.06	138592.40	20.390	9201.23	187610.30
A_68_P31144954	chr17:32457616-32457660	NM_019774:460	Akap8	INSIDE	2.308	6.815	5331.38	36334.12	15.732	3796.01	59720.41
A_68_P20149055	chr1:36615091-36615135	NM_001126047:114	Sema4c	INSIDE	2.308	2.850	1328.56	3786.16	6.578	972.00	6393.64
A_68_P32340723	chrX:39421307-39421351	NM_009688:316	Xiap	INSIDE	2.308	3.837	2381.77	9138.39	8.854	1191.40	10548.87
A_68_P32365932	chrX:46048174-46048218	NM_173376:16	Rbmx2	INSIDE	2.307	1.483	755.30	1119.85	3.421	464.12	1587.86
A_68_P29342439	chr13:114584551-114584595	NM_172595:-143	Arl15	PROMOTER	2.306	6.894	13305.65	91725.86	15.896	9055.61	143951.40
A_68_P25176629	chr7:71518985-71519029	NM_177893:-25	Fan1	PROMOTER	2.306	4.347	1205.52	5239.99	10.023	908.82	9109.01
A_68_P27302613	chr10:83903670-83903714	NM_001004363:-476	Nuak1	PROMOTER	2.305	2.296	907.95	2084.57	5.293	794.46	4204.96
A_68_P32260816	chrX:11737647-11737691	NM_001168321:-187	Bcor	PROMOTER	2.303	3.008	999.15	3005.25	6.928	525.11	3638.03
A_68_P30596436	chr16:22163233-22163277	NM_183029:118	Igf2bp2	INSIDE	2.303	7.747	847.67	6567.12	17.840	768.85	13716.50
A_68_P21571253	chr2:119569096-119569140	NM_146125:1046	Itpka	INSIDE	2.303	3.874	2504.23	9700.66	8.922	1955.76	17450.11
A_68_P21013699	chr2:12932692-12932736	NM_153155:-223	C1ql3	PROMOTER	2.302	10.537	2128.50	22428.25	24.254	1494.20	36239.69
A_68_P32263512	chrX:12339036-12339080	NM_001048208:41	Med14	INSIDE	2.302	6.479	885.86	5739.19	14.914	563.91	8410.04
A_68_P27856224	chr11:62692825-62692869	NM_026210:-145	Fam18b	PROMOTER	2.301	8.002	44876.32	359089.20	18.410	25812.74	475218.60
A_68_P22085568	chr3:41368782-41368826	NM_001130186:3	Phf17	INSIDE	2.300	18.229	4332.09	78968.20	41.924	2483.05	104099.50
A_68_P32683852	chrX:133584183-133584227	NM_146261:72	Fam199x	INSIDE	2.299	5.605	36252.91	203197.50	12.886	25460.36	328071.30
A_68_P21820794	chr2:164793741-164793785	NM_020333:275	Slc12a5	INSIDE	2.299	8.368	8253.59	69064.27	19.241	5190.38	99869.07
A_68_P28183801	chr11:120166516-120166560			Unknown	2.298	12.608	2249.12	28357.44	28.973	1397.42	40487.78
A_68_P23262658	chr4:123089142-123089186	NM_001167918:-10	D830031N03Rik	PROMOTER	2.296	9.442	1728.54	16320.16	21.680	1397.75	30303.05
A_68_P32240004	chrX:7327982-7328026	NR_030454:-2210	Mir684-1	DIVERGENT_PROMOTER	2.296	3.799	1605.13	6098.03	8.723	894.64	7803.66
A_68_P31253474	chr17:56175980-56176024	NM_013664:-3	Sh3gl1	DIVERGENT_PROMOTER	2.295	5.057	8492.46	42943.44	11.605	6803.83	78960.70
A_68_P26658155	chr9:77956059-77956103	NM_023605:383	Fbxo9	INSIDE	2.294	9.040	3947.31	35683.72	20.740	3181.35	65981.75
A_68_P29055232	chr13:55574226-55574270	NM_001030296:8621	Prr7	INSIDE	2.293	2.788	1306.19	3641.47	6.394	1054.80	6744.14
A_68_P31838828	chr18:75857092-75857136	NM_201354:236	Ctif	INSIDE	2.291	9.102	4442.49	40434.40	20.853	3496.62	72913.37
A_68_P24449533	chr6:52211079-52211123	NM_008264:-226	Hoxa13	PROMOTER	2.290	6.551	2969.10	19450.39	15.000	2271.12	34065.81
A_68_P23325610	chr4:134487232-134487276	NM_026780:360	Syf2	INSIDE	2.288	21.890	11179.55	244721.20	50.094	7846.17	393047.30
A_68_P31764312	chr18:62708242-62708286	NM_134136:133	Fbxo38	INSIDE	2.287	2.829	9614.08	27195.70	6.469	6425.64	41568.23
A_68_P25766302	chr8:33994797-33994841	NM_001177589:65680	Gm3985	DOWNSTREAM	2.287	9.404	1069.61	10058.46	21.510	750.44	16141.86
A_68_P20455835	chr1:95374821-95374865	NM_133808:543	Hdlbp	INSIDE	2.286	5.679	1908.50	10839.24	12.985	1421.38	18456.94
A_68_P26772513	chr9:100935215-100935259	NM_025835:58	Pccb	INSIDE	2.286	4.099	7042.17	28866.25	9.370	5402.54	50619.91
A_68_P25809870	chr8:42325280-42325324	NM_023662:190	Pcm1	INSIDE	2.286	10.549	531.79	5609.94	24.115	415.82	10027.66
A_68_P25499304	chr7:133344026-133344070	NM_028816:-126	Xpo6	PROMOTER	2.285	19.109	8771.90	167619.40	43.660	5610.62	244958.70
A_68_P23366440	chr4:141430540-141430584	NM_025994:273	Efhd2	INSIDE	2.283	2.694	1008.85	2717.95	6.150	893.14	5493.12
A_68_P32265729	chrX:12858825-12858869	NM_010028:699	Ddx3x	INSIDE	2.282	1.824	882.91	1610.03	4.162	582.92	2425.88
A_68_P22487800	chr3:123088652-123088696	NM_201638:234	Mettl14	INSIDE	2.281	7.737	8006.62	61947.64	17.649	5831.80	102926.20
A_68_P30244836	chr15:57723668-57723712	NM_024207:283	Derl1	INSIDE	2.280	1.624	1458.51	2367.91	3.701	1125.77	4166.54
A_68_P20849641	chr1:177622831-177622875	NM_010098:-131	Opn3	DIVERGENT_PROMOTER	2.280	1.833	6986.01	12806.43	4.180	5290.64	22112.28
A_68_P27965917	chr11:82200919-82200963	NM_023438:-1461	Tmem132e	PROMOTER	2.280	7.265	2269.87	16491.30	16.564	1718.62	28467.81
A_68_P20023664	chr1:9690196-9690240	NM_008651:72	Mybl1	INSIDE	2.277	6.956	950.56	6612.18	15.839	788.81	12494.10
A_68_P25262217	chr7:86762595-86762639	NM_019799:-73	Rhcg	PROMOTER	2.277	16.815	2412.43	40564.86	38.284	1425.80	54585.64
A_68_P23322032	chr4:133843514-133843558	NM_001163794:-368	Pdik1l	PROMOTER	2.276	2.424	1209.39	2931.15	5.516	959.27	5291.41
A_68_P23927384	chr5:100467950-100467994	NM_016690:269	Hnrpdl	INSIDE	2.275	5.958	5826.38	34711.57	13.556	4005.52	54299.33
A_68_P28538319	chr12:74685927-74685971	NM_008856:-79	Prkch	PROMOTER	2.273	3.609	351.00	1266.84	8.205	326.89	2682.09
A_68_P27083521	chr10:40069136-40069180	NM_001168304:45	Cdk19	INSIDE	2.272	7.152	461.33	3299.64	16.254	351.42	5711.81
A_68_P27937689	chr11:77275784-77275828	NM_139128:-1608	Coro6	PROMOTER	2.271	3.704	1483.14	5493.90	8.411	1145.14	9631.95
A_68_P27095712	chr10:42303728-42303772	NM_152229:-356	Nr2e1	PROMOTER	2.271	12.858	11284.84	145096.10	29.199	7978.87	232972.60

						Sham group			TiO$_2$-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28598113	chr12:85749685-85749729	NM_001026214:273	Entpd5	INSIDE	2.269	3.661	3028.24	11086.95	8.308	2223.13	18468.75
A_68_P27185080	chr10:61732562-61732606	NM_001146100:70585	Hk1	INSIDE	2.269	10.646	2773.56	29527.97	24.158	2096.18	50638.62
A_68_P28159656	chr11:116351010-116351061	NM_026364:625	Prpsap1	INSIDE	2.269	17.758	4033.71	71630.06	40.290	2464.90	99310.50
A_68_P25616602	chr8:4217183-4217227	NM_207203:108	BC068157	INSIDE	2.268	2.780	1157.85	3218.82	6.304	970.70	6119.43
A_68_P31948062	chr19:10115784-10115828	NM_021890:-231	Fads3	PROMOTER	2.268	7.995	626.39	5008.14	18.133	509.60	9240.45
A_68_P27558730	chr11:4537928-4537972	NM_029291:155	Ascc2	INSIDE	2.265	8.303	1676.18	13917.18	18.803	1201.82	22597.63
A_68_P31499629	chr18:12395086-12395130	NM_008720:-213	Npc1	PROMOTER	2.263	5.827	3711.66	21629.28	13.187	2940.31	38774.14
A_68_P20088280	A_68_P20088280			Unknown	2.263	6.286	1897.88	11930.69	14.227	1381.63	19656.91
A_68_P31152238	chr17:34259488-34259532	NM_010238:-818	Brd2	PROMOTER	2.262	8.753	1863.76	16313.88	19.798	1695.39	33564.70
A_68_P24338521	chr6:31513401-31513445	NM_013723:515	Podxl	INSIDE	2.261	5.210	1194.73	6224.80	11.778	960.89	11317.24
A_68_P21625558	chr2:129418959-129419003	NM_001177647:50	Sirpa	INSIDE	2.259	2.888	1133.84	3275.07	6.526	933.94	6095.30
A_68_P29308205	chr13:108680813-108680857	NM_145456:-576	Zswim6	PROMOTER	2.259	1.450	1072.99	1555.79	3.276	830.04	2719.13
A_68_P22450560	chr3:116365543-116365587	NM_008246:31	Hiat1	INSIDE	2.258	4.123	1719.69	7090.76	9.309	1240.40	11546.41
A_68_P25023454	chr7:29551526-29551579	NM_010908:-9	Nfkbib	DIVERGENT_PROMOTER	2.257	8.477	713.98	6052.27	19.133	530.50	10149.87
A_68_P25837064	chr8:47702719-47702763	NM_009810:-62	Casp3	DIVERGENT_PROMOTER	2.255	8.065	13019.36	104998.00	18.182	9442.59	171689.80
A_68_P32464980	chrX:71069698-71069742	NM_001029868:588	Pdzd4	INSIDE	2.253	5.144	453.64	2333.58	11.591	243.90	2826.91
A_68_P23749456	chr5:64551627-64551671	NM_019636:199	Tbc1d1	INSIDE	2.251	6.568	13603.88	89353.73	14.786	9241.51	136648.90
A_68_P27921611	chr11:74451961-74452005	NM_001013784:18876	E130309D14Rik	INSIDE	2.250	5.916	3541.95	20954.34	13.311	2760.39	36744.42
A_68_P22481653	chr3:121996304-121996348	NR_030439:295	Mir760	DOWNSTREAM	2.249	3.528	297.41	1049.11	7.933	238.92	1895.23
A_68_P28909030	chr13:29051600-29051644	NM_009238:-6071	Sox4	PROMOTER	2.248	3.638	3625.39	13187.66	8.177	2539.05	20760.84
A_68_P25761256	chr8:33120256-33120300	ENSMUST00000080782:-697		PROMOTER	2.247	4.259	4672.03	19896.15	9.570	3228.37	30896.25
A_68_P23873662	chr5:89150059-89150103	NM_026735:185	Mobkl1a	INSIDE	2.246	6.208	3024.03	18774.60	13.943	2380.22	33186.33
A_68_P23176712	chr4:104782284-104782328	NM_178143:197	Prkaa2	INSIDE	2.246	5.210	21364.40	111304.50	11.704	15131.89	177100.10
A_68_P27338390	chr10:90291759-90291803	NM_001177396:252345	Anks1b	INSIDE	2.245	4.521	1258.95	5692.26	10.151	946.42	9607.50
A_68_P29144056	chr13:74199745-74199789	NM_028959:-33	Cep72	PROMOTER	2.243	5.603	3753.23	21030.95	12.567	2544.14	31972.55
A_68_P21492621	chr2:104966817-104966861	NM_144783:153	Wt1	INSIDE	2.243	4.140	9624.40	39847.81	9.288	6641.61	61684.67
A_68_P27850822	chr11:61668093-61668137	NM_013881:480	Ulk2	INSIDE	2.241	12.017	5428.39	65234.44	26.936	3559.78	95885.15
A_68_P29011797	chr13:47218039-47218083	NM_146042:-28	Rnf144b	PROMOTER	2.239	1.629	928.54	1512.30	3.647	772.40	2816.58
A_68_P33007144	chr9_random:49674-49720	NR_015516:-3712	4930526I15Rik	PROMOTER	2.238	20.949	646.83	13550.10	46.880	431.58	20232.68
A_68_P23297034	chr4:129190844-129190888	NM_010807:42	Marcksl1	INSIDE	2.238	6.078	31663.01	192442.20	13.600	21299.62	289684.00
A_68_P30337605	chr15:74348245-74348289	NM_174991:1641	Bai1	INSIDE	2.237	5.632	3019.87	17008.45	12.598	1874.84	23618.98
A_68_P32031149	chr19:25746643-25746687	NM_145831:-236	Dmrt2	PROMOTER	2.234	3.449	1352.47	4664.11	7.702	1112.55	8569.35
A_68_P26221254	chr8:123113358-123113402	NM_178856:-405	Gins2	PROMOTER	2.234	8.182	5236.56	42846.61	18.278	3565.24	65164.01
A_68_P23397206	chr4:148265535-148265579	NM_027195:87056	Casz1	INSIDE	2.233	5.561	2267.31	12607.68	12.418	1606.26	19945.99
A_68_P30356228	chr15:77672759-77672803	NM_022410:-235	Myh9	PROMOTER	2.233	5.791	8131.65	47090.36	12.930	5925.98	76623.80
A_68_P30481633	chr15:99501487-99501531	NM_009597:360	Accn2	INSIDE	2.232	1.473	1396.71	2057.16	3.287	1251.13	4112.21
A_68_P32260247	chrX:11654044-11654088	NM_029510:3613	Bcor	INSIDE	2.232	1.501	1387.28	2082.41	3.351	649.41	2176.05
A_68_P28047527	chr11:96777858-96777902	NM_030248:-85	Cdk5rap3	PROMOTER	2.231	9.254	3176.78	29398.85	20.649	1753.53	36208.26
A_68_P31147212	chr17:32966976-32967020	NM_177359:195	Zfp799	INSIDE	2.230	7.205	2501.50	18022.65	16.067	1776.93	28549.85
A_68_P28080239	chr11:102417477-102417521	NM_001159492:-26	Gpatch8	PROMOTER	2.229	6.312	7420.54	46836.99	14.069	5185.46	72952.94
A_68_P32506209	chrX:82819101-82819145	NM_025729:-238	Tab3	PROMOTER	2.228	5.900	2141.79	12636.44	13.145	1254.89	16495.16
A_68_P28053229	chr11:97745535-97745579	NM_001081435:-88	Fbxo47	PROMOTER	2.226	7.628	7635.22	58240.73	16.982	4804.99	81599.95
A_68_P25279941	chr7:90014673-90014717	NM_175366:-1148	Mex3b	PROMOTER	2.224	5.070	4959.03	25142.20	11.274	3753.77	42319.18
A_68_P32583453	chrX:103415136-103415180	NM_001001176:23	Taf9b	INSIDE	2.223	6.738	958.05	6455.48	14.979	638.42	9563.02
A_68_P26017904	chr8:86591013-86591057	NM_009055:300	Rfx1	INSIDE	2.220	4.457	1742.64	7766.47	9.895	1449.24	14340.14
A_68_P26247734	chr8:127317918-127317962	NM_198632:1022	Trim67	INSIDE	2.219	5.090	4707.86	23962.96	11.297	3622.37	40921.94
A_68_P23693365	chr5:52581836-52581880	NR_015537:-61	9230114K14Rik	DIVERGENT_PROMOTER	2.218	6.219	1084.17	6742.91	13.793	995.51	13731.22
A_68_P28575798	chr12:81564728-81564777	NM_133798:671	Exd2	INSIDE	2.218	7.448	1524.74	11356.43	16.524	1070.78	17693.19
A_68_P31158869	chr17:35457566-35457610	NM_010390:86	H2-Q1	INSIDE	2.218	3.214	2869.99	9224.70	7.128	2234.57	15927.74
A_68_P32265730	chrX:12858920-12858964	NM_010028:795	Ddx3x	INSIDE	2.217	1.889	385.98	729.24	4.188	219.21	918.16
A_68_P23513990	chr5:18732536-18732580	NM_001170746:-305	Magi2	PROMOTER	2.216	6.205	10538.73	65397.65	13.752	8258.67	113576.80

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P32700325	chrX:137200051-137200095	ENSMUST00000112988:462		INSIDE	2.216	6.332	1007.94	6382.27	14.033	816.09	11452.23
A_68_P20645803	chr1:138311898-138311942	NM_026500:73	Ddx59	INSIDE	2.215	2.243	339.36	761.23	4.969	308.46	1532.86
A_68_P27901829	chr11:70460462-70460506	NM_024211:11	Slc25a11	INSIDE	2.215	1.633	1156.52	1888.88	3.617	951.49	3441.89
A_68_P25091867	chr7:52471545-52471589	NM_011565:444	Tead2	INSIDE	2.215	15.992	4898.00	78330.04	35.420	3007.66	106531.60
A_68_P31619415	chr18:35812025-35812069	NM_027222:-3025	2010001M09Rik	PROMOTER	2.214	6.357	1547.49	9837.17	14.072	1207.65	16994.20
A_68_P21103096	chr2:30271133-30271177	NM_007760:114	Crat	INSIDE	2.214	7.925	3581.49	28381.88	17.546	2493.99	43759.89
A_68_P33007796	chr4_random:129068-129112	NM_001033326:19289	Dhrsx	INSIDE	2.214	6.689	9324.57	62374.43	14.813	5853.14	86702.44
A_68_P23592057	chr5:34343782-34343826	NM_001001985:5172	Nat8l	INSIDE	2.214	8.208	19505.54	160108.10	18.177	11137.08	202440.10
A_68_P24920738	chr6:144997199-144997243	NM_001024468:112	Bcat1	INSIDE	2.213	2.887	1538.27	4441.50	6.390	1136.41	7261.59
A_68_P22861615	chr4:41261631-41261675	NM_026893:282	Dcaf12	INSIDE	2.213	9.114	4804.62	43790.81	20.168	3504.05	70669.71
A_68_P27943494	chr11:78279579-78279623	NM_026740:398	Slc46a1	INSIDE	2.212	5.310	7800.47	41419.02	11.745	5159.24	60594.41
A_68_P31093720	chr17:23940883-23940927	NM_175229:751	Srrm2	INSIDE	2.212	2.483	1982.45	4923.18	5.494	1454.97	7994.04
A_68_P20742449	chr1:158233625-158233669	NM_001134741:-167	Tdrd5	DIVERGENT_PROMOTER	2.212	9.538	2976.99	28395.71	21.102	2346.43	49515.32
A_68_P25360757	chr7:106417697-106417741	NM_001043355:863	Mtap6	INSIDE	2.210	4.630	2563.91	11870.65	10.232	1820.63	18628.00
A_68_P22737302	chr4:12833974-12834018	NM_001171801:13	Gm11818	INSIDE	2.209	5.015	1959.85	9827.78	11.076	1368.52	15158.08
A_68_P28751776	chr12:113916958-113917002	NM_001100460:-70	Zbtb42	DIVERGENT_PROMOTER	2.209	2.980	806.11	2402.03	6.582	700.69	4611.84
A_68_P29080348	chr13:59686650-59686694	NM_030153:-21	Naa35	PROMOTER	2.207	6.748	1745.08	11775.43	14.893	1380.05	20552.67
A_68_P31951139	chr19:10599956-10600000	NM_001164272:245	Cpsf7	INSIDE	2.206	15.169	6442.48	97726.43	33.464	3939.70	131838.40
A_68_P20337461	chr1:72582629-72582673	NM_001045533:488	Marchf4	INSIDE	2.205	8.769	4635.05	40642.45	19.337	3125.23	60432.55
A_68_P20335713	chr1:72290528-72290572	ENSMUST00000123654:-44		PROMOTER	2.205	3.019	1186.36	3581.85	6.658	844.95	5625.61
A_68_P24591289	chr6:83027770-83027814	NM_197992:-591	Pcgf1	DIVERGENT_PROMOTER	2.204	2.692	354.10	953.35	5.934	302.72	1796.48
A_68_P28606270	chr12:87166109-87166153	NM_001081423:231	Ttll5	INSIDE	2.203	1.934	783.80	1515.98	4.262	601.72	2564.47
A_68_P28712200	chr12:107200958-107201002	BC156654:163120		INSIDE	2.203	8.056	7461.56	60109.60	17.745	5395.10	95735.46
A_68_P27279294	chr10:79318023-79318067	NR_029447:-328	E130317F20Rik	PROMOTER	2.202	5.706	1545.56	8818.27	12.562	1215.69	15271.43
A_68_P26169432	chr8:114167808-114167852	NM_001037665:488	Zfp1	INSIDE	2.202	5.107	2651.81	13541.72	11.244	1977.35	22233.90
A_68_P24603559	chr6:85137815-85137859	NM_010131:-88	Emx1	PROMOTER	2.198	6.948	2502.06	17385.39	15.275	1965.77	30027.50
A_68_P25032021	chr7:31320496-31320540	NM_178252:-490	Arhgap33	PROMOTER	2.197	5.889	4112.22	24218.15	12.937	2604.63	33696.82
A_68_P27503761	chr10:120913745-120913792	NM_138956:-462	Rassf3	PROMOTER	2.197	2.114	470.03	993.45	4.644	376.06	1746.53
A_68_P26398844	chr9:30939486-30939530	NM_011176:-124	St14	PROMOTER	2.197	4.125	7544.95	31124.72	9.064	5133.42	46531.13
A_68_P30960416	chr16:91010827-91010871	NM_001045515:492	Synj1	INSIDE	2.196	7.714	957.87	7388.76	16.937	792.63	13424.86
A_68_P31306319	chr17:66798578-66798622	NM_001114098:490	1110012J17Rik	INSIDE	2.195	10.809	9897.40	106984.90	23.727	6523.10	154776.90
A_68_P31143302	chr17:32173587-32173631	NM_028244:502	Rrp1b	INSIDE	2.195	6.110	3200.19	19554.71	13.412	2348.29	31494.87
A_68_P25505623	chr7:134587980-134588024	NM_175163:4670	Zfp689	INSIDE	2.195	6.386	1233.58	7878.17	14.018	1140.67	15989.94
A_68_P30478229	chr15:98928779-98928823	NM_176835:-1114	Dnajc22	PROMOTER	2.194	8.321	7380.07	61409.06	18.254	5468.03	99815.07
A_68_P28067852	chr11:100258833-100258877	NM_010593:250	Jup	INSIDE	2.193	5.577	3327.06	18556.04	12.233	2328.22	28480.36
A_68_P25716360	chr8:24521956-24522000	NM_013834:5	Sfrp1	INSIDE	2.193	9.499	2326.53	22099.39	20.830	1818.84	37887.13
A_68_P30668269	A_68_P30668269			Unknown	2.193	10.012	1958.33	19606.21	21.951	1317.28	28916.10
A_68_P32672214	chrX:131010586-131010630	NM_028958:421	Taf7l	INSIDE	2.192	4.631	1820.18	8429.86	10.151	797.38	8094.39
A_68_P20303908	chr1:66724124-66724168	NM_175510:209126	Unc80	INSIDE	2.192	12.767	15968.88	203869.80	27.990	10327.29	289058.50
A_68_P29578138	chr14:47380037-47380081	NM_028222:-157	Cdkn3	PROMOTER	2.191	1.390	1576.79	2191.73	3.046	1182.31	3601.48
A_68_P32226993	chr19:60831736-60831780	NM_178421:-131	Nanos1	PROMOTER	2.190	5.397	11809.73	63740.95	11.823	8903.57	105264.20
A_68_P31784091	chr18:66094837-66094881	NM_013833:3885	Rax	INSIDE	2.190	7.709	3926.57	30268.81	16.880	2989.95	50470.21
A_68_P28595531	chr12:85291747-85291791	NM_023633:211	2410016O06Rik	INSIDE	2.188	2.421	371.70	899.87	5.298	458.78	2430.71
A_68_P27681337	chr11:30854282-30854326	NM_023906:-93	Asb3	DIVERGENT_PROMOTER	2.186	6.686	9808.72	65585.14	14.615	7228.55	105644.30
A_68_P23057175	chr4:82151052-82151103	NM_001113209:135	Nfib	INSIDE	2.186	12.701	2331.78	29615.98	27.759	1593.57	44235.74
A_68_P22336399	chr3:93248419-93248463	NM_001163098:2189	Tchh	INSIDE	2.183	41.121	2242.23	92201.51	89.767	1225.81	110037.50
A_68_P29614877	chr14:55513260-55513304	NM_019402:303	Pabpn1	INSIDE	2.182	9.221	2638.58	24330.46	20.124	1966.61	39576.81
A_68_P27804178	chr11:53138130-53138174	NM_026479:-38	Zcchc10	PROMOTER	2.182	3.232	3439.26	11114.35	7.051	2390.08	16853.17
A_68_P24134134	chr5:139677035-139677079	NM_024451:433	Sun1	INSIDE	2.181	5.783	2783.77	16099.74	12.615	1839.83	23209.33
A_68_P24327113	chr6:29477125-29477169	NM_012057:414	Irf5	INSIDE	2.180	6.727	2168.97	14589.91	14.666	1359.43	19936.89
A_68_P25056449	chr7:37481732-37481776	NM_172298:-1382	Tshz3	PROMOTER	2.179	4.522	6942.59	31394.05	9.853	5384.81	53058.30

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28752833	chr12:114067608-114067652	NM_028023:-30	Cdca4	PROMOTER	2.176	4.177	2559.35	10690.00	9.089	1848.78	16804.37
A_68_P22422570	chr3:109945667-109945711	NM_001163348:702	Ntng1	INSIDE	2.176	1.821	2038.86	3713.60	3.963	1614.34	6397.87
A_68_P27290790	chr10:81063642-81063689	NM_053254:-20	Tle6	DIVERGENT_PROMOTER	2.176	4.811	8247.25	39678.77	10.468	6013.28	62949.87
A_68_P31922938	chr19:4397627-4397671	NM_001001984:-571	Kdm2a	PROMOTER	2.175	3.087	1795.80	5543.40	6.715	1491.27	10014.01
A_68_P21780563	chr2:157854132-157854176	NM_027434:-375	Rprd1b	PROMOTER	2.174	3.021	1078.36	3258.04	6.568	867.01	5694.82
A_68_P32099202	chr19:38129262-38129306	NM_028293:-230	Cep55	PROMOTER	2.173	8.598	14671.61	126142.50	18.683	9111.35	170231.80
A_68_P28048173	chr11:96879906-96879950	NM_031183:5046	Sp6	INSIDE	2.171	8.587	6504.89	55854.27	18.644	4870.51	90804.01
A_68_P32242174	chrX:7769836-7769880	NM_007898:780	Ebp	INSIDE	2.170	1.795	3484.43	6255.21	3.896	1401.56	5460.34
A_68_P29615096	chr14:55545666-55545710	NM_010112:-63	Efs	DIVERGENT_PROMOTER	2.169	18.040	3597.05	64890.58	39.131	2404.11	94075.39
A_68_P23344531	chr4:137772915-137772959	NM_001122897:-109	Hp1bp3	PROMOTER	2.169	16.862	7205.96	121509.40	36.582	4534.79	165892.40
A_68_P22894261	chr4:47365847-47365891	NM_009370:-308	Tgfbr1	PROMOTER	2.169	5.306	1036.17	5498.30	11.508	847.24	9749.72
A_68_P21587592	chr2:122528587-122528631	NM_011774:-209	Slc30a4	PROMOTER	2.167	4.479	2103.53	9422.12	9.705	1687.24	16374.21
A_68_P32742983	chrX:147247480-147247524	NM_001199246:744	Maged2	INSIDE	2.161	4.903	2403.16	11783.38	10.596	1585.60	16800.76
A_68_P21204319	chr2:49643540-49643584	NM_027990:357	Lypd6b	INSIDE	2.160	4.204	1901.65	7994.55	9.081	1433.64	13018.78
A_68_P25266551	chr7:87547096-87547140	NM_011046:530	Furin	INSIDE	2.159	12.930	2107.76	27252.24	27.910	1267.94	35387.98
A_68_P20556970	chr1:121318089-121318133	NM_008381:715	Inhbb	INSIDE	2.159	5.335	1743.08	9299.56	11.520	1390.23	16015.89
A_68_P27846103	chr11:60835840-60835884	ENSMUST00000089184:-203		PROMOTER	2.159	4.342	8041.17	34914.08	9.374	6184.87	57977.20
A_68_P24624506	chr6:88791877-88791921	NM_030251:31	Abtb1	INSIDE	2.158	5.442	15857.65	86291.89	11.741	10489.90	123163.10
A_68_P28175309	chr11:118884826-118884870	NM_007623:506	Cbx2	INSIDE	2.158	2.545	1722.26	4382.75	5.492	1449.00	7957.76
A_68_P31114505	chr17:27270655-27270699	NM_026063:160	2900010M23Rik	INSIDE	2.157	9.667	6284.28	60751.19	20.850	4279.05	89217.88
A_68_P27537125	chr10:127058908-127058952	NM_008512:-726	Lrp1	PROMOTER	2.156	5.585	2639.93	14743.96	12.043	1960.62	23611.85
A_68_P21722283	chr2:146909704-146909748	NM_023504:1355	Nkx2-4	INSIDE	2.154	8.276	3101.29	25666.94	17.826	2213.60	39460.62
A_68_P27332821	chr10:89207726-89207770	NM_029166:13	Uhrf1bp1l	INSIDE	2.154	3.424	2654.20	9088.83	7.375	2280.54	16819.81
A_68_P28873012	chr13:21560534-21560582	NM_025719:-188	Nkapl	PROMOTER	2.153	4.725	1181.67	5583.63	10.174	928.73	9449.34
A_68_P21250388	chr2:58999667-58999711	NM_026361:782	Pkp4	INSIDE	2.153	7.303	2391.43	17465.64	15.726	1956.02	30760.24
A_68_P21103442	chr2:30328841-30328885	NM_030244:857	Ier5l	INSIDE	2.152	11.581	3520.79	40775.03	24.925	2959.60	73769.32
A_68_P31731070	chr18:56721947-56721991	NM_138600:-16	Aldh7a1	DIVERGENT_PROMOTER	2.150	8.615	28263.35	243484.30	18.524	18196.29	337068.80
A_68_P30625227	chr16:27388952-27388996	NM_001025615:-88	Ccdc50	PROMOTER	2.147	4.727	892.50	4218.57	10.148	820.82	8329.36
A_68_P32463053	chrX:70748921-70748965	NM_177236:518	Atp2b3	INSIDE	2.146	1.750	5188.54	9081.27	3.756	2355.67	8846.92
A_68_P32383369	chrX:49967083-49967127	NM_016697:47	Gpc3	INSIDE	2.146	3.528	4704.13	16596.20	7.570	2240.78	16963.39
A_68_P23931499	chr5:101227260-101227304	NM_001081107:337	Helq	INSIDE	2.145	2.896	2065.63	5982.98	6.212	1669.15	10368.86
A_68_P31420283	chr17:87362407-87362451	NM_145491:-22	Rhoq	PROMOTER	2.143	2.059	433.01	891.59	4.412	401.47	1771.37
A_68_P25174406	chr7:71083847-71083891	NM_021366:-67	Klf13	PROMOTER	2.142	5.907	1489.42	8798.10	12.651	1164.39	14731.24
A_68_P31020947	chr17:6079672-6079716	NM_001111017:45	Serac1	INSIDE	2.142	2.556	2521.73	6444.82	5.475	1977.12	10824.66
A_68_P30580079	chr16:18499124-18499168	NM_023120:183	Gnb1l	INSIDE	2.141	2.844	1859.81	5289.01	6.089	1442.04	8781.04
A_68_P22752524	chr4:15885248-15885292	NM_013752:157	Nbn	INSIDE	2.141	2.779	1457.00	4048.50	5.948	1231.65	7325.64
A_68_P24116580	chr5:135964648-135964692	NM_146001:56322	Hip1	INSIDE	2.140	5.409	3084.15	16682.53	11.576	2262.33	26188.17
A_68_P23232782	chr4:116828713-116828757	NR_030704:-281	Snord55	PROMOTER	2.140	3.084	637.06	1964.47	6.599	492.18	3247.96
A_68_P31116177	chr17:27552104-27552148	NM_001013385:88123	Grm4	DOWNSTREAM	2.139	12.359	2346.81	29005.04	26.430	1264.59	33423.64
A_68_P27776272	chr11:47802609-47802653	ENSMUST00000128558:-159		PROMOTER	2.139	4.332	1174.70	5089.32	9.265	917.71	8502.75
A_68_P26710370	chr9:88377975-88378019	NM_019796:-761	Syncrip	PROMOTER	2.138	5.150	1514.87	7801.64	11.009	1191.15	13113.61
A_68_P26405232	chr9:32217116-32217162	AK146406:436717		INSIDE	2.138	3.197	3016.19	9643.67	6.836	2325.43	15897.00
A_68_P28175799	chr11:118951917-118951961	NM_007625:-4387	Cbx4	PROMOTER	2.137	5.608	3193.53	17908.29	11.981	2453.76	29398.49
A_68_P22202889	chr3:65762508-65762552	NM_019937:-383	Ccnl1	PROMOTER	2.137	1.533	854.67	1310.43	3.276	727.96	2384.86
A_68_P27448186	chr10:110735503-110735547	NM_027914:-210	Bbs10	PROMOTER	2.136	4.699	6265.44	29444.31	10.038	4580.95	45985.56
A_68_P24046831	chr5:122293021-122293065	NM_175474:-5994	Fam109a	DIVERGENT_PROMOTER	2.136	2.255	193.72	436.93	4.817	167.27	805.78
A_68_P23164325	chr4:102787321-102787365	NM_001039081:-4652	Mier1	PROMOTER	2.136	7.582	18637.64	141316.60	16.193	13089.85	211962.50
A_68_P30959119	chr16:90810476-90810520	NM_029497:160	Urb1	INSIDE	2.136	3.049	1905.85	5811.50	6.515	1616.24	10529.11
A_68_P23260191	chr4:122672828-122672872	NM_008506:-491	Mycl1	PROMOTER	2.135	12.888	3988.63	51404.12	27.511	2697.48	74210.26
A_68_P24535485	chr6:71222087-71222131	NM_145568:96	Krcc1	INSIDE	2.134	11.063	1731.55	19155.50	23.604	1167.46	27557.14
A_68_P20457529	chr1:95700443-95700487	NM_025454:-77	Ing5	DIVERGENT_PROMOTER	2.133	9.915	5255.68	52111.82	21.145	2649.65	56025.88

						Sham group			TiO$_2$-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P29075350	chr13:58908196-58908240	NM_001025074:-975	Ntrk2	PROMOTER	2.133	15.813	9970.56	157660.40	33.725	6282.78	211887.50
A_68_P29237599	chr13:95653816-95653860	NM_011021:8257	Otp	DOWNSTREAM	2.133	2.276	7639.08	17383.48	4.854	5327.65	25861.44
A_68_P26138122	chr8:108692733-108692777	NM_178798:-20	Slc7a6	PROMOTER	2.133	9.459	3267.93	30911.10	20.172	2009.26	40530.44
A_68_P32168785	chr19:50752526-50752570	NM_021377:554	Sorcs1	INSIDE	2.133	7.067	4953.93	35007.53	15.071	3490.88	52610.12
A_68_P32026831	chr19:25036147-25036191	NM_146097:-62	Cbwd1	PROMOTER	2.132	6.201	3613.13	22406.37	13.219	2745.31	36290.47
A_68_P24783935	chr6:117857266-117857310	NM_001166428:-533	Hnrnpf	PROMOTER	2.132	4.289	3396.15	14566.89	9.143	2523.63	23072.58
A_68_P26221734	chr8:123191897-123191941	NM_010926:94	Cox4nb	INSIDE	2.130	2.268	6911.12	15675.39	4.830	4809.16	23230.14
A_68_P31866342	chr18:80909356-80909400	NM_001164111:-4466	Nfatc1	PROMOTER	2.130	3.279	1050.27	3443.57	6.983	910.41	6357.55
A_68_P27289987	chr10:80945075-80945119	NM_176954:358	Celf5	INSIDE	2.128	8.817	8860.98	78128.69	18.767	4829.56	90637.92
A_68_P25850572	chr8:49928690-49928734	AK013771:-216		PROMOTER	2.127	7.939	5676.85	45068.92	16.886	4392.61	74172.80
A_68_P32533270	chrX:90542781-90542825	NM_007492:10818	Arx	INSIDE	2.126	3.577	832.85	2978.70	7.604	439.74	3344.00
A_68_P25009418	chr7:26067028-26067072	NM_001110131:-147	Cic	PROMOTER	2.126	4.923	27867.04	137201.80	10.469	18156.34	190086.60
A_68_P28153958	chr11:115374907-115374951	NM_008258:756	Hn1	INSIDE	2.126	17.486	989.68	17305.50	37.177	683.54	25411.86
A_68_P27561184	chr11:4965305-4965349	NM_001190406:4	Gas2l1	INSIDE	2.125	7.670	8270.87	63438.54	16.302	5486.54	89440.16
A_68_P32573188	chrX:100689079-100689123	NR_015508:186	Enox	INSIDE	2.124	3.962	3243.02	12847.80	8.416	2143.69	18040.59
A_68_P28470083	chr12:60168415-60168459	NM_008891:531	Pnn	INSIDE	2.123	1.820	544.02	990.33	3.864	511.63	1976.88
A_68_P27693355	chr11:33102836-33102880	NM_019916:730	Tlx3	INSIDE	2.123	3.391	1478.25	5012.70	7.199	1172.83	8443.77
A_68_P30747800	chr16:49855504-49855548	NM_010581:-240	Cd47	PROMOTER	2.122	2.349	1331.03	3126.76	4.984	933.56	4653.28
A_68_P22032039	chr3:31048745-31048789	NM_008770:-75	Cldn11	PROMOTER	2.122	1.605	1227.26	1969.46	3.405	969.49	3301.02
A_68_P25098823	chr7:53653169-53653213	NM_001112739:1324	Kcnc1	INSIDE	2.122	1.801	902.15	1624.83	3.822	1053.18	4025.32
A_68_P29055349	chr13:55589582-55589626	NM_001177371:-167	Dbn1	PROMOTER	2.120	8.125	3720.33	30227.89	17.225	2832.48	48789.15
A_68_P29726978	chr14:75684076-75684120	NM_026083:-81	Zc3h13	PROMOTER	2.120	8.539	2031.43	17345.71	18.101	1558.55	28211.02
A_68_P27939273	chr11:77580346-77580390	ENSMUST00000102488:-5284		PROMOTER	2.119	6.643	2128.84	14141.13	14.075	1689.26	23776.24
A_68_P26866698	chr9:118416014-118416060	NM_018748:601	Golga4	INSIDE	2.118	11.798	3642.19	42970.34	24.992	2297.60	57421.75
A_68_P28977626	chr13:41454570-41454617	NM_017464:-223	Nedd9	PROMOTER	2.118	8.738	800.33	6993.42	18.504	665.69	12317.74
A_68_P20148714	chr1:36568619-36568663	NM_001039551:-80	Cnnm3	PROMOTER	2.117	8.917	14587.91	130076.10	18.878	10155.26	191711.20
A_68_P24295432	chr6:23203617-23203661	NM_028462:-5374	Fezf1	PROMOTER	2.117	4.889	2303.60	11263.08	10.350	1828.01	18919.61
A_68_P24477003	chr6:56781975-56782019	NM_012056:-56	Fkbp9	PROMOTER	2.117	2.955	752.71	2224.52	6.256	588.64	3682.38
A_68_P25343512	chr7:103359060-103359104	NM_011858:-64	Odz4	PROMOTER	2.117	11.052	2664.60	29448.01	23.391	2126.61	49742.89
A_68_P25354353	chr7:105326510-105326554	NM_007602:171	Capn5	INSIDE	2.116	4.262	3205.06	13658.50	9.017	2370.02	21370.70
A_68_P25274817	chr7:89079514-89079558	NM_013886:-191	Hdgfrp3	PROMOTER	2.116	6.283	3031.88	19048.71	13.295	2230.02	29648.19
A_68_P24697529	chr6:101327967-101328012	NM_018884:-98	Pdzrn3	PROMOTER	2.116	3.642	1129.20	4112.31	7.704	922.39	7106.53
A_68_P20354818	chr1:75543316-75543360	NM_009208:498	Slc4a3	INSIDE	2.116	4.675	6516.45	30464.92	9.891	4369.35	43216.35
A_68_P23154908	chr4:101093069-101093113	NM_009647:783	Ak4	INSIDE	2.114	2.054	374.05	768.22	4.343	300.11	1303.25
A_68_P31428328	chr17:88929429-88929473	NM_028658:-13	Klraq1	PROMOTER	2.114	6.174	817.38	5046.29	13.049	621.87	8114.53
A_68_P27995861	chr11:87550950-87550994	NM_009296:-94	Supt4h1	PROMOTER	2.114	6.564	2326.72	15273.06	13.877	1692.93	23493.62
A_68_P28578489	chr12:82047116-82047160	NM_001079694:648	Srsf5	INSIDE	2.113	3.899	533.87	2081.51	8.237	451.24	3716.87
A_68_P31013736	chr17:4994894-4994938	NM_001085355:-157	Arid1b	PROMOTER	2.112	7.097	7741.52	54941.16	14.990	5329.90	79894.54
A_68_P21767078	chr2:155518080-155518124	NM_001163452:18	Trpc4ap	INSIDE	2.112	3.247	805.77	2616.47	6.857	678.22	4650.51
A_68_P32362520	chrX:45387716-45387760	NM_013912:291	Apln	INSIDE	2.111	11.695	2906.03	33987.15	24.693	1701.13	42005.98
A_68_P23332310	chr4:135700553-135700600	NM_008321:840	Id3	INSIDE	2.111	4.020	265.91	1068.88	8.487	194.28	1648.92
A_68_P21081484	chr2:26819762-26819806	NM_207234:122	Rexo4	INSIDE	2.111	1.454	1049.76	1526.60	3.069	779.46	2392.39
A_68_P21932364	chr3:8463041-8463085	NR_033512:36	Gm6194	INSIDE	2.110	4.809	7173.47	34497.75	10.146	5470.79	55505.08
A_68_P26580032	chr9:63932502-63932546	AK011166:3957		INSIDE	2.110	8.689	923.42	8023.56	18.334	876.07	16061.57
A_68_P31106282	chr17:25929216-25929260	NM_145410:-9	Fam173a	PROMOTER	2.109	4.902	4593.98	22517.64	10.336	3445.66	35614.77
A_68_P24859175	chr6:133985925-133985969	NM_007961:222	Etv6	INSIDE	2.108	3.752	3350.18	12571.15	7.911	2729.27	21590.99
A_68_P23296217	chr4:129012516-129012560	NM_009030:76	Rbbp4	INSIDE	2.108	2.519	1338.36	3371.92	5.310	1049.62	5573.84
A_68_P21212091	chr2:51004685-51004729	NM_028810:-75	Rnd3	PROMOTER	2.108	2.277	362.08	824.64	4.800	271.24	1301.97
A_68_P28159663	chr11:116351729-116351773	NM_026364:-90	Prpsap1	PROMOTER	2.107	11.663	4378.77	51068.54	24.577	3204.24	78750.14
A_68_P31152236	chr17:34259233-34259277	NM_010238:-562	Brd2	PROMOTER	2.106	10.329	4117.14	42527.06	21.755	2698.80	58712.71
A_68_P30447922	chr15:93426512-93426556	NM_001033217:-212	Prickle1	PROMOTER	2.106	6.137	74837.32	459288.20	12.924	48581.46	627876.40

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25457391	chr7:125387085-125387129	NM_001031814:45	Smg1	INSIDE	2.106	4.551	16026.86	72944.30	9.587	11915.57	114231.50
A_68_P31120338	chr17:28217573-28217617	NM_001085555:-10	Tcp11	PROMOTER	2.106	4.187	3641.41	15248.33	8.819	2657.60	23437.56
A_68_P23272064	chr4:124762396-124762440	NM_027310:28	Meaf6	INSIDE	2.105	4.439	2277.95	10112.16	9.343	1719.31	16064.02
A_68_P24611353	chr6:86619098-86619142	NM_010751:33	Mxd1	INSIDE	2.105	4.756	11879.78	56499.76	10.010	9280.46	92901.41
A_68_P22682770	chr3:157610734-157610778	NM_001013806:327	Ankrd13c	INSIDE	2.104	9.504	13866.58	131786.90	19.996	9715.78	194280.20
A_68_P22319131	chr3:89200123-89200167	NM_009565:-3019	Zbtb7b	PROMOTER	2.104	1.910	3518.56	6721.41	4.019	2746.25	11038.09
A_68_P21108244	chr2:31169965-31170009	ENSMUST00000113532:52		INSIDE	2.104	8.863	1254.86	11121.21	18.649	932.21	17385.19
A_68_P27924602	chr11:74984051-74984095	NM_010430:-315	Hic1	DIVERGENT_PROMOTER	2.102	5.021	1961.59	9850.01	10.557	1570.80	16583.45
A_68_P30156691	chr15:39775111-39775155	NM_172814:171	Lrp12	INSIDE	2.102	11.020	1141.73	12582.07	23.167	888.50	20584.27
A_68_P24116035	chr5:135845821-135845865	NM_145414:20	Nsun5	INSIDE	2.102	17.612	2746.94	48380.36	37.014	1782.24	65968.27
A_68_P27265105	chr10:76424885-76424929	NM_021568:-214	Pcbp3	PROMOTER	2.101	15.355	9942.78	152671.90	32.260	6191.69	199742.50
A_68_P31422209	chr17:87682307-87682351	NM_028639:103	Ttc7	INSIDE	2.100	3.330	695.26	2315.04	6.993	552.07	3860.37
A_68_P28057142	chr11:98412381-98412425	NM_001166494:-8	Zpbp2	DIVERGENT_PROMOTER	2.100	7.127	4869.52	34703.67	14.967	3233.09	48389.12
A_68_P25365140	chr7:107154438-107154482	NM_133709:-453	Chrdl2	PROMOTER	2.099	6.849	440.36	3016.19	14.378	378.06	5435.81
A_68_P29958335	chr14:122277673-122277717	NM_026861:-133	Ubac2	PROMOTER	2.099	1.758	1369.19	2407.09	3.691	1136.02	4192.80
A_68_P26373433	chr9:26807126-26807170	NM_025862:-14	Acad8	DIVERGENT_PROMOTER	2.098	5.345	17294.92	92433.87	11.212	11665.23	130790.60
A_68_P31879479	chr18:83126499-83126543	NM_001177464:42497	Zfp516	INSIDE	2.098	9.025	2560.18	23104.84	18.937	2102.69	39819.04
A_68_P22589086	chr3:141832410-141832454	ENSMUST00000106230:-43		PROMOTER	2.098	5.085	1374.40	6989.17	10.667	1016.87	10846.50
A_68_P31465581	chr18:4922333-4922377	ENSMUST00000143254:631		INSIDE	2.098	4.943	1041.55	5148.69	10.369	737.86	7651.00
A_68_P24157329	chr5:144383488-144383532	NM_011182:195	Cyth3	INSIDE	2.097	5.682	2773.18	15757.80	11.913	2014.79	24002.08
A_68_P32056099	chr19:30105106-30105150	NM_144873:126	Uhrf2	INSIDE	2.097	6.089	1920.53	11693.79	12.766	1554.80	19847.81
A_68_P26217005	chr8:122480667-122480711	NM_009462:45937	Usp10	INSIDE	2.097	5.459	7807.56	42622.45	11.448	5530.16	63309.99
A_68_P25097409	chr7:53435456-53435500	NM_011510:-75	Abcc8	PROMOTER	2.095	2.714	766.06	2078.86	5.685	662.42	3765.95
A_68_P29750657	chr14:79700949-79700993	NM_025427:472	1190002H23Rik	INSIDE	2.094	3.449	1577.46	5439.92	7.221	1229.53	8878.49
A_68_P22752864	chr4:15941113-15941157	NM_145950:-110	Osgin2	PROMOTER	2.094	4.203	1844.34	7752.34	8.800	1498.32	13185.35
A_68_P25747455	chr8:30329725-30329769	NM_153135:362	Unc5d	INSIDE	2.094	7.058	8318.20	58706.24	14.778	6527.83	96467.42
A_68_P30141373	chr15:36868452-36868496			Unknown	2.093	6.700	1134.05	7597.84	14.025	878.71	12323.46
A_68_P29257223	chr13:99136439-99136483	NM_008242:12261	Foxd1	DOWNSTREAM	2.092	8.661	2174.59	18833.71	18.116	1799.01	32590.48
A_68_P29044041	chr13:53558129-53558173	NM_013601:9999	Msx2	DOWNSTREAM	2.092	5.217	933.42	4869.21	10.914	666.32	7272.46
A_68_P31092441	chr17:23713283-23713327	NM_011747:23150	Zfp13	INSIDE	2.092	1.581	1651.05	2609.73	3.307	1243.51	4112.10
A_68_P31099001	chr17:24824425-24824469	NM_011522:2448	Syngr3	INSIDE	2.091	8.282	15324.02	126913.40	17.318	9704.87	168065.90
A_68_P21114610	chr2:32168059-32168103	NR_029811:-5899	Mir199b	PROMOTER	2.090	4.476	10196.84	45644.87	9.354	6842.97	64010.85
A_68_P28073802	chr11:101286306-101286350	NM_172566:-70	Rundc1	PROMOTER	2.090	4.644	5587.40	25946.09	9.706	3826.56	37141.60
A_68_P30791337	chr16:58408386-58408430	NM_028523:-239	Dcbld2	PROMOTER	2.089	3.420	3208.27	10970.76	7.142	2683.72	19168.06
A_68_P22293161	chr3:84619085-84619129	NM_001177773:-392	Fbxw7	PROMOTER	2.089	7.473	3528.14	26366.72	15.611	2725.81	42552.94
A_68_P27921682	chr11:74463075-74463119	NM_001081158:100	1300001I01Rik	INSIDE	2.088	2.414	680.04	1641.56	5.039	534.85	2695.16
A_68_P27257833	chr10:75130195-75130239	NM_172549:96886	Cabin1	INSIDE	2.088	4.864	1348.50	6558.82	10.158	1195.82	12146.99
A_68_P27579284	chr11:8564125-8564169	NM_001083587:392	Tns3	INSIDE	2.088	6.420	1932.44	12405.84	13.402	1474.21	19757.56
A_68_P20637774	chr1:137044071-137044115	NM_026823:682	Arl8a	INSIDE	2.086	7.376	14805.20	109197.40	15.389	10138.97	156028.00
A_68_P29651397	chr14:62301793-62301837	NR_028264:-604	Dleu2	PROMOTER	2.086	5.959	1659.98	9891.50	12.430	1475.76	18342.94
A_68_P22101775	chr3:45185176-45185220	NM_011043:2879	Pcdh10	INSIDE	2.086	3.350	1178.34	3947.95	6.990	865.17	6047.41
A_68_P32603687	chrX:109715096-109715140	NM_177747:984	Zfp711	INSIDE	2.086	6.119	1571.52	9616.70	12.767	999.78	12764.45
A_68_P30540368	chr16:9995820-9995865	NM_008170:-3216	Grin2a	PROMOTER	2.085	12.926	6410.38	82858.78	26.947	4763.33	128356.60
A_68_P28956451	chr13:37870397-37870441	ENSMUST00000122842:150		INSIDE	2.085	7.454	6420.13	47855.92	15.540	4503.02	69975.92
A_68_P32957122	A_68_P32957122			Unknown	2.083	2.877	2800.99	8058.38	5.992	2104.57	12611.20
A_68_P21576252	chr2:120435142-120435186	NM_025475:-7	Haus2	DIVERGENT_PROMOTER	2.082	2.017	670.15	1351.97	4.200	563.13	2365.28
A_68_P31161375	chr17:36002953-36002997	NM_001146710:-98	2310014H01Rik	PROMOTER	2.081	4.776	4697.04	22432.44	9.940	3457.88	34370.91
A_68_P27278520	chr10:79187527-79187571	NM_008226:8170	Hcn2	INSIDE	2.081	10.178	1515.88	15429.29	21.186	1116.24	23649.08
A_68_P22601420	chr3:143865390-143865434	NM_001161769:-52	Lmo4	PROMOTER	2.081	4.028	7512.89	30265.03	8.383	5764.40	48324.41
A_68_P23334806	chr4:136158309-136158353	NM_133872:308	Kdm1a	INSIDE	2.080	7.767	4209.78	32698.79	16.158	3270.28	52841.38
A_68_P25349892	chr7:104473950-104473994	NM_001177412:502	Usp35	INSIDE	2.080	2.019	288.84	583.25	4.200	214.06	899.00

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P32751751	chrX:149472100-149472144	NM_023788:-16	Mageh1	PROMOTER	2.079	7.842	12021.86	94269.69	16.303	7384.41	120391.60
A_68_P24877027	chr6:137200894-137200938	NM_001164401:97	Ptpro	INSIDE	2.079	5.823	4168.49	24271.80	12.108	3191.65	38642.87
A_68_P32008156	chr19:21853273-21853317	NM_001033759:463	Tmem2	INSIDE	2.079	7.297	4595.47	33532.42	15.169	3279.14	49740.42
A_68_P20268947	chr1:60467002-60467046	NM_001198570:562	Abi2	INSIDE	2.078	4.564	2869.41	13096.93	9.483	2330.68	22101.92
A_68_P23271474	chr4:124663490-124663534	NM_138683:-161	Rspo1	PROMOTER	2.078	4.498	1224.00	5505.66	9.348	917.28	8574.29
A_68_P24118747	chr5:136438697-136438741	NM_001160366:11628	Srcrb4d	INSIDE	2.078	3.036	1843.78	5597.98	6.308	1464.81	9240.73
A_68_P21338948	chr2:74542744-74542788	NM_008276:-779	Hoxd8	PROMOTER	2.077	4.821	1280.62	6174.19	10.013	960.79	9620.80
A_68_P20599489	chr1:130140741-130140785	NM_026390:5	Ubxn4	INSIDE	2.077	1.596	867.00	1383.46	3.314	766.74	2541.27
A_68_P27186303	chr10:61949193-61949237	NM_001113355:132	Vps26a	INSIDE	2.075	17.294	1212.62	20971.44	35.885	866.21	31083.98
A_68_P26847149	chr9:114843024-114843068	NM_175380:59	Gpd1l	INSIDE	2.074	4.714	2036.36	9598.68	9.776	1631.58	15950.71
A_68_P25016218	chr7:28013554-28013598	NM_181593:40	Itpkc	INSIDE	2.074	7.976	939.09	7490.48	16.541	687.48	11371.60
A_68_P30278749	chr15:63829759-63829803	NM_144846:62230	Fam49b	INSIDE	2.073	3.646	2844.80	10373.26	7.558	2230.18	16854.81
A_68_P26814202	chr9:108209138-108209182	NM_016802:625	Rhoa	INSIDE	2.073	11.208	7900.79	88551.97	23.233	4693.18	109038.70
A_68_P25549531	chr7:142129256-142129301	NM_001143802:835	Fam196a	INSIDE	2.072	3.078	1300.45	4002.22	6.375	952.86	6074.71
A_68_P25992689	chr8:81636479-81636523	NM_178267:84165	Zfp827	INSIDE	2.072	12.786	10404.52	133037.20	26.490	6169.84	163436.70
A_68_P27787453	chr11:50044668-50044712	NM_145926:5854	Mgat4b	INSIDE	2.071	2.420	1573.74	3808.69	5.012	1234.71	6187.88
A_68_P20585375	chr1:127456906-127456950	NM_028787:-664	Slc35f5	PROMOTER	2.071	5.325	2201.21	11722.48	11.029	1528.85	16862.37
A_68_P21571594	chr2:119625143-119625187	NM_019392:-85	Tyro3	PROMOTER	2.071	8.860	3983.38	35291.72	18.347	3170.68	58172.74
A_68_P31678555	chr18:46901926-46901970	NM_009681:378	Ap3s1	INSIDE	2.070	5.852	3619.77	21183.18	12.116	2582.15	31286.58
A_68_P22323963	chr3:90017329-90017373	NM_001190258:219	Gm9846	INSIDE	2.068	0.262	1139.06	298.86	0.543	1169.11	634.28
A_68_P28202486	chr12:4824316-4824360	NM_025323:-75	0610009D07Rik	PROMOTER	2.066	5.998	7074.81	42438.20	12.391	5053.47	62617.15
A_68_P25263207	chr7:86938148-86938192	NM_008588:306	Mesp1	INSIDE	2.066	1.675	913.13	1529.48	3.460	931.29	3222.05
A_68_P23962136	chr5:107003898-107003942	ENSMUST00000124394:-185		PROMOTER	2.066	9.107	6108.38	55630.31	18.816	4224.86	79494.57
A_68_P28842022	chr13:15555028-15555072	NM_008130:-505	Gli3	PROMOTER	2.065	6.713	2389.98	16043.20	13.862	1884.57	26123.75
A_68_P25092565	chr7:52602361-52602407	NM_029741:20005	Ppfia3	INSIDE	2.064	16.737	4118.57	68931.68	34.541	2615.55	90342.51
A_68_P29270336	chr13:101602642-101602692	NM_022885:716	Slc30a5	INSIDE	2.064	4.883	1259.48	6149.51	10.078	939.30	9466.16
A_68_P26468513	chr9:44413201-44413245	NM_001110826:248	Ddx6	INSIDE	2.063	4.714	9476.98	44677.44	9.726	6618.62	64370.16
A_68_P31100482	chr17:25073578-25073622	NM_001163447:322	Mapk8ip3	INSIDE	2.063	1.495	880.29	1315.95	3.084	628.83	1939.61
A_68_P31161218	chr17:35978447-35978494	NM_001010833:28	Mdc1	INSIDE	2.063	6.398	6929.61	44333.91	13.196	5328.21	70309.10
A_68_P25797392	chr8:39723329-39723373	NM_145841:1212	Sgcz	INSIDE	2.063	33.866	2213.30	74955.73	69.872	1292.88	90336.10
A_68_P22878938	chr4:44769794-44769838	NM_138590:386	Zcchc7	INSIDE	2.063	3.570	1474.78	5264.24	7.363	1251.77	9216.30
A_68_P27887968	chr11:68026330-68026374	NM_008744:173976	Ntn1	INSIDE	2.061	8.672	4533.14	39310.19	17.872	3242.41	57949.74
A_68_P22215798	chr3:68299063-68299107	NR_036665:970	Schip1	INSIDE	2.061	4.193	1799.08	7543.33	8.640	1428.43	12341.43
A_68_P30478150	chr15:98918593-98918637	NM_001024702:-455	C1ql4	PROMOTER	2.059	1.825	1640.51	2993.20	3.756	1345.67	5054.11
A_68_P25273848	chr7:88908491-88908535	NM_025997:674	Fam103a1	INSIDE	2.059	5.435	741.82	4031.91	11.189	588.81	6587.93
A_68_P27556422	chr11:4118442-4118486	NM_028022:211	Gatsl3	INSIDE	2.059	7.708	1310.88	10104.72	15.868	1024.76	16260.78
A_68_P32463876	chrX:70882705-70882749	NM_029352:-2053	Dusp9	PROMOTER	2.058	3.948	1322.13	5219.25	8.125	759.53	6171.13
A_68_P23440042	chr4:155069270-155069314	NM_178699:842	B930041F14Rik	INSIDE	2.057	2.160	3207.52	6928.72	4.444	2257.47	10031.80
A_68_P29249638	chr13:97907886-97907931	NM_177266:17	Gfm2	INSIDE	2.057	6.374	600.32	3826.62	13.115	435.69	5714.06
A_68_P25008850	chr7:25963997-25964041	X53654:548352		INSIDE	2.057	5.198	4666.59	24258.15	10.691	3443.42	36814.72
A_68_P26068970	chr8:95484812-95484856	NM_009209:-111	Slc6a2	PROMOTER	2.056	2.600	328.68	854.73	5.348	259.54	1387.98
A_68_P31385961	A_68_P31385961			Unknown	2.056	9.617	10513.88	101112.50	19.776	6821.81	134906.90
A_68_P32260645	chrX:11714194-11714238	NM_001168321:23265	Bcor	INSIDE	2.055	1.644	1945.12	3196.98	3.377	960.88	3245.06
A_68_P20644756	chr1:138131091-138131135	NM_028872:-271	5730559C18Rik	PROMOTER	2.054	5.740	1343.02	7709.17	11.789	979.59	11548.56
A_68_P31214913	chr17:48046778-48046822	NM_001110824:14781	Foxp4	INSIDE	2.054	5.738	6145.33	35262.75	11.786	4375.44	51567.38
A_68_P28290823	chr12:25335979-25336023	NM_178357:-235	Klf11	PROMOTER	2.054	4.846	5228.33	25336.60	9.953	3774.20	37564.05
A_68_P23397279	chr4:148275001-148275045	NM_027195:96522	Casz1	INSIDE	2.053	5.719	3282.49	18772.41	11.740	2431.91	28550.31
A_68_P30630406	chr16:28445546-28445590	NM_183064:-255	Fgf12	PROMOTER	2.053	2.897	1614.92	4677.83	5.947	1132.49	6734.62
A_68_P21902328	chr2:179960330-179960374	NM_001081171:212	Lama5	INSIDE	2.052	2.789	706.81	1971.49	5.724	600.12	3434.97
A_68_P31928180	chr19:5349389-5349433	NM_028623:164	Cst6	INSIDE	2.051	6.540	14012.71	91648.82	13.412	10206.67	136892.60
A_68_P28525473	chr12:72410602-72410646	NM_001190466:-246	Dact1	PROMOTER	2.051	4.733	4828.66	22854.24	9.709	3756.42	36472.19

						Sham group			TiO$_2$-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P24382228	chr6:39206775-39206819	ENSMUST00000158797:9145		DOWNSTREAM	2.051	8.436	13139.72	110850.80	17.307	8633.86	149423.40
A_68_P26685702	chr9:83699787-83699831	NM_001145974:41	Elovl4	INSIDE	2.050	7.487	9488.45	71038.47	15.349	7623.95	117020.20
A_68_P23968450	chr5:108155208-108155253	NM_010278:-1867	Gfi1	PROMOTER	2.050	3.755	599.09	2249.65	7.697	495.49	3813.81
A_68_P31411779	chr17:86022957-86023001	NM_011381:2805	Six3	INSIDE	2.050	2.885	1519.99	4385.06	5.913	1232.54	7288.03
A_68_P25926494	chr8:67471391-67471435	NM_001163747:329	Tmem192	INSIDE	2.049	1.823	3191.17	5815.94	3.734	2491.95	9305.58
A_68_P25844867	chr8:49075341-49075385	NM_133791:543	Wwc2	INSIDE	2.049	5.154	5036.50	25958.43	10.560	3628.59	38319.47
A_68_P32698227	chrX:136812773-136812817	ENSMUST00000130153:-393		PROMOTER	2.049	4.073	7538.47	30704.72	8.344	4410.05	36799.63
A_68_P30375392	chr15:80778891-80778935	NM_009634:-36	Adsl	PROMOTER	2.048	5.773	6612.32	38176.14	11.822	4842.27	57243.28
A_68_P22310062	chr3:87599138-87599182	NM_001033124:-76	Ntrk1	DIVERGENT_PROMOTER	2.048	4.535	1048.11	4753.37	9.290	851.34	7908.49
A_68_P27340135	chr10:90586440-90586484	NM_133668:246	Slc25a3	INSIDE	2.048	3.639	885.81	3223.11	7.451	782.32	5828.85
A_68_P26500013	chr9:49606044-49606088	NM_001081445:1108	Ncam1	INSIDE	2.047	6.334	6147.30	38938.26	12.967	4556.04	59078.64
A_68_P31415137	chr17:86567183-86567227	NM_011104:80	Prkce	INSIDE	2.047	2.450	2244.27	5497.38	5.015	1805.14	9053.30
A_68_P27953576	chr11:80114526-80114570	NM_139228:135	Rhbdl3	INSIDE	2.047	5.408	2493.11	13483.69	11.071	1887.05	20891.68
A_68_P23430520	chr4:153674348-153674392	NM_001112744:-366	Arhgef16	PROMOTER	2.046	6.781	4768.04	32330.88	13.874	3046.91	42272.60
A_68_P24160214	chr5:145016060-145016104	NM_018772:-11	Bri3	PROMOTER	2.046	3.409	1012.84	3452.90	6.976	891.10	6216.12
A_68_P20266458	chr1:59969786-59969830	NM_001037725:-41	Fam117b	PROMOTER	2.045	6.604	2387.87	15770.47	13.504	1898.02	25630.46
A_68_P20828236	chr1:173433692-173433736	NM_019484:106	Refbp2	INSIDE	2.045	2.577	711.82	1834.64	5.271	588.31	3101.00
A_68_P28195044	chr12:3426740-3426784	NR_030694:-15	1110002L01Rik	DIVERGENT_PROMOTER	2.044	6.470	2368.60	15325.50	13.224	1639.16	21676.61
A_68_P29683667	chr14:67850834-67850879	NM_010095:-1272	Ebf2	PROMOTER	2.044	7.888	448.05	3534.34	16.125	291.83	4705.88
A_68_P24535484	chr6:71221790-71221834	NM_145568:-200	Krcc1	DIVERGENT_PROMOTER	2.044	6.040	3652.61	22061.07	12.346	2689.46	33203.28
A_68_P23985069	chr5:111760075-111760119	NM_019640:314	Pitpnb	INSIDE	2.044	3.246	1597.28	5185.40	6.636	1287.60	8543.96
A_68_P24536895	chr6:71493871-71493915	NM_025783:45	Vps24	INSIDE	2.044	6.284	3257.70	20471.36	12.844	2453.21	31509.98
A_68_P26253528	chr8:128258194-128258238	NM_025636:114	Ntpcr	INSIDE	2.043	4.405	4197.86	18493.38	8.999	3121.18	28087.87
A_68_P27096130	chr10:42398668-42398712	NM_172416:-31	Ostm1	PROMOTER	2.043	8.153	7419.15	60484.62	16.654	5007.72	83396.75
A_68_P24769157	chr6:115084895-115084939	NM_013681:-3	Syn2	PROMOTER	2.043	2.768	1816.41	5028.12	5.654	1390.76	7863.42
A_68_P29449771	chr14:21748812-21748856	NM_009502:180	Vcl	INSIDE	2.043	1.657	1740.03	2882.66	3.385	1324.16	4482.62
A_68_P22947351	chr4:57795187-57795231	ENSMUST00000124581:157		INSIDE	2.043	4.310	5761.20	24831.12	8.805	3955.52	34829.01
A_68_P27230702	chr10:70061703-70061747	NM_001162846:-6164	Phyhipl	PROMOTER	2.042	3.479	2120.64	7376.67	7.102	1778.00	12627.91
A_68_P31839435	chr18:75979484-75979528	NM_145356:-325	Zbtb7c	PROMOTER	2.041	4.500	2203.19	9914.56	9.184	1824.68	16758.33
A_68_P21394209	chr2:84555435-84555479	NM_144887:-135	Zdhhc5	PROMOTER	2.041	7.232	8025.09	58033.93	14.762	6272.09	92586.57
A_68_P20252736	chr1:57434804-57434848	NM_028546:363	1700066M21Rik	INSIDE	2.040	7.560	1416.99	10712.47	15.420	1205.70	18591.62
A_68_P24002947	chr5:114723893-114723937	NM_148935:-144	Foxn4	PROMOTER	2.040	1.930	249.67	481.97	3.938	173.95	684.94
A_68_P22321899	chr3:89635034-89635078	NM_172530:-235	She	PROMOTER	2.040	5.853	1470.83	8608.54	11.942	1263.72	15091.48
A_68_P23351277	chr4:138908735-138908779	NM_001039200:249	C230096C10Rik	INSIDE	2.039	5.358	960.53	5146.29	10.923	813.03	8880.43
A_68_P20135584	chr1:33964894-33964938	NM_177235:-450	Bend6	PROMOTER	2.037	3.894	1308.53	5095.77	7.934	871.14	6911.80
A_68_P30349855	chr15:76502255-76502299	NM_033371:167	Ppp1r16a	INSIDE	2.037	5.148	4503.69	23185.47	10.486	3132.18	32843.45
A_68_P31126789	chr17:29374780-29374824	NM_153166:-67	Cpne5	PROMOTER	2.036	2.750	5129.96	14108.92	5.599	4116.55	23049.87
A_68_P32281785	chrX:17740258-17740302	NM_009483:488	Kdm6a	INSIDE	2.036	2.133	1484.78	3166.69	4.342	891.83	3872.13
A_68_P25588869	chr7:148633509-148633553	NM_026020:-18	Rplp2	DIVERGENT_PROMOTER	2.036	1.443	1519.74	2192.72	2.938	1093.90	3214.10
A_68_P30255506	chr15:59479250-59479294	NM_144549:-936	Trib1	PROMOTER	2.036	6.079	9403.85	57161.85	12.376	6351.70	78609.39
A_68_P20259677	chr1:58643036-58643080	NM_172513:119	Fam126b	INSIDE	2.034	5.228	4857.54	25394.96	10.635	3718.15	39544.05
A_68_P24839014	chr6:128387845-128387889	NM_010219:783	Fkbp4	INSIDE	2.034	8.102	3964.90	32121.93	16.475	2576.69	42451.57
A_68_P30349763	chr15:76491001-76491045	NM_010630:-48	Kifc2	DIVERGENT_PROMOTER	2.034	5.654	3010.19	17019.65	11.499	2241.26	25773.16
A_68_P21753788	chr2:153067075-153067119	NM_018807:-2	Plagl2	DIVERGENT_PROMOTER	2.034	5.406	1530.17	8272.83	10.998	1242.41	13664.06
A_68_P32576283	chrX:101395692-101395736	NM_001077354:742	C77370	INSIDE	2.033	6.035	5902.41	35622.69	12.267	3428.34	42055.65
A_68_P23695553	chr5:52957300-52957344	NM_144945:197	Lgi2	INSIDE	2.033	6.026	7794.77	46973.65	12.249	6150.40	75336.94
A_68_P26021886	chr8:87308677-87308721	NM_001081982:15541	Nfix	INSIDE	2.033	3.153	2950.03	9300.15	6.408	2216.58	14204.27
A_68_P21888793	chr2:177877242-177877286	NM_028806:627	Phactr3	INSIDE	2.033	15.233	3107.48	47336.47	30.969	1919.41	59441.49
A_68_P31122921	chr17:28660085-28660129	NM_026290:-7699	4930511I11Rik	PROMOTER	2.032	1.699	1585.67	2693.97	3.452	1228.85	4241.70
A_68_P30560747	chr16:14163515-14163559	NM_001114085:169	Nde1	INSIDE	2.032	5.369	18178.12	97589.71	10.906	11694.21	127539.10
A_68_P31013265	chr17:4907805-4907849	AK186662:128019		INSIDE	2.032	5.461	2831.22	15461.30	11.095	2051.46	22761.46

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P21113215	chr2:31939833-31939877	NM_175511:-629	Fam78a	PROMOTER	2.031	5.322	1178.34	6271.46	10.808	1047.04	11316.20
A_68_P27893219	chr11:68936458-68936502	NM_033041:2526	Hes7	INSIDE	2.031	4.211	3734.43	15726.52	8.552	2629.86	22489.56
A_68_P31496424	chr18:11815840-11815884	NM_001081223:-488	Rbbp8	PROMOTER	2.031	5.306	1302.81	6913.15	10.775	937.39	10100.56
A_68_P24328142	chr6:29685305-29685349	NM_176996:-170	Smo	PROMOTER	2.031	6.080	4339.25	26382.27	12.347	3096.61	38233.21
A_68_P30596851	chr16:22265603-22265647	NM_009186:378	Tra2b	INSIDE	2.031	3.657	723.92	2647.65	7.430	568.60	4224.62
A_68_P21813623	chr2:163470481-163470525	NR_028113:-83	0610039K10Rik	PROMOTER	2.030	6.080	3175.66	19308.06	12.340	2365.83	29194.46
A_68_P27569029	chr11:6447001-6447045	NM_001190343:133	Ccm2	INSIDE	2.030	7.059	1906.52	13457.51	14.326	1432.75	20526.24
A_68_P33007786	chr4_random:127770-127814	NM_001033326:17991	Dhrsx	INSIDE	2.030	7.054	14713.05	103787.70	14.321	9700.82	138923.80
A_68_P33007785	chr4_random:127689-127733	NM_001033326:17909	Dhrsx	INSIDE	2.029	9.778	14226.98	139116.50	19.840	9243.32	183387.90
A_68_P22899537	chr4:48292195-48292239	NM_029572:245	Erp44	INSIDE	2.029	6.351	2110.38	13402.42	12.888	1564.24	20159.97
A_68_P22934435	chr4:55545469-55545513	NM_010637:-143	Klf4	PROMOTER	2.029	4.472	1865.43	8341.62	9.073	1581.81	14351.88
A_68_P27285555	chr10:80260794-80260838	NM_023900:555	Plekhj1	INSIDE	2.029	5.818	14811.46	86178.09	11.803	10962.46	129386.30
A_68_P21754954	chr2:153270097-153270141	NM_001001986:97	8430427H17Rik	INSIDE	2.028	6.050	1367.93	8276.38	12.269	1143.90	14034.44
A_68_P28997663	chr13:44826717-44826761	NM_001205043:99	Jarid2	INSIDE	2.028	5.777	5348.99	30900.59	11.717	3961.04	46412.44
A_68_P30514378	chr16:5203992-5204036	NM_013796:91	Nagpa	INSIDE	2.028	3.462	3483.62	12060.51	7.023	2716.12	19074.05
A_68_P27497678	chr10:119913602-119913646	NM_010441:367	Hmga2	INSIDE	2.027	10.620	1669.67	17732.25	21.526	1108.46	23860.40
A_68_P27788199	chr11:50190689-50190733	NM_021510:-510	Hnrnph1	PROMOTER	2.027	5.389	4503.43	24268.11	10.925	3367.63	36792.22
A_68_P25962148	chr8:75095909-75095953	NM_144534:-71	Tmem38a	DIVERGENT_PROMOTER	2.027	3.910	3988.38	15596.27	7.928	3405.73	27001.85
A_68_P30436287	chr15:91403612-91403656	NM_001033633:58	Slc2a13	INSIDE	2.026	8.109	4830.94	39175.08	16.427	3504.49	57568.49
A_68_P20621314	chr1:134314077-134314121	NM_172516:69	Dstyk	INSIDE	2.025	8.533	658.52	5619.20	17.275	566.30	9782.98
A_68_P32555655	chrX:96666023-96666067	NM_001083110:30	Pja1	INSIDE	2.025	2.458	1745.67	4290.00	4.976	972.49	4838.95
A_68_P32320545	chrX:34415031-34415075	NM_019668:692	Ube2a	INSIDE	2.025	3.110	1464.24	4554.02	6.297	822.03	5176.49
A_68_P24619664	chr6:88035091-88035135	NM_133933:646	Rpn1	INSIDE	2.023	2.406	687.90	1655.17	4.867	583.12	2838.15
A_68_P23468796	chr5:8622618-8622662	NM_198620:312	Rundc3b	INSIDE	2.023	2.921	1876.82	5481.80	5.908	1531.02	9044.67
A_68_P23440100	chr4:155079091-155079135	NM_026899:189	Ssu72	INSIDE	2.023	4.457	9756.79	43489.91	9.016	7677.19	69218.56
A_68_P25232263	chr7:81157988-81158032	NM_009181:558	St8sia2	INSIDE	2.023	4.807	8465.95	40693.13	9.725	6151.28	59819.75
A_68_P32258635	chrX:11384158-11384202			Unknown	2.023	3.830	857.33	3283.38	7.748	470.95	3649.06
A_68_P23297489	chr4:129278119-129278163	NM_029748:190	2510006D16Rik	INSIDE	2.022	9.500	6864.88	65215.47	19.211	6025.84	115762.80
A_68_P23925841	chr5:100157706-100157750	NR_030692:351	A930011G23Rik	INSIDE	2.022	3.906	1456.65	5689.62	7.898	1228.64	9704.30
A_68_P26137548	chr8:108583970-108584014	NM_010901:490	Nfatc3	INSIDE	2.022	5.688	2426.16	13798.89	11.497	1782.99	20499.86
A_68_P29455871	chr14:22804612-22804656	NM_145459:4189	Zfp503	INSIDE	2.022	3.937	2979.74	11729.99	7.960	2329.53	18543.92
A_68_P25297066	chr7:94395079-94395123	NM_015760:-204	Nox4	PROMOTER	2.021	2.806	1848.01	5184.78	5.670	1421.14	8058.25
A_68_P25505272	chr7:134489178-134489222	NM_146202:-372	Zfp768	PROMOTER	2.021	1.770	593.28	1049.86	3.577	545.91	1952.67
A_68_P29018253	chr13:48323422-48323466	ENSMUST00000143259:34548		INSIDE	2.021	6.626	8014.06	53098.56	13.390	6186.98	82841.30
A_68_P26741575	chr9:95307812-95307856	NM_018763:-145	Chst2	PROMOTER	2.020	6.357	3712.67	23602.70	12.843	2845.78	36548.30
A_68_P23440105	chr4:155079607-155079651	NM_026899:705	Ssu72	INSIDE	2.020	6.071	1128.51	6850.95	12.263	891.79	10935.81
A_68_P32749012	chrX:148777026-148777070	NM_029836:-21	Tspyl2	PROMOTER	2.020	6.415	31502.22	202084.40	12.961	19139.72	248069.50
A_68_P30588341	chr16:20591588-20591632	NM_182636:1956	Vwa5b2	INSIDE	2.020	2.519	1889.99	4761.39	5.088	1498.07	7621.73
A_68_P21736747	chr2:149656520-149656564	NM_001085521:24	Tmem90b	INSIDE	2.019	14.996	3615.40	54215.89	30.269	2609.57	78989.27
A_68_P24064187	chr5:125491813-125491857	NM_028443:7990	Fam101a	INSIDE	2.018	3.517	2606.98	9168.48	7.098	1942.22	13786.55
A_68_P26693194	chr9:85220859-85220903	NM_001160379:-123	Fam46a	PROMOTER	2.018	2.016	961.09	1937.50	4.067	820.03	3335.24
A_68_P28036776	chr11:94982434-94982478	NM_010055:1026	Dlx3	INSIDE	2.017	2.367	3116.23	7376.19	4.774	2074.45	9904.28
A_68_P26588443	chr9:65427955-65427999	NM_153119:-135	Plekho2	DIVERGENT_PROMOTER	2.017	3.347	4537.00	15184.92	6.750	3697.39	24956.61
A_68_P29236942	chr13:95558754-95558798	NM_009321:-121	Tbca	PROMOTER	2.017	4.511	2758.98	12446.79	9.101	2323.29	21144.94
A_68_P27532842	chr10:126338342-126338386	NM_026858:63	Xrcc6bp1	INSIDE	2.017	4.400	3059.98	13463.66	8.873	2300.66	20414.17
A_68_P30578494	chr16:18234940-18234984	NM_172151:267	Zdhhc8	INSIDE	2.017	3.442	5731.05	19726.11	6.943	4192.76	29109.48
A_68_P21099935	chr2:29724646-29724690	NM_207298:-345	Cercam	PROMOTER	2.016	4.334	846.01	3666.90	8.736	713.80	6236.04
A_68_P29020011	chr13:48641397-48641441	NR_029725:-7777	Mirlet7a-1	PROMOTER	2.016	5.034	3588.40	18065.04	10.151	2852.00	28949.53
A_68_P32540976	chrX:92391835-92391879	ENSMUST00000113884:304		INSIDE	2.016	7.714	9301.38	71751.77	15.552	6043.94	93993.33
A_68_P22882382	chr4:45355016-45355060	NM_153167:66	Dcaf10	INSIDE	2.015	1.758	1505.23	2646.64	3.543	1371.16	4857.88
A_68_P20451399	chr1:94728353-94728397	NM_016696:112	Gpc1	INSIDE	2.015	7.014	1900.79	13332.30	14.136	1221.02	17260.24

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P21747518	chr2:151908021-151908065	NM_001160410:778	Scrt2	INSIDE	2.015	5.702	6790.30	38718.10	11.488	4305.90	49465.33
A_68_P28881600	chr13:23556264-23556308	NM_013483:1484	Btn1a1	INSIDE	2.014	3.623	1561.40	5656.95	7.296	1294.60	9445.96
A_68_P27542462	chr10:128082827-128082871	NM_011772:201	Ikzf4	INSIDE	2.014	6.594	3300.43	21761.88	13.277	2547.16	33818.33
A_68_P22413373	chr3:108365105-108365149	NM_026198:258	Tmem167b	INSIDE	2.014	5.899	11035.30	65100.15	11.883	7806.95	92767.71
A_68_P32054917	chr19:29880262-29880306	NM_172836:215	9930021J03Rik	INSIDE	2.013	8.406	1611.24	13543.82	16.922	1113.14	18836.77
A_68_P23430516	chr4:153673821-153673865	NM_001112744:162	Arhgef16	INSIDE	2.012	3.473	3277.71	11382.83	6.988	2371.01	16569.62
A_68_P26015683	chr8:86132210-86132254	NM_018808:159	Dnajb1	INSIDE	2.012	3.343	2738.47	9154.51	6.726	2170.21	14596.54
A_68_P26224550	chr8:123632450-123632508	NM_001166482:-199	Mthfsd	DIVERGENT_PROMOTER	2.012	13.659	8664.67	118351.90	27.485	5760.48	158325.40
A_68_P29596330	chr14:50682188-50682232	AK041390:1176		INSIDE	2.012	2.046	949.94	1944.02	4.118	747.94	3080.16
A_68_P24608765	chr6:86145281-86145325	NM_031199:58	Tgfa	INSIDE	2.011	4.196	265.89	1115.69	8.439	229.08	1933.18
A_68_P32326603	chrX:35543022-35543066	NM_001079513:75	Zbtb33	INSIDE	2.011	4.310	831.73	3584.55	8.668	491.76	4262.69
A_68_P24864944	chr6:135015833-135015878	NM_181444:176	Gprc5a	INSIDE	2.010	8.465	1809.30	15316.48	17.014	1441.62	24527.37
A_68_P33005811	A_68_P33005811			Unknown	2.010	7.835	405.82	3179.55	15.748	365.25	5751.97
A_68_P26022583	chr8:87432507-87432551	NM_010062:6	Dnase2a	INSIDE	2.009	11.553	2603.56	30078.45	23.214	1599.71	37136.06
A_68_P24784010	chr6:117867385-117867429	NM_001166427:95	Hnrnpf	INSIDE	2.009	4.788	2320.95	11113.62	9.618	1897.26	18248.16
A_68_P22696144	chr4:4066014-4066058	NM_001002927:-444	Penk	PROMOTER	2.009	5.062	1845.48	9341.22	10.168	1526.33	15519.67
A_68_P27564785	chr11:5641343-5641387	NM_178623:-185	Urgcp	PROMOTER	2.009	0.300	1036.82	310.68	0.602	1175.91	707.96
A_68_P25616898	chr8:4259319-4259363	NM_183315:-66	Ctxn1	PROMOTER	2.007	4.280	4968.20	21264.26	8.592	3603.90	30964.43
A_68_P31156111	chr17:34987166-34987210	NM_021337:-39	Skiv2l	DIVERGENT_PROMOTER	2.007	5.126	962.58	4934.17	10.287	766.37	7883.27
A_68_P20614481	chr1:133141395-133141439	NM_018750:339	Rassf5	INSIDE	2.006	1.595	980.47	1563.95	3.200	835.62	2674.01
A_68_P25670551	chr8:13785477-13785521	NM_025924:-116	Upf3a	PROMOTER	2.006	1.435	1349.51	1936.78	2.880	977.43	2814.58
A_68_P29024653	chr13:49436665-49436709	NM_001039179:-231	Bicd2	PROMOTER	2.005	1.473	918.00	1352.30	2.953	718.95	2123.30
A_68_P31836381	chr18:75502057-75502101			Unknown	2.005	5.647	7194.94	40631.71	11.322	5950.74	67373.66
A_68_P28328448	chr12:31596461-31596505	NM_001110239:-5	Acp1	DIVERGENT_PROMOTER	2.003	3.807	1330.58	5065.67	7.626	1077.42	8216.80
A_68_P26571039	chr9:62384681-62384725	NM_175484:149	Coro2b	INSIDE	2.003	9.729	15328.83	149132.30	19.488	12051.50	234861.50
A_68_P26658192	chr9:77961262-77961306	NM_019987:240	Ick	INSIDE	2.003	10.295	19505.51	200801.00	20.621	11145.86	229837.30
A_68_P21906908	chr2:180628801-180628845	NR_029538:78	Mir124a-3	DOWNSTREAM	2.003	1.584	457.25	724.51	3.173	393.78	1249.64
A_68_P21152636	chr2:39045852-39045896	NM_178778:376	Scai	INSIDE	2.003	6.019	21465.77	129193.80	12.053	15269.99	184042.30
A_68_P28080444	chr11:102467782-102467826	NM_020510:2060	Fzd2	INSIDE	2.002	1.520	598.43	909.33	3.043	460.34	1400.67
A_68_P26588687	chr9:65478956-65479000	NM_028030:590	Rbpms2	INSIDE	2.002	7.101	1348.61	9576.98	14.215	1028.12	14614.30
A_68_P27842891	chr11:60230619-60230663	NM_025757:-6	4933439F18Rik	DIVERGENT_PROMOTER	2.001	5.082	6324.86	32141.10	10.170	4611.32	46897.03
A_68_P23447093	chr5:3802955-3802999	NM_001003909:133	Ankib1	INSIDE	2.001	4.414	2001.52	8835.30	8.832	1594.37	14080.72
A_68_P25264893	chr7:87260180-87260224	NM_173011:34	Idh2	INSIDE	2.001	5.771	760.03	4386.16	11.547	694.19	8015.83
A_68_P27901897	chr11:70468130-70468174	NM_011072:0	Pfn1	INSIDE	2.001	12.585	2812.51	35396.18	25.178	2091.82	52667.40
A_68_P24816773	chr6:124696183-124696227	NM_007881:10301	Atn1	INSIDE	2.000	4.992	1835.22	9160.55	9.981	1390.13	13875.38
A_68_P32380519	chrX:49518713-49518757	NM_008150:-634	Gpc4	PROMOTER	2.000	3.934	2022.85	7957.44	7.869	1423.61	11202.84
A_68_P24176699	chr5:148769334-148769378	NM_029920:461	Mtus2	INSIDE	2.000	5.862	4947.09	28999.70	11.723	3794.87	44486.85
A_68_P21359595	chr2:77654503-77654547	NM_178723:349	Zfp385b	INSIDE	2.000	4.636	925.18	4289.04	9.270	697.33	6464.28
A_68_P23658789	chr5:46248126-46248170	NM_172153:-357	Lcorl	PROMOTER	1.999	2.835	1420.42	4026.53	5.666	1124.72	6372.68
A_68_P20998559	chr2:9970073-9970117	NM_027748:142	Taf3	INSIDE	1.999	3.882	2680.44	10404.16	7.759	2242.04	17396.16
A_68_P23447098	chr5:3803414-3803458	NR_033173:256	Krit1	INSIDE	1.998	5.399	2144.76	11579.96	10.788	1737.16	18740.61
A_68_P24804564	chr6:121423714-121423758	NM_001033354:-40	Iqsec3	PROMOTER	1.997	3.206	1771.26	5679.11	6.403	1380.83	8841.48
A_68_P25507242	chr7:134920047-134920091	NM_178029:-834	Setd1a	PROMOTER	1.997	4.883	785.76	3837.16	9.754	536.84	5236.52
A_68_P32766764	chrX:153929309-153929353	NM_009214:648	Sms	INSIDE	1.997	4.112	1440.88	5924.68	8.211	837.57	6877.17
A_68_P20012423	chr1:6373229-6373273	NM_001195732:23839	Fam150a	INSIDE	1.996	3.088	938.57	2898.62	6.165	860.84	5306.75
A_68_P21221051	chr2:52531541-52531585	NM_001037099:539	Cacnb4	INSIDE	1.994	6.214	1722.92	10705.97	12.392	1153.42	14292.68
A_68_P21418382	chr2:90519554-90519598	NM_021512:2205	Nup160	INSIDE	1.994	5.312	8159.69	43345.81	10.590	6258.95	66281.53
A_68_P26140014	chr8:109035535-109035580	NM_001037809:745	Cdh3	INSIDE	1.993	3.372	10881.57	36690.04	6.721	7717.80	51872.65
A_68_P22378552	chr3:101816741-101816785	NM_178777:2695	Nhlh2	INSIDE	1.993	4.711	4515.17	21271.37	9.388	3478.52	32656.96
A_68_P23018376	chr4:73436995-73437039	NM_001017427:-510	Rasef	PROMOTER	1.993	7.837	1435.05	11246.82	15.617	1145.53	17889.46
A_68_P20877753	chr1:182708067-182708111	AK013590:116		INSIDE	1.993	2.064	359.44	741.95	4.115	393.88	1620.70

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P32321491	chrX:34588512-34588556	NM_173779:-305	Ankrd58	PROMOTER	1.991	3.764	4900.57	18445.54	7.492	3053.16	22875.36
A_68_P25505711	chr7:134615245-134615289	NM_145589:139	Prr14	INSIDE	1.991	1.548	1093.16	1692.00	3.081	841.95	2593.98
A_68_P28175491	chr11:118907932-118907976	NM_013926:-5727	Cbx8	PROMOTER	1.989	1.758	536.84	943.64	3.497	458.11	1601.84
A_68_P33008826	chr4_random:110027-110071	NM_001033326:247	Dhrsx	INSIDE	1.989	5.009	2018.28	10110.10	9.965	1605.78	16000.96
A_68_P24942904	chr6:148895207-148895251	NM_019643:-274	Fam60a	PROMOTER	1.989	4.671	2575.90	12031.24	9.289	2051.98	19060.53
A_68_P23029295	chr4:76095885-76095929	NM_011211:144297	Ptprd	INSIDE	1.989	6.927	2157.13	14942.00	13.775	1517.81	20907.64
A_68_P27177056	chr10:60293675-60293719	NM_029770:633	Unc5b	INSIDE	1.989	3.673	1451.34	5330.04	7.303	1228.29	8970.39
A_68_P22319097	chr3:89196146-89196190	NM_009565:957	Zbtb7b	INSIDE	1.989	0.704	1297.39	913.61	1.400	1152.06	1613.43
A_68_P24774306	chr6:115943883-115943927	NM_026376:1119	Plxnd1	INSIDE	1.988	5.492	1597.59	8773.58	10.917	1045.67	11415.58
A_68_P20294265	chr1:64784540-64784584	NM_001042659:-238	Fzd5	PROMOTER	1.987	4.693	1117.88	5245.69	9.322	838.15	7813.62
A_68_P29369781	chr13:119503243-119503287	NM_008002:-241	Fgf10	PROMOTER	1.986	4.921	7424.08	36535.57	9.775	5894.22	57617.72
A_68_P26430635	chr9:37240928-37240972	NM_001164767:-190	Robo3	PROMOTER	1.986	5.036	3993.54	20110.91	10.002	2951.93	29524.69
A_68_P32557243	chrX:97015613-97015657	NM_001081283:-773	Tmem28	PROMOTER	1.986	2.695	738.08	1989.24	5.353	374.47	2004.59
A_68_P30593952	chr16:21695060-21695104	NM_001001881:-344	2510009E07Rik	PROMOTER	1.985	1.567	1249.70	1958.13	3.110	936.20	2911.16
A_68_P30958538	chr16:90727762-90727806	NM_025642:-168	2610039C10Rik	PROMOTER	1.985	7.148	6153.67	43986.93	14.192	4023.20	57098.84
A_68_P21419450	chr2:90726161-90726205	NM_026161:240	C1qtnf4	INSIDE	1.985	3.211	2122.23	6815.20	6.373	1771.75	11291.25
A_68_P21613749	chr2:127308338-127308382	NM_001111331:-125	Kcnip3	PROMOTER	1.984	9.371	1665.44	15607.18	18.594	1049.56	19515.72
A_68_P24537770	chr6:71657709-71657753	NM_178608:56	Reep1	INSIDE	1.984	8.149	1094.29	8917.83	16.167	912.91	14759.37
A_68_P31411712	chr17:86014601-86014645	NR_038085:3114	Six3os1	INSIDE	1.984	4.684	10986.84	51460.60	9.291	7340.72	68205.52
A_68_P28154074	chr11:115397049-115397093	NM_133354:474	Sumo2	INSIDE	1.984	7.154	14395.30	102980.70	14.191	11130.77	157957.40
A_68_P25958256	chr8:74203690-74203734	NM_001190830:3431	Jak3	INSIDE	1.983	3.564	823.69	2935.98	7.070	656.49	4641.15
A_68_P32140500	chr19:45857855-45857899	NM_023799:-95	Mgea5	PROMOTER	1.983	7.289	757.01	5518.17	14.456	564.55	8161.40
A_68_P31609277	chr18:33954596-33954640	NR_038151:73	2410004N09Rik	INSIDE	1.982	1.727	3048.18	5263.10	3.423	2411.34	8253.95
A_68_P28078744	chr11:102157408-102157452	NM_001098836:513	Atxn7l3	INSIDE	1.982	2.125	1191.74	2532.41	4.212	930.26	3917.90
A_68_P27804074	chr11:53113101-53113145	NM_008300:859	Hspa4	INSIDE	1.982	3.316	6412.82	21267.40	6.574	5187.91	34105.70
A_68_P26345150	chr9:20836502-20836546	NM_008319:43	Icam5	INSIDE	1.982	4.277	4438.10	18981.33	8.477	3506.13	29722.46
A_68_P25807719	chr8:41947388-41947432	NM_007514:-310	Slc7a2	PROMOTER	1.982	6.030	7612.40	45905.08	11.954	5257.46	62847.22
A_68_P30363493	chr15:78798329-78798373	NM_001039155:20197	Triobp	INSIDE	1.982	11.133	1510.57	16816.93	22.062	976.39	21540.76
A_68_P28156930	chr11:115891653-115891697	NM_172569:39	Unk	INSIDE	1.982	3.224	656.27	2115.97	6.391	542.34	3466.17
A_68_P23962878	chr5:107125443-107125487	NM_026856:385	Zfp644	INSIDE	1.982	5.364	4973.92	26679.75	10.633	4228.15	44958.50
A_68_P26543338	chr9:57556763-57556807	NM_153799:409	Edc3	INSIDE	1.980	7.076	3933.06	27831.33	14.009	2928.64	41028.03
A_68_P26622301	chr9:71333539-71333583	NM_001164793:-795	Grinl1a	PROMOTER	1.980	2.353	1200.03	2824.26	4.660	1053.28	4908.56
A_68_P25005776	chr7:25396309-25396353	NM_001102613:-16	Phldb3	PROMOTER	1.980	6.753	6453.48	43581.39	13.373	4202.48	56201.35
A_68_P28595369	chr12:85262700-85262744	ENSMUST00000085215:72		INSIDE	1.980	3.043	16786.27	51079.68	6.026	12030.00	72496.26
A_68_P27900652	chr11:70246079-70246123	NM_145429:-54	Arrb2	PROMOTER	1.979	2.610	1169.34	3052.36	5.167	916.74	4736.55
A_68_P21395110	chr2:84712227-84712271	NM_199223:14601	Rtn4rl2	INSIDE	1.979	6.057	2764.73	16746.15	11.988	2317.19	27778.80
A_68_P25370744	chr7:108123196-108123240			Unknown	1.979	2.486	1180.31	2934.71	4.921	930.79	4580.85
A_68_P25911981	chr8:64238686-64238730	NM_001081390:142779	Palld	INSIDE	1.978	2.275	971.13	2209.05	4.500	779.80	3508.97
A_68_P21042876	chr2:18919881-18919925	NR_024323:-43	4930426L09Rik	DIVERGENT_PROMOTER	1.977	7.301	2991.97	21843.57	14.432	2189.70	31602.67
A_68_P20016449	chr1:7388374-7388418	ENSMUST00000138711:-514		PROMOTER	1.977	4.924	4200.99	20683.63	9.733	3349.27	32597.71
A_68_P20240346	chr1:55145446-55145490	NM_008303:477	Hspe1	INSIDE	1.976	4.193	1419.21	5951.07	8.284	985.84	8167.04
A_68_P21070656	chr2:25080752-25080796	NM_146116:-552	Tubb2c	PROMOTER	1.976	4.220	2765.86	11672.93	8.339	2234.63	18633.69
A_68_P30433473	chr15:90880476-90880520	NM_001109040:-119	Kif21a	PROMOTER	1.975	4.611	5323.48	24544.24	9.106	4245.04	38656.75
A_68_P23006650	chr4:70195415-70195459	NM_172694:526	Megf9	INSIDE	1.975	3.715	8274.32	30737.56	7.336	6416.84	47074.16
A_68_P30650846	chr16:32079318-32079362	NM_177326:19	Pak2	INSIDE	1.975	8.408	4276.72	35957.81	16.607	3448.53	57270.10
A_68_P27921681	chr11:74462947-74462991	NM_001081158:-28	1300001I01Rik	PROMOTER	1.974	4.812	4348.74	20926.06	9.500	3488.37	33138.09
A_68_P25088286	chr7:51846961-51847005	NM_008422:727	Kcnc3	INSIDE	1.974	6.215	2829.89	17588.75	12.271	2291.82	28124.06
A_68_P31110054	chr17:26552202-26552246	NM_001081656:315	Neurl1b	INSIDE	1.974	5.321	1188.55	6323.81	10.504	1036.44	10886.31
A_68_P27278802	chr10:79229397-79229442	NM_144528:247	Rnf126	INSIDE	1.974	4.084	5437.70	22205.53	8.062	4054.43	32684.99
A_68_P31479225	chr18:7869058-7869102	NM_001146298:-114	Wac	PROMOTER	1.974	4.017	3388.04	13608.31	7.928	2757.80	21863.00
A_68_P23396578	chr4:148179082-148179126	NM_027195:604	Casz1	INSIDE	1.973	5.530	2948.56	16304.53	10.908	2126.42	23195.85

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P20963945	chr2:3630790-3630834	NM_025626:83	Fam107b	INSIDE	1.973	1.721	749.08	1289.47	3.396	585.50	1988.33
A_68_P21783928	chr2:158436941-158436985	NM_009508:469	Slc32a1	INSIDE	1.973	5.667	21029.26	119167.00	11.180	15800.81	176658.30
A_68_P22630556	chr3:148650621-148650665	ENSMUST00000098518:1638		INSIDE	1.973	2.845	6332.89	18017.74	5.614	4669.41	26214.69
A_68_P28432636	chr12:53071968-53072012	NM_177171:318	Heatr5a	INSIDE	1.972	2.436	3384.93	8244.91	4.803	2605.10	12511.36
A_68_P28053756	chr11:97847867-97847911	NM_001163608:-128	Plxdc1	PROMOTER	1.972	4.486	1026.12	4602.73	8.846	764.65	6763.79
A_68_P25412183	chr7:117365487-117365531	NM_009302:292	Swap70	INSIDE	1.972	5.336	5679.82	30307.86	10.520	4381.06	46089.90
A_68_P24124224	chr5:137507416-137507460	NM_001039385:1274	Vgf	INSIDE	1.972	7.730	2393.17	18499.10	15.247	1785.80	27227.51
A_68_P27591949	chr11:11585605-11585649	NM_001025597:-589	Ikzf1	PROMOTER	1.971	6.461	328.40	2121.91	12.737	332.67	4237.04
A_68_P31992368	chr19:18745200-18745244	NM_026120:-47	2410127L17Rik	PROMOTER	1.970	8.119	1112.52	9032.07	15.996	768.74	12296.69
A_68_P27788005	chr11:50138862-50138906	NM_001110499:291	Canx	INSIDE	1.970	3.156	5574.41	17595.39	6.220	4426.17	27529.64
A_68_P26242535	chr8:126473140-126473184	NM_172288:3	Nup133	INSIDE	1.970	3.959	1555.56	6157.81	7.800	1160.78	9054.05
A_68_P23245805	chr4:119164931-119164975	NM_177572:251	Rimkla	INSIDE	1.970	1.959	817.12	1601.11	3.860	738.33	2849.76
A_68_P28152781	chr11:115183238-115183282	NM_176847:-28	Ush1g	PROMOTER	1.970	9.441	10000.64	94413.83	18.600	6015.03	111879.70
A_68_P29615089	chr14:55545056-55545100	NM_010112:547	Efs	INSIDE	1.969	2.680	3959.09	10609.07	5.277	2914.31	15377.54
A_68_P29152220	chr13:76081481-76081525	NM_028493:-230	Rhobtb3	PROMOTER	1.969	2.960	1198.54	3547.32	5.827	851.95	4963.87
A_68_P28515845	chr12:70782400-70782444	NM_001135559:417	Sos2	INSIDE	1.969	2.541	1958.50	4975.69	5.001	1528.15	7642.91
A_68_P21330556	chr2:73115402-73115446	NM_001005343:5442	Sp9	DOWNSTREAM	1.969	4.836	4620.55	22345.30	9.521	3436.51	32718.53
A_68_P29449770	chr14:21748700-21748744	NM_009502:68	Vcl	INSIDE	1.969	3.193	4035.96	12886.43	6.286	3134.26	19703.38
A_68_P23381901	chr4:144785001-144785047	NM_001128198:-4529	Vps13d	PROMOTER	1.969	2.303	958.14	2206.35	4.534	812.58	3684.09
A_68_P23897553	chr5:93473897-93473941	NM_175270:130	Ankrd56	INSIDE	1.968	1.785	1103.52	1970.25	3.513	847.35	2977.09
A_68_P30991207	chr16:96348653-96348697	NM_008251:658	Hmgn1	INSIDE	1.968	2.602	5404.50	14060.23	5.121	4000.73	20487.47
A_68_P27349651	chr10:92185236-92185280	NM_008682:-95	Nedd1	PROMOTER	1.968	4.104	1115.32	4576.96	8.076	934.49	7546.94
A_68_P29023779	chr13:49283004-49283048	NM_013610:111	Ninj1	INSIDE	1.968	4.358	3369.18	14682.72	8.576	2531.85	21712.21
A_68_P28533645	chr12:73862367-73862411	NM_008910:191	Ppm1a	INSIDE	1.968	4.045	3217.29	13015.10	7.962	2569.35	20457.82
A_68_P28192906	chr11:121691796-121691840	NM_029049:287	Ptchd3	INSIDE	1.968	3.225	1636.76	5277.73	6.345	1415.98	8984.10
A_68_P32197338	chr19:55969833-55969892	NM_001142924:52	Tcf7l2	INSIDE	1.968	5.017	167.54	840.57	9.872	114.89	1134.25
A_68_P30959222	chr16:90831079-90831123	NM_001199210:-3	4931408A02Rik	PROMOTER	1.967	1.517	905.38	1373.80	2.985	747.69	2231.93
A_68_P28115686	chr11:108782547-108782591	NM_015732:906	Axin2	INSIDE	1.967	3.863	1652.35	6382.81	7.597	1331.82	10117.39
A_68_P23350166	chr4:138748616-138748660	NM_009798:-207	Capzb	PROMOTER	1.967	3.798	6080.09	23094.74	7.471	4908.49	36671.62
A_68_P29614701	chr14:55482992-55483036	NM_001177705:-19	Homez	PROMOTER	1.967	3.067	3193.56	9795.99	6.033	2541.20	15329.78
A_68_P28099140	chr11:105881863-105881907	NM_001037712:12368	Kcnh6	INSIDE	1.967	7.729	2711.08	20953.02	15.199	1794.72	27278.05
A_68_P24954294	chr7:6107601-6107645	NM_001013012:-49	Zfp787	PROMOTER	1.967	4.333	5409.37	23436.41	8.522	4239.71	36128.89
A_68_P32477697	chrX:74679072-74679116			Unknown	1.967	4.351	10388.98	45204.71	8.559	7505.05	64237.52
A_68_P21752520	chr2:152857602-152857646	NM_001011732:37	Xkr7	INSIDE	1.966	7.358	1460.41	10745.14	14.466	1068.59	15458.44
A_68_P32730437	chrX:143988143-143988187	NM_001081173:460	Lrch2	INSIDE	1.965	4.409	9704.97	42791.58	8.664	6149.70	53283.79
A_68_P28615786	chr12:88729140-88729184	NM_011479:18	Sptlc2	INSIDE	1.965	7.386	683.93	5051.85	14.516	646.96	9391.54
A_68_P27644168	chr11:22967930-22967974	ENSMUST00000128996:-45		DIVERGENT_PROMOTER	1.965	6.515	903.14	5884.30	12.805	735.16	9413.94
A_68_P27289148	chr10:80827041-80827085	NM_001014836:1503	4930404N11Rik	INSIDE	1.964	4.488	7214.34	32377.00	8.812	5305.63	46755.12
A_68_P29620076	chr14:56445768-56445812	NM_001168346:2159	Nfatc4	INSIDE	1.964	6.334	3968.26	25134.45	12.440	2785.42	34650.17
A_68_P26464014	chr9:43611501-43611545	NM_021424:58864	Pvrl1	INSIDE	1.964	6.335	2397.16	15184.99	12.442	1497.26	18628.77
A_68_P22606649	chr3:144781741-144781785	NM_025714:199	Odf2l	INSIDE	1.963	4.343	4977.82	21616.42	8.526	3841.15	32748.48
A_68_P31256055	chr17:56568653-56568712	NM_011218:47221	Ptprs	INSIDE	1.963	9.451	507.20	4793.44	18.548	389.72	7228.65
A_68_P27040510	chr10:30337995-30338039	NM_025798:156	Hint3	INSIDE	1.962	3.176	1065.95	3384.99	6.229	904.96	5637.29
A_68_P20173639	chr1:40847463-40847507	NM_172499:18	Mfsd9	INSIDE	1.962	7.038	1091.71	7683.65	13.809	885.85	12232.37
A_68_P22341853	chr3:94819143-94819187	NM_030074:-4	Zfp687	PROMOTER	1.962	4.849	808.04	3917.86	9.511	672.38	6395.29
A_68_P33012155	chr9_random:54509-54553	NR_027950:-162	4930526I15Rik	PROMOTER	1.961	3.299	5356.65	17673.86	6.469	3968.95	25675.00
A_68_P22130346	chr3:51364011-51364056	NR_033624:355	5031434O11Rik	INSIDE	1.960	3.201	3208.33	10271.15	6.274	2445.68	15345.16
A_68_P26659639	chr9:78296196-78296240	NM_026658:202	Mto1	INSIDE	1.960	1.795	397.62	713.77	3.518	481.25	1693.03
A_68_P24850990	chr6:131383791-131383835			Unknown	1.960	3.368	888.30	2991.42	6.601	808.91	5339.71
A_68_P25953242	chr8:73183309-73183353	NM_023217:250	Pgpep1	INSIDE	1.959	1.778	3492.00	6208.53	3.483	2420.79	8431.85
A_68_P25276873	chr7:89483916-89483960	NM_001190374:-265	Adamtsl3	PROMOTER	1.957	2.496	301.10	751.49	4.885	287.88	1406.35

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27365029	chr10:94878409-94878453	NM_001168656:-312	Socs2	PROMOTER	1.957	3.650	1261.25	4603.74	7.144	1029.49	7354.78
A_68_P24946816	chr7:3637239-3637283	NM_029934:7867	Mboat7	INSIDE	1.956	4.635	2593.16	12018.65	9.064	2031.67	18415.71
A_68_P31140911	chr17:31773548-31773592	NM_178224:506	Cbs	INSIDE	1.954	3.316	7744.08	25678.94	6.479	5771.70	37394.65
A_68_P22942460	chr4:56960340-56960384	NM_175518:-61	D730040F13Rik	PROMOTER	1.954	3.183	1863.90	5932.74	6.221	1527.94	9504.93
A_68_P30343819	chr15:75578604-75578648	NM_194350:-274	Mafa	PROMOTER	1.953	3.653	1220.29	4457.21	7.135	915.27	6530.09
A_68_P24951794	chr7:5004858-5004902	NM_026900:1747	Zfp580	INSIDE	1.953	11.439	6702.51	76672.71	22.347	4388.05	98058.91
A_68_P22060448	chr3:36762071-36762115	NM_172679:65	4932438A13Rik	INSIDE	1.952	2.163	1441.07	3116.81	4.222	1152.18	4864.87
A_68_P23361905	chr4:140616349-140616393	NM_172122:-6794	Crocc	PROMOTER	1.952	1.574	3797.77	5976.06	3.071	3180.60	9768.25
A_68_P25005645	chr7:25370764-25370808	NM_023154:-1775	Ethe1	PROMOTER	1.952	5.784	9677.20	55972.42	11.292	6298.59	71125.48
A_68_P23807625	chr5:75548984-75549028	NM_001083316:-3184	Pdgfra	PROMOTER	1.952	3.211	2425.96	7790.23	6.267	1751.08	10974.80
A_68_P28598116	chr12:85750091-85750135	NM_025525:-8037	Rnf113a2	PROMOTER	1.952	7.688	929.08	7143.04	15.009	656.03	9846.31
A_68_P31163327	chr17:36394876-36394920	NM_026308:-107	Rpp21	PROMOTER	1.952	6.137	1187.76	7289.19	11.981	1029.28	12331.59
A_68_P26158736	chr8:112261757-112261801	NM_001080930:-139	Atxn1l	PROMOTER	1.951	1.963	1818.15	3569.42	3.830	1494.02	5721.52
A_68_P27788006	chr11:50138948-50138992	NM_001110499:205	Canx	INSIDE	1.951	4.085	5502.89	22480.34	7.970	3802.85	30309.46
A_68_P21134366	chr2:35438211-35438255	NM_001114125:24255	Dab2ip	INSIDE	1.951	9.744	1321.86	12879.94	19.014	1073.76	20416.14
A_68_P21978078	chr3:19957968-19958012	NM_144959:180	Hltf	INSIDE	1.951	4.988	7603.38	37929.07	9.733	5994.60	58346.11
A_68_P31097493	chr17:24606963-24607007	NM_025954:-433	Pgp	PROMOTER	1.951	7.982	4367.45	34859.26	15.570	2531.42	39413.34
A_68_P21769931	chr2:156005366-156005410	NM_133242:588	Rbm39	INSIDE	1.951	4.336	1368.97	5936.39	8.462	1195.59	10116.89
A_68_P24459338	chr6:53768811-53768855	NM_025817:1987	Tril	INSIDE	1.951	6.346	4390.67	27862.05	12.382	3566.54	44159.98
A_68_P26238816	chr8:125778247-125778291	NM_020497:174	Zfp276	INSIDE	1.951	7.620	4136.00	31517.69	14.868	3031.78	45076.72
A_68_P29996479	chr15:7760686-7760730	NM_010275:-302	Gdnf	PROMOTER	1.950	9.773	1415.04	13828.45	19.057	1081.20	20604.19
A_68_P30500682	chr15:102752309-102752353	NM_010464:769	Hoxc13	INSIDE	1.950	2.090	437.20	913.94	4.076	393.05	1601.97
A_68_P24448786	chr6:52122729-52122773	NM_010452:40316	Hoxa3	INSIDE	1.949	3.590	2816.44	10111.45	6.999	2194.43	15358.72
A_68_P32239859	chrX:7305710-7305754	NM_138602:36	Praf2	INSIDE	1.949	1.561	944.87	1475.33	3.044	603.67	1837.49
A_68_P21819631	chr2:164595113-164595157	NM_026785:-294	Ube2c	PROMOTER	1.949	1.547	2320.10	3588.52	3.015	1901.78	5734.30
A_68_P27543031	chr10:128185237-128185281	NM_001170869:-319	Wibg	PROMOTER	1.949	1.732	406.22	703.63	3.376	336.20	1134.90
A_68_P30371091	chr15:80086279-80086325	NM_009716:689	Atf4	INSIDE	1.948	3.218	1720.78	5537.99	6.270	1305.60	8185.62
A_68_P24060833	chr5:124803880-124803924	NM_013812:735	Cdk2ap1	INSIDE	1.948	8.285	867.65	7188.25	16.135	691.74	11161.30
A_68_P29330297	chr13:112515612-112515656	NM_172593:39249	Mier3	DOWNSTREAM	1.948	3.136	4485.94	14066.93	6.108	3426.27	20927.12
A_68_P32464061	chrX:70918592-70918636	NM_001142809:143	Slc6a8	INSIDE	1.948	4.473	1953.12	8735.75	8.713	1190.32	10371.57
A_68_P31147009	chr17:32924787-32924831	NM_172458:424	Zfp871	INSIDE	1.948	4.509	5798.67	26143.80	8.782	5006.12	43964.92
A_68_P25715145	chr8:24268305-24268349	NM_029002:4584	Nkx6-3	INSIDE	1.947	5.658	1617.56	9152.92	11.019	1197.01	13189.99
A_68_P32260286	chrX:11658874-11658919	NM_029510:-1217	Bcor	PROMOTER	1.946	2.868	401.28	1150.87	5.582	234.46	1308.67
A_68_P29639452	chr14:60216844-60216888	NM_001168535:-70	Cdadc1	PROMOTER	1.946	9.593	6488.31	62244.12	18.664	3827.68	71440.31
A_68_P20192816	chr1:44204826-44204870	NM_011729:260	Ercc5	INSIDE	1.946	6.459	1824.46	11783.62	12.569	1452.81	18260.66
A_68_P30686476	chr16:38522756-38522801	NM_024273:-31	4930455C21Rik	PROMOTER	1.945	6.413	5617.05	36021.49	12.474	3776.73	47112.65
A_68_P25508222	chr7:135079466-135079510	NM_001081374:10751	Prss36	INSIDE	1.945	3.919	2482.62	9729.37	7.622	1728.10	13170.75
A_68_P28119629	chr11:109472837-109472881	NM_145940:-155	Wipi1	PROMOTER	1.945	2.160	5773.50	12469.26	4.201	4146.90	17421.64
A_68_P28177063	chr11:119161761-119161805	NM_138669:-425	Eif4a3	PROMOTER	1.944	7.417	3705.01	27478.19	14.417	2789.51	40215.82
A_68_P21843420	chr2:168591529-168591573	NM_175303:1151	Sall4	INSIDE	1.944	2.326	400.24	930.99	4.522	339.93	1537.30
A_68_P23701554	chr5:53982361-53982405	NM_001080927:570	Rbpj	INSIDE	1.943	2.359	2601.07	6135.06	4.584	2146.76	9839.79
A_68_P31921054	chr19:4101079-4101123	NM_008851:479	Pitpnm1	INSIDE	1.942	3.118	795.68	2480.76	6.056	677.00	4099.75
A_68_P21622283	chr2:128792891-128792935	NM_178404:-225	Zc3h6	PROMOTER	1.942	7.387	16791.77	124034.50	14.346	11192.29	160559.10
A_68_P27842896	chr11:60231205-60231249	NM_025757:580	4933439F18Rik	INSIDE	1.941	6.392	6265.28	40045.30	12.409	5241.96	65047.20
A_68_P24786758	chr6:118369210-118369254	NM_194339:203	Bms1	INSIDE	1.941	1.975	2909.05	5744.70	3.833	2374.51	9101.42
A_68_P26983892	chr10:19653936-19653980	NM_008580:-373	Map3k5	PROMOTER	1.941	2.801	2266.02	6346.81	5.436	1777.92	9664.64
A_68_P26041379	chr8:91045377-91045421	NM_001163660:-6133	Nkd1	PROMOTER	1.941	4.503	5556.83	25021.48	8.741	4103.47	35867.01
A_68_P20506810	chr1:108069429-108069473	NM_133821:1005	Phlpp1	INSIDE	1.941	3.369	2493.42	8399.51	6.540	2097.84	13719.55
A_68_P27185081	chr10:61732662-61732706	NM_001146100:70485	Hk1	INSIDE	1.940	4.623	1350.81	6244.16	8.967	1020.86	9154.55
A_68_P24086564	chr5:129526514-129526558	NM_009391:506	Ran	INSIDE	1.940	3.942	1831.96	7220.91	7.645	1437.02	10986.09
A_68_P30544459	chr16:10785615-10785659	NM_009896:-7	Socs1	PROMOTER	1.940	4.714	4002.87	18868.14	9.143	3241.30	29633.88

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P29605230	chr14:52816435-52816479	NM_033618:458	Supt16h	INSIDE	1.940	4.812	2932.18	14109.05	9.334	2379.69	22211.42
A_68_P30114905	chr15:31461133-31461177	NM_172606:-362	Marchf6	PROMOTER	1.939	1.837	568.10	1043.48	3.561	476.87	1698.37
A_68_P28726319	chr12:109416700-109416744	NM_028262:772	Setd3	INSIDE	1.939	4.260	1042.01	4439.33	8.260	798.11	6592.16
A_68_P20267395	chr1:60155522-60155566	NM_001199060:-200	Wdr12	PROMOTER	1.939	3.578	1891.30	6767.76	6.938	1500.30	10409.78
A_68_P27534905	chr10:126703422-126703466	NM_001190453:127	Dctn2	INSIDE	1.938	3.315	3380.69	11207.19	6.425	2486.22	15973.56
A_68_P26352003	chr9:22272492-22272536	NM_018739:286	Rp9	INSIDE	1.937	6.711	2403.58	16130.31	13.000	1977.00	25701.63
A_68_P25357073	chr7:105804516-105804560	NM_172280:541	2210018M11Rik	INSIDE	1.936	5.040	31781.32	160178.50	9.757	23016.13	224567.40
A_68_P28123546	chr11:110199057-110199101	NM_147219:-48	Abca5	PROMOTER	1.936	6.585	5276.42	34744.38	12.751	3677.97	46899.50
A_68_P31119196	chr17:28046558-28046602	NM_181413:296	Anks1	INSIDE	1.936	1.807	794.26	1435.62	3.500	648.57	2270.05
A_68_P32144718	chr19:46647649-46647693	NM_019718:-95	Arl3	DIVERGENT_PROMOTER	1.936	5.303	2710.10	14370.72	10.264	2159.84	22168.29
A_68_P29140001	chr13:73605046-73605090	NM_145376:238	Lpcat1	INSIDE	1.936	4.602	5042.49	23207.43	8.909	3905.21	34793.18
A_68_P24591144	chr6:83005100-83005144	NM_007517:476	Aup1	INSIDE	1.935	1.746	1460.28	2549.64	3.378	1153.78	3897.89
A_68_P31117117	chr17:27694485-27694529	NM_001166476:909	Hmga1-rs1	INSIDE	1.935	3.854	4656.86	17945.86	7.456	3396.56	25324.85
A_68_P29309087	chr13:108834557-108834601	NM_001048250:-89	2810008M24Rik	PROMOTER	1.934	4.845	3948.98	19133.40	9.369	3266.40	30603.79
A_68_P24482547	chr6:58590413-58590457	NM_011920:43769	Abcg2	INSIDE	1.934	4.525	2139.50	9681.96	8.751	1636.83	14324.60
A_68_P31208112	chr17:46787505-46787549	NM_025611:240	Cul7	INSIDE	1.934	4.597	1458.98	6707.18	8.893	1174.54	10445.09
A_68_P30361559	chr15:78502925-78502969	NM_183141:45597	Elfn2	INSIDE	1.934	7.718	1295.22	9996.63	14.929	1026.00	15316.62
A_68_P25609917	chr7:152082446-152082490	NM_008003:32	Fgf15	INSIDE	1.934	2.354	2711.42	6383.42	4.554	2263.15	10306.32
A_68_P31236178	chr17:51952223-51952267	NM_001163630:-865	Satb1	PROMOTER	1.934	4.659	2674.30	12459.88	9.009	2114.51	19049.22
A_68_P25086963	chr7:51608090-51608134	NM_001034115:42479	Shank1	INSIDE	1.934	1.856	483.92	897.95	3.589	416.06	1493.20
A_68_P25947613	chr8:72178336-72178380	NM_001177527:-96	Zfp964	PROMOTER	1.934	5.353	2590.06	13863.49	10.354	1969.80	20395.55
A_68_P30160398	chr15:40486792-40486836	NM_011766:227	Zfpm2	INSIDE	1.934	4.138	7704.09	31875.86	8.003	5311.51	42509.08
A_68_P22376195	chr3:101408231-101408275	NM_144900:328	Atp1a1	INSIDE	1.933	5.227	2297.12	12008.18	10.104	1986.01	20065.78
A_68_P26808316	chr9:107302358-107302402	NM_001174047:170	Cacna2d2	INSIDE	1.933	3.324	3446.50	11455.10	6.425	2700.40	17350.81
A_68_P26591015	chr9:65917041-65917085	NM_001025612:476	Snx22	INSIDE	1.933	3.673	1247.31	4581.80	7.101	1043.81	7412.32
A_68_P25408016	chr7:116582357-116582401	NM_054103:189	Stk33	INSIDE	1.933	3.287	1844.54	6063.05	6.353	1448.65	9202.64
A_68_P28183963	chr11:120210170-120210214	NR_038126:201	0610009L18Rik	INSIDE	1.932	3.213	1826.02	5866.26	6.205	1558.40	9670.64
A_68_P27566544	chr11:5965149-5965193	NM_001174053:581	Camk2b	INSIDE	1.932	3.324	2280.29	7579.09	6.420	1796.50	11533.69
A_68_P27091229	chr10:41530226-41530270	NM_001162908:-131	Sesn1	DIVERGENT_PROMOTER	1.930	4.951	3065.18	15175.30	9.557	2488.78	23786.35
A_68_P21752521	chr2:152857720-152857764	NM_001011732:155	Xkr7	INSIDE	1.930	4.795	3267.73	15669.96	9.254	2596.29	24027.08
A_68_P28291023	chr12:25365989-25366033	NM_001004455:650	Cys1	INSIDE	1.929	13.581	9472.94	128648.20	26.192	5382.13	140967.50
A_68_P28457808	chr12:57713134-57713178	NM_008701:1115	Nkx2-9	INSIDE	1.929	4.516	1026.23	4634.92	8.713	885.78	7718.13
A_68_P30646578	chr16:31275334-31275378	NM_025800:7	Ppp1r2	INSIDE	1.929	3.705	2474.18	9166.92	7.148	2077.06	14846.63
A_68_P30349758	chr15:76490310-76490354	NM_019396:159	Cyhr1	INSIDE	1.928	3.640	4666.59	16984.62	7.018	3324.48	23331.03
A_68_P27765093	chr11:45758539-45758583	NM_028185:-123	Lsm11	PROMOTER	1.928	3.590	3657.32	13130.18	6.923	2701.76	18704.49
A_68_P28195719	chr12:3572230-3572274	NM_001162465:-138	Dtnb	PROMOTER	1.927	2.025	1262.01	2555.32	3.901	913.73	3564.66
A_68_P25392116	chr7:112548270-112548314	NM_199009:233	Fam160a2	INSIDE	1.927	3.135	3303.29	10354.85	6.040	2514.41	15186.65
A_68_P32571132	chrX:100129205-100129249	NR_026596:336	Gm5126	INSIDE	1.927	2.774	1584.24	4393.93	5.345	859.88	4595.98
A_68_P24863969	chr6:134820135-134820179	NM_001167697:17721	Gpr19	INSIDE	1.927	4.853	539.59	2618.65	9.351	411.50	3847.75
A_68_P27796195	chr11:51671777-51671821	NM_199299:-815	Phf15	PROMOTER	1.927	3.621	11034.72	39960.52	6.977	7949.07	55458.77
A_68_P22149943	chr3:54611747-54611791	NM_133231:-55	Rfxap	PROMOTER	1.927	4.905	1112.94	5459.44	9.453	945.98	8942.71
A_68_P30390278	chr15:83555204-83555248	NM_022723:225	Scube1	INSIDE	1.927	4.462	1759.53	7850.47	8.596	1610.50	13843.26
A_68_P20005810	chr1:4483711-4483755	NM_011441:2762	Sox17	INSIDE	1.927	4.121	693.64	2858.49	7.941	700.21	5560.40
A_68_P27896951	chr11:69579684-69579728	NM_029348:293	Zbtb4	INSIDE	1.927	6.578	853.34	5613.07	12.676	665.38	8434.45
A_68_P24973956	chr7:13563487-13563531	NM_001168561:312	Zfp446	INSIDE	1.927	4.269	926.05	3952.94	8.225	813.97	6694.80
A_68_P32488667	chrX:78316560-78316604	NM_138751:600	Tmem47	INSIDE	1.926	4.390	5758.30	25281.21	8.457	3130.92	26478.88
A_68_P23195047	chr4:107889859-107889903	NM_001167936:647	Zyg11a	INSIDE	1.926	5.752	19495.88	112147.10	11.079	13845.63	153397.70
A_68_P30459959	chr15:95620940-95620984	NM_175344:-311	Ano6	PROMOTER	1.925	3.162	2819.28	8914.46	6.086	2292.31	13950.27
A_68_P28175418	chr11:118898955-118898999	NM_013926:3251	Cbx8	DOWNSTREAM	1.925	5.303	2342.48	12422.04	10.206	1877.46	19160.97
A_68_P30183902	chr15:44945966-44946010	NM_026200:492	Kcnv1	INSIDE	1.925	7.547	2060.05	15548.16	14.527	1203.61	17485.23
A_68_P29330800	chr13:112598036-112598080	NM_011945:1133	Map3k1	INSIDE	1.925	3.844	1210.59	4652.97	7.400	1025.67	7589.61

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31258630	chr17:56969214-56969258	NM_009056:1195	Rfx2	INSIDE	1.925	6.313	5662.42	35747.04	12.150	4694.45	57039.64
A_68_P21116393	chr2:32468028-32468072	NM_001025310:5570	St6galnac6	INSIDE	1.925	8.406	3661.88	30782.19	16.185	2404.68	38920.51
A_68_P23588493	chr5:33721117-33721161	NM_001081101:-206	4933407H18Rik	PROMOTER	1.924	5.062	8181.42	41417.93	9.741	5614.39	54690.28
A_68_P22659834	chr3:153607495-153607539	NM_007382:-120	Acadm	PROMOTER	1.924	3.919	2766.09	10839.68	7.540	2240.55	16892.71
A_68_P29752204	chr14:79987400-79987444	NM_026474:-75	Sugt1	PROMOTER	1.924	4.763	3302.53	15728.79	9.163	2623.06	24035.36
A_68_P24133861	chr5:139626021-139626065	NM_001081265:-134	Heatr2	PROMOTER	1.923	5.203	17869.78	92974.62	10.007	11113.70	111213.60
A_68_P25005398	chr7:25318769-25318814	NM_153134:3125	Irgq	INSIDE	1.923	3.356	458.84	1539.90	6.454	324.51	2094.37
A_68_P27648126	chr11:23795318-23795362	NM_172555:-70	Papolg	PROMOTER	1.923	3.254	5338.37	17370.64	6.258	3939.80	24656.64
A_68_P30345853	chr15:75900100-75900144	NM_134089:38	Scrib	INSIDE	1.923	4.663	3776.94	17610.21	8.966	3372.04	30235.25
A_68_P21782539	chr2:158187061-158187105	NR_015463:163	9430008C03Rik	INSIDE	1.922	4.489	4847.02	21757.79	8.630	4715.69	40694.87
A_68_P28752186	chr12:113977208-113977252	NM_001024602:16846	AW555464	INSIDE	1.922	4.566	3478.97	15886.58	8.777	2592.08	22749.48
A_68_P28153096	chr11:115229081-115229125	NM_175454:-69	C630004H02Rik	PROMOTER	1.922	6.389	5115.22	32680.12	12.279	3916.94	48094.92
A_68_P24683080	chr6:98978547-98978591	NM_001197322:-276	Foxp1	PROMOTER	1.922	1.899	1475.64	2802.18	3.650	1327.61	4846.05
A_68_P27932457	chr11:76308492-76308536	NM_198018:14407	Abr	INSIDE	1.921	9.569	21667.79	207339.50	18.381	18186.63	334294.90
A_68_P26132026	chr8:107695072-107695119	NM_001161456:522	Cbfb	INSIDE	1.921	1.830	668.55	1223.14	3.515	622.51	2188.07
A_68_P32573186	chrX:100688845-100688889	NR_015508:-48	Enox	PROMOTER	1.921	6.156	1849.84	11386.70	11.827	1373.86	16248.66
A_68_P24942897	chr6:148894399-148894443	NM_019643:534	Fam60a	INSIDE	1.921	4.150	1979.80	8216.13	7.973	1511.82	12053.87
A_68_P31201735	chr17:45686486-45686530	NM_001013749:118	Tmem151b	INSIDE	1.921	4.523	4033.96	18243.61	8.688	2866.15	24900.98
A_68_P28225578	chr12:8980743-8980787	NM_001159527:-42	Wdr35	PROMOTER	1.921	2.640	7446.62	19660.79	5.071	5556.74	28180.03
A_68_P29975444	chr15:3533365-3533409	NM_010284:-156	Ghr	PROMOTER	1.920	7.272	941.81	6848.65	13.961	869.39	12137.41
A_68_P23573590	chr5:30925082-30925126	NM_010608:34562	Kcnk3	INSIDE	1.920	5.787	2350.06	13599.97	11.110	1736.33	19291.40
A_68_P20282811	chr1:62749708-62749752	NM_001077406:-160	Nrp2	PROMOTER	1.920	8.010	3164.47	25348.92	15.380	2494.48	38364.67
A_68_P24428260	chr6:48552305-48552349	NM_001079901:8445	Repin1	DOWNSTREAM	1.920	5.777	379.35	2191.66	11.091	284.25	3152.55
A_68_P27286394	chr10:80391549-80391593	NM_008655:-1265	Gadd45b	PROMOTER	1.918	1.815	1699.65	3085.00	3.482	1370.18	4771.14
A_68_P28164254	chr11:117151837-117151881	NM_001113487:24299	Septin9	INSIDE	1.918	4.704	4337.00	20399.80	9.019	3424.73	30888.83
A_68_P28739824	chr12:111934703-111934747	NM_010480:-119	Hsp90aa1	PROMOTER	1.917	11.944	1915.98	22884.25	22.896	1402.99	32122.28
A_68_P24052813	chr5:123350619-123350663	NM_013910:-281	Kdm2b	PROMOTER	1.917	2.640	545.58	1440.33	5.060	392.77	1987.24
A_68_P23757989	chr5:66155461-66155505	NM_001024917:723	N4bp2	INSIDE	1.917	2.979	1575.15	4692.02	5.709	1233.33	7041.59
A_68_P25445817	chr7:123177303-123177347	NM_001025560:-2763	Sox6	PROMOTER	1.917	3.509	3173.69	11135.04	6.726	2390.20	16075.83
A_68_P27289055	chr10:80813338-80813382	NM_001163166:-158	Hmg20b	DIVERGENT_PROMOTER	1.916	3.014	4739.46	14285.52	5.774	3859.24	22283.48
A_68_P30395524	chr15:84388079-84388123	NM_177630:153	Ldoc1l	INSIDE	1.916	7.935	2483.85	19709.22	15.205	2070.29	31478.86
A_68_P20148355	chr1:36502065-36502109	NM_001013374:-2	Lman2l	PROMOTER	1.916	2.963	7704.43	22829.15	5.678	5809.89	32991.37
A_68_P24132971	chr5:139470887-139470931	NM_008808:-1	Pdgfa	PROMOTER	1.916	6.049	10464.92	63300.49	11.592	10109.40	117188.10
A_68_P21774858	chr2:156866344-156866388	NM_001164663:38635	9830001H06Rik	INSIDE	1.915	3.175	3202.56	10167.64	6.079	2541.60	15449.53
A_68_P24205536	chr6:4550713-4550757	NM_145398:-331	Casd1	PROMOTER	1.915	5.905	4018.61	23729.76	11.305	3300.47	37312.12
A_68_P25565202	chr7:144505325-144505370	NM_001113414:781	Ebf3	INSIDE	1.915	5.902	4572.39	26987.78	11.301	3496.84	39517.37
A_68_P32281782	chrX:17739949-17739993	NM_009483:178	Kdm6a	INSIDE	1.915	1.913	2267.29	4337.15	3.663	1308.27	4792.41
A_68_P21204312	chr2:49642923-49642967	NM_027990:-261	Lypd6b	PROMOTER	1.915	2.123	464.44	986.20	4.067	405.43	1648.96
A_68_P32582402	chrX:103206930-103206974	NM_001190409:286	Magt1	INSIDE	1.915	1.775	471.25	836.39	3.398	285.08	968.83
A_68_P28107262	chr11:107332069-107332113	NM_145823:-56	Pitpnc1	DIVERGENT_PROMOTER	1.915	11.985	2125.28	25472.22	22.948	1793.44	41155.20
A_68_P26529571	chr9:54996925-54996969	NM_180600:-229	Ube2q2	PROMOTER	1.914	7.210	1010.45	7285.18	13.799	790.60	10909.70
A_68_P25065443	chr7:38893032-38893076	NM_007633:-545	Ccne1	PROMOTER	1.913	1.928	2996.29	5777.92	3.690	2226.80	8216.66
A_68_P21102300	chr2:30141879-30141923	NM_177648:-26	Dolk	DIVERGENT_PROMOTER	1.913	2.441	2439.73	5955.30	4.670	1879.60	8778.17
A_68_P23814358	chr5:76569347-76569391	NM_020611:71	Srd5a3	INSIDE	1.913	3.279	1314.92	4311.92	6.273	972.42	6100.40
A_68_P23190148	chr4:107040619-107040663	NM_028355:252	Tmem48	INSIDE	1.913	8.198	1328.94	10894.72	15.684	1001.80	15712.00
A_68_P31621446	chr18:36177796-36177840	NM_001167891:178996	Nrg2	INSIDE	1.912	6.614	1194.95	7903.79	12.650	1049.81	13279.96
A_68_P24057004	chr5:124133945-124133989	NM_019765:334	Clip1	INSIDE	1.911	2.160	864.01	1865.97	4.126	813.86	3358.04
A_68_P31864634	chr18:80666119-80666163	NM_026295:266	Ctdp1	INSIDE	1.911	4.138	713.39	2952.12	7.909	717.95	5678.08
A_68_P23320471	chr4:133556862-133556906	NM_026144:-105	Dhdds	PROMOTER	1.911	6.695	713.05	4773.77	12.792	604.67	7734.84
A_68_P24908780	chr6:143116314-143116358	NM_029250:587	Etnk1	INSIDE	1.911	4.120	8609.83	35470.89	7.873	6271.76	49378.43
A_68_P23681258	chr5:50449746-50449790	NM_133911:467	Gpr125	INSIDE	1.910	2.700	4056.12	10949.92	5.155	3147.75	16226.96

						Sham group			TiO$_2$-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P21536555	chr2:113598914-113598958	NM_011824:-131	Grem1	PROMOTER	1.910	6.201	10172.87	63086.12	11.843	7495.12	88766.02
A_68_P28671841	chr12:99975831-99975875	NM_001146199:-237	Ptpn21	DIVERGENT_PROMOTER	1.910	3.169	3504.26	11104.89	6.054	2752.12	16661.96
A_68_P21285107	chr2:65077163-65077207	NM_027225:-501	Cobll1	PROMOTER	1.909	4.523	6122.86	27694.30	8.633	4521.21	39031.95
A_68_P23657737	chr5:46030747-46030791	NM_021416:-28	Fam184b	PROMOTER	1.909	1.799	1547.18	2783.68	3.435	1287.38	4422.59
A_68_P32743933	chrX:147481461-147481505	NM_008001:-293	Fgd1	PROMOTER	1.909	4.057	3063.49	12429.23	7.745	1840.37	14252.89
A_68_P23296219	chr4:129012748-129012792	NM_009030:-156	Rbbp4	DIVERGENT_PROMOTER	1.909	4.649	4131.98	19209.22	8.876	3331.75	29571.28
A_68_P30499546	chr15:102577711-102577755			Unknown	1.909	1.480	2355.57	3485.49	2.824	1811.15	5114.82
A_68_P27784450	chr11:49525550-49525594	NM_212484:640	Cnot6	INSIDE	1.908	2.634	3975.65	10469.93	5.025	3106.29	15610.64
A_68_P26983894	chr10:19654073-19654117	NM_008580:-237	Map3k5	PROMOTER	1.908	4.715	1137.39	5362.66	8.995	869.16	7818.51
A_68_P28726327	chr12:109417619-109417664	NM_028262:-147	Setd3	DIVERGENT_PROMOTER	1.908	4.603	1903.06	8759.66	8.782	1566.38	13755.89
A_68_P26880499	chr9:120842203-120842247	NM_007614:-293	Ctnnb1	PROMOTER	1.907	3.489	2486.61	8675.34	6.652	1765.98	11746.72
A_68_P25644704	chr8:9771350-9771394	NM_173446:-349	Fam155a	PROMOTER	1.907	12.194	23543.03	287086.60	23.250	14771.44	343435.70
A_68_P25266552	chr7:87547168-87547212	NM_011046:458	Furin	INSIDE	1.907	4.974	1206.48	6001.21	9.487	1020.22	9678.73
A_68_P30243544	chr15:57525714-57525758	NM_199449:-485	Zhx2	PROMOTER	1.907	2.755	1625.86	4478.68	5.253	1339.99	7039.37
A_68_P29049835	chr13:54605357-54605401	NM_176987:213	4732471D19Rik	INSIDE	1.906	4.028	1786.81	7197.41	7.678	1384.65	10630.74
A_68_P23647569	chr5:44173172-44173216	NM_001159963:194	Fbxl5	INSIDE	1.905	5.037	4066.60	20482.39	9.597	2939.28	28208.15
A_68_P23350170	chr4:138749124-138749168	NM_001037761:253	Capzb	INSIDE	1.904	3.333	401.15	1336.85	6.346	334.45	2122.53
A_68_P27930557	chr11:76015854-76015898	NM_027773:319	Fam57a	INSIDE	1.904	3.875	1497.57	5802.80	7.379	1271.09	9379.09
A_68_P31162404	chr17:36221085-36221129	NM_008199:88	H2-Bl	INSIDE	1.904	2.502	2933.75	7341.23	4.765	2115.03	10078.02
A_68_P30601918	chr16:23225193-23225237	NM_145933:380	St6gal1	INSIDE	1.904	2.661	1893.74	5038.34	5.066	1478.16	7487.62
A_68_P32553141	chrX:96238064-96238108	NM_199018:167	Stard8	INSIDE	1.904	4.549	2633.26	11979.79	8.662	1594.17	13808.89
A_68_P24735989	chr6:108778919-108778963	NM_138677:306	Edem1	INSIDE	1.903	3.777	394.52	1490.21	7.189	410.65	2952.03
A_68_P27091644	chr10:41607176-41607220	NM_001013370:-46	Sesn1	PROMOTER	1.903	6.522	2943.93	19199.99	12.412	2476.28	30734.88
A_68_P30128581	chr15:34373372-34373416	NM_001163485:-363	Rpl30	DIVERGENT_PROMOTER	1.902	2.460	2857.63	7030.14	4.679	2030.46	9500.08
A_68_P30380067	chr15:81688792-81688836	NM_020507:-58	Tob2	PROMOTER	1.902	4.656	2525.26	11757.26	8.854	1887.14	16709.04
A_68_P29134822	chr13:72768633-72768679	NM_010574:2231	Irx2	INSIDE	1.901	2.271	4470.84	10154.53	4.319	3365.33	14533.82
A_68_P20456742	chr1:95532281-95532325	NM_021537:2	Stk25	INSIDE	1.901	5.375	5391.60	28979.31	10.220	4104.03	41941.65
A_68_P30230212	chr15:54903756-54903800	NM_001081288:-71	Taf2	PROMOTER	1.901	4.632	1981.73	9179.20	8.804	1705.00	15010.15
A_68_P23608585	chr5:36924742-36924786	NM_133910:282	Tbc1d14	INSIDE	1.901	2.812	13547.19	38091.92	5.346	9749.13	52114.66
A_68_P32258637	chrX:11384409-11384453			Unknown	1.901	1.417	1543.52	2187.58	2.694	810.68	2183.79
A_68_P24995433	chr7:20408093-20408137	NM_033601:-10	Bcl3	PROMOTER	1.900	4.210	710.19	2990.18	8.001	585.96	4688.00
A_68_P27111732	chr10:45297581-45297625	NM_172473:-32	Hace1	PROMOTER	1.900	2.556	1049.71	2683.25	4.857	871.12	4231.03
A_68_P29237544	chr13:95647510-95647554	NM_011021:1951	Otp	INSIDE	1.900	3.442	1352.07	4653.63	6.541	951.11	6220.87
A_68_P27898391	chr11:69810124-69810168	NM_030064:874	Phf23	INSIDE	1.900	6.188	16696.39	103321.70	11.758	11612.96	136541.00
A_68_P23609090	chr5:37086922-37086966	NM_001081232:264	D5Ertd579e	INSIDE	1.899	4.942	5250.33	25945.60	9.383	4159.62	39028.77
A_68_P28174620	chr11:118768747-118768791	NM_001024931:2118	Rbfox3	INSIDE	1.899	5.324	5970.48	31785.57	10.112	4426.10	44755.41
A_68_P31659996	chr18:43367102-43367146	NM_178749:-226	Stk32a	PROMOTER	1.899	6.224	3351.87	20860.38	11.820	2474.30	29245.91
A_68_P32709174	chrX:139116023-139116067	NM_001199360:-224	Tmem164	PROMOTER	1.899	4.862	2349.83	11425.20	9.232	1450.14	13387.17
A_68_P32578104	chrX:101866109-101866153	NM_175358:273	Zdhhc15	INSIDE	1.899	3.304	4590.08	15164.50	6.274	2668.97	16744.35
A_68_P21762932	chr2:154718551-154718596	NM_026030:69	Eif2s2	INSIDE	1.898	3.101	2784.28	8634.70	5.886	2108.86	12413.38
A_68_P20506808	chr1:108069211-108069255	NM_133821:787	Phlpp1	INSIDE	1.898	7.316	1813.92	13270.07	13.888	1509.26	20961.24
A_68_P32234207	chrX:5977686-5977730	NM_001040459:446	Shroom4	INSIDE	1.898	3.037	992.20	3013.76	5.764	637.73	3675.91
A_68_P24019920	chr5:117769201-117769245	NM_001033311:-52	Vsig10	PROMOTER	1.898	1.432	926.32	1326.26	2.717	833.12	2263.95
A_68_P24098738	chr5:132013832-132013876	NM_177047:1004359	Auts2	INSIDE	1.897	3.105	2416.69	7504.06	5.891	1923.10	11328.58
A_68_P30667506	chr16:35022484-35022528	NM_023587:0	Ptplb	INSIDE	1.897	2.685	1062.16	2851.96	5.094	902.45	4597.00
A_68_P22382656	chr3:102538778-102538822	NM_027533:108	Tspan2	INSIDE	1.897	4.171	9887.21	41239.90	7.911	7434.75	58815.90
A_68_P21117289	chr2:32612990-32613034	NM_152800:222	Tor2a	INSIDE	1.896	6.493	1602.39	10403.93	12.309	1213.79	14940.74
A_68_P32700327	chrX:137200260-137200304	ENSMUST00000112988:672		INSIDE	1.896	2.665	1016.59	2709.60	5.053	477.49	2412.85
A_68_P23222359	chr4:114597578-114597622	NM_015758:1018	Foxe3	DOWNSTREAM	1.895	11.062	1484.95	16425.86	20.962	1203.20	25221.92
A_68_P26538932	chr9:56712960-56713004	NM_139001:72	Cspg4	INSIDE	1.894	4.386	10522.96	46156.43	8.309	7877.12	65451.70
A_68_P25766300	chr8:33994475-33994519	NM_001177589:66002	Gm3985	DOWNSTREAM	1.894	2.241	608.52	1363.70	4.244	521.65	2213.84

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28450733	chr12:56225550-56225594	NM_001100116:58	1700047I17Rik2	INSIDE	1.893	4.739	1177.94	5581.73	8.969	972.67	8724.30
A_68_P27914258	chr11:72775141-72775185	NM_001163336:492	Atp2a3	INSIDE	1.893	2.324	1220.11	2835.14	4.398	1120.16	4926.22
A_68_P23361673	chr4:140581289-140581333	NM_172122:28266	Crocc	INSIDE	1.893	5.666	2665.13	15100.28	10.727	2182.63	23412.04
A_68_P26348962	chr9:21602957-21603001	NM_145611:12	Kank2	INSIDE	1.893	2.623	1978.53	5190.52	4.966	1544.30	7669.06
A_68_P27283985	chr10:80024218-80024262	NM_025852:65	Rexo1	INSIDE	1.893	1.853	1490.13	2761.57	3.509	1217.01	4270.00
A_68_P26079748	chr8:97362202-97362246	NM_134141:16	Ciapin1	INSIDE	1.892	2.871	431.89	1240.15	5.432	323.32	1756.29
A_68_P28732711	chr12:110692025-110692069	NM_001190703:382	Dlk1	INSIDE	1.892	2.773	11271.12	31256.75	5.247	7974.42	41839.52
A_68_P20636645	chr1:136884255-136884299	NM_001033409:117577	Lgr6	INSIDE	1.892	14.177	2442.11	34620.74	26.820	1778.74	47705.97
A_68_P22341452	chr3:94758251-94758295	NM_017395:-664	Rfx5	PROMOTER	1.892	1.986	1160.58	2305.20	3.759	985.55	3704.39
A_68_P23442283	chr4:155452135-155452179			Unknown	1.892	3.276	2422.93	7938.13	6.200	1916.25	11880.43
A_68_P21900913	chr2:179759394-179759438	NM_177727:-275	Lsm14b	PROMOTER	1.891	4.621	5053.95	23356.44	8.741	3956.25	34580.53
A_68_P25578901	chr7:146768634-146768678	NR_027857:40	Nkx6-2	INSIDE	1.891	4.355	4487.96	19544.00	8.234	3456.28	28458.97
A_68_P28039255	chr11:95375266-95375310	NM_130858:591	Nxph3	INSIDE	1.891	6.571	8238.62	54137.48	12.429	6016.37	74779.02
A_68_P31713385	chr18:53624187-53624231	NM_001033281:9	Prdm6	INSIDE	1.891	2.311	1897.82	4386.30	4.371	1358.76	5938.95
A_68_P31121831	chr17:28465275-28465320	NM_011287:-118	Rpl10a	PROMOTER	1.891	8.952	1034.42	9260.53	16.925	734.71	12435.11
A_68_P32564024	chrX:98615209-98615253	NM_001177985:23	Zmym3	INSIDE	1.891	2.856	582.27	1662.67	5.400	372.25	2010.15
A_68_P30246249	chr15:57966345-57966389	NM_027435:271	Atad2	INSIDE	1.890	8.349	2043.61	17062.91	15.779	1656.81	26143.28
A_68_P29530305	chr14:35315556-35315600	NM_009758:154	Bmpr1a	INSIDE	1.890	3.798	2069.87	7862.13	7.178	1766.58	12680.11
A_68_P28167547	chr11:117710471-117710515	NM_001012273:-58	Birc5	PROMOTER	1.889	4.570	1254.99	5735.76	8.632	1037.63	8956.98
A_68_P25354355	chr7:105326695-105326739	NM_007602:-13	Capn5	PROMOTER	1.889	3.757	1433.93	5386.78	7.097	1113.74	7904.33
A_68_P24359955	chr6:35083485-35083529	NM_001164412:231	Cnot4	INSIDE	1.889	3.638	4126.95	15015.24	6.874	3480.07	23921.77
A_68_P30093655	chr15:27560477-27560521	NM_001013792:-50	Fam105b	PROMOTER	1.889	3.790	4711.05	17853.99	7.158	3397.60	24320.69
A_68_P27924667	chr11:74992384-74992428	NM_027136:-96	Ovca2	PROMOTER	1.889	6.221	3563.75	22170.42	11.753	2485.00	29206.57
A_68_P30678526	chr16:37011868-37011912	NM_001159369:19	Polq	INSIDE	1.889	2.244	1247.87	2800.29	4.240	1016.30	4308.64
A_68_P26569971	chr9:62191474-62191518	NM_009672:2347	Anp32a	INSIDE	1.888	1.626	2462.56	4004.47	3.070	2044.89	6278.80
A_68_P23763603	chr5:67136839-67136883	NM_001001980:-218	Limch1	PROMOTER	1.888	5.879	1443.65	8487.48	11.099	1197.28	13288.10
A_68_P28604394	chr12:86827035-86827079	NM_010234:12206	Fos	DOWNSTREAM	1.887	3.215	1472.75	4735.17	6.066	1107.98	6721.43
A_68_P30367903	chr15:79518094-79518138	NM_028792:186	Josd1	INSIDE	1.887	3.055	1146.51	3502.77	5.766	919.95	5304.26
A_68_P20723965	chr1:154802917-154802961	NM_175460:708	Nmnat2	INSIDE	1.887	7.197	5326.04	38330.74	13.580	3487.41	47358.05
A_68_P29624997	chr14:57483807-57483852	AK209334:-895		PROMOTER	1.887	1.472	811.40	1194.05	2.778	730.58	2029.25
A_68_P21438176	chr2:93816807-93816851	NM_026944:34059	Alkbh3	DOWNSTREAM	1.886	5.584	1256.48	7015.68	10.528	1153.90	12148.56
A_68_P31152221	chr17:34257414-34257458	NR_037970:-591	Brd2	PROMOTER	1.886	4.785	791.53	3787.67	9.025	636.70	5746.45
A_68_P27262526	chr10:75994451-75994495	NM_146006:101	Lss	INSIDE	1.886	5.474	6782.44	37124.20	10.325	5005.00	51676.57
A_68_P29054388	chr13:55431309-55431353	NM_016662:-239	Mxd3	PROMOTER	1.886	4.408	1313.53	5789.64	8.315	1065.03	8855.45
A_68_P32118295	chr19:42056730-42056774	NM_145500:500	Ubtd1	INSIDE	1.886	6.127	949.72	5818.85	11.553	816.00	9427.02
A_68_P25734548	chr8:27891120-27891164			Unknown	1.886	2.789	931.33	2597.80	5.262	886.53	4664.93
A_68_P29470473	chr14:25064406-25064450	NM_001163513:714	Dlg5	INSIDE	1.884	21.987	778.65	17120.00	41.423	520.80	21572.99
A_68_P20451406	chr1:94729272-94729316	NM_016696:1032	Gpc1	INSIDE	1.884	4.338	2033.27	8819.41	8.171	1598.45	13060.72
A_68_P25394537	chr7:112959576-112959620	NM_025301:3	Mrpl17	INSIDE	1.884	3.020	2285.66	6902.31	5.690	1763.25	10032.24
A_68_P28246269	chr12:12944121-12944165	NM_008709:4500	Mycn	INSIDE	1.884	3.332	931.52	3104.13	6.278	767.56	4818.81
A_68_P28950705	chr13:36816445-36816489	NM_153529:9857	Nrn1	DOWNSTREAM	1.884	8.358	4570.60	38201.00	15.746	3319.36	52265.63
A_68_P20085264	chr1:22812557-22812601	NM_001012623:-15	Rims1	PROMOTER	1.884	3.168	5138.64	16277.20	5.969	3944.43	23542.48
A_68_P23468797	chr5:8622724-8622768	NM_198620:206	Rundc3b	INSIDE	1.884	1.793	6375.10	11431.71	3.379	5084.04	17177.17
A_68_P28724517	chr12:109154270-109154314	NM_001079883:87332	Bcl11b	INSIDE	1.883	5.082	2190.88	11133.18	9.566	1718.68	16441.20
A_68_P30362680	chr15:78673148-78673192	NM_027219:94	Cdc42ep1	INSIDE	1.883	4.258	1830.06	7792.26	8.016	1529.47	12260.21
A_68_P25598742	chr7:150293216-150293260	NM_008434:80	Kcnq1	INSIDE	1.883	8.553	779.08	6663.79	16.107	603.76	9724.83
A_68_P30421719	chr15:88693018-88693062	NM_145478:417	Pim3	INSIDE	1.883	4.203	734.95	3088.77	7.913	589.31	4663.15
A_68_P27541275	chr10:127848643-127848687	NM_001164237:-7	Rnf41	DIVERGENT_PROMOTER	1.883	5.832	1251.46	7299.10	10.982	997.40	10953.87
A_68_P27836028	chr11:59103858-59103902	NM_009522:373	Wnt3a	INSIDE	1.883	2.885	1333.86	3847.79	5.431	1095.47	5949.46
A_68_P29631470	chr14:58691022-58691066	NM_013518:-478	Fgf9	PROMOTER	1.882	5.806	1512.20	8780.06	10.924	1230.13	13438.37
A_68_P23787605	chr5:72049192-72049236	NM_010251:333	Gabra4	INSIDE	1.882	5.032	905.66	4556.89	9.471	750.11	7104.47

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P24774311	chr6:115944633-115944678	NM_026376:368	Plxnd1	INSIDE	1.882	6.530	3149.31	20564.84	12.291	2421.41	29761.64
A_68_P21812328	chr2:163244957-163245001	NM_025699:228	3230401D17Rik	INSIDE	1.881	7.426	2014.28	14958.86	13.971	1569.90	21933.65
A_68_P32775148	chrX:155970504-155970548	NM_001033472:-73	A830080D01Rik	PROMOTER	1.881	4.182	1734.44	7253.34	7.867	1002.59	7887.70
A_68_P27512350	chr10:122513515-122513559	NM_001163024:25	Mon2	INSIDE	1.881	4.934	2975.86	14683.41	9.281	2372.94	22023.12
A_68_P30463766	chr15:96290439-96290483	NM_028148:814	Scaf11	INSIDE	1.881	1.929	1477.99	2851.50	3.629	1168.09	4239.56
A_68_P29051405	chr13:54890823-54890867	NM_028841:79	Tspan17	INSIDE	1.881	3.452	458.95	1584.22	6.494	329.33	2138.76
A_68_P30346013	chr15:75920805-75920849	NM_144847:-383	Nrbp2	PROMOTER	1.880	2.482	2490.06	6180.14	4.665	1969.62	9188.98
A_68_P22398585	chr3:105490135-105490179	NM_017397:333	Ddx20	INSIDE	1.879	2.525	1089.30	2750.84	4.746	942.09	4471.30
A_68_P20877951	chr1:182742690-182742734	NM_008210:1022	H3f3a	INSIDE	1.879	2.919	2269.28	6623.75	5.485	1821.43	9991.04
A_68_P30346762	chr15:76028710-76028754	NM_201393:-93	Plec	PROMOTER	1.879	3.238	2210.87	7157.92	6.082	1649.76	10033.85
A_68_P32567036	chrX:99266249-99266293	NM_183318:376	Rgag4	INSIDE	1.879	8.946	4538.15	40597.66	16.807	2317.83	38955.67
A_68_P22872576	chr4:43591441-43591485	NM_172866:-144	Rgp1	PROMOTER	1.879	2.255	663.43	1495.70	4.236	480.39	2035.06
A_68_P21266440	chr2:61650101-61650145	NM_009322:7613	Tbr1	INSIDE	1.879	2.100	424.79	892.06	3.945	412.76	1628.36
A_68_P26554375	chr9:59465216-59465260	NM_001205239:148	Parp6	INSIDE	1.878	4.980	2916.91	14526.13	9.350	2137.24	19983.87
A_68_P23062645	chr4:83131826-83131870	NM_133948:446	Psip1	INSIDE	1.878	2.791	1459.70	4074.48	5.242	1255.71	6581.91
A_68_P26290461	chr9:8004643-8004687	NM_001171147:-68	Yap1	PROMOTER	1.878	5.407	3903.80	21106.63	10.155	3228.67	32788.72
A_68_P32565199	chrX:98892409-98892453	ENSMUST00000073812:-5241		PROMOTER	1.878	6.112	8917.51	54505.77	11.481	3674.32	42184.32
A_68_P27563898	chr11:5441853-5441897	NM_134033:346	Ccdc117	INSIDE	1.877	5.498	3920.15	21554.59	10.319	3139.07	32391.51
A_68_P30490489	chr15:101062456-101062514	NM_019518:7847	Grasp	INSIDE	1.877	9.892	1964.82	19435.55	18.567	1397.98	25956.94
A_68_P30337599	chr15:74347574-74347618	NM_174991:971	Bai1	INSIDE	1.876	5.979	1825.93	10917.73	11.217	1386.24	15550.12
A_68_P26756440	chr9:97933663-97933707	NM_022319:-98	Clstn2	PROMOTER	1.876	9.816	3587.04	35211.04	18.414	3006.61	55364.42
A_68_P25092690	chr7:52622810-52622854	NR_027802:230	Mtag2	INSIDE	1.876	3.324	2610.46	8676.44	6.236	1965.83	12259.79
A_68_P23328804	chr4:135050696-135050741	NM_028995:-299	Nipal3	DIVERGENT_PROMOTER	1.876	2.629	2957.08	7775.38	4.932	2108.10	10397.66
A_68_P26783904	chr9:103014963-103015007	NM_173781:581	Rab6b	INSIDE	1.876	6.996	3134.89	21931.57	13.124	2261.49	29680.34
A_68_P27693347	chr11:33101808-33101852	NM_019916:1758	Tlx3	INSIDE	1.876	2.938	673.36	1978.25	5.511	549.92	3030.69
A_68_P29751622	chr14:79881067-79881111	NM_018765:-13	Wbp4	PROMOTER	1.876	0.357	1577.79	563.98	0.670	1430.02	958.78
A_68_P27788008	chr11:50139149-50139193	NM_001110499:5	Canx	INSIDE	1.875	2.514	5536.90	13918.62	4.712	4124.56	19436.10
A_68_P31112726	chr17:26978463-26978507	NM_008700:26	Nkx2-5	INSIDE	1.875	3.055	1100.14	3361.00	5.729	941.99	5396.80
A_68_P26015929	chr8:86192596-86192640	NM_013641:2080	Ptger1	INSIDE	1.875	5.992	6861.71	41111.95	11.236	4744.67	53309.83
A_68_P27996402	chr11:87630757-87630801	NM_080420:8838	Lpo	INSIDE	1.874	3.124	2302.41	7193.28	5.856	1764.87	10335.15
A_68_P28376737	chr12:40860793-40860837	NM_001146196:1	Scin	INSIDE	1.874	8.543	1868.55	15962.97	16.011	1151.05	18429.85
A_68_P27167594	chr10:58684574-58684618	NM_001024910:-1	Septin10	DIVERGENT_PROMOTER	1.874	6.097	4520.24	27558.99	11.425	3322.33	37957.26
A_68_P22338534	chr3:94167626-94167670	NM_001136117:1283	C2cd4d	INSIDE	1.873	6.728	2320.94	15615.16	12.603	1545.88	19482.20
A_68_P32185492	chr19:54018463-54018507	NM_001168505:-311	Shoc2	PROMOTER	1.873	3.317	398.42	1321.74	6.212	340.43	2114.92
A_68_P27456596	chr10:112366019-112366063	NM_001033474:42	Atxn7l3b	INSIDE	1.872	2.055	1150.38	2364.14	3.846	889.33	3420.50
A_68_P22045621	chr3:33919264-33919308	NM_001113188:286	Fxr1	INSIDE	1.872	5.067	1615.59	8186.84	9.487	1389.21	13179.17
A_68_P26974637	chr10:18039197-18039241			Unknown	1.872	4.510	1580.08	7125.83	8.444	1398.48	11808.21
A_68_P20453775	chr1:95073064-95073108			Unknown	1.872	4.538	4204.56	19080.88	8.496	3052.39	25933.24
A_68_P30594370	chr16:21794748-21794792	NR_037957:351	1300002E11Rik	INSIDE	1.871	2.126	2580.94	5487.07	3.977	1897.25	7546.25
A_68_P31350938	chr17:74715809-74715853	NM_001146223:-57	Dpy30	PROMOTER	1.871	3.740	704.95	2636.74	7.000	589.60	4127.01
A_68_P21683849	chr2:140221825-140221869	NM_028387:676	Macrod2	INSIDE	1.871	6.341	1384.22	8776.69	11.861	1025.84	12167.25
A_68_P26590952	chr9:65908094-65908138	NM_011149:141	Ppib	INSIDE	1.871	4.387	1835.70	8054.00	8.209	1472.92	12091.40
A_68_P23362920	chr4:140804003-140804047	NM_172520:5226	Arhgef19	INSIDE	1.870	5.882	3780.71	22238.90	11.000	2681.58	29498.68
A_68_P24993125	chr7:19989502-19989546	NM_146182:-4319	Klc3	DIVERGENT_PROMOTER	1.870	5.073	605.74	3072.82	9.488	524.06	4972.47
A_68_P30759540	chr16:52031753-52031797	NM_001033238:113	Cblb	INSIDE	1.869	5.433	3786.69	20574.64	10.156	2974.85	30212.40
A_68_P21478262	chr2:102499332-102499376	NM_001077514:515	Slc1a2	INSIDE	1.869	1.470	1996.54	2934.82	2.748	1860.15	5111.37
A_68_P31560905	chr18:24761962-24762006	NM_139143:334	Slc39a6	INSIDE	1.868	2.161	1272.21	2749.55	4.037	1035.29	4179.32
A_68_P31204664	chr17:46168459-46168503	NM_001110266:-6368	Vegfa	PROMOTER	1.868	3.938	2692.61	10604.08	7.358	1954.89	14383.83
A_68_P21072052	chr2:25283953-25283999	NM_007379:-217	Abca2	PROMOTER	1.867	6.187	1092.36	6758.71	11.554	738.63	8533.92
A_68_P22878646	chr4:44717054-44717098	NM_008782:6236	Pax5	INSIDE	1.867	3.219	1464.92	4715.36	6.011	1183.08	7111.31
A_68_P26931630	chr10:9394840-9394884	NM_177271:144	Samd5	INSIDE	1.867	2.575	252.30	649.59	4.807	193.73	931.21

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26399336	chr9:31018727-31018771	NM_001102455:652	Aplp2	INSIDE	1.866	3.500	1846.08	6460.53	6.530	1573.87	10276.76
A_68_P31933966	chr19:6320610-6320654	NM_001033342:14176	Cdc42bpg	INSIDE	1.866	2.451	1328.64	3256.35	4.573	993.63	4544.01
A_68_P28143851	chr11:113612678-113612722	NM_020006:-226	Cdc42ep4	PROMOTER	1.866	5.437	4581.48	24908.34	10.143	3566.82	36177.86
A_68_P32815030	chrX:164561176-164561220	NM_001033330:453967	Frmpd4	INSIDE	1.866	1.925	4121.47	7933.14	3.592	2105.63	7564.06
A_68_P27850828	chr11:61668703-61668747	NM_013881:-130	Ulk2	PROMOTER	1.866	9.965	2530.43	25216.61	18.596	1822.22	33886.04
A_68_P23231372	chr4:116550094-116550138	NM_001029912:110	Zswim5	INSIDE	1.866	3.471	2852.81	9901.03	6.476	2279.39	14761.92
A_68_P29243355	chr13:96661950-96661994	NM_027711:-95	Iqgap2	PROMOTER	1.865	7.954	4160.49	33091.43	14.837	3280.77	48675.82
A_68_P28587837	chr12:83718482-83718526	NM_015812:480	Rgs6	INSIDE	1.865	4.469	5923.59	26471.32	8.335	4024.42	33544.94
A_68_P24153558	chr5:143580250-143580294	NM_001122730:-1206	Tnrc18	PROMOTER	1.865	3.080	1012.96	3120.38	5.746	755.98	4343.72
A_68_P26242187	chr8:126416382-126416426	NM_009606:2232	Acta1	INSIDE	1.864	5.940	2048.63	12168.98	11.070	1536.20	17005.65
A_68_P25017319	chr7:28232977-28233021	NM_144923:2	Blvrb	INSIDE	1.864	5.626	831.95	4680.16	10.488	640.99	6722.65
A_68_P21871012	chr2:173485328-173485372	NM_024436:5	Rab22a	INSIDE	1.864	3.810	1753.20	6679.06	7.102	1469.63	10436.92
A_68_P30379103	chr15:81524969-81525013	NM_001164320:2727	Chadl	INSIDE	1.863	5.182	1487.64	7708.88	9.656	1312.39	12672.07
A_68_P31933641	chr19:6277445-6277489	NM_010119:571	Ehd1	INSIDE	1.863	2.535	2307.03	5847.36	4.723	1920.83	9072.38
A_68_P23416733	chr4:151506350-151506394	NM_019585:-3338	Espn	PROMOTER	1.863	2.714	1723.10	4676.52	5.057	1235.44	6248.09
A_68_P21820992	chr2:164823190-164823234	NM_020333:29725	Slc12a5	INSIDE	1.863	4.280	1560.22	6677.49	7.972	1157.02	9223.73
A_68_P31932456	chr19:6060898-6060957	NM_013859:-279	Znhit2-ps	PROMOTER	1.863	9.177	22684.11	208180.60	17.096	12764.16	218213.80
A_68_P26542457	chr9:57408653-57408697	NM_022813:-76	Scamp2	DIVERGENT_PROMOTER	1.862	8.524	2860.02	24377.60	15.873	2166.72	34391.44
A_68_P28778754	chr12:119539626-119539670	NM_001166385:265	Sp4	INSIDE	1.862	2.643	5538.52	14636.78	4.922	3708.25	18250.32
A_68_P28871505	chr13:21272743-21272787	NM_009054:937	Trim27	INSIDE	1.862	3.993	1642.00	6556.20	7.435	1345.09	10000.14
A_68_P26844412	chr9:114299556-114299600	NM_019922:252	Crtap	INSIDE	1.861	2.317	304.24	704.96	4.312	255.06	1099.81
A_68_P24859179	chr6:133986298-133986342	NM_007961:596	Etv6	INSIDE	1.861	4.825	3201.66	15448.10	8.981	2185.86	19630.72
A_68_P31136610	chr17:31038660-31038704	NM_021332:-129	Glp1r	PROMOTER	1.861	3.103	1597.84	4957.41	5.775	1231.07	7109.74
A_68_P24005520	chr5:115141122-115141166	NM_019821:-200	Gltp	PROMOTER	1.861	14.750	2824.25	41658.07	27.452	1892.70	51959.08
A_68_P30348856	chr15:76348296-76348340	NM_130893:4241	Scrt1	INSIDE	1.861	1.663	646.71	1075.76	3.096	568.99	1761.59
A_68_P33005878	A_68_P33005878			Unknown	1.861	2.483	1273.31	3161.72	4.622	1150.16	5316.27
A_68_P32288523	chrX:20003140-20003184	ENSMUST00000136093:249		INSIDE	1.861	2.307	1224.44	2824.45	4.292	634.04	2721.51
A_68_P30093919	chr15:27611395-27611439	NM_198301:-163	Fam105a	PROMOTER	1.860	6.742	2286.11	15412.02	12.541	1862.41	23356.17
A_68_P30137020	chr15:36094444-36094488	NM_001081253:173	Fbxo43	INSIDE	1.860	5.797	2825.11	16376.00	10.784	2325.91	25082.19
A_68_P32127978	chr19:43749225-43749269	NM_145156:125	Slc25a28	INSIDE	1.860	3.834	4546.31	17431.31	7.130	3722.09	26537.24
A_68_P22411695	chr3:108086638-108086682	NM_019972:-389	Sort1	PROMOTER	1.860	12.153	4225.97	51358.98	22.603	3331.36	75298.24
A_68_P27907296	chr11:71564250-71564294	NM_177618:68	Wscd1	INSIDE	1.860	4.496	4666.83	20981.39	8.363	3397.05	28410.13
A_68_P26036153	chr8:90184081-90184125	NM_033327:299392	Zfp423	DOWNSTREAM	1.860	2.586	2470.14	6388.56	4.811	1808.14	8699.09
A_68_P26617803	chr9:70527024-70527068	NM_007399:239	Adam10	INSIDE	1.859	3.341	3327.19	11116.75	6.210	2658.10	16507.02
A_68_P29629464	chr14:58318596-58318640	NM_015771:46342	Lats2	INSIDE	1.859	4.525	1145.35	5183.03	8.411	850.90	7156.64
A_68_P29055172	chr13:55565926-55565970	NM_001030296:321	Prr7	INSIDE	1.859	1.859	1462.78	2719.55	3.456	1167.23	4034.24
A_68_P21641570	chr2:132512792-132512837	NM_028637:-3204	1110034G24Rik	PROMOTER	1.858	6.225	4805.88	29915.80	11.569	3480.64	40266.74
A_68_P28576807	chr12:81744426-81744470	NM_007951:400	Erh	INSIDE	1.857	8.037	3705.65	29783.34	14.922	2743.77	40942.16
A_68_P20942041	chr1:194014550-194014594	NM_001038607:-181	Kcnh1	PROMOTER	1.857	6.657	1568.79	10443.24	12.363	1127.88	13944.47
A_68_P20877047	chr1:182571834-182571878	NM_175186:392	Lin9	INSIDE	1.857	3.800	539.78	2051.03	7.055	419.29	2957.95
A_68_P26500017	chr9:49606485-49606529	NM_001081445:668	Ncam1	INSIDE	1.857	2.717	2069.79	5624.12	5.047	1608.35	8117.62
A_68_P30176273	chr15:43308698-43308742	NM_025736:-54	Ttc35	PROMOTER	1.857	2.199	1903.70	4185.70	4.083	1443.41	5892.75
A_68_P32203587	chr19:56948670-56948714	NM_172840:-213	Vwa2	PROMOTER	1.857	2.149	2555.17	5491.18	3.992	1976.20	7888.36
A_68_P32245740	chrX:8777550-8777594	NM_173414:474	Lancl3	INSIDE	1.856	3.553	2031.89	7220.04	6.594	1133.27	7472.63
A_68_P27812425	chr11:54674397-54674456	NM_029327:-333	Lyrm7	DIVERGENT_PROMOTER	1.856	6.650	561.10	3731.56	12.345	393.08	4852.51
A_68_P20929010	chr1:191746024-191746068	NM_026796:121	Smyd2	INSIDE	1.856	1.637	1106.26	1810.60	3.039	961.74	2922.27
A_68_P29030706	chr13:51195741-51195786	NR_029463:333	9430083A17Rik	INSIDE	1.855	7.570	295.35	2235.85	14.039	200.59	2816.15
A_68_P24798780	chr6:120442970-120443014	NM_033567:833	Cecr6	INSIDE	1.855	9.906	4627.20	45837.77	18.374	3197.85	58756.19
A_68_P28152301	chr11:115111293-115111337	NM_010350:17243	Grin2c	INSIDE	1.855	4.543	821.35	3731.26	8.426	625.37	5269.14
A_68_P25088285	chr7:51846895-51846939	NM_008422:661	Kcnc3	INSIDE	1.855	1.592	1174.97	1870.06	2.953	960.40	2835.96
A_68_P31150844	chr17:34027540-34027584	NM_001195298:16	Kifc1	INSIDE	1.855	2.792	4744.51	13244.59	5.177	3568.63	18475.69

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28781893	chr12:120087514-120087558	NM_177082:2735	Sp8	INSIDE	1.855	6.228	2260.85	14079.59	11.549	1813.01	20938.56
A_68_P21117286	chr2:32612762-32612806	NM_152800:-6	Tor2a	PROMOTER	1.855	3.906	1786.12	6976.17	7.247	1455.65	10548.40
A_68_P26826440	chr9:110782793-110782837	NM_001146060:-11	Als2cl	PROMOTER	1.854	2.810	1878.69	5278.63	5.210	1557.45	8114.97
A_68_P32563078	chrX:98450245-98450289	NM_018789:400	Foxo4	INSIDE	1.854	2.398	2878.19	6901.22	4.445	1681.25	7473.24
A_68_P25022784	chr7:29383198-29383242	NM_027470:-17	Pak4	PROMOTER	1.853	2.382	1554.18	3702.31	4.414	1320.10	5827.10
A_68_P24631961	chr6:90319416-90319460	NM_030260:-49	Zxdc	PROMOTER	1.853	2.577	1348.62	3475.42	4.775	1139.85	5442.93
A_68_P26897431	A_68_P26897431			Unknown	1.853	3.957	2107.03	8337.27	7.333	1705.38	12505.80
A_68_P22312502	chr3:88018703-88018747	NR_037276:-368	Mir3093	PROMOTER	1.852	2.529	1938.75	4903.30	4.684	1457.09	6825.26
A_68_P27980115	chr11:84693687-84693731	NM_027388:-11	Pigw	DIVERGENT_PROMOTER	1.852	5.805	4740.80	27519.45	10.748	3448.08	37060.13
A_68_P21307670	chr2:69044152-69044196	NM_001199123:73	Spc25	INSIDE	1.852	3.706	1585.79	5877.44	6.865	1353.50	9291.82
A_68_P29560590	chr14:41779806-41779850	NM_145928:268	Tspan14	INSIDE	1.852	3.937	6353.90	25015.85	7.292	5038.57	36742.06
A_68_P28172267	chr11:118430861-118430905	NM_001024931:340004	Rbfox3	INSIDE	1.851	7.994	1742.26	13928.25	14.799	1321.84	19561.59
A_68_P23588840	chr5:33775538-33775582	ENSMUST00000030994:-1716		PROMOTER	1.851	3.157	943.98	2980.57	5.843	721.78	4217.52
A_68_P22128839	chr3:51081429-51081473	NM_023502:48459	Elf2	INSIDE	1.850	5.104	1669.02	8517.86	9.439	1364.87	12883.47
A_68_P26248330	chr8:127421598-127421642	NM_198103:-15	Exoc8	DIVERGENT_PROMOTER	1.850	4.396	1582.35	6956.78	8.135	1298.63	10564.61
A_68_P23195768	chr4:108055890-108055934	NM_001099303:42	Fam159a	INSIDE	1.850	3.727	1717.43	6400.97	6.893	1331.16	9176.22
A_68_P27997843	chr11:87912671-87912715	NM_198013:45	Cuedc1	INSIDE	1.849	4.175	3123.06	13039.48	7.721	2763.17	21333.33
A_68_P27681336	chr11:30854073-30854117	NM_025745:37	Erlec1	INSIDE	1.849	8.253	1290.17	10647.89	15.262	994.76	15181.97
A_68_P22481656	chr3:121996594-121996638	NR_030439:5	Mir760	INSIDE	1.849	3.682	1919.95	7068.63	6.809	1611.73	10973.93
A_68_P23230191	chr4:116299963-116300007	NM_001081475:118	Nasp	INSIDE	1.849	1.862	608.42	1132.81	3.442	451.71	1554.89
A_68_P21780565	chr2:157854409-157854453	NM_027434:-99	Rprd1b	PROMOTER	1.849	2.117	3552.85	7520.53	3.913	2754.84	10779.73
A_68_P23778454	chr5:69948402-69948446	NM_172711:244	Guf1	INSIDE	1.848	11.820	651.41	7699.92	21.844	469.40	10253.48
A_68_P27628926	chr11:19825568-19825612	NM_033523:1146	Spred2	INSIDE	1.848	5.940	1757.69	10440.87	10.975	1358.52	14909.89
A_68_P20268943	chr1:60466325-60466369	NM_001198570:-116	Abi2	PROMOTER	1.847	3.771	2029.17	7651.42	6.965	1746.26	12163.37
A_68_P28725240	chr12:109244557-109244601	NM_001079883:-2954	Bcl11b	PROMOTER	1.847	10.113	8411.21	85064.03	18.677	6212.44	116032.30
A_68_P24112800	chr5:135164852-135164896	NM_010717:-414	Limk1	PROMOTER	1.847	3.153	1731.17	5458.42	5.825	1224.90	7134.82
A_68_P29700473	chr14:70689417-70689461	NM_008915:-182	Ppp3cc	PROMOTER	1.847	1.470	711.29	1045.58	2.714	616.46	1673.29
A_68_P20796837	chr1:167775393-167775437	NM_001113391:56603	Cd247	INSIDE	1.846	3.316	1024.24	3396.84	6.123	945.61	5790.05
A_68_P31092997	chr17:23816594-23816638	NM_018777:285	Cldn6	INSIDE	1.846	2.792	6471.81	18068.45	5.154	4832.01	24904.13
A_68_P32798239	chrX:160857687-160857731	NM_011081:-10	Piga	PROMOTER	1.846	2.501	1866.07	4667.41	4.618	951.22	4392.61
A_68_P27560706	chr11:4886974-4887018	NM_007454:89	Ap1b1	INSIDE	1.845	5.714	2772.77	15842.99	10.541	2186.53	23047.61
A_68_P26814987	chr9:108362953-108362997	NM_133744:126	Ccdc71	INSIDE	1.845	3.061	1718.26	5258.97	5.647	1503.95	8493.19
A_68_P25005401	chr7:25319057-25319101	NM_153134:3412	Irgq	INSIDE	1.845	7.348	962.25	7071.03	13.556	824.30	11174.33
A_68_P24322963	chr6:28783645-28783689	NM_138682:-1919	Lrrc4	PROMOTER	1.845	3.671	1049.16	3851.39	6.772	1235.47	8367.10
A_68_P31621448	chr18:36178193-36178239	NM_001167891:178598	Nrg2	INSIDE	1.845	5.845	6052.49	35379.04	10.786	4628.59	49921.89
A_68_P23618578	chr5:38668746-38668790	NM_172709:126	Otop1	INSIDE	1.845	3.000	1919.11	5756.51	5.536	1513.31	8377.17
A_68_P30729955	chr16:46010463-46010507	NM_001134480:42	Plcxd2	INSIDE	1.845	4.883	876.34	4279.17	9.008	681.15	6135.69
A_68_P21566993	chr2:118752216-118752260	NM_028117:6	Chst14	INSIDE	1.844	4.062	1825.71	7415.99	7.491	1518.00	11371.36
A_68_P32229410	chr19:61301151-61301195	NM_009970:3149	Csf2ra	INSIDE	1.844	8.907	12157.54	108287.80	16.425	7752.53	127333.40
A_68_P31122728	chr17:28622553-28622597	NM_010220:483	Fkbp5	INSIDE	1.844	2.440	266.10	649.29	4.499	246.20	1107.77
A_68_P22483661	chr3:122321647-122321691	NM_001114665:917	Fnbp1l	INSIDE	1.844	6.922	969.79	6713.12	12.762	832.67	10626.89
A_68_P23261234	chr4:122866488-122866532	NM_174998:5764	Hpcal4	INSIDE	1.844	7.354	10025.79	73731.62	13.561	6913.90	93759.12
A_68_P23373724	chr4:142752116-142752160	NM_001081355:50474	Prdm2	INSIDE	1.844	3.720	941.81	3503.25	6.859	847.18	5811.11
A_68_P31162032	chr17:36116207-36116251	NR_028516:-260	Prr3	PROMOTER	1.844	4.839	2099.54	10159.79	8.921	1578.09	14077.99
A_68_P25103254	chr7:54387461-54387505	NM_001163565:486	Ptpn5	INSIDE	1.844	3.412	2019.97	6892.19	6.290	1577.30	9921.40
A_68_P26574053	chr9:62986483-62986527	NM_172446:8283	Skor1	INSIDE	1.844	6.491	392.52	2547.85	11.969	308.45	3691.74
A_68_P21844247	chr2:168760922-168760966	NM_009564:20143	Zfp64	INSIDE	1.844	7.758	353.32	2740.99	14.308	325.64	4659.13
A_68_P32565200	chrX:98892529-98892573	ENSMUST00000073812:-5361		PROMOTER	1.844	7.736	2925.10	22628.70	14.269	1541.65	21997.32
A_68_P31939711	chr19:7496090-7496134	NM_175381:3998	2700081O15Rik	INSIDE	1.843	5.555	2835.16	15749.15	10.237	1880.48	19250.76
A_68_P26073617	chr8:96334994-96335038	NM_001113384:279	Gnao1	INSIDE	1.843	6.583	10465.44	68894.13	12.130	7446.55	90329.10
A_68_P26258433	chr8:129118351-129118402	NM_001164598:-1040	Irf2bp2	PROMOTER	1.843	3.789	2286.39	8663.45	6.982	1790.20	12499.77

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31777744	chr18:65047479-65047523	NM_001114386:91	Nedd4l	INSIDE	1.843	10.346	942.70	9753.45	19.064	714.87	13628.62
A_68_P28457438	chr12:57634665-57634709	NM_001146198:1407	Nkx2-1	INSIDE	1.843	2.491	2084.61	5193.37	4.591	1654.48	7596.10
A_68_P21820797	chr2:164794239-164794283	NM_020333:773	Slc12a5	INSIDE	1.843	2.128	874.21	1860.62	3.922	698.46	2739.65
A_68_P29718152	chr14:73952682-73952726	NM_011506:112	Sucla2	INSIDE	1.843	4.831	1652.03	7980.50	8.905	1393.34	12407.05
A_68_P32906197	A_68_P32906197			Unknown	1.843	5.241	235.53	1234.33	9.660	181.13	1749.76
A_68_P23093082	chr4:88584489-88584533			Unknown	1.843	2.136	260.76	556.96	3.937	258.24	1016.83
A_68_P23253636	chr4:120527346-120527390	ENSMUST00000132895:-52		PROMOTER	1.843	5.879	13179.14	77479.07	10.837	9680.76	104913.40
A_68_P24004680	chr5:115017431-115017475	NM_001004180:-807	BC057022	PROMOTER	1.842	14.251	1361.17	19397.40	26.247	916.41	24053.55
A_68_P24388784	chr6:40385730-40385774	NM_175528:380	E330009J07Rik	INSIDE	1.842	8.401	5482.20	46054.93	15.474	4148.33	64192.08
A_68_P26554373	chr9:59464987-59465031	NM_001205239:-82	Parp6	PROMOTER	1.842	4.992	752.76	3758.08	9.197	605.13	5565.22
A_68_P21556050	chr2:116946481-116946525	NM_033524:-683	Spred1	PROMOTER	1.842	3.294	4864.40	16025.06	6.069	4099.83	24880.16
A_68_P26143096	chr8:109620241-109620285	NM_009353:183	Terf2	INSIDE	1.842	7.143	4769.95	34073.04	13.156	3569.45	46958.07
A_68_P29385917	chr14:8624251-8624295	ENSMUST00000081331:-107		DIVERGENT_PROMOTER	1.842	2.171	1122.88	2438.04	4.000	1068.56	4274.30
A_68_P26863467	chr9:117781995-117782039	ENSMUST00000126482:-245		PROMOTER	1.841	2.890	892.04	2577.83	5.319	690.12	3670.96
A_68_P20897790	chr1:186669470-186669514	NM_133684:234	Mosc2	INSIDE	1.840	1.853	1126.79	2088.49	3.410	827.00	2819.66
A_68_P27168078	chr10:58786437-58786481	NM_011030:415	P4ha1	INSIDE	1.840	4.803	4662.90	22393.81	8.836	3461.32	30584.71
A_68_P20740950	chr1:157820522-157820566	NM_001039184:-159	Cep350	PROMOTER	1.839	2.129	1799.19	3830.65	3.916	1451.01	5682.19
A_68_P25661493	chr8:12431257-12431301	NR_027975:45508	Gm5607	INSIDE	1.839	6.119	16899.96	103403.30	11.255	12229.55	137644.50
A_68_P32137222	chr19:45309238-45309283	NM_010691:466	Lbx1	INSIDE	1.839	4.671	1595.40	7451.81	8.589	1245.19	10695.25
A_68_P28086889	chr11:103611261-103611305	NM_011719:-147	Wnt9b	PROMOTER	1.839	4.097	1081.37	4430.58	7.536	805.24	6068.44
A_68_P25727484	chr8:26629202-26629246	NM_001079908:-19	Fgfr1	PROMOTER	1.838	2.463	1456.02	3585.62	4.527	1219.57	5521.00
A_68_P30547082	chr16:11253796-11253840	NM_001130008:600	Gspt1	INSIDE	1.838	1.881	1209.07	2273.78	3.456	1042.67	3603.49
A_68_P31715736	chr18:54022224-54022268	NM_152809:480	Csnk1g3	INSIDE	1.837	4.968	577.16	2867.29	9.127	430.82	3931.94
A_68_P24004046	chr5:114894276-114894320	NM_023556:-16	Mvk	DIVERGENT_PROMOTER	1.837	4.580	511.99	2345.05	8.414	406.64	3421.63
A_68_P25088136	chr7:51808933-51808977	NM_009473:339	Nr1h2	INSIDE	1.837	5.913	15841.82	93679.72	10.861	11014.63	119635.30
A_68_P26017663	chr8:86545319-86545363	NM_028877:-32	Palm3	DIVERGENT_PROMOTER	1.837	4.553	2619.26	11926.44	8.366	2019.89	16899.13
A_68_P29699987	chr14:70606016-70606060	NM_011366:1406	Sorbs3	INSIDE	1.837	4.285	2648.09	11346.76	7.872	2086.17	16422.34
A_68_P25017170	chr7:28193438-28193482	NM_032610:38148	Spnb4	INSIDE	1.837	3.254	1617.69	5263.61	5.977	1239.79	7410.37
A_68_P24671729	chr6:97155626-97155670	NM_001111106:-12	Uba3	DIVERGENT_PROMOTER	1.837	4.483	7712.25	34570.24	8.234	5398.68	44452.74
A_68_P21664157	chr2:136504412-136504456			Unknown	1.837	7.495	4216.07	31601.16	13.766	2972.39	40917.96
A_68_P20087502	chr1:23263626-23263674	ENSMUST00000097807:-405		PROMOTER	1.837	2.686	714.35	1918.87	4.933	620.39	3060.58
A_68_P26820784	chr9:109778541-109778586	NM_007658:481	Cdc25a	INSIDE	1.836	7.655	2446.19	18725.75	14.054	1806.42	25386.49
A_68_P28221329	chr12:8309070-8309114	NM_013527:-332	Gdf7	PROMOTER	1.836	2.722	5774.15	15716.10	4.998	4784.64	23914.52
A_68_P23590298	chr5:33995400-33995444	NM_009193:-467	Slbp	PROMOTER	1.836	2.597	4361.04	11323.66	4.766	3399.33	16202.53
A_68_P26494143	chr9:48643240-48643284	NM_001033324:788	Zbtb16	INSIDE	1.836	5.724	2309.58	13219.75	10.510	1649.43	17335.96
A_68_P24111498	chr5:134575433-134575477	NM_030719:-163	Gatsl2	PROMOTER	1.835	4.963	1362.28	6761.22	9.107	1124.35	10239.46
A_68_P25095389	chr7:53088549-53088593	NM_008172:33481	Grin2d	INSIDE	1.835	6.204	1118.06	6936.44	11.385	875.81	9971.39
A_68_P23264212	chr4:123341892-123341936	NM_001199136:19689	Macf1	INSIDE	1.835	6.225	2756.08	17155.80	11.422	2142.75	24474.07
A_68_P27080350	chr10:39452886-39452930	NM_011264:943	Rev3l	INSIDE	1.835	9.042	2510.01	22694.51	16.596	1771.06	29392.16
A_68_P27504343	chr10:121023890-121023934	NM_019786:-62	Tbk1	PROMOTER	1.835	6.046	1165.23	7045.24	11.095	1100.61	12211.23
A_68_P32016047	chr19:23210802-23210846	NM_010638:-4891	Klf9	PROMOTER	1.834	3.797	3494.13	13267.89	6.963	2747.09	19127.36
A_68_P24973639	chr7:13507675-13507719	NM_009095:37	Rps5	INSIDE	1.834	2.127	320.23	681.01	3.899	316.64	1234.64
A_68_P31560903	chr18:24761642-24761686	NM_139143:654	Slc39a6	INSIDE	1.834	2.435	2444.17	5951.24	4.466	2013.51	8992.61
A_68_P28752030	chr12:113959942-113959986	NM_001024602:-420	AW555464	PROMOTER	1.833	5.367	1685.78	9047.25	9.838	1290.79	12699.32
A_68_P21897030	chr2:179177570-179177614	NM_009867:410	Cdh4	INSIDE	1.833	3.684	2559.17	9428.91	6.755	2105.20	14221.06
A_68_P20437267	chr1:92500071-92500115	NM_133805:93	Cops8	INSIDE	1.833	5.807	2421.48	14062.52	10.645	1968.22	20952.55
A_68_P29445598	chr14:21001028-21001072	NM_021542:-46	Kcnk5	PROMOTER	1.833	3.715	4890.28	18167.01	6.809	3684.25	25086.54
A_68_P26818267	chr9:108998137-108998181	NM_172775:209	Plxnb1	INSIDE	1.833	3.745	978.86	3665.46	6.864	845.62	5804.39
A_68_P32143181	chr19:46392296-46392341	NM_028627:9328	Psd	INSIDE	1.833	2.663	1490.81	3969.84	4.881	1320.65	6445.94
A_68_P31791603	chr18:67550248-67550292	NM_026473:-114	Tubb6	PROMOTER	1.833	2.112	1364.48	2881.84	3.872	1120.72	4339.74
A_68_P30605892	chr16:23988103-23988147	NM_009744:574	Bcl6	INSIDE	1.832	5.444	3908.90	21278.28	9.974	3111.28	31031.68

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31600224	chr18:32070540-32070584	NM_026006:995	Sft2d3	INSIDE	1.832	5.139	2574.66	13231.95	9.415	2098.93	19762.36
A_68_P21017264	chr2:13495981-13496025	NM_011701:65	Vim	INSIDE	1.832	3.783	3082.57	11659.97	6.931	2498.75	17319.85
A_68_P31022093	chr17:6256852-6256896	ENSMUST00000121576:2972		DOWNSTREAM	1.832	3.733	1974.82	7371.73	6.840	1596.63	10920.47
A_68_P21115867	chr2:32391280-32391324	NM_153560:424	Fam102a	INSIDE	1.831	2.476	1103.59	2732.88	4.533	852.12	3863.05
A_68_P24611767	chr6:86683275-86683319	NM_011818:76	Gmcl1	INSIDE	1.831	6.282	6492.21	40784.11	11.502	4673.24	53751.74
A_68_P21093574	chr2:28695671-28695715	NM_001166033:188	Gtf3c4	INSIDE	1.831	6.435	1088.97	7007.60	11.785	913.34	10763.79
A_68_P29117527	chr13:69878894-69878938	NM_001145162:-141	Ube2ql1	PROMOTER	1.831	1.454	759.42	1103.94	2.661	644.53	1715.34
A_68_P23880187	chr5:90311691-90311735	NM_001081401:647	Adamts3	INSIDE	1.830	5.079	4130.18	20975.32	9.291	3425.03	31823.61
A_68_P30490425	chr15:101054602-101054646	NM_019518:-13	Grasp	PROMOTER	1.830	1.605	841.61	1350.63	2.937	635.77	1867.57
A_68_P21339341	chr2:74591156-74591200	NM_010467:-9858	Hoxd1	PROMOTER	1.830	4.738	3235.33	15329.05	8.673	2385.13	20685.77
A_68_P23399812	chr4:148681667-148681711	NM_207682:119	Kif1b	INSIDE	1.830	4.570	1413.26	6458.18	8.364	1189.26	9946.59
A_68_P25411827	chr7:117266477-117266521	NM_009516:926	Wee1	INSIDE	1.830	1.663	628.36	1044.80	3.043	619.02	1883.92
A_68_P20611349	chr1:132613579-132613625	NM_178691:-301	Yod1	DIVERGENT_PROMOTER	1.830	2.158	504.55	1088.79	3.949	468.83	1851.55
A_68_P20720544	chr1:154247140-154247184	NM_177756:166	Glt25d2	INSIDE	1.829	2.208	4633.39	10228.90	4.038	3755.72	15165.27
A_68_P29023967	chr13:49311401-49311447	NM_026738:-29	1110007C09Rik	PROMOTER	1.828	3.956	6255.04	24744.55	7.232	4536.90	32809.15
A_68_P26890105	chr9:122478146-122478190	NR_015610:-3450	9530059O14Rik	PROMOTER	1.828	3.077	1268.86	3904.14	5.625	1337.99	7526.78
A_68_P20351513	chr1:74998432-74998476	NM_010544:-229	Ihh	PROMOTER	1.828	1.985	2593.05	5147.28	3.629	2305.65	8366.79
A_68_P30295269	chr15:66800435-66800479	NM_008681:747	Ndrg1	INSIDE	1.828	6.584	2811.46	18509.54	12.036	2244.93	27019.44
A_68_P24213704	chr6:5955887-5955931	NM_001191023:280270	Dync1i1	INSIDE	1.827	3.203	1241.53	3976.49	5.851	992.91	5809.75
A_68_P21420369	chr2:90894125-90894169	NM_008948:-26	Psmc3	PROMOTER	1.827	5.506	33165.50	182611.90	10.061	22661.42	227992.10
A_68_P20411724	chr1:88255322-88255366	NR_002851:-2442	Snord82	PROMOTER	1.827	5.464	1772.42	9685.24	9.982	1286.89	12845.70
A_68_P23819150	chr5:77403737-77403781	NM_025691:33	Srp72	INSIDE	1.827	5.143	3782.81	19453.76	9.396	2820.82	26505.70
A_68_P24160101	chr5:144984767-144984811	NM_027410:-341	Tecpr1	PROMOTER	1.827	1.830	1178.84	2157.15	3.343	846.77	2831.13
A_68_P24979381	chr7:16646861-16646906			Unknown	1.827	4.435	3850.42	17074.98	8.102	2834.25	22963.00
A_68_P23797913	chr5:73883146-73883190	NM_001190733:904	Dcun1d4	INSIDE	1.826	10.139	17685.04	179306.30	18.515	10597.88	196224.10
A_68_P27921465	chr11:74424335-74424379	NM_001013784:-8750	E130309D14Rik	PROMOTER	1.826	5.392	1636.03	8821.58	9.847	1314.62	12944.86
A_68_P24171749	chr5:147887960-147888004	NM_080795:166	Lnx2	INSIDE	1.826	3.175	1701.57	5403.14	5.797	1544.24	8952.35
A_68_P26044646	chr8:91549828-91549872	NM_021390:18211	Sall1	DOWNSTREAM	1.826	1.816	777.09	1411.38	3.317	681.97	2261.82
A_68_P28078909	chr11:102180488-102180532	NM_011551:-100	Ubtf	PROMOTER	1.826	2.132	552.33	1177.68	3.893	399.39	1554.76
A_68_P27228617	chr10:69707740-69707784	NM_025807:-261	Slc16a9	PROMOTER	1.825	3.012	3026.06	9114.75	5.497	2482.91	13648.79
A_68_P23444287	chr5:3341583-3341627	NM_009873:-2707	Cdk6	PROMOTER	1.824	3.467	2545.92	8825.46	6.323	1807.56	11428.91
A_68_P29053522	chr13:55254151-55254195	NM_008011:-6	Fgfr4	PROMOTER	1.824	5.512	1658.26	9140.76	10.054	1504.20	15122.59
A_68_P20187367	chr1:43220695-43220739	NM_010212:90	Fhl2	INSIDE	1.824	6.556	1156.88	7584.06	11.958	1018.56	12180.28
A_68_P25010202	chr7:26180987-26181031	NM_010719:-2	Lipe	PROMOTER	1.824	3.873	4065.25	15743.27	7.063	3161.08	22325.43
A_68_P27171931	chr10:59465553-59465597	NM_026937:22	Ascc1	INSIDE	1.823	3.303	1913.76	6322.08	6.023	1652.32	9952.06
A_68_P32567806	chrX:99447101-99447145	NM_007709:-14	Cited1	PROMOTER	1.823	2.299	570.23	1310.75	4.190	323.08	1353.75
A_68_P32140683	chr19:45890581-45890625	NM_030716:-309	Kcnip2	PROMOTER	1.823	1.932	2746.60	5307.61	3.524	2147.02	7565.05
A_68_P21418380	chr2:90519239-90519283	NM_021512:1889	Nup160	INSIDE	1.823	5.490	7728.86	42429.44	10.009	6169.66	61751.11
A_68_P30489504	chr15:100908526-100908570	AK078004:-921		PROMOTER	1.823	1.626	3698.21	6011.74	2.964	2761.17	8183.88
A_68_P32572442	chrX:100551806-100551850	NM_009767:14	Chic1	INSIDE	1.822	3.938	3190.05	12563.39	7.174	1466.11	10517.46
A_68_P22319359	chr3:89234506-89234550	NM_026869:-230	Pygo2	PROMOTER	1.822	4.307	2831.88	12197.24	7.846	2355.22	18479.47
A_68_P27468929	chr10:114752147-114752191	NM_024454:479	Rab21	INSIDE	1.822	1.708	878.80	1500.72	3.111	731.83	2276.69
A_68_P31929627	chr19:5602038-5602082	NM_026616:188	Rnaseh2c	INSIDE	1.822	5.312	2264.08	12027.24	9.679	1871.49	18114.83
A_68_P26344894	chr9:20780852-20780896	NM_010333:363	S1pr2	INSIDE	1.822	15.703	5257.87	82562.47	28.611	3131.07	89583.18
A_68_P31097620	chr17:24626114-24626158	NM_027937:409	Caskin1	INSIDE	1.821	1.379	1840.28	2537.41	2.510	1442.13	3620.09
A_68_P21497226	chr2:105744559-105744603	NM_023876:77	Elp4	INSIDE	1.821	4.077	3355.27	13680.51	7.425	2790.48	20720.57
A_68_P23314731	chr4:132478927-132478977	NM_001163792:-486	Fam76a	PROMOTER	1.821	2.349	1010.77	2374.41	4.277	696.91	2980.48
A_68_P28066375	chr11:100006570-100006614	NM_008471:641	Krt19	INSIDE	1.821	2.693	5241.41	14114.38	4.905	4115.85	20188.17
A_68_P31336379	chr17:72131880-72131924	NM_030179:616	Clip4	INSIDE	1.820	4.744	765.70	3632.43	8.635	671.28	5796.46
A_68_P27756942	chr11:44432030-44432075	NM_007897:417	Ebf1	INSIDE	1.820	1.507	645.68	973.03	2.742	504.33	1383.01
A_68_P23250319	chr4:119941839-119941885	NM_194060:18004	Foxo6	INSIDE	1.820	3.106	574.76	1785.39	5.655	460.56	2604.27

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P24064307	chr5:125507269-125507313	NM_011424:152294	Ncor2	INSIDE	1.820	5.340	9566.43	51080.29	9.717	7206.32	70024.62
A_68_P24771681	chr6:115494875-115494919	NM_199033:175	Tsen2	INSIDE	1.820	7.577	2438.08	18473.32	13.787	1654.35	22808.57
A_68_P24152591	chr5:143105523-143105567	NM_178398:7	Wipi2	INSIDE	1.820	3.101	1127.27	3495.87	5.644	958.11	5407.37
A_68_P22630575	chr3:148652818-148652862	ENSMUST00000098518:-560		PROMOTER	1.820	9.814	1470.88	14435.63	17.863	1052.46	18800.46
A_68_P20726280	chr1:155180208-155180252	NM_010683:-314	Lamc1	PROMOTER	1.819	7.614	27733.70	211155.70	13.851	15482.40	214448.20
A_68_P30363283	chr15:78765483-78765527	NM_133800:142	Nol12	INSIDE	1.819	3.125	1896.06	5924.42	5.685	1496.31	8506.16
A_68_P28442990	chr12:54808173-54808232	NM_013780:458539	Npas3	INSIDE	1.819	5.224	899.58	4699.41	9.504	716.61	6810.66
A_68_P25011329	chr7:26472470-26472514	NM_011577:472	Tgfb1	INSIDE	1.819	2.718	5512.94	14984.39	4.943	4060.73	20072.39
A_68_P27630622	chr11:20149303-20149348	NM_172260:102	Cep68	INSIDE	1.818	6.231	2082.62	12977.22	11.331	1861.11	21088.80
A_68_P32378028	chrX:49034553-49034597	NM_015819:-920	Hs6st2	PROMOTER	1.818	2.100	1353.54	2842.92	3.817	739.84	2824.33
A_68_P31130464	chr17:30025085-30025129	NM_001081160:-279	Mdga1	PROMOTER	1.818	4.836	2874.13	13899.56	8.792	2325.88	20449.59
A_68_P28449264	chr12:55896516-55896560	NM_026998:111	Snx6	INSIDE	1.818	4.739	1566.84	7425.23	8.616	1292.67	11137.82
A_68_P29080191	chr13:59658571-59658615	NM_023328:88	Agtpbp1	INSIDE	1.817	6.266	4305.05	26975.86	11.388	3358.48	38245.19
A_68_P20405120	chr1:84692097-84692141	NM_152915:678	Dner	INSIDE	1.817	2.089	1042.51	2177.44	3.794	810.47	3075.12
A_68_P21345223	chr2:75497311-75497355	NR_033513:-14	Gm6793	PROMOTER	1.817	3.214	715.56	2299.70	5.840	502.90	2936.75
A_68_P31412114	chr17:86086928-86086972	NM_011380:644	Six2	INSIDE	1.817	4.305	1547.01	6659.82	7.824	1263.46	9885.38
A_68_P24134133	chr5:139676870-139676914	NM_024451:269	Sun1	INSIDE	1.817	1.607	767.61	1233.68	2.920	1083.62	3164.28
A_68_P29024152	chr13:49343166-49343210	NM_025491:344	Susd3	INSIDE	1.817	1.837	1441.29	2648.13	3.338	1207.12	4029.69
A_68_P23196094	chr4:108132526-108132570	NM_175472:518	Zcchc11	INSIDE	1.817	10.177	5197.71	52899.47	18.496	3681.07	68086.84
A_68_P23201928	chr4:109330089-109330133	NM_007671:7867	Cdkn2c	DOWNSTREAM	1.816	2.840	954.42	2710.40	5.157	785.33	4050.01
A_68_P27163123	chr10:57786395-57786439	NM_026148:203	Lims1	INSIDE	1.816	4.775	3182.08	15193.93	8.672	2345.80	20343.02
A_68_P24053482	chr5:123464905-123464949	NM_175423:-156	Orai1	PROMOTER	1.816	2.677	906.36	2426.00	4.861	846.86	4116.84
A_68_P22317129	chr3:88894411-88894455	NM_001083808:-479	Rusc1	PROMOTER	1.816	3.505	2746.83	9627.80	6.364	2121.72	13503.65
A_68_P24631649	chr6:90275213-90275257	NM_027928:-55	Chst13	DIVERGENT_PROMOTER	1.815	1.643	880.04	1445.53	2.982	709.33	2115.11
A_68_P21909702	chr2:181022305-181022349	NM_198169:345	Gmeb2	INSIDE	1.815	1.560	1875.56	2926.55	2.832	1427.15	4041.51
A_68_P24784006	chr6:117866996-117867040	NM_001166427:-293	Hnrnpf	PROMOTER	1.815	3.705	2777.20	10289.67	6.726	2018.60	13576.17
A_68_P26346115	chr9:21043701-21043745	NM_001110305:54	Keap1	INSIDE	1.815	1.799	2047.85	3683.26	3.264	1688.13	5510.34
A_68_P24764867	chr6:114233070-114233114	NM_178703:464	Slc6a1	INSIDE	1.815	2.185	1964.99	4292.57	3.964	1703.19	6751.78
A_68_P26804662	chr9:106587823-106587867	NM_011573:154	Tex264	INSIDE	1.815	2.861	632.52	1809.56	5.192	463.35	2405.94
A_68_P26232970	chr8:124900378-124900422	NM_001029993:-115	Zc3h18	PROMOTER	1.815	4.101	833.27	3417.54	7.443	688.30	5123.13
A_68_P28050431	chr11:97276806-97276850	ENSMUST00000121799:-18		PROMOTER	1.815	3.825	2894.65	11072.80	6.942	2139.59	14852.50
A_68_P30361566	chr15:78503626-78503670	NM_183141:44895	Elfn2	INSIDE	1.814	6.596	1520.94	10032.69	11.964	1350.77	16160.51
A_68_P25644699	chr8:9770615-9770659	NM_173446:387	Fam155a	INSIDE	1.814	5.687	3346.03	19027.70	10.313	2684.47	27685.74
A_68_P31311922	chr17:67703725-67703769	NM_008984:53	Ptprm	INSIDE	1.814	7.137	1696.55	12107.99	12.949	1365.94	17687.68
A_68_P23457345	chr5:5749151-5749195	NM_027399:145	Steap1	INSIDE	1.814	5.963	5147.22	30691.20	10.818	4433.72	47962.54
A_68_P24383759	chr6:39523831-39523875	NM_178873:-22	Adck2	PROMOTER	1.813	3.292	2014.29	6630.83	5.969	1485.03	8863.72
A_68_P22317617	chr3:88973343-88973387	NM_001163432:4638	Clk2	INSIDE	1.813	7.739	6628.02	51296.66	14.031	4272.64	59947.78
A_68_P28396964	chr12:45311296-45311340	NM_013760:-263	Dnajb9	PROMOTER	1.813	1.965	1056.58	2076.00	3.562	892.34	3178.07
A_68_P21722817	chr2:147019650-147019694	NM_001077632:-7534	Nkx2-2	PROMOTER	1.813	2.371	1751.40	4151.79	4.299	1341.88	5768.45
A_68_P32183826	chr19:53751832-53751876	NM_001170847:59	Rbm20	INSIDE	1.813	6.095	2886.04	17589.61	11.050	2309.40	25517.88
A_68_P22128834	chr3:51080739-51080783	NM_023502:49149	Elf2	INSIDE	1.812	5.068	3293.52	16690.08	9.184	2567.56	23580.83
A_68_P32016039	chr19:23209957-23210001	NM_010638:-5737	Klf9	PROMOTER	1.812	4.846	4436.94	21499.29	8.780	3414.58	29979.51
A_68_P23544552	chr5:24414202-24414246	NM_001170555:103	Prkag2	INSIDE	1.812	7.118	8413.99	59892.39	12.900	7495.71	96696.36
A_68_P27833411	chr11:58717772-58717816	NM_011758:-67	Zfp39	PROMOTER	1.812	5.846	8399.74	49106.03	10.592	6079.29	64392.64
A_68_P29703311	A_68_P29703311			Unknown	1.812	7.959	3332.17	26519.53	14.422	2490.01	35910.79
A_68_P31019376	A_68_P31019376			Unknown	1.812	3.074	1463.58	4499.53	5.571	1156.81	6444.19
A_68_P31961511	chr19:12670617-12670661	NR_015503:418	A330040F15Rik	INSIDE	1.811	6.470	2292.64	14834.32	11.717	1846.29	21632.64
A_68_P31790565	chr18:67365128-67365172	NM_024190:138	Chmp1b	INSIDE	1.811	3.225	4755.01	15334.68	5.839	3568.63	20838.37
A_68_P32464984	chrX:71070091-71070135	NM_001029868:196	Pdzd4	INSIDE	1.811	4.937	765.24	3778.22	8.939	576.34	5152.02
A_68_P30927986	chr16:85173922-85173966	NM_001198823:8	App	INSIDE	1.810	4.246	1445.59	6137.72	7.684	1257.78	9665.34
A_68_P29699040	chr14:70480133-70480177	NM_018781:2903	Egr3	DOWNSTREAM	1.810	6.388	3054.13	19508.73	11.561	2484.02	28717.76

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27274519	chr10:77945016-77945060	ENSMUST00000069431:5549		DOWNSTREAM	1.810	1.673	1145.55	1916.89	3.028	1011.16	3061.94
A_68_P28684687	chr12:102146364-102146408	NM_001177674:-8652	Gpr68	PROMOTER	1.809	3.695	1650.80	6100.38	6.684	1533.07	10246.92
A_68_P21339240	chr2:74578542-74578586	NM_010468:28515	Hoxd3	INSIDE	1.809	2.036	1647.74	3355.21	3.683	1258.03	4633.65
A_68_P23094194	chr4:88783218-88783262	NM_024433:-33	Mtap	PROMOTER	1.809	3.549	5045.36	17904.92	6.418	3626.40	23275.54
A_68_P20134295	chr1:33727422-33727466	NR_033199:776	1700001G17Rik	INSIDE	1.808	8.194	2704.50	22161.41	14.814	1913.03	28339.87
A_68_P30476326	chr15:98593248-98593292	NM_007478:279	Arf3	INSIDE	1.808	1.391	2235.94	3111.08	2.516	1636.95	4118.23
A_68_P32260334	chrX:11664151-11664195	NM_029510:-6493	Bcor	PROMOTER	1.808	2.229	1356.47	3024.10	4.031	815.61	3287.47
A_68_P22338541	chr3:94168285-94168329	NM_001136117:1941	C2cd4d	INSIDE	1.808	5.376	5230.63	28118.47	9.722	4155.52	40398.62
A_68_P28990871	chr13:43655098-43655142	NM_001081059:440	Ccdc90a	INSIDE	1.808	4.884	2329.94	11379.26	8.831	1930.50	17047.94
A_68_P25954496	chr8:73376577-73376621	NM_032397:4309	Kcnn1	INSIDE	1.808	5.381	1881.59	10125.04	9.727	1305.40	12698.01
A_68_P26985109	chr10:19868572-19868616	NM_001198635:-131	Mtap7	PROMOTER	1.808	5.214	1052.75	5489.10	9.426	892.38	8411.77
A_68_P30000055	chr15:8395316-8395364	NM_027707:-877	Nipbl	PROMOTER	1.807	10.334	11522.38	119074.30	18.676	6922.61	129285.00
A_68_P27965931	chr11:82202507-82202551	NM_023438:127	Tmem132e	INSIDE	1.807	5.438	5787.76	31475.98	9.825	4556.78	44770.51
A_68_P24638016	chr6:91235548-91235592			Unknown	1.807	3.859	1017.61	3927.24	6.973	821.14	5725.42
A_68_P24992765	chr7:19927675-19927719	NM_001127324:-2723	Ercc1	PROMOTER	1.806	8.013	991.82	7947.64	14.469	840.64	12163.27
A_68_P21765995	chr2:155340656-155340700	NM_144786:-96	Ggt7	DIVERGENT_PROMOTER	1.806	2.951	1077.94	3180.74	5.328	842.32	4487.81
A_68_P30556199	chr16:13256418-13256462	NM_001122667:-133	Mkl2	PROMOTER	1.806	2.014	1559.34	3140.77	3.637	1310.82	4767.44
A_68_P32150744	chr19:47653811-47653855	NM_001164639:-676	Slk	PROMOTER	1.806	1.474	1101.74	1624.42	2.663	969.80	2583.01
A_68_P25502305	chr7:133942445-133942489	NM_001177307:226	Aldoa	INSIDE	1.805	2.341	2242.61	5249.11	4.224	1800.05	7603.52
A_68_P22085575	chr3:41369640-41369684	NM_001130186:861	Phf17	INSIDE	1.805	7.734	1394.73	10786.45	13.960	1101.00	15370.41
A_68_P30346613	chr15:76011583-76011627	NM_201394:14536	Plec	INSIDE	1.805	1.900	565.89	1075.26	3.429	411.97	1412.72
A_68_P28426162	chr12:51750316-51750360	NM_008858:-128	Prkd1	PROMOTER	1.804	2.988	3996.06	11938.92	5.389	3237.18	17445.42
A_68_P27635752	chr11:21139299-21139343	NM_139061:429	Vps54	INSIDE	1.804	4.071	1720.94	7005.72	7.344	1344.29	9872.08
A_68_P25581873	chr7:147222902-147222946	NM_027201:635	Zfp511	INSIDE	1.804	2.157	2142.84	4623.02	3.891	1510.89	5879.04
A_68_P31782005	chr18:65740650-65740694	NM_207255:789	Zfp532	INSIDE	1.804	4.365	4337.80	18933.93	7.874	3516.66	27688.88
A_68_P33012150	chr9_random:53992-54036	NR_027950:-678	4930526I15Rik	PROMOTER	1.803	7.605	24634.84	187359.00	13.714	15139.21	207618.50
A_68_P27975235	chr11:83881690-83881734	NM_019819:147	Dusp14	INSIDE	1.803	2.054	1290.16	2649.80	3.702	1035.86	3834.90
A_68_P25910880	chr8:64070053-64070097	NM_001081390:311413	Palld	INSIDE	1.803	5.859	3203.60	18770.66	10.564	2389.29	25240.59
A_68_P26464017	chr9:43611785-43611829	NM_021424:59148	Pvrl1	INSIDE	1.803	5.219	1554.17	8111.24	9.408	1038.88	9773.69
A_68_P25576307	chr7:146374240-146374284	NM_021302:131	Stk32c	INSIDE	1.803	4.492	1127.51	5065.01	8.099	961.82	7790.11
A_68_P31124371	chr17:28938550-28938594	NM_001081315:502	Brpf3	INSIDE	1.802	6.412	13892.16	89073.98	11.552	9383.17	108395.60
A_68_P25780173	chr8:36558550-36558594	NM_026067:15	Eri1	INSIDE	1.802	2.449	747.61	1830.80	4.413	663.58	2928.45
A_68_P30246699	chr15:58046420-58046464	NM_026346:-9	Fbxo32	PROMOTER	1.802	1.596	1220.54	1947.77	2.876	1004.10	2888.22
A_68_P23392700	chr4:147525826-147525870	NM_001163704:186	Fbxo6	INSIDE	1.802	5.283	4542.00	23995.44	9.522	3913.81	37267.97
A_68_P21420493	chr2:90910689-90910733	NM_026721:-332	Slc39a13	PROMOTER	1.802	3.480	3319.90	11553.43	6.269	2783.38	17450.22
A_68_P21438071	chr2:93797315-93797359	NM_001145034:-79	Gm13889	PROMOTER	1.801	2.816	3220.82	9068.87	5.071	2565.75	13010.32
A_68_P31781218	chr18:65590541-65590585	NM_172833:-88	Malt1	PROMOTER	1.801	4.774	13185.43	62940.98	8.596	9108.70	78301.18
A_68_P21261140	chr2:60719287-60719331	NM_001141931:187	Rbms1	INSIDE	1.801	2.769	209.34	579.69	4.988	235.88	1176.47
A_68_P21580978	chr2:121275537-121275581	NM_011354:595	Serf2	INSIDE	1.801	2.582	3099.68	8003.43	4.651	2734.38	12717.10
A_68_P30605897	chr16:23988863-23988907	NM_009744:-186	Bcl6	PROMOTER	1.800	15.406	1820.78	28050.26	27.729	1472.85	40839.93
A_68_P29713892	chr14:73109778-73109822	NM_207636:10	Fndc3a	INSIDE	1.800	3.666	15386.09	56402.37	6.598	12880.93	84987.90
A_68_P31258174	chr17:56896255-56896299	NM_008738:677	Nrtn	INSIDE	1.800	9.627	1392.79	13407.73	17.330	1188.08	20589.48
A_68_P23999133	chr5:114064391-114064435	NM_008153:35987	Cmklr1	INSIDE	1.799	5.553	1505.92	8362.64	9.989	1033.77	10325.81
A_68_P31620539	chr18:36020271-36020315	NM_133687:30821	Cxxc5	INSIDE	1.799	4.958	1846.83	9156.90	8.922	1356.72	12104.51
A_68_P21278824	chr2:63936695-63936739	NM_021716:-647	Fign	PROMOTER	1.799	1.562	572.22	893.92	2.810	476.20	1338.03
A_68_P30349539	chr15:76462358-76462402	NM_183091:7979	Tonsl	INSIDE	1.799	6.542	8551.76	55942.93	11.767	6017.12	70801.82
A_68_P29257361	chr13:99161507-99161552	BC059100:739690		INSIDE	1.799	5.081	3273.53	16631.91	9.141	2534.57	23167.47
A_68_P24004989	chr5:115060757-115060801	NM_001004180:42519	BC057022	INSIDE	1.798	4.701	4257.35	20015.41	8.454	3149.22	26623.86
A_68_P24449229	chr6:52175914-52175958	NM_010456:1433	Hoxa9	INSIDE	1.798	1.819	1546.09	2811.78	3.269	1279.83	4184.40
A_68_P28236792	chr12:11157416-11157460	NM_173417:-259	Kcns3	PROMOTER	1.798	12.300	3004.88	36959.76	22.110	2237.03	49461.30
A_68_P32050808	chr19:29122130-29122174	NR_028360:180	1700018L02Rik	INSIDE	1.797	3.071	3532.99	10850.38	5.520	2811.40	15519.09

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27810090	chr11:54251929-54251973	NM_173753:270	Fnip1	INSIDE	1.797	3.055	1965.54	6005.08	5.491	1626.28	8930.19
A_68_P21765994	chr2:155340501-155340545	NM_144786:60	Ggt7	INSIDE	1.797	1.723	1515.62	2611.59	3.096	1202.00	3721.77
A_68_P31933357	chr19:6235648-6235692	NM_198168:170	Ppp2r5b	INSIDE	1.796	1.849	688.63	1273.17	3.320	592.64	1967.48
A_68_P22383780	chr3:102799614-102799658	NM_025679:-26	Sike1	PROMOTER	1.796	1.652	1622.33	2680.09	2.967	1345.94	3993.37
A_68_P21147548	chr2:38195289-38195333	ENSMUST00000133661:-1301		PROMOTER	1.796	2.717	1425.62	3873.62	4.880	1225.15	5978.96
A_68_P29656173	chr14:63174404-63174448	ENSMUST00000162987:-147		PROMOTER	1.796	1.704	6632.57	11303.29	3.060	4694.28	14364.54
A_68_P25708990	chr8:23170949-23170993	NM_183142:-221	Alg11	DIVERGENT_PROMOTER	1.795	2.373	2983.00	7078.50	4.259	2521.59	10738.91
A_68_P32117489	chr19:41921912-41921956	NM_177603:688	Frat2	INSIDE	1.795	3.395	963.77	3271.91	6.093	735.76	4482.62
A_68_P30139530	chr15:36539045-36539089	NM_008774:-338	Pabpc1	PROMOTER	1.795	1.615	1468.37	2370.92	2.898	1265.04	3665.54
A_68_P20800091	chr1:168339580-168339624	NM_001142948:357	Pogk	INSIDE	1.795	4.313	8825.38	38061.16	7.740	6802.34	52653.14
A_68_P21782725	chr2:158235581-158235625	NM_177658:14	Ralgapb	INSIDE	1.795	2.817	1325.13	3733.54	5.058	1159.90	5866.99
A_68_P25994476	chr8:81922795-81922839	NM_008539:551	Smad1	INSIDE	1.795	10.589	3319.82	35154.77	19.006	2493.42	47388.88
A_68_P31675573	chr18:46358367-46358411	NM_001170855:84	Trim36	INSIDE	1.795	2.018	1190.25	2402.41	3.623	1052.42	3813.30
A_68_P28613117	chr12:88289051-88289098	NM_173735:782	2310044G17Rik	INSIDE	1.794	4.048	1247.68	5050.33	7.262	971.94	7058.25
A_68_P20633265	chr1:136312273-136312317	NM_028320:251	Adipor1	INSIDE	1.794	4.207	10396.44	43740.06	7.547	7847.36	59223.02
A_68_P22899538	chr4:48292337-48292381	NM_029572:103	Erp44	INSIDE	1.794	2.440	5149.30	12565.52	4.377	3986.47	17447.60
A_68_P30478814	chr15:99054189-99054233	NM_010601:-1196	Kcnh3	PROMOTER	1.794	4.971	3105.74	15437.94	8.916	2434.66	21707.96
A_68_P28600848	chr12:86217110-86217154	NM_013589:313	Ltbp2	INSIDE	1.794	1.754	853.83	1497.77	3.146	705.49	2219.75
A_68_P32567492	chrX:99352458-99352502	NM_146235:-50	Ercc6l	PROMOTER	1.793	4.973	810.47	4030.48	8.915	463.28	4129.97
A_68_P22082256	chr3:40753573-40753617	NM_001040399:-958	Larp1b	PROMOTER	1.793	2.331	22714.34	52937.90	4.178	16691.41	69733.62
A_68_P28351016	chr12:35731926-35731970	NM_001014973:88	Snx13	INSIDE	1.793	5.061	1661.88	8411.34	9.077	1424.16	12927.00
A_68_P22345154	chr3:95491735-95491779	NM_144899:25	Adamtsl4	INSIDE	1.792	1.859	2073.84	3854.71	3.330	1714.80	5711.03
A_68_P25498532	chr7:133225682-133225726	NM_001101488:221	Gsg1l	INSIDE	1.792	5.769	15276.74	88131.47	10.340	11739.08	121378.90
A_68_P20778372	chr1:164478561-164478605	NM_144877:-106	Mettl13	PROMOTER	1.791	2.885	7977.41	23018.06	5.169	5991.19	30966.64
A_68_P25948621	chr8:72427093-72427137	NM_023312:-657	Ndufa13	PROMOTER	1.791	1.527	619.53	946.15	2.735	577.30	1579.17
A_68_P29682917	chr14:67690619-67690663	NM_001205188:668	Ppp2r2a	INSIDE	1.791	7.070	3368.81	23816.75	12.659	2318.52	29350.15
A_68_P32710882	chrX:139400446-139400490	NM_019496:803	Ammecr1	INSIDE	1.790	3.226	976.55	3150.72	5.775	511.66	2954.91
A_68_P28598112	chr12:85749605-85749649	NM_001026214:353	Entpd5	INSIDE	1.790	3.507	2023.75	7097.12	6.279	1689.57	10608.28
A_68_P27500779	chr10:120416497-120416541	NM_001081193:-132	Lemd3	PROMOTER	1.790	4.313	931.72	4018.41	7.721	825.94	6376.93
A_68_P22340919	chr3:94642155-94642199	NM_001165948:688	Pogz	INSIDE	1.790	7.624	1520.61	11592.56	13.646	1173.41	16012.30
A_68_P25092685	chr7:52622314-52622358	NM_029741:53	Ppfia3	INSIDE	1.790	3.630	1450.59	5264.91	6.498	1233.06	8011.86
A_68_P27277985	chr10:79100697-79100741	NM_001024539:-55	Shc2	PROMOTER	1.790	3.240	1741.42	5642.11	5.799	1450.86	8414.19
A_68_P24008929	chr5:115751222-115751266	NM_019682:-245	Dynll1	PROMOTER	1.789	4.209	2244.59	9447.12	7.528	1866.35	14049.56
A_68_P32386813	chrX:50622802-50622846	NM_001166365:158	Fam122b	INSIDE	1.789	8.506	5647.04	48031.03	15.218	2876.24	43771.99
A_68_P32457442	chrX:69520267-69520311	NM_017369:-228	Gabre	PROMOTER	1.789	4.370	3001.36	13115.06	7.817	2007.83	15694.92
A_68_P28029575	chr11:93747831-93747875	NM_134012:320	Mbtd1	INSIDE	1.789	4.285	2190.93	9388.97	7.668	1775.23	13611.80
A_68_P25588870	chr7:148633634-148633678	NR_034049:-1075	Snora52	PROMOTER	1.789	2.259	6061.79	13694.99	4.041	4450.07	17984.60
A_68_P26134826	chr8:108129362-108129406	NR_035492:-9981	Mir1966	PROMOTER	1.788	3.411	2337.21	7972.16	6.098	1612.29	9831.01
A_68_P23991577	chr5:112772027-112772071	NM_027323:12	Srrd	INSIDE	1.788	3.757	18048.04	67814.54	6.717	14956.85	100468.50
A_68_P25328173	chr7:100228372-100228416	NM_021427:6	Fam181b	INSIDE	1.787	2.659	1172.86	3119.18	4.753	871.74	4143.13
A_68_P29575892	chr14:47000105-47000149	NR_037981:928	Gm15217	INSIDE	1.787	3.607	2919.11	10529.17	6.446	2186.72	14096.10
A_68_P28067972	chr11:100275705-100275749	NM_176830:407	Leprel4	INSIDE	1.787	4.906	930.00	4562.88	8.768	870.89	7635.61
A_68_P27288382	chr10:80720130-80720174	NM_010768:-137	Matk	PROMOTER	1.787	7.778	2735.01	21273.82	13.898	2288.70	31808.01
A_68_P28748036	chr12:113368595-113368639	NR_029590:-474	Mir203	PROMOTER	1.787	2.450	281.02	688.43	4.378	193.24	845.98
A_68_P25948620	chr8:72427025-72427069	NM_023312:-589	Ndufa13	PROMOTER	1.787	3.236	714.39	2311.79	5.783	683.51	3952.85
A_68_P20421182	chr1:89904977-89905021	NM_001033291:128	Usp40	INSIDE	1.787	3.697	4393.92	16244.86	6.605	3280.38	21667.59
A_68_P31148785	chr17:33495528-33495572	NM_207541:273	Zfp81	INSIDE	1.787	2.112	3403.81	7188.31	3.773	2674.22	10090.12
A_68_P31561526	chr18:24868000-24868044	NM_175276:77	Fhod3	INSIDE	1.786	4.266	1651.68	7046.32	7.617	1352.02	10298.76
A_68_P30424721	chr15:89186360-89186404	NM_001115132:230	Ncaph2	INSIDE	1.786	4.363	3195.59	13942.59	7.793	2602.19	20277.78
A_68_P24872958	chr6:136467356-136467400	NM_019426:7	Atf7ip	INSIDE	1.785	3.282	2891.36	9490.11	5.858	2247.19	13163.42
A_68_P26825039	chr9:110558909-110558957	NM_028312:-74	Ccdc12	DIVERGENT_PROMOTER	1.785	1.894	1145.22	2168.99	3.380	928.34	3138.11

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P22301528	chr3:86028273-86028317	NM_001077687:-317	Lrba	PROMOTER	1.785	3.658	708.35	2591.21	6.529	653.27	4265.14
A_68_P24362057	chr6:35489865-35489909	NM_008098:2	Mtpn	INSIDE	1.785	3.996	2129.43	8508.36	7.134	1659.27	11837.30
A_68_P31098019	chr17:24687487-24687532	NM_013630:615	Pkd1	INSIDE	1.785	5.306	1287.64	6831.75	9.469	1086.78	10290.64
A_68_P25960292	chr8:74764393-74764437	NM_007456:384	Ap1m1	INSIDE	1.784	2.981	740.71	2207.94	5.317	583.61	3102.99
A_68_P24397660	chr6:42274774-42274818	NM_001113327:-157	Fam131b	PROMOTER	1.784	2.154	2777.70	5982.65	3.841	2513.41	9655.11
A_68_P24154219	chr5:143723667-143723712	NM_007984:1656	Fscn1	INSIDE	1.784	4.276	1532.87	6554.20	7.628	1125.17	8582.46
A_68_P28744403	chr12:112723947-112723992	NM_001033248:65	Gm266	INSIDE	1.784	1.381	2131.22	2942.41	2.463	1768.10	4355.31
A_68_P29863087	chr14:103381523-103381567	NM_177715:310	Kctd12	INSIDE	1.784	8.827	2400.30	21187.50	15.751	1800.82	28365.41
A_68_P21099263	chr2:29602898-29602942	NM_001039086:127681	Rapgef1	DOWNSTREAM	1.784	1.437	1080.70	1553.22	2.563	938.01	2404.52
A_68_P31412120	chr17:86087935-86087979	NM_011380:-362	Six2	PROMOTER	1.784	7.698	5465.70	42077.02	13.734	4681.46	64296.65
A_68_P21631241	chr2:130523070-130523114	NM_001081162:163	Slc4a11	INSIDE	1.784	2.805	856.46	2402.29	5.003	680.46	3404.16
A_68_P26581054	chr9:64129658-64129702	NM_025372:267	Tipin	INSIDE	1.784	1.772	3811.93	6754.17	3.161	3116.88	9853.57
A_68_P25940715	chr8:70586499-70586543	ENSMUST00000150169:-335		PROMOTER	1.784	5.329	693.49	3695.53	9.509	526.22	5003.90
A_68_P24000798	chr5:114359230-114359275	NM_011779:-537	Coro1c	PROMOTER	1.783	5.286	11332.47	59901.40	9.423	7656.87	72153.48
A_68_P25641012	chr8:9207827-9207871	NM_173446:563175	Fam155a	INSIDE	1.783	2.152	310.81	668.92	3.836	231.54	888.28
A_68_P29094155	chr13:63664480-63664524	NM_008957:2326	Ptch1	INSIDE	1.783	5.078	1136.97	5773.54	9.054	940.38	8514.46
A_68_P25032744	chr7:31435111-31435155	NM_133693:115	Rbm42	INSIDE	1.783	4.162	759.76	3161.83	7.420	589.95	4377.41
A_68_P21580976	chr2:121275325-121275369	NM_011354:383	Serf2	INSIDE	1.783	2.627	1183.49	3109.35	4.685	1067.15	4999.11
A_68_P25091507	chr7:52417775-52417819	NM_182993:-1494	Slc17a7	PROMOTER	1.783	4.040	3391.39	13699.88	7.203	2543.47	18320.64
A_68_P24766862	chr6:114688350-114688394	NM_028835:95230	Atg7	INSIDE	1.782	3.117	2619.62	8164.55	5.554	2153.76	11961.65
A_68_P31929035	chr19:5490695-5490739	NM_007687:262	Cfl1	INSIDE	1.782	3.659	3764.08	13772.99	6.520	2853.19	18602.65
A_68_P23416903	chr4:151532635-151532679	NM_008236:-319	Hes2	DIVERGENT_PROMOTER	1.782	2.676	1085.29	2904.61	4.769	811.53	3870.50
A_68_P22530177	chr3:130815462-130815506	NM_010703:2096	Lef1	INSIDE	1.782	3.664	2595.49	9508.91	6.530	2057.48	13436.06
A_68_P31774692	chr18:64500898-64500942	NM_194268:903	Onecut2	INSIDE	1.782	3.177	1989.72	6321.43	5.662	1432.33	8109.73
A_68_P26591323	chr9:65972506-65972550	NM_019727:165	Snx1	INSIDE	1.782	2.993	1149.29	3439.90	5.332	971.18	5178.63
A_68_P31197210	chr17:44914016-44914060	NM_178652:-81	Supt3h	PROMOTER	1.782	4.329	2694.77	11664.92	7.713	2128.74	16418.48
A_68_P27269640	chr10:77140522-77140570			Unknown	1.782	2.558	3658.89	9360.00	4.557	2742.95	12500.90
A_68_P22340674	chr3:94590393-94590437	NM_001037711:23	Cgn	INSIDE	1.781	2.740	3234.59	8862.34	4.881	2421.32	11818.44
A_68_P23873660	chr5:89149794-89149838	NM_026735:-79	Mobkl1a	PROMOTER	1.781	1.972	1492.65	2944.13	3.513	1281.13	4500.88
A_68_P27281785	chr10:79689246-79689290	NM_023431:-74	Mum1	PROMOTER	1.780	3.402	6975.63	23734.06	6.057	5170.10	31312.73
A_68_P23435277	chr4:154338248-154338292	NM_172990:29	Pank4	INSIDE	1.780	5.935	6193.36	36759.48	10.566	4696.39	49623.53
A_68_P21250385	chr2:58999390-58999434	NM_026361:506	Pkp4	INSIDE	1.780	4.497	4161.06	18710.84	8.005	2857.20	22872.33
A_68_P28159934	chr11:116403055-116403099	NM_173755:39685	Ube2o	INSIDE	1.780	3.415	1066.32	3641.22	6.080	893.63	5433.21
A_68_P30484704	chr15:100058837-100058881	NM_007497:569	Atf1	INSIDE	1.779	3.069	632.44	1941.20	5.461	547.45	2989.56
A_68_P23203774	chr4:109655335-109655379	NM_172296:4727	Dmrta2	INSIDE	1.779	4.383	3173.67	13908.76	7.797	2499.63	19489.75
A_68_P22722447	chr4:9771366-9771410	NM_013526:-130	Gdf6	PROMOTER	1.779	2.585	23523.29	60796.56	4.598	16395.60	75387.85
A_68_P20372363	chr1:78654178-78654222	NM_001001981:-199	Utp14b	PROMOTER	1.779	2.805	1095.37	3072.37	4.989	992.11	4949.18
A_68_P20880195	chr1:183141802-183141846	NM_145514:285	Wdr26	INSIDE	1.779	4.212	2162.58	9109.20	7.493	1734.85	12999.94
A_68_P31150957	chr17:34053104-34053148	NM_020625:6	Zbtb22	INSIDE	1.779	4.398	11456.48	50390.67	7.827	8771.91	68655.84
A_68_P25008269	chr7:25866719-25866763	NM_175477:4476	Zfp574	INSIDE	1.779	4.221	4048.08	17085.21	7.509	3275.89	24598.20
A_68_P26055737	chr8:93432164-93432208	NM_177224:79453	Chd9	INSIDE	1.778	5.839	1278.96	7467.43	10.384	1034.28	10739.74
A_68_P23365645	chr4:141279495-141279539	NM_001017966:-182	Ddi2	PROMOTER	1.778	2.405	1101.33	2649.11	4.276	961.04	4109.56
A_68_P28055686	chr11:98188438-98188482	NM_010895:2499	Neurod2	INSIDE	1.778	5.624	3157.40	17755.68	10.001	1993.02	19932.24
A_68_P28053984	chr11:97883326-97883370	NM_001159320:-3662	Cacnb1	PROMOTER	1.777	3.533	2587.31	9140.65	6.279	1866.76	11721.27
A_68_P28528483	chr12:72932910-72932958	NM_026102:870	Daam1	INSIDE	1.777	7.692	781.12	6008.10	13.668	536.03	7326.51
A_68_P25672261	chr8:14096967-14097011	NM_001145965:1114	Dlgap2	INSIDE	1.777	3.076	3873.43	11915.11	5.468	2879.39	15743.16
A_68_P29250236	chr13:98010968-98011012	NM_007930:-69	Enc1	PROMOTER	1.777	7.313	1585.24	11593.63	12.995	1275.24	16571.48
A_68_P21367543	chr2:79095483-79095527	NM_010576:-78	Itga4	PROMOTER	1.777	3.658	2017.49	7379.30	6.500	1621.43	10538.48
A_68_P22572454	chr3:138738598-138738642	NM_001040690:-457	Rap1gds1	PROMOTER	1.777	6.223	1452.24	9037.25	11.060	1227.37	13575.00
A_68_P24541704	chr6:72389176-72389220	NM_145569:354	Mat2a	INSIDE	1.776	3.581	1968.78	7050.07	6.361	1773.17	11279.90
A_68_P27568398	chr11:6316069-6316113	NM_008907:218	Ppia	INSIDE	1.776	4.454	3774.27	16809.61	7.911	3015.41	23855.94

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31791990	chr18:67624448-67624492	NM_144867:-32	Slmo1	PROMOTER	1.776	1.828	573.52	1048.66	3.248	617.54	2005.65
A_68_P20863553	chr1:180299131-180299175			Unknown	1.776	4.221	3754.06	15846.01	7.498	3098.90	23236.86
A_68_P24791280	chr6:119057361-119057405	NM_001159533:825	Cacna1c	INSIDE	1.775	3.638	2783.45	10125.32	6.457	2185.01	14109.12
A_68_P31565714	chr18:25645254-25645298	NM_001146292:267208	Celf4	INSIDE	1.775	2.149	1952.48	4194.93	3.813	1584.88	6043.79
A_68_P26504861	chr9:50467491-50467535	NM_145614:373	Dlat	INSIDE	1.775	3.414	2240.05	7647.12	6.059	1937.02	11735.53
A_68_P31333820	chr17:71660018-71660062	NM_145158:265	Emilin2	INSIDE	1.775	3.943	1298.83	5121.79	7.000	1128.92	7902.88
A_68_P30261330	chr15:60655945-60655989	NM_001162926:669	Fam84b	INSIDE	1.775	3.498	751.96	2630.19	6.210	645.31	4007.21
A_68_P23609897	chr5:37221748-37221792	NM_008550:118	Man2b2	INSIDE	1.775	2.479	395.33	980.03	4.399	374.60	1648.01
A_68_P25046332	chr7:35697322-35697366	NM_008820:-81	Pepd	PROMOTER	1.775	4.026	3483.89	14027.35	7.147	2496.64	17842.52
A_68_P23308821	chr4:131429974-131430018	NM_020587:443	Srsf4	INSIDE	1.775	1.555	884.71	1375.62	2.760	827.18	2283.21
A_68_P32707838	chrX:138825108-138825152	NM_001033600:-52	Acsl4	PROMOTER	1.774	2.727	1079.84	2945.22	4.840	552.09	2671.95
A_68_P28154359	chr11:115465196-115465240	NM_173048:2	Gga3	INSIDE	1.774	3.264	732.95	2392.19	5.789	639.72	3703.54
A_68_P24382000	chr6:39157044-39157088	NM_001033430:-294	Jhdm1d	PROMOTER	1.774	8.461	8493.65	71863.49	15.006	8119.38	121837.70
A_68_P32579463	chrX:102347552-102347596	AK136781:-2464		PROMOTER	1.774	2.645	1412.04	3734.71	4.692	791.80	3715.44
A_68_P32287125	chrX:19638017-19638061	NM_021715:1343	Chst7	INSIDE	1.773	2.989	484.37	1447.95	5.301	264.32	1401.23
A_68_P30659187	chr16:33684576-33684620	NM_175256:47	Heg1	INSIDE	1.773	6.285	2971.27	18674.29	11.145	2361.20	26314.81
A_68_P24383009	chr6:39369612-39369656	NM_018810:734	Mkrn1	INSIDE	1.773	4.571	1184.49	5414.21	8.105	871.42	7062.48
A_68_P30782600	chr16:56717318-56717362	NM_019678:127	Tfg	INSIDE	1.773	2.471	835.50	2064.67	4.382	706.35	3094.87
A_68_P22347225	chr3:95861928-95861972	NM_013841:428	Vps45	INSIDE	1.773	1.463	941.12	1376.55	2.593	861.27	2233.70
A_68_P32351254	chrX:42143356-42143400	NM_178739:-4	Dcaf12l1	PROMOTER	1.772	2.845	4125.07	11736.55	5.042	2258.89	11388.94
A_68_P31928602	chr19:5424535-5424579	NM_024176:360	Drap1	INSIDE	1.772	3.070	6270.42	19247.44	5.439	4578.67	24902.28
A_68_P32095553	chr19:37509433-37509477	NM_008245:124	Hhex	INSIDE	1.772	3.525	3556.33	12536.69	6.247	2918.16	18228.33
A_68_P29469015	chr14:24824174-24824218	NM_010610:-769	Kcnma1	PROMOTER	1.772	3.849	993.01	3822.26	6.822	802.86	5476.86
A_68_P26344985	chr9:20807480-20807524	NM_023167:322	Mrpl4	INSIDE	1.772	1.812	959.47	1738.23	3.210	728.81	2339.48
A_68_P29453038	chr14:22320578-22320622	NM_017479:1594	Myst4	INSIDE	1.772	10.363	8250.98	85508.03	18.364	5000.42	91827.39
A_68_P32148144	chr19:47253081-47253125	NM_021360:-207	Neurl1a	PROMOTER	1.772	2.016	1665.95	3358.83	3.572	1310.60	4681.33
A_68_P25088125	chr7:51807692-51807736	NM_009473:1579	Nr1h2	INSIDE	1.772	8.216	7542.10	61962.49	14.558	5015.40	73015.23
A_68_P24061285	chr5:124889815-124889859	NM_030241:-102	Setd8	PROMOTER	1.772	6.736	706.20	4756.98	11.934	574.76	6858.93
A_68_P27165498	chr10:58275060-58275104	NM_172788:-1024	Sh3rf3	PROMOTER	1.772	1.997	6835.60	13649.97	3.539	5808.04	20551.85
A_68_P24951825	chr7:5008460-5008504	NM_146178:155	Ccdc106	INSIDE	1.771	2.209	1864.31	4118.27	3.912	1406.04	5500.30
A_68_P26375208	chr9:27107222-27107266	NM_001033323:432	Igsf9b	INSIDE	1.771	11.717	1501.62	17594.76	20.756	1142.28	23708.96
A_68_P32565869	chrX:99044829-99044873	NM_001163610:127	Nhsl2	INSIDE	1.771	4.869	967.20	4709.58	8.623	694.45	5988.30
A_68_P29258499	chr13:99359027-99359071	AK135687:168913		INSIDE	1.771	14.231	1753.95	24959.88	25.208	1094.15	27581.51
A_68_P31610600	chr18:34165600-34165644	NM_013512:1238	Epb4.1l4a	INSIDE	1.770	4.669	7245.25	33830.49	8.266	5145.26	42531.44
A_68_P31873837	chr18:82113134-82113178	AK046168:311		INSIDE	1.770	1.694	1350.04	2286.41	2.998	1131.40	3392.14
A_68_P23770428	chr5:68238336-68238380	NM_001038999:312	Atp8a1	INSIDE	1.769	2.920	5059.10	14771.55	5.165	4019.53	20760.05
A_68_P28047199	chr11:96723478-96723522	NM_019877:12311	Copz2	DOWNSTREAM	1.769	2.368	1123.29	2659.94	4.189	762.30	3193.24
A_68_P32128434	chr19:43827858-43827902	NM_001113562:368	Cutc	INSIDE	1.769	2.558	2374.32	6072.97	4.525	1895.91	8578.58
A_68_P31161104	chr17:35960060-35960104	NM_008027:-219	Flot1	PROMOTER	1.769	5.447	1552.32	8455.38	9.634	1231.80	11866.98
A_68_P27921007	chr11:74336152-74336196	NM_001015046:67486	Rap1gap2	INSIDE	1.769	3.183	828.38	2636.47	5.632	709.37	3994.99
A_68_P27804722	chr11:53244281-53244325	NM_025352:31	Uqcrq	INSIDE	1.769	1.652	602.65	995.78	2.923	574.97	1680.60
A_68_P30149946	chr15:38448361-38448405	NM_001102458:639	Azin1	INSIDE	1.768	2.411	2801.07	6754.27	4.263	2330.83	9935.58
A_68_P25015934	chr7:27963629-27963675	NR_037283:-2540	Mir3101	PROMOTER	1.768	3.211	11134.92	35755.86	5.678	7580.22	43038.60
A_68_P30382971	chr15:82184657-82184701	NM_025987:43	Ndufa6	INSIDE	1.768	7.264	5277.33	38335.13	12.840	3633.10	46648.45
A_68_P31117838	chr17:27822326-27822370	NM_178365:150	Pacsin1	INSIDE	1.768	3.552	4612.42	16382.12	6.279	3523.84	22124.95
A_68_P27311153	chr10:85391455-85391499	NM_001163614:241	Ascl4	INSIDE	1.767	4.192	1634.87	6853.41	7.406	1314.91	9737.78
A_68_P28727037	chr12:109513497-109513541	NM_001159910:109	Ccdc85c	INSIDE	1.767	4.478	592.81	2654.85	7.911	592.78	4689.72
A_68_P22728457	chr4:11118468-11118512	NM_001037134:-10	Ccne2	PROMOTER	1.767	2.141	909.54	1947.35	3.783	756.22	2860.48
A_68_P23269776	chr4:124378137-124378181	NM_010213:216	Fhl3	INSIDE	1.767	3.462	657.54	2276.40	6.116	625.75	3826.93
A_68_P26018642	chr8:86707908-86707952	NR_029821:-5070	Mir181c	PROMOTER	1.767	5.718	2600.84	14870.92	10.102	2267.63	22907.50
A_68_P30368655	chr15:79634703-79634747	NM_030689:415	Nptxr	INSIDE	1.767	8.180	2599.79	21265.87	14.457	2031.04	29361.75

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P30436282	chr15:91402943-91402987	NM_001033633:728	Slc2a13	INSIDE	1.767	3.345	1912.48	6397.63	5.912	1714.23	10134.76
A_68_P32393600	chrX:52896641-52896685	ENSMUST00000163353:91930		INSIDE	1.767	3.118	1362.56	4247.89	5.508	790.77	4355.57
A_68_P23262662	chr4:123089650-123089695	NM_001167918:-518	D830031N03Rik	PROMOTER	1.766	3.937	2775.83	10928.71	6.954	2219.30	15433.61
A_68_P24138256	chr5:140384605-140384649	NM_175522:730	Elfn1	INSIDE	1.766	9.868	2008.19	19816.30	17.424	1874.43	32660.71
A_68_P21814796	chr2:163684382-163684426	NM_001030292:4919	Kcnk15	INSIDE	1.766	2.761	1864.02	5147.25	4.876	1411.23	6881.10
A_68_P25230185	chr7:80763469-80763513	AK158912:-221		PROMOTER	1.766	7.062	5298.66	37420.68	12.469	4235.27	52810.32
A_68_P27288028	chr10:80657209-80657253	NR_015477:-205	2310050B05Rik	PROMOTER	1.765	2.499	2529.81	6320.77	4.411	2017.03	8896.69
A_68_P26505081	chr9:50506728-50506772	NM_178118:29339	Dixdc1	INSIDE	1.765	1.817	1669.25	3032.53	3.207	1162.67	3728.34
A_68_P23590169	chr5:33972359-33972403	NM_178390:-96	Fam53a	PROMOTER	1.765	2.637	5515.12	14543.40	4.654	4415.98	20551.40
A_68_P32805174	chrX:162677268-162677312	NM_001177961:416	Gpm6b	INSIDE	1.765	1.759	1334.09	2347.25	3.106	749.12	2326.47
A_68_P27910209	chr11:72028885-72028929	NM_026068:188	Med31	INSIDE	1.765	1.777	736.61	1308.89	3.136	608.92	1909.51
A_68_P24164494	chr5:145900797-145900843	NM_001033313:138	Pdap1	INSIDE	1.765	2.842	4990.32	14183.28	5.016	3663.46	18375.68
A_68_P32054980	chr19:29887444-29887488	NM_177721:-2	Ranbp6	PROMOTER	1.765	2.134	1348.08	2877.14	3.766	1137.32	4283.48
A_68_P23597150	chr5:35292277-35292321	NM_173402:202	Rgs12	INSIDE	1.765	6.421	322.42	2070.34	11.335	287.78	3261.91
A_68_P32168791	chr19:50753028-50753072	NM_021377:52	Sorcs1	INSIDE	1.765	5.090	1771.47	9017.51	8.987	1696.90	15249.77
A_68_P27542559	chr10:128105989-128106033	NM_173733:4964	Suox	DOWNSTREAM	1.765	4.909	11211.50	55040.77	8.663	7886.81	68326.57
A_68_P26804666	chr9:106588275-106588319	NM_001081654:-17	Tex264	PROMOTER	1.765	2.185	1727.76	3774.92	3.855	1342.99	5177.58
A_68_P21911521	chr2:181327466-181327510	NM_001164597:-322	Znf512b	PROMOTER	1.765	3.573	1536.04	5488.81	6.305	1321.95	8335.16
A_68_P29940452	chr14:119105540-119105584	NM_001033336:-121	Abcc4	PROMOTER	1.764	1.368	1461.86	1999.96	2.413	1301.71	3141.45
A_68_P24372708	chr6:37392303-37392347	NM_178661:-176	Creb3l2	PROMOTER	1.764	2.324	991.77	2304.44	4.098	853.65	3498.34
A_68_P21438069	chr2:93797146-93797190	NM_001145034:89	Gm13889	INSIDE	1.764	3.176	1991.48	6325.51	5.604	1596.99	8949.92
A_68_P22133096	chr3:51811618-51811662	NM_001004176:97288	Maml3	INSIDE	1.764	4.761	566.37	2696.29	8.396	443.15	3720.85
A_68_P31612548	chr18:34533141-34533185	NM_007874:-93	Reep5	PROMOTER	1.764	4.572	1898.17	8677.73	8.066	1528.25	12326.48
A_68_P20149049	chr1:36614326-36614370	NM_001126047:878	Sema4c	INSIDE	1.764	7.297	6518.75	47565.21	12.870	4549.54	58550.61
A_68_P29055901	chr13:55672343-55672387	NM_001162881:-1028	Fam193b	PROMOTER	1.763	2.951	2122.69	6264.39	5.202	1772.94	9223.40
A_68_P30955189	chr16:90144198-90144242	NR_033476:1739	Gm10789	INSIDE	1.763	6.303	1076.13	6783.06	11.115	799.09	8881.84
A_68_P23978770	chr5:110715093-110715137	NM_008993:73	Pxmp2	INSIDE	1.763	2.563	2154.39	5520.74	4.518	1822.63	8234.37
A_68_P21151631	chr2:38860577-38860621	NM_025592:53	Rpl35	INSIDE	1.763	2.925	2620.19	7663.81	5.157	2061.53	10630.55
A_68_P30779064	chr16:56075886-56075930	NM_001003972:387	Senp7	INSIDE	1.763	6.223	2092.73	13022.48	10.970	1717.71	18843.10
A_68_P31118768	chr17:27977231-27977275	NM_011432:221	Snrpc	INSIDE	1.763	5.799	496.83	2881.28	10.226	367.40	3757.01
A_68_P26242940	chr8:126544834-126544878	NM_133966:353	Taf5l	INSIDE	1.763	4.722	1079.06	5094.78	8.322	864.28	7192.74
A_68_P24006959	chr5:115392406-115392450	NM_028211:218	2210016L21Rik	INSIDE	1.762	2.075	3762.48	7807.39	3.655	2626.23	9600.08
A_68_P21483989	chr2:103406800-103406844	NM_178890:356	Abtb2	INSIDE	1.762	2.160	513.43	1109.03	3.805	462.30	1759.28
A_68_P26220483	chr8:123012034-123012078	NM_198671:-709	Gse1	PROMOTER	1.762	4.405	1205.27	5309.66	7.762	902.80	7007.95
A_68_P28043336	chr11:96132754-96132798	NM_008270:133	Hoxb9	INSIDE	1.762	2.702	1478.87	3996.34	4.761	1167.08	5556.00
A_68_P27180703	chr10:60938705-60938749	NM_153542:146	Lrrc20	INSIDE	1.762	16.348	1322.90	21626.74	28.805	1006.90	29004.18
A_68_P25435757	chr7:121559995-121560039	NM_011055:1249	Pde3b	INSIDE	1.762	3.398	1535.25	5217.14	5.987	1224.88	7333.25
A_68_P20157818	chr1:38186099-38186143	NM_019570:387	Rev1	INSIDE	1.762	4.318	390.96	1688.19	7.608	378.46	2879.32
A_68_P26983377	chr10:19570989-19571033	NM_029529:255	Slc35d3	INSIDE	1.762	1.437	1770.66	2545.16	2.533	1354.11	3430.35
A_68_P31347831	chr17:74059828-74059872	NM_027864:-59	Galnt14	PROMOTER	1.761	2.701	2475.44	6685.55	4.756	1800.05	8561.73
A_68_P31205409	chr17:46297933-46297979	NM_001145979:-24	Gtpbp2	DIVERGENT_PROMOTER	1.761	4.260	3135.28	13356.36	7.504	2415.30	18123.83
A_68_P28166383	chr11:117515888-117515933	NM_198022:308	Tnrc6c	INSIDE	1.761	3.753	1659.74	6229.66	6.610	1320.71	8729.71
A_68_P20622147	chr1:134439405-134439449	NM_177129:91	Cntn2	INSIDE	1.760	7.013	3736.09	26202.98	12.345	2879.07	35542.74
A_68_P22391858	chr3:104315425-104315469	NM_001025067:333	Lrig2	INSIDE	1.760	5.016	599.41	3006.70	8.827	522.51	4612.18
A_68_P27892954	chr11:68901870-68901914	NM_009497:-137	Vamp2	PROMOTER	1.760	1.492	1659.78	2477.16	2.626	1196.24	3141.60
A_68_P27083322	chr10:40020722-40020766	NM_007444:1248	Amd2	INSIDE	1.759	1.725	617.62	1065.22	3.034	556.90	1689.59
A_68_P21094080	chr2:28763906-28763951	NM_019446:8013	Barhl1	INSIDE	1.759	1.881	359.60	676.37	3.309	188.20	622.75
A_68_P26159425	chr8:112392612-112392656	NM_001122594:132	Phlpp2	INSIDE	1.759	3.602	1589.73	5726.16	6.337	1426.80	9041.23
A_68_P27327917	chr10:88348711-88348755	NM_145423:-4	Slc5a8	PROMOTER	1.759	5.743	1545.80	8878.18	10.104	1367.68	13818.54
A_68_P26218688	chr8:122754127-122754171	ENSMUST00000127664:319408		INSIDE	1.759	4.700	1631.72	7669.08	8.267	1341.60	11090.44
A_68_P21958958	chr3:14886343-14886387	NM_009801:-61	Car2	PROMOTER	1.758	1.790	329.27	589.39	3.146	299.56	942.43

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26526109	chr9:54349056-54349100	NM_172771:355	Dmxl2	INSIDE	1.758	3.148	2854.95	8988.13	5.534	2120.01	11732.20
A_68_P26905236	chr10:4522611-4522655	NM_175374:35	Mtrf1l	INSIDE	1.758	3.434	1637.50	5622.63	6.037	1288.35	7777.73
A_68_P30346633	chr15:76014154-76014198	NM_201394:11964	Plec	INSIDE	1.758	3.607	1900.53	6855.42	6.341	1385.38	8784.31
A_68_P31488614	chr18:10181658-10181702	NM_009071:110	Rock1	INSIDE	1.758	5.975	3034.69	18133.36	10.504	2295.97	24116.75
A_68_P22923084	chr4:53453754-53453798	NM_001159633:492	Slc44a1	INSIDE	1.758	4.226	3284.90	13883.52	7.429	2686.04	19955.22
A_68_P23607369	chr5:36740782-36740826	NM_030889:-16	Sorcs2	PROMOTER	1.758	6.372	4995.22	31827.52	11.198	4038.19	45221.17
A_68_P20946920	chr1:194861857-194861901	NM_181546:14	Syt14	INSIDE	1.758	3.505	904.97	3171.63	6.162	732.36	4513.01
A_68_P29509885	chr14:31944046-31944090	NR_024069:-1952	2010107H07Rik	DIVERGENT_PROMOTER	1.757	3.885	1220.48	4741.76	6.827	944.05	6444.63
A_68_P27351976	chr10:92623453-92623497	NM_146239:-146	Cdk17	PROMOTER	1.757	4.366	815.31	3559.77	7.669	642.05	4924.18
A_68_P24859169	chr6:133985084-133985128	NM_007961:-618	Etv6	PROMOTER	1.757	1.842	1887.56	3476.45	3.235	1459.11	4720.73
A_68_P23681262	chr5:50450445-50450489	NM_133911:-231	Gpr125	PROMOTER	1.757	7.745	1505.05	11656.69	13.611	1198.64	16314.77
A_68_P21078497	chr2:26264502-26264546	NM_033134:184	Inpp5e	INSIDE	1.757	1.686	929.83	1567.59	2.963	841.93	2494.54
A_68_P26270749	chr8:131209761-131209805	NM_010578:229	Itgb1	INSIDE	1.757	2.130	3422.29	7289.03	3.743	2642.46	9891.32
A_68_P25713191	chr8:23969515-23969559	NM_001081149:-474	Myst3	PROMOTER	1.757	1.557	599.52	933.45	2.735	404.86	1107.42
A_68_P28029989	chr11:93817362-93817406	NM_008705:-63	Nme2	PROMOTER	1.757	4.151	3025.34	12559.02	7.295	2391.06	17443.98
A_68_P31196995	chr17:44873188-44873232	NM_001145920:387	Runx2	INSIDE	1.757	2.269	882.30	2001.78	3.986	705.48	2812.18
A_68_P27278356	chr10:79167062-79167106	NM_001077184:-18	Bsg	PROMOTER	1.756	1.921	932.44	1791.45	3.373	697.13	2351.69
A_68_P26132023	chr8:107694748-107694792	NM_001161456:197	Cbfb	INSIDE	1.756	4.825	1548.46	7471.14	8.475	1377.88	11677.23
A_68_P30895867	chr16:78376777-78376821	NR_002700:204	Gm7334	INSIDE	1.756	5.544	4323.13	23966.56	9.736	3610.15	35150.07
A_68_P29530592	chr14:35362336-35362380	NM_001039074:39435	Ldb3	INSIDE	1.756	1.541	946.64	1459.23	2.707	874.65	2367.60
A_68_P24894485	chr6:140373203-140373247	NM_144920:605	Plekha5	INSIDE	1.756	1.787	4206.33	7516.88	3.138	3331.26	10452.47
A_68_P31934467	chr19:6399578-6399622	NM_011242:-982	Rasgrp2	PROMOTER	1.756	4.373	2869.09	12545.09	7.679	2161.16	16595.64
A_68_P27507134	chr10:121533967-121534011	NM_153059:170	Tmem5	INSIDE	1.756	2.901	22532.79	65360.53	5.093	17904.44	91188.08
A_68_P21782542	chr2:158187327-158187371	NR_027887:-90	9430008C03Rik	PROMOTER	1.755	4.200	1215.00	5103.27	7.372	959.59	7073.91
A_68_P31162860	chr17:36305369-36305413	NM_001081032:92	Gm8909	INSIDE	1.755	2.647	5455.52	14440.49	4.646	4867.99	22619.08
A_68_P30497013	chr15:102110024-102110068	NM_134100:160	Mfsd5	INSIDE	1.755	10.569	1150.96	12164.70	18.546	955.38	17718.13
A_68_P26492138	chr9:48303203-48303247	NM_144948:211	Rbm7	INSIDE	1.755	2.232	1857.66	4146.27	3.916	1461.89	5724.85
A_68_P29605237	chr14:52817103-52817147	NM_033618:-210	Supt16h	PROMOTER	1.755	1.527	2216.53	3384.63	2.681	1820.08	4878.78
A_68_P25983698	chr8:80041949-80041993	NM_030113:-164	Arhgap10	PROMOTER	1.754	7.007	3126.51	21906.85	12.292	2424.09	29797.49
A_68_P29005205	chr13:46060754-46060798	NM_009124:-431	Atxn1	PROMOTER	1.754	3.197	1185.29	3789.79	5.607	956.20	5361.12
A_68_P27385039	chr10:98569849-98569893	NM_015737:-898	Galnt4	PROMOTER	1.754	2.881	597.56	1721.78	5.053	546.34	2760.79
A_68_P20457526	chr1:95700053-95700097	NM_025454:-467	Ing5	DIVERGENT_PROMOTER	1.754	3.519	1095.13	3853.92	6.171	890.34	5494.47
A_68_P25736226	chr8:28152855-28152901	NM_001039077:-148	Prosc	PROMOTER	1.754	3.824	3213.83	12289.94	6.708	2627.55	17626.44
A_68_P26875613	chr9:119920587-119920631	NM_011724:12108	Xirp1	DOWNSTREAM	1.754	2.196	2506.01	5503.35	3.852	2088.07	8042.98
A_68_P31758329	chr18:61715242-61715286	NM_146087:29	Csnk1a1	INSIDE	1.753	2.001	1909.97	3822.75	3.509	1370.39	4808.15
A_68_P30287852	chr15:65618774-65618818	NM_133766:194	Efr3a	INSIDE	1.753	1.928	260.85	502.80	3.380	253.86	858.03
A_68_P23681257	chr5:50449672-50449716	NM_133911:541	Gpr125	INSIDE	1.753	3.106	6380.11	19814.98	5.445	5137.68	27974.89
A_68_P24449528	chr6:52210288-52210332	NM_008264:564	Hoxa13	INSIDE	1.753	7.221	591.44	4270.79	12.660	478.78	6061.55
A_68_P26951412	chr10:13194053-13194097	NM_001195065:128	Phactr2	INSIDE	1.753	1.737	792.22	1376.34	3.045	676.01	2058.35
A_68_P24001851	chr5:114541342-114541386	NM_026805:25	Svop	INSIDE	1.753	5.740	2988.43	17153.90	10.061	2550.77	25662.82
A_68_P26421598	chr9:35075374-35075418	NM_175411:-31	Fam118b	DIVERGENT_PROMOTER	1.752	1.543	895.51	1381.34	2.703	863.11	2333.18
A_68_P26132587	chr8:107788500-107788544	NM_015821:-25	Fbxl8	DIVERGENT_PROMOTER	1.752	3.803	715.63	2721.64	6.664	631.31	4207.03
A_68_P26643861	chr9:75257109-75257153	NM_027418:36	Mapk6	INSIDE	1.752	6.242	804.80	5023.46	10.938	682.80	7468.18
A_68_P29051301	chr13:54867120-54867164	NM_033610:659	Sncb	INSIDE	1.752	3.620	2927.26	10596.65	6.343	2313.86	14677.38
A_68_P20022045	chr1:9289343-9289387	NM_027671:447	Sntg1	INSIDE	1.752	5.857	3617.91	21188.75	10.260	2628.46	26966.77
A_68_P28118792	chr11:109334732-109334776	NM_028710:67	Arsg	INSIDE	1.751	1.983	2131.27	4227.17	3.474	1811.40	6292.14
A_68_P22859197	chr4:40800680-40800724	NM_022305:329	B4galt1	INSIDE	1.751	3.145	1556.87	4896.93	5.509	1299.73	7159.97
A_68_P25952284	chr8:73027155-73027199	NM_018827:10122	Crlf1	INSIDE	1.751	3.433	2378.66	8165.82	6.011	1884.88	11330.54
A_68_P25089584	chr7:52095285-52095329	NM_010215:3649	Il4i1	INSIDE	1.751	2.596	1830.05	4751.35	4.547	1424.35	6476.19
A_68_P30453398	chr15:94459261-94459305	NM_178789:-333	Tmem117	PROMOTER	1.751	4.555	9344.40	42566.47	7.978	6963.78	55556.36
A_68_P20262088	chr1:59177273-59177317	NM_001033449:-354	Als2cr4	PROMOTER	1.750	4.488	745.12	3344.05	7.854	631.06	4956.38

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P29413810	chr14:13654360-13654404	NM_001042617:1211	Cadps	INSIDE	1.750	3.642	2671.56	9730.57	6.374	2240.68	14281.93
A_68_P23892215	chr5:92512150-92512194	NM_001080797:-229	G3bp2	PROMOTER	1.750	2.949	1937.02	5713.11	5.163	1664.45	8593.41
A_68_P30961697	chr16:91226847-91226891	NM_016967:1074	Olig2	INSIDE	1.750	3.045	5236.27	15942.01	5.329	4041.84	21540.29
A_68_P23402215	chr4:149111795-149111839	NM_001025106:327	Tmem201	INSIDE	1.750	6.996	1464.17	10243.76	12.245	1030.76	12621.58
A_68_P30096385	chr15:27954397-27954441	NM_001081302:1185	Trio	INSIDE	1.750	1.463	4319.80	6321.36	2.561	3326.99	8521.62
A_68_P32795839	chrX:160396590-160396634	NM_009453:-14	Zrsr2	PROMOTER	1.750	2.246	2229.98	5007.44	3.929	1201.96	4722.33
A_68_P21722826	chr2:147020543-147020587	NM_001077632:-8426	Nkx2-2	PROMOTER	1.749	5.439	1090.25	5929.85	9.512	881.94	8388.93
A_68_P27614819	chr11:17111398-17111442	NM_025443:172	Pno1	INSIDE	1.749	2.061	1394.34	2873.63	3.605	1113.56	4013.90
A_68_P29428731	chr14:17197979-17198023	NM_009409:281	Top2b	INSIDE	1.749	2.011	1529.45	3075.09	3.516	1246.60	4382.69
A_68_P27445213	chr10:110182319-110182363	NM_178609:-180	E2f7	PROMOTER	1.748	4.159	772.89	3214.54	7.272	770.36	5602.23
A_68_P32213515	chr19:58529618-58529662	NM_010279:-684	Gfra1	PROMOTER	1.748	1.741	4343.45	7562.41	3.044	2798.64	8517.84
A_68_P25954584	chr8:73389578-73389623	NM_032397:-8693	Kcnn1	PROMOTER	1.748	1.511	1699.52	2567.57	2.641	1171.95	3095.36
A_68_P26039507	chr8:90723531-90723575	NM_001164497:441	Papd5	INSIDE	1.748	5.336	3155.94	16841.30	9.330	2634.39	24579.68
A_68_P24956659	chr7:6682310-6682354	NM_008817:798	Peg3	INSIDE	1.748	1.520	829.29	1260.71	2.657	758.86	2016.08
A_68_P25265832	chr7:87439097-87439141	NM_145150:-232	Prc1	PROMOTER	1.748	5.867	2742.61	16091.81	10.254	2081.05	21339.65
A_68_P23236664	chr4:117508530-117508574	NM_008135:690	Slc6a9	INSIDE	1.748	2.240	1988.17	4452.72	3.914	1745.17	6830.68
A_68_P25958205	chr8:74195695-74195739	NM_001029873:-60	Unc13a	DIVERGENT_PROMOTER	1.748	3.016	8338.50	25152.77	5.272	6293.49	33177.18
A_68_P32477696	chrX:74678992-74679036			Unknown	1.748	4.677	553.98	2590.80	8.177	333.85	2729.94
A_68_P27900882	chr11:70279513-70279557	NM_023158:-6048	Cxcl16	PROMOTER	1.747	1.427	1830.22	2611.27	2.493	1401.27	3492.97
A_68_P23103735	chr4:91038685-91038729	NM_010486:40	Elavl2	INSIDE	1.747	4.653	2752.25	12806.90	8.127	2275.41	18493.30
A_68_P28033280	chr11:94352619-94352663	NM_027984:8648	Epn3	INSIDE	1.747	14.019	1245.75	17463.81	24.492	945.71	23162.58
A_68_P25953980	chr8:73300616-73300660	NM_008841:-27	Pik3r2	DIVERGENT_PROMOTER	1.747	3.516	669.06	2352.54	6.141	614.17	3771.75
A_68_P25354354	chr7:105326624-105326668	NM_007602:57	Capn5	INSIDE	1.746	5.034	1591.36	8011.50	8.790	1263.09	11102.05
A_68_P31565718	chr18:25645741-25645785	NM_001146292:266722	Celf4	INSIDE	1.746	1.912	1475.53	2821.49	3.339	1166.82	3896.56
A_68_P25957751	chr8:74126551-74126595	NM_001166213:5028	Fam129c	INSIDE	1.746	2.904	1868.37	5424.90	5.071	1476.20	7485.77
A_68_P24005517	chr5:115140712-115140756	NM_019821:210	Gltp	INSIDE	1.746	3.422	3875.07	13262.26	5.977	2524.78	15089.95
A_68_P25095297	chr7:53075356-53075400	NM_145963:4739	Kcnj14	INSIDE	1.746	3.039	3221.66	9789.23	5.306	2632.50	13967.01
A_68_P23577316	chr5:31554254-31554298	NM_027221:198	Krtcap3	INSIDE	1.746	5.588	2563.92	14326.24	9.756	2030.20	19806.48
A_68_P21149827	chr2:38544490-38544534	NM_139051:25550	Nr5a1	DOWNSTREAM	1.746	3.993	1793.33	7161.53	6.972	1423.96	9927.68
A_68_P26429021	chr9:36954305-36954349	NM_001029838:525	Pknox2	INSIDE	1.746	3.693	1007.30	3720.30	6.447	818.84	5279.12
A_68_P32268351	chrX:13424038-13424082	NM_009806:-393	Cask	PROMOTER	1.745	2.623	3604.11	9455.09	4.577	2141.76	9802.92
A_68_P26249219	chr8:127578258-127578302	NM_174853:186	Disc1	INSIDE	1.745	4.120	16321.94	67241.74	7.190	12123.42	87166.19
A_68_P25495415	chr7:132725071-132725115	NM_001008700:29297	Il4ra	DOWNSTREAM	1.745	4.300	3635.17	15632.42	7.503	2918.89	21900.68
A_68_P28291793	chr12:25515677-25515721	NM_001083341:-765	Mboat2	PROMOTER	1.745	14.968	1756.93	26296.92	26.116	1229.01	32097.13
A_68_P24981209	chr7:16973109-16973153	NM_019748:4	Sae1	INSIDE	1.745	2.708	1486.23	4024.38	4.726	1180.87	5580.70
A_68_P30496205	chr15:101966489-101966533	NM_001033277:136	Spryd3	INSIDE	1.745	2.590	3279.72	8492.93	4.519	2677.66	12099.03
A_68_P31326352	chr17:70318650-70318694	ENSMUST00000155823:-35		PROMOTER	1.745	2.085	673.37	1403.79	3.638	630.45	2293.40
A_68_P26814990	chr9:108363250-108363294	NM_133744:424	Ccdc71	INSIDE	1.744	2.571	1714.86	4409.18	4.485	1407.04	6309.96
A_68_P33007798	chr4_random:129389-129433	NM_001033326:19609	Dhrsx	INSIDE	1.744	5.327	2192.86	11680.33	9.290	1601.36	14876.20
A_68_P20442011	chr1:93263227-93263272	NM_173395:243	Fam132b	INSIDE	1.744	3.148	2766.94	8709.43	5.489	2276.05	12492.45
A_68_P28177386	chr11:119217235-119217283	NM_178743:388	Slc26a11	INSIDE	1.744	3.869	1785.95	6909.52	6.749	1449.59	9782.59
A_68_P22015873	chr3:28161770-28161814	NM_001163009:-343	Tnik	PROMOTER	1.744	3.559	324.25	1153.94	6.206	261.68	1623.89
A_68_P22674484	chr3:156225009-156225062	NM_177274:113	Negr1	INSIDE	1.743	6.651	2013.48	13392.34	11.594	1409.31	16339.35
A_68_P26021287	chr8:87230962-87231012	NM_001081981:67282	Nfix	DOWNSTREAM	1.743	5.485	1102.57	6047.57	9.561	909.77	8698.03
A_68_P30559120	chr16:13819791-13819845	NM_010946:449	Ntan1	INSIDE	1.743	2.431	941.21	2287.75	4.237	752.84	3189.89
A_68_P31117527	chr17:27760515-27760559	NM_019837:-139	Nudt3	PROMOTER	1.743	1.917	633.10	1213.82	3.342	554.31	1852.33
A_68_P21768463	chr2:155755683-155755727	NM_018888:342	Uqcc	INSIDE	1.743	3.108	3340.04	10381.87	5.418	2243.48	12155.32
A_68_P27787099	chr11:49988480-49988526	NM_026543:150	3010026O09Rik	INSIDE	1.742	1.554	3080.89	4787.81	2.707	2253.64	6101.51
A_68_P26890130	chr9:122481560-122481604	NR_015610:-36	9530059O14Rik	PROMOTER	1.742	2.246	822.11	1846.18	3.911	742.78	2905.29
A_68_P29526837	chr14:34736673-34736717	NM_145741:-78	Gdf10	PROMOTER	1.742	2.152	3153.19	6786.21	3.750	2573.87	9651.14
A_68_P30778982	chr16:56037716-56037760	NM_029092:149	Rg9mtd1	INSIDE	1.742	2.409	1190.64	2868.44	4.197	1272.69	5341.78

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25102500	chr7:54263669-54263713	NM_175318:94	Spty2d1	INSIDE	1.742	3.016	3244.63	9784.45	5.252	2553.17	13408.54
A_68_P31315914	chr17:68353306-68353350	NM_172964:120	Arhgap28	INSIDE	1.741	3.659	2455.65	8984.22	6.368	2022.42	12879.14
A_68_P24603556	chr6:85137482-85137526	NM_010131:-420	Emx1	PROMOTER	1.741	1.686	1548.80	2610.51	2.934	1261.23	3700.15
A_68_P27856227	chr11:62693165-62693209	NM_026210:195	Fam18b	INSIDE	1.741	6.334	2125.21	13461.23	11.029	1638.86	18075.66
A_68_P24535482	chr6:71221514-71221558	NM_145568:-476	Krcc1	DIVERGENT_PROMOTER	1.741	4.318	2746.85	11859.56	7.516	1893.83	14233.44
A_68_P24133762	chr5:139605565-139605609	NM_008923:120	Prkar1b	INSIDE	1.741	4.090	4595.71	18798.29	7.122	3413.53	24310.10
A_68_P29612660	chr14:55098640-55098684	NM_080726:3726	Rem2	INSIDE	1.741	2.457	334.13	820.80	4.277	262.63	1123.22
A_68_P27633577	chr11:20730971-20731015	NM_173752:119	1110067D22Rik	INSIDE	1.740	5.809	1800.24	10457.74	10.107	1463.09	14786.97
A_68_P23991928	chr5:112823693-112823737	NM_028386:-2481	Asphd2	PROMOTER	1.740	4.992	2724.62	13601.48	8.687	2226.16	19338.16
A_68_P22222029	chr3:69402614-69402658	NM_020026:147	B3galnt1	INSIDE	1.740	2.676	1545.57	4135.28	4.657	1385.46	6451.65
A_68_P24995306	chr7:20382177-20382221	NM_001161844:-40	Cblc	PROMOTER	1.740	2.603	3012.08	7840.71	4.530	2502.69	11336.44
A_68_P20391720	chr1:82288083-82288127	NM_010570:-90	Irs1	PROMOTER	1.740	6.741	738.79	4980.22	11.731	618.89	7260.25
A_68_P27631991	chr11:20443663-20443707	NM_021372:429	Sertad2	INSIDE	1.740	1.563	615.95	962.46	2.718	770.09	2093.18
A_68_P30574719	chr16:17619415-17619459	NM_001164609:-10	Smpd4	PROMOTER	1.740	3.457	1114.97	3854.16	6.013	928.41	5582.68
A_68_P29599187	chr14:51550282-51550326	NM_001033271:220	Tmem55b	INSIDE	1.740	8.543	1131.21	9664.49	14.870	707.37	10518.48
A_68_P29682512	chr14:67627253-67627297	NM_009761:440	Bnip3l	INSIDE	1.739	3.096	1938.77	6002.12	5.383	2240.87	12063.71
A_68_P23279343	chr4:125978444-125978488	NM_199473:14429	Col8a2	INSIDE	1.739	1.434	1429.27	2050.07	2.494	1206.55	3008.88
A_68_P20168277	chr1:39957569-39957613	NM_008696:-167	Map4k4	PROMOTER	1.739	6.591	1829.38	12056.65	11.462	1482.10	16987.39
A_68_P24758832	chr6:113276968-113277012	NM_010957:21	Ogg1	INSIDE	1.739	4.601	10666.25	49076.78	8.002	7706.41	61667.74
A_68_P29701956	chr14:70944977-70945021	NM_180588:-59	Reep4	PROMOTER	1.739	1.515	696.61	1055.02	2.634	767.89	2022.35
A_68_P26555222	chr9:59598670-59598714	NM_001172068:-236	Senp8	DIVERGENT_PROMOTER	1.739	3.056	1609.98	4920.90	5.317	1312.18	6976.36
A_68_P31385967	chr17:81344527-81344571	NM_026516:577	Tmem178	INSIDE	1.739	2.003	790.27	1582.55	3.483	671.56	2339.01
A_68_P20936661	chr1:193006674-193006718	NM_007498:516	Atf3	INSIDE	1.738	7.410	4368.87	32372.21	12.876	3330.41	42883.92
A_68_P29011719	chr13:47201171-47201215	NM_025900:397	Dek	INSIDE	1.738	1.560	990.11	1544.24	2.711	764.35	2072.05
A_68_P32364765	chrX:45806673-45806717	NM_019680:9615	Elf4	INSIDE	1.738	1.635	1048.84	1715.36	2.842	569.64	1619.14
A_68_P26550030	chr9:58670732-58670776	NM_001081192:-564	Hcn4	PROMOTER	1.738	2.314	463.53	1072.60	4.022	400.76	1611.96
A_68_P20556969	chr1:121317983-121318027	NM_008381:821	Inhbb	INSIDE	1.738	5.199	2087.36	10852.02	9.033	1599.33	14447.15
A_68_P24142218	chr5:141083418-141083462	NM_008494:146	Lfng	INSIDE	1.738	3.087	2249.66	6945.00	5.366	1855.84	9959.10
A_68_P31130455	chr17:30024049-30024093	NM_001081160:757	Mdga1	INSIDE	1.738	2.851	1712.55	4882.18	4.954	1318.07	6529.20
A_68_P27950601	chr11:79525364-79525408	NR_029579:-84	Mir193	PROMOTER	1.738	2.793	2055.00	5739.78	4.854	1642.00	7969.79
A_68_P30480085	chr15:99256217-99256261	NM_001001884:31941	Nckap5l	INSIDE	1.738	4.114	1881.69	7740.46	7.150	1425.95	10195.16
A_68_P28566637	chr12:80012969-80013013	NM_013738:-5065	Plek2	PROMOTER	1.738	2.300	3127.95	7195.06	3.997	2381.41	9519.02
A_68_P23234760	chr4:117167587-117167631	NM_025739:1912	Rnf220	INSIDE	1.738	3.133	2488.25	7795.60	5.446	2043.22	11127.02
A_68_P27787321	chr11:50023806-50023850	NM_011018:464	Sqstm1	INSIDE	1.738	4.742	6644.51	31510.94	8.244	4503.50	37125.14
A_68_P23298058	chr4:129373895-129373939	NM_199305:166	Tmem39b	INSIDE	1.738	2.740	2790.29	7644.16	4.761	2354.98	11212.01
A_68_P26871705	chr9:119231516-119231560	ENSMUST00000128880:-98		PROMOTER	1.738	5.111	4707.16	24057.97	8.881	3557.34	31594.19
A_68_P20165362	chr1:39424508-39424553	NM_053257:-165	Rpl31	PROMOTER	1.737	3.441	688.17	2368.01	5.977	527.67	3153.77
A_68_P26397640	chr9:30729401-30729445	NM_001024139:615	Adamts15	INSIDE	1.736	2.378	1314.66	3126.25	4.129	962.94	3976.27
A_68_P31762242	chr18:62339733-62339777	NM_007420:-141	Adrb2	PROMOTER	1.736	3.893	1542.63	6005.45	6.760	1271.57	8595.79
A_68_P28688785	chr12:103214150-103214194	NM_016856:-11	Cpsf2	PROMOTER	1.736	1.425	1111.50	1583.51	2.474	1079.73	2670.99
A_68_P26926726	chr10:8605914-8605958	NM_175155:-68	Sash1	PROMOTER	1.736	2.375	1853.06	4400.32	4.123	1678.72	6920.83
A_68_P20453778	chr1:95073519-95073563			Unknown	1.736	7.128	2346.40	16725.72	12.378	1903.78	23564.98
A_68_P32127475	chr19:43674323-43674367			Unknown	1.736	3.029	4914.69	14886.60	5.260	3642.82	19160.25
A_68_P31259473	chr17:57136900-57136944	NM_025538:161	Alkbh7	INSIDE	1.735	2.983	1175.23	3506.23	5.178	897.02	4644.46
A_68_P21102918	chr2:30248319-30248363	NM_020329:405	Dolpp1	INSIDE	1.735	4.161	1997.38	8310.37	7.217	1574.57	11363.04
A_68_P26659818	chr9:78329691-78329735	NM_010106:-181	Eef1a1	PROMOTER	1.735	1.761	947.75	1669.34	3.056	778.65	2379.18
A_68_P30261334	chr15:60656407-60656451	NM_001162926:207	Fam84b	INSIDE	1.735	2.756	867.52	2391.32	4.784	695.50	3327.13
A_68_P26803570	chr9:106367374-106367418	NM_001159652:875	Gpr62	INSIDE	1.735	4.565	756.92	3455.63	7.923	673.99	5340.17
A_68_P23812530	chr5:76374553-76374597	NM_010612:-121	Kdr	PROMOTER	1.735	4.224	6303.13	26622.36	7.328	4621.05	33863.12
A_68_P27287865	chr10:80630602-80630646	NM_021501:-159	Pias4	DIVERGENT_PROMOTER	1.735	3.750	3317.59	12442.19	6.506	2416.58	15721.63
A_68_P31295069	chr17:64681315-64681359	NM_001025309:-113	Pja2	PROMOTER	1.735	2.178	911.66	1985.96	3.779	794.14	3001.14

						Sham group			TiO$_2$-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26725648	chr9:92145271-92145315	NM_011636:261	Plscr1	INSIDE	1.735	3.586	4101.69	14709.23	6.221	3012.57	18741.24
A_68_P26574057	chr9:62986883-62986927	NM_172446:7883	Skor1	INSIDE	1.735	6.931	588.37	4077.83	12.028	469.55	5647.64
A_68_P25537056	chr7:140005623-140005667	NM_212473:-765	Fam53b	PROMOTER	1.734	2.759	1651.86	4558.12	4.785	1316.60	6299.36
A_68_P20967784	chr2:4322707-4322751	NM_001177843:707	Frmd4a	INSIDE	1.734	4.722	12366.15	58388.60	8.189	8550.72	70023.36
A_68_P24904258	chr6:142336086-142336130	NM_025872:346	Golt1b	INSIDE	1.734	1.677	823.66	1381.09	2.908	721.84	2098.75
A_68_P30482738	chr15:99705731-99705775	NM_001113545:135	Lima1	INSIDE	1.734	5.138	2702.22	13884.57	8.908	2227.72	19845.29
A_68_P22313622	chr3:88214207-88214256	NM_025928:7	Pmf1	INSIDE	1.734	3.408	876.38	2986.69	5.908	678.82	4010.58
A_68_P30013962	chr15:10966866-10966910	NM_178717:835	Rxfp3	INSIDE	1.734	6.001	3825.75	22960.00	10.408	2752.13	28644.35
A_68_P20505897	chr1:107890521-107890565	NM_001122675:3560	Zcchc2	INSIDE	1.734	3.021	2180.83	6589.31	5.239	1749.16	9164.54
A_68_P23282958	chr4:126644783-126644827	NM_001114399:363	Zmym4	INSIDE	1.734	6.315	4207.22	26569.82	10.948	3446.79	37736.43
A_68_P23542143	chr5:23988482-23988526	NM_139153:30510	Agap3	INSIDE	1.733	5.843	4665.00	27259.61	10.129	3513.02	35584.60
A_68_P25022916	chr7:29415707-29415751	NM_175319:306	C330005M16Rik	INSIDE	1.733	1.796	1168.65	2099.07	3.113	1029.93	3205.78
A_68_P32380511	chrX:49517673-49517717	NM_008150:406	Gpc4	INSIDE	1.733	3.289	1340.52	4408.65	5.699	855.74	4877.06
A_68_P25952867	chr8:73118782-73118826	NM_023627:425	Isyna1	INSIDE	1.733	1.577	1487.43	2345.26	2.732	1207.58	3299.13
A_68_P24946817	chr7:3637393-3637437	NM_029934:7713	Mboat7	INSIDE	1.733	4.064	2244.83	9124.02	7.046	1661.51	11706.57
A_68_P31929629	chr19:5602275-5602319	NM_026616:424	Rnaseh2c	INSIDE	1.733	2.818	461.91	1301.47	4.883	438.90	2143.20
A_68_P31209382	chr17:47026332-47026376	NM_178385:-1215	Tbcc	PROMOTER	1.733	4.014	1076.92	4322.30	6.957	914.68	6363.05
A_68_P33005868	A_68_P33005868			Unknown	1.733	6.745	406.82	2743.92	11.687	336.19	3929.21
A_68_P26469462	chr9:44575608-44575652	NM_145985:261	Arcn1	INSIDE	1.732	4.073	1190.06	4847.60	7.057	1021.52	7208.99
A_68_P22971150	chr4:63206034-63206078	NM_024173:258	Atp6v1g1	INSIDE	1.732	4.331	2368.67	10258.41	7.501	2015.75	15119.91
A_68_P27003030	chr10:23069823-23069869	NM_010167:-137	Eya4	PROMOTER	1.732	3.286	434.32	1427.34	5.692	439.18	2499.66
A_68_P28745894	chr12:112997376-112997420	NM_008450:339	Klc1	INSIDE	1.732	1.607	6227.53	10010.32	2.783	4582.88	12756.15
A_68_P20797864	chr1:167933679-167933723	NM_011137:-935	Pou2f1	PROMOTER	1.732	4.747	1600.53	7598.07	8.223	1240.42	10199.96
A_68_P22182581	chr3:61168376-61168420	NM_028712:-30	Rap2b	PROMOTER	1.732	3.914	4615.79	18064.14	6.779	3329.52	22571.76
A_68_P23402414	chr4:149148446-149148491	NM_027460:-92	Slc25a33	PROMOTER	1.732	6.311	5319.73	33572.15	10.928	4115.00	44966.77
A_68_P27935204	chr11:76811878-76811922	NM_010484:-198	Slc6a4	PROMOTER	1.732	2.191	1262.92	2767.27	3.795	1066.19	4046.40
A_68_P23310689	chr4:131767916-131767960	NM_145393:233	Ythdf2	INSIDE	1.732	4.831	8487.61	41002.43	8.366	6485.99	54258.90
A_68_P26237605	chr8:125566196-125566241	NM_001081379:-34	Ankrd11	PROMOTER	1.731	2.847	2956.92	8417.35	4.926	2522.15	12425.07
A_68_P20101394	chr1:25886869-25886913	NM_175642:-338	Bai3	PROMOTER	1.731	6.315	3410.04	21533.82	10.933	2400.03	26238.94
A_68_P25609544	chr7:152024886-152024930	NM_008007:392	Fgf3	INSIDE	1.731	2.429	1335.04	3242.95	4.204	1106.16	4650.24
A_68_P21078770	chr2:26301305-26301349	NM_153125:-590	Sec16a	PROMOTER	1.731	2.186	792.56	1732.82	3.784	665.25	2517.04
A_68_P24432387	chr6:49345594-49345638	NM_029916:14	Stk31	INSIDE	1.731	6.766	7487.28	50658.23	11.713	5534.60	64827.12
A_68_P26242939	chr8:126544720-126544764	NM_133966:467	Taf5l	INSIDE	1.731	7.775	676.84	5262.41	13.462	525.48	7074.04
A_68_P22449315	chr3:116126619-116126663	NM_001080818:310	Cdc14a	INSIDE	1.730	3.289	1221.99	4019.51	5.690	1102.08	6270.97
A_68_P27094083	chr10:41996329-41996375	NM_019740:196	Foxo3	INSIDE	1.730	2.798	733.02	2050.96	4.841	674.74	3266.23
A_68_P31632704	chr18:38371400-38371444	NM_029357:-2006	Pcdh1	PROMOTER	1.730	3.324	1831.38	6088.28	5.751	1438.68	8273.75
A_68_P26773477	chr9:101153798-101153842	NM_001161362:342	Ppp2r3a	INSIDE	1.730	1.698	791.47	1343.88	2.937	672.35	1974.64
A_68_P27311096	chr10:85379833-85379877	NM_181650:-164	Prdm4	PROMOTER	1.730	3.434	1386.39	4760.46	5.939	1135.23	6742.20
A_68_P31513736	chr18:14841066-14841110	NM_001161369:335	Ss18	INSIDE	1.730	1.539	893.89	1376.05	2.663	779.30	2075.10
A_68_P24760447	chr6:113554719-113554763	NM_133937:-25	6720456B07Rik	DIVERGENT_PROMOTER	1.729	29.247	415.36	12148.19	50.565	408.90	20675.97
A_68_P31760609	chr18:62071314-62071358	NM_198649:142	Ablim3	INSIDE	1.729	2.646	1903.66	5036.37	4.575	1574.24	7201.53
A_68_P29047192	chr13:54150550-54150594	NM_010076:455	Drd1a	INSIDE	1.729	3.605	1644.59	5928.09	6.233	1271.41	7925.09
A_68_P23513989	chr5:18732427-18732471	NM_001170746:-415	Magi2	PROMOTER	1.729	5.351	1454.92	7784.77	9.253	1263.72	11692.73
A_68_P24537769	chr6:71657624-71657668	NM_178608:-28	Reep1	PROMOTER	1.729	4.365	558.91	2439.40	7.545	446.64	3369.74
A_68_P32906199	A_68_P32906199			Unknown	1.729	8.050	1059.06	8524.89	13.918	818.63	11394.02
A_68_P24980671	chr7:16871769-16871813	NM_172297:-1782	Ccdc9	PROMOTER	1.728	4.829	18022.74	87028.16	8.343	12430.23	103702.10
A_68_P32539664	chrX:91881437-91881481	NM_008179:51	Gspt2	INSIDE	1.728	1.532	1092.11	1672.96	2.647	546.98	1447.80
A_68_P28693227	chr12:103943323-103943367	NM_172584:-265	Itpk1	PROMOTER	1.728	5.248	811.62	4259.30	9.070	709.53	6435.19
A_68_P23253010	chr4:120419437-120419481	NM_001081142:323	Kcnq4	INSIDE	1.728	2.460	1299.17	3195.38	4.251	1082.81	4602.51
A_68_P22157978	chr3:55987140-55987184	NM_030595:461	Nbea	INSIDE	1.728	4.480	1138.19	5099.45	7.741	981.53	7598.19
A_68_P29599189	chr14:51550570-51550614	NM_001033271:-68	Tmem55b	PROMOTER	1.728	6.256	6967.38	43587.79	10.809	5207.44	56284.93

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P29509872	chr14:31942367-31942412	NR_024069:-273	2010107H07Rik	DIVERGENT_PROMOTER	1.727	3.207	2485.55	7970.80	5.539	2061.63	11419.23
A_68_P30150544	chr15:38591583-38591627	NM_025494:-54	Atp6v1c1	PROMOTER	1.727	3.206	1534.77	4919.78	5.535	1234.99	6835.11
A_68_P32130475	chr19:44181890-44181934	NM_001162410:55	Chuk	INSIDE	1.727	3.622	678.44	2457.12	6.254	590.49	3693.13
A_68_P22752471	chr4:15872402-15872446	NM_026172:230	Decr1	INSIDE	1.727	2.505	2768.71	6935.72	4.326	2314.43	10012.17
A_68_P28266974	chr12:16817834-16817878	NM_033270:86	E2f6	INSIDE	1.727	3.658	1329.30	4862.99	6.319	1114.54	7042.68
A_68_P29059430	chr13:56236999-56237043	NM_001159513:-109	H2afy	PROMOTER	1.727	2.959	648.32	1918.32	5.110	510.41	2608.02
A_68_P26954148	chr10:13684931-13684975	NM_010437:-1232	Hivep2	PROMOTER	1.727	4.565	2223.13	10147.80	7.885	1782.67	14056.88
A_68_P23288232	chr4:127666279-127666323	ENSMUST00000144298:1013		INSIDE	1.727	2.333	1772.54	4135.39	4.030	1329.21	5356.51
A_68_P29410675	chr14:13178814-13178858	NM_080433:-457	Fezf2	PROMOTER	1.726	2.747	1144.71	3144.30	4.740	883.06	4185.46
A_68_P28691644	chr12:103707806-103707850	NM_013747:-291	Golga5	PROMOTER	1.726	2.151	1836.11	3949.73	3.712	1527.76	5671.67
A_68_P22448215	chr3:115955466-115955511	NM_022427:914	Gpr88	INSIDE	1.726	2.313	6031.43	13952.53	3.992	4318.84	17240.68
A_68_P22393109	chr3:104584285-104584329	NM_027982:333	Ppm1j	INSIDE	1.726	8.053	2584.88	20816.80	13.897	2145.43	29815.76
A_68_P31341464	chr17:72953935-72953979	NM_007439:-309	Alk	PROMOTER	1.725	3.540	6394.26	22635.29	6.108	5150.08	31456.16
A_68_P27234932	chr10:70807397-70807441	NM_134007:179	Cisd1	INSIDE	1.725	5.434	743.69	4041.59	9.376	605.45	5676.99
A_68_P28974187	chr13:40826726-40826770	NM_001122948:-936	Tcfap2a	PROMOTER	1.725	2.982	3597.64	10726.98	5.142	2801.51	14405.41
A_68_P22708703	chr4:6917953-6917997	NM_145711:-104	Tox	PROMOTER	1.725	3.353	5320.50	17841.79	5.786	4525.23	26181.49
A_68_P29733553	chr14:76816095-76816139	NM_207652:489	Tsc22d1	INSIDE	1.725	3.435	3654.98	12555.67	5.926	2628.47	15576.82
A_68_P24152597	chr5:143106025-143106069	NM_178398:509	Wipi2	INSIDE	1.725	2.031	1971.87	4004.07	3.502	1589.00	5564.96
A_68_P20350627	chr1:74849814-74849858	NM_009518:11244	Wnt10a	INSIDE	1.725	3.465	3093.07	10717.89	5.977	2626.35	15696.38
A_68_P23865427	chr5:87233816-87233860	NM_177680:324	Ythdc1	INSIDE	1.725	1.739	413.95	720.01	3.000	361.58	1084.78
A_68_P31620318	chr18:35991596-35991640	NM_133687:2147	Cxxc5	INSIDE	1.724	1.975	1603.91	3166.95	3.404	1180.80	4019.63
A_68_P24620361	chr6:88149067-88149115	NM_008090:433	Gata2	INSIDE	1.724	1.904	294.63	560.86	3.281	247.73	812.77
A_68_P31127484	chr17:29484749-29484793	NM_019880:79	Mtch1	INSIDE	1.724	3.035	1442.67	4378.91	5.232	1135.57	5941.51
A_68_P27483044	chr10:117229909-117229953	NM_134010:-169	Nup107	PROMOTER	1.724	2.587	4878.89	12620.43	4.460	3749.15	16720.20
A_68_P31654583	chr18:42435328-42435372	NM_172626:344	Rbm27	INSIDE	1.724	3.406	3192.91	10873.86	5.870	2639.01	15490.72
A_68_P23331724	chr4:135577368-135577412	NM_013736:174	Tceb3	INSIDE	1.724	5.009	4526.26	22670.37	8.633	3689.98	31854.49
A_68_P23982393	chr5:111308521-111308565	NM_024477:-279	Ttc28	PROMOTER	1.724	6.433	286.30	1841.66	11.088	176.30	1954.72
A_68_P31464043	chr18:4635545-4635589	NM_001081963:640	9430020K01Rik	INSIDE	1.723	2.340	2351.10	5500.43	4.031	2007.10	8090.87
A_68_P26954155	chr10:13685730-13685774	NM_010437:-432	Hivep2	PROMOTER	1.723	4.479	4379.25	19614.59	7.715	3569.73	27541.79
A_68_P24624872	chr6:88848652-88848696	NM_008564:100	Mcm2	INSIDE	1.723	2.710	2143.08	5807.63	4.668	1669.78	7794.48
A_68_P29613302	chr14:55236499-55236543	NR_030457:-898	Mir686	PROMOTER	1.723	4.302	368.61	1585.89	7.412	316.57	2346.51
A_68_P20147266	chr1:36326391-36326435	NM_153408:3858	Neurl3	INSIDE	1.723	2.008	1892.51	3800.04	3.460	1405.54	4862.79
A_68_P32201471	chr19:56623197-56623241	NM_025811:468	Nhlrc2	INSIDE	1.723	2.753	677.65	1865.37	4.743	532.80	2526.87
A_68_P21871010	chr2:173484993-173485037	NR_027957:26	Ppp4r1l-ps	INSIDE	1.723	4.435	2241.73	9941.73	7.641	1850.19	14137.33
A_68_P23393512	chr4:147662081-147662125	NM_001083342:-28	Ptchd2	PROMOTER	1.723	2.265	1585.17	3590.51	3.903	1302.94	5085.97
A_68_P27234632	chr10:70747404-70747448	NM_145420:584	Ube2d1	INSIDE	1.723	4.515	3345.42	15106.07	7.781	2432.05	18923.28
A_68_P23409805	chr4:150432256-150432300	NM_009498:-216	Vamp3	PROMOTER	1.723	5.061	4467.10	22606.50	8.719	3000.37	26159.48
A_68_P31154661	A_68_P31154661			Unknown	1.723	5.020	1377.34	6913.80	8.649	935.76	8093.31
A_68_P21071854	chr2:25251918-25251962	NM_009849:547	Entpd2	INSIDE	1.722	4.180	2448.06	10232.39	7.196	1935.00	13923.72
A_68_P29644193	chr14:60997735-60997779	NM_001164705:634	Fam123a	INSIDE	1.722	3.402	1085.16	3691.29	5.858	923.00	5406.96
A_68_P28084547	chr11:103173618-103173663			Unknown	1.722	1.532	679.97	1041.72	2.638	547.69	1444.83
A_68_P28859763	chr13:19040669-19040713	NM_175007:451	Amph	INSIDE	1.721	4.158	662.80	2756.07	7.158	559.15	4002.62
A_68_P24172967	chr5:148116571-148116615	NM_007673:2233	Cdx2	INSIDE	1.721	4.316	1295.33	5590.72	7.427	1017.59	7557.83
A_68_P30588586	chr16:20630082-20630126	NM_139293:181	Ece2	INSIDE	1.721	2.516	2058.37	5178.35	4.328	1688.09	7306.66
A_68_P28334082	chr12:32634899-32634943	NM_153198:480	Hbp1	INSIDE	1.721	1.569	1598.61	2508.49	2.700	1307.28	3530.14
A_68_P25474216	chr7:128643864-128643910	NM_001081327:108077	Hs3st2	INSIDE	1.721	7.977	1898.20	15141.20	13.728	1434.35	19691.47
A_68_P25168663	chr7:69493375-69493419	NM_010882:234	Ndn	INSIDE	1.721	5.983	1564.06	9357.36	10.297	1409.83	14516.67
A_68_P29117519	chr13:69878102-69878146	NM_001145162:651	Ube2ql1	INSIDE	1.721	3.906	4725.31	18459.07	6.724	3879.84	26087.56
A_68_P32573117	chrX:100677336-100677380	NR_001463:1214	Xist	INSIDE	1.721	2.053	4041.71	8298.95	3.533	1728.31	6105.93
A_68_P27287617	chr10:80598897-80598941	NM_010731:-97	Zbtb7a	PROMOTER	1.721	3.469	1436.35	4982.19	5.968	1224.08	7305.29
A_68_P26217897	chr8:122625576-122625620	NM_133967:-226	Zdhhc7	PROMOTER	1.721	1.447	1487.66	2151.96	2.490	1206.32	3003.91

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26721663	chr9:91278946-91278990	NM_009576:15159	Zic4	INSIDE	1.721	2.922	909.30	2656.60	5.028	697.42	3506.49
A_68_P30534202	A_68_P30534202			Unknown	1.721	3.265	1026.16	3350.15	5.619	897.05	5040.94
A_68_P28736910	chr12:111426306-111426350	AK044800:543		INSIDE	1.721	12.342	2821.20	34819.40	21.240	1891.38	40173.25
A_68_P22888792	chr4:46464440-46464484	NM_130889:474	Anp32b	INSIDE	1.720	3.243	3492.38	11327.10	5.578	2955.22	16483.79
A_68_P26846741	chr9:114753280-114753324	NM_027294:-32	Cmtm8	PROMOTER	1.720	4.235	8858.42	37512.78	7.283	7283.97	53046.75
A_68_P22318578	chr3:89126786-89126830	NM_010108:-7	Efna3	PROMOTER	1.720	1.555	6323.19	9831.44	2.675	4671.38	12494.26
A_68_P24329145	chr6:29866863-29866907	NM_001037740:-128	Fam40b	PROMOTER	1.720	3.229	355.25	1147.20	5.556	308.76	1715.42
A_68_P23929939	chr5:100929613-100929657	NM_001115010:-2042	Lin54	PROMOTER	1.720	3.153	2338.54	7372.86	5.423	1885.87	10226.99
A_68_P25375583	chr7:108967177-108967221	NM_008887:372	Phox2a	INSIDE	1.720	5.525	3288.44	18167.43	9.503	2745.79	26092.66
A_68_P28203004	chr12:4924079-4924123	NM_001099628:-58	Atad2b	DIVERGENT_PROMOTER	1.719	5.477	1128.71	6182.38	9.415	915.99	8624.10
A_68_P23647570	chr5:44173303-44173347	NM_001159963:64	Fbxl5	INSIDE	1.719	3.873	1869.08	7238.82	6.659	1685.32	11222.52
A_68_P29928904	chr14:117325550-117325594	NM_001079844:1036	Gpc6	INSIDE	1.719	2.874	1535.27	4413.00	4.941	1284.53	6347.51
A_68_P30577450	chr16:18088960-18089004	NM_011172:301	Prodh	INSIDE	1.719	2.615	2729.88	7138.39	4.496	2107.54	9475.10
A_68_P23236670	chr4:117509289-117509333	NM_008135:1448	Slc6a9	INSIDE	1.719	3.621	3065.86	11101.40	6.224	2295.46	14288.00
A_68_P25005464	chr7:25332066-25332110	NM_009532:-80	Xrcc1	DIVERGENT_PROMOTER	1.719	2.836	1884.27	5344.33	4.875	1417.59	6910.93
A_68_P24624504	chr6:88791715-88791759	NM_030251:193	Abtb1	INSIDE	1.718	3.548	10382.55	36839.75	6.095	6985.27	42572.99
A_68_P25578895	chr7:146768050-146768094	NR_027857:624	Nkx6-2	INSIDE	1.718	3.426	1968.92	6745.40	5.887	1554.74	9153.31
A_68_P28781792	chr12:120075230-120075274	NM_177082:-9549	Sp8	PROMOTER	1.718	2.608	3721.05	9704.84	4.481	2814.29	12609.79
A_68_P21568536	chr2:119063328-119063372	NM_016907:255	Spint1	INSIDE	1.718	2.031	3187.21	6473.42	3.490	2311.72	8067.09
A_68_P21075771	chr2:25877080-25877124	NM_133835:178	Ubac1	INSIDE	1.718	3.692	611.91	2259.37	6.342	595.33	3775.64
A_68_P22483663	chr3:122321938-122321982	NM_001114665:625	Fnbp1l	INSIDE	1.717	5.718	894.16	5113.21	9.819	840.35	8251.31
A_68_P28540462	chr12:75009562-75009606	NM_010431:731	Hif1a	INSIDE	1.717	3.450	1890.74	6523.81	5.924	1556.06	9217.74
A_68_P23936334	chr5:102093547-102093591	NM_144955:162	Nkx6-1	INSIDE	1.717	1.920	2360.88	4532.33	3.297	1938.13	6389.91
A_68_P30344883	chr15:75740087-75740131	NM_178646:-56	Tigd5	DIVERGENT_PROMOTER	1.717	4.105	2199.15	9027.46	7.048	1901.13	13399.69
A_68_P27693346	chr11:33101716-33101763	NM_019916:1849	Tlx3	INSIDE	1.717	4.968	736.97	3661.61	8.529	543.56	4636.17
A_68_P24091293	chr5:130418207-130418251	NM_001001327:246	Vkorc1l1	INSIDE	1.717	6.268	943.56	5914.16	10.764	1054.67	11352.37
A_68_P30481041	chr15:99414682-99414726	NM_009699:5218	Aqp2	INSIDE	1.716	3.349	1478.19	4949.91	5.747	1177.19	6764.97
A_68_P26727067	chr9:92437602-92437647	NR_029474:83	B430319G15Rik	INSIDE	1.716	3.978	2810.97	11182.00	6.828	2049.32	13992.34
A_68_P24607367	chr6:85911667-85911711	NM_028099:-27	Dusp11	PROMOTER	1.716	2.947	1375.74	4054.99	5.058	1093.69	5531.42
A_68_P20849151	chr1:177555721-177555765	NM_010209:24	Fh1	INSIDE	1.716	3.071	7119.66	21865.76	5.271	5290.52	27886.33
A_68_P24449298	chr6:52184077-52184121	NM_008263:840	Hoxa10	INSIDE	1.716	5.558	1152.59	6405.71	9.538	928.05	8852.16
A_68_P31515584	chr18:15221979-15222023	NM_001142731:91	Kctd1	INSIDE	1.716	3.299	1144.74	3776.04	5.660	975.32	5519.95
A_68_P23399809	chr4:148681348-148681392	NM_207682:437	Kif1b	INSIDE	1.716	3.683	258.15	950.86	6.319	229.26	1448.71
A_68_P28915541	chr13:30228560-30228604	NM_153546:224	Mboat1	INSIDE	1.716	4.650	5057.74	23518.34	7.979	3984.22	31790.67
A_68_P23985683	chr5:111849467-111849511	NM_001081235:2303	Mn1	INSIDE	1.716	3.154	537.33	1694.76	5.412	481.21	2604.08
A_68_P24904253	chr6:142335519-142335563	NM_001204907:67	Recql	INSIDE	1.716	2.797	4496.67	12578.37	4.800	3780.54	18145.67
A_68_P26890104	chr9:122477963-122478007	NR_015610:-3634	9530059O14Rik	PROMOTER	1.715	2.017	1416.52	2857.29	3.459	1128.93	3905.17
A_68_P23612481	chr5:37633390-37633434	NM_007765:-3618	Crmp1	PROMOTER	1.715	4.336	649.92	2817.97	7.435	538.48	4003.66
A_68_P30253796	chr15:59205558-59205602	NM_153548:127	E430025E21Rik	INSIDE	1.715	7.918	3792.74	30030.63	13.577	2640.05	35843.98
A_68_P22509722	chr3:127335595-127335641	NM_009718:-444	Neurog2	PROMOTER	1.715	2.334	539.14	1258.42	4.004	417.61	1672.11
A_68_P30353507	chr15:77137504-77137548	NM_001110827:-43	Rbfox2	PROMOTER	1.715	2.280	405.10	923.60	3.911	360.13	1408.46
A_68_P21527966	chr2:112105941-112105985	NM_133649:-508	Slc12a6	PROMOTER	1.715	1.556	781.59	1216.41	2.669	608.90	1625.27
A_68_P25261701	chr7:86680448-86680492	ENSMUST00000141822:35468		DOWNSTREAM	1.715	3.255	1707.77	5559.10	5.582	1369.99	7646.90
A_68_P20827009	chr1:173200884-173200928	NM_020579:448	B4galt3	INSIDE	1.714	5.863	2039.79	11958.50	10.047	1518.05	15252.02
A_68_P25009419	chr7:26067406-26067450	NM_001110131:231	Cic	INSIDE	1.714	5.002	3250.76	16259.68	8.575	2867.73	24589.71
A_68_P23254538	chr4:120690017-120690061	NM_133716:-186	Smap2	PROMOTER	1.714	4.098	636.02	2606.32	7.024	524.34	3683.03
A_68_P23817348	chr5:77086896-77086940	ENSMUST00000125922:173		INSIDE	1.714	2.665	1380.62	3679.33	4.568	1126.22	5144.39
A_68_P23644443	chr5:43625072-43625116	NM_001177379:393	Cpeb2	INSIDE	1.713	5.653	2539.23	14353.61	9.685	1936.44	18754.98
A_68_P29403726	chr14:11994369-11994413	NM_010210:156	Fhit	INSIDE	1.713	3.069	5639.46	17306.04	5.257	4585.36	24106.61
A_68_P32385145	chrX:50341393-50341437	NM_013556:160	Hprt	INSIDE	1.713	5.394	1232.71	6648.69	9.240	713.22	6590.19
A_68_P26764036	chr9:99336932-99336976	NM_008624:177	Mras	INSIDE	1.713	3.924	3458.26	13570.25	6.722	2687.56	18066.21

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P29001576	chr13:45485361-45485405	NM_181043:57	Mylip	INSIDE	1.713	1.479	1688.38	2496.84	2.533	1298.46	3288.58
A_68_P28039252	chr11:95374960-95375004	NM_130858:897	Nxph3	INSIDE	1.713	3.388	3144.62	10653.15	5.802	2466.83	14312.08
A_68_P23584119	chr5:32761375-32761419	NM_172707:54	Ppp1cb	INSIDE	1.713	3.796	5314.37	20175.38	6.503	4182.75	27199.38
A_68_P27926352	chr11:75300162-75300206	NM_138659:-94	Prpf8	PROMOTER	1.713	2.584	2946.26	7613.67	4.425	2454.06	10860.23
A_68_P21902494	chr2:179991894-179991938	NM_025587:-167	Rps21	PROMOTER	1.713	9.493	3506.19	33283.25	16.258	2557.31	41577.61
A_68_P26847329	chr9:114887053-114887097	CCDS52952.1:4751		DOWNSTREAM	1.713	7.635	2948.35	22510.50	13.079	1995.00	26092.04
A_68_P28706885	chr12:106248338-106248382	NM_172500:-341	4831426I19Rik	PROMOTER	1.712	5.463	6987.51	38171.76	9.353	5071.87	47438.28
A_68_P24127315	chr5:138182692-138182736	NM_175521:-1488	6430598A04Rik	DIVERGENT_PROMOTER	1.712	3.004	1293.54	3886.35	5.143	1008.95	5189.40
A_68_P20268944	chr1:60466493-60466537	NM_001198570:52	Abi2	INSIDE	1.712	4.100	1797.03	7367.11	7.017	1504.43	10555.97
A_68_P31126791	chr17:29375001-29375045	NM_153166:-287	Cpne5	PROMOTER	1.712	2.642	673.07	1778.26	4.523	569.70	2576.69
A_68_P26234161	chr8:125074980-125075024	NM_001037298:227	Fam38a	INSIDE	1.712	3.407	554.37	1888.59	5.832	500.29	2917.83
A_68_P21932363	chr3:8462950-8462994	NR_033512:126	Gm6194	INSIDE	1.712	4.894	2868.01	14035.36	8.377	2247.66	18829.32
A_68_P27537124	chr10:127058798-127058842	NM_008512:-616	Lrp1	PROMOTER	1.712	2.092	4941.30	10335.66	3.581	4217.40	15102.89
A_68_P30447388	chr15:93349565-93349609	NM_001033217:76736	Prickle1	INSIDE	1.712	1.704	1895.94	3231.44	2.918	1539.71	4493.14
A_68_P31107655	chr17:26122056-26122100	NM_153140:36727	Rab11fip3	DOWNSTREAM	1.712	6.619	986.65	6530.67	11.332	855.11	9690.13
A_68_P22315261	chr3:88520728-88520772	NM_001163310:-25	Rit1	PROMOTER	1.712	4.393	2291.16	10065.31	7.521	1802.82	13558.61
A_68_P28277266	chr12:19710348-19710392	BC012645:386747		INSIDE	1.712	5.328	2009.26	10704.84	9.122	1558.95	14220.18
A_68_P23678475	chr5:49916199-49916243	ENSMUST00000087395:-280		PROMOTER	1.712	1.441	1179.39	1699.97	2.468	1102.21	2719.84
A_68_P26867372	chr9:118515925-118515969	NM_133721:120	Itga9	INSIDE	1.711	3.220	367.80	1184.40	5.510	296.16	1631.77
A_68_P21322072	chr2:71711713-71711757	NM_172665:406	Pdk1	INSIDE	1.711	2.500	555.31	1388.44	4.279	440.50	1884.90
A_68_P21836025	chr2:167363730-167363774	NM_011427:26	Snai1	INSIDE	1.711	1.602	1591.40	2549.53	2.740	1316.52	3607.71
A_68_P29672987	chr14:65977066-65977114	NM_199029:-422	Zfp395	PROMOTER	1.711	3.926	498.77	1958.26	6.719	434.67	2920.36
A_68_P24954136	chr7:6083754-6083798	NM_001013012:23797	Zfp787	INSIDE	1.711	3.719	1970.48	7328.70	6.364	1617.93	10296.73
A_68_P24864304	chr6:134878874-134878918	NR_037955:-213	1190002F15Rik	PROMOTER	1.710	3.687	1160.62	4279.02	6.305	851.08	5366.07
A_68_P23753715	chr5:65361156-65361200	NM_026667:-135	Fam114a1	DIVERGENT_PROMOTER	1.710	4.115	2530.52	10412.20	7.037	2134.05	15016.51
A_68_P25096865	chr7:53356200-53356244	NM_001204411:-88	Kcnj11	PROMOTER	1.710	7.334	10124.04	74246.41	12.539	6198.09	77718.21
A_68_P30397291	chr15:84684245-84684289	NM_001081166:2293	Phf21b	INSIDE	1.710	4.195	3058.48	12831.61	7.173	2343.68	16811.35
A_68_P23531274	chr5:21850512-21850556	NM_011261:-11	Reln	PROMOTER	1.710	5.008	3601.55	18035.54	8.563	3038.50	26017.57
A_68_P25102011	chr7:54175094-54175138	NM_021884:184	Tsg101	INSIDE	1.710	3.474	1126.98	3915.36	5.942	917.98	5454.39
A_68_P23317755	chr4:133024124-133024168			Unknown	1.710	2.913	1711.16	4983.75	4.982	1437.64	7161.96
A_68_P31157497	chr17:35226598-35226642	NM_178592:385	Abhd16a	INSIDE	1.709	2.371	2002.65	4748.68	4.052	1436.97	5822.04
A_68_P22415887	chr3:108830521-108830565	NM_001163567:-17	Fam102b	PROMOTER	1.709	30.067	421.02	12658.99	51.391	305.92	15721.46
A_68_P21078285	chr2:26236006-26236050	NM_172339:145	Snapc4	INSIDE	1.709	3.792	4307.71	16333.25	6.478	3441.90	22297.41
A_68_P28974164	chr13:40824040-40824084	NM_001122948:1750	Tcfap2a	INSIDE	1.709	4.053	3801.80	15408.83	6.928	3002.30	20798.76
A_68_P21741665	chr2:150730549-150730593	NM_024465:-103	Abhd12	DIVERGENT_PROMOTER	1.708	3.632	2876.84	10449.71	6.204	2289.56	14203.41
A_68_P29619756	chr14:56381232-56381276	NM_020490:990	Ltb4r2	INSIDE	1.708	1.671	743.80	1242.88	2.855	716.65	2045.84
A_68_P26079854	chr8:97381360-97381404	NM_009090:33	Polr2c	INSIDE	1.708	8.059	1623.42	13082.40	13.768	1177.99	16217.94
A_68_P23317106	chr4:132895104-132895148	NM_199306:104	Wdtc1	INSIDE	1.708	4.498	11435.70	51436.61	7.681	8078.16	62051.66
A_68_P21419479	chr2:90729985-90730029	NM_026161:4064	C1qtnf4	INSIDE	1.707	11.448	561.15	6424.04	19.545	476.10	9305.58
A_68_P24864235	chr6:134870715-134870759	NM_009875:318	Cdkn1b	INSIDE	1.707	1.405	1767.54	2483.14	2.397	1419.21	3402.40
A_68_P27173119	chr10:59681994-59682038	NM_016803:-8	Chst3	PROMOTER	1.707	1.891	3067.53	5801.21	3.228	2489.26	8036.45
A_68_P23280751	chr4:126234084-126234128	NM_175554:-117	Clspn	PROMOTER	1.707	5.348	1230.34	6580.06	9.127	1117.06	10195.26
A_68_P30672037	chr16:35769289-35769333	NM_153550:132	Dirc2	INSIDE	1.707	3.802	1819.91	6918.94	6.491	1445.82	9384.94
A_68_P22271218	chr3:80717646-80717690	NM_010298:-122	Glrb	PROMOTER	1.707	3.883	2691.97	10453.05	6.627	2172.05	14394.29
A_68_P25023658	chr7:29594290-29594344	NM_177301:-1592	Hnrnpl	PROMOTER	1.707	4.797	1710.77	8206.30	8.186	1221.68	10000.86
A_68_P24171753	chr5:147888406-147888450	NM_080795:-280	Lnx2	DIVERGENT_PROMOTER	1.707	3.199	8652.25	27677.32	5.461	6559.61	35820.20
A_68_P23609096	A_68_P23609096			Unknown	1.707	2.868	253.04	725.71	4.895	223.66	1094.77
A_68_P31376853	chr17:79753911-79753955	NM_026514:499	Cdc42ep3	INSIDE	1.706	1.929	1057.53	2040.31	3.292	870.61	2866.13
A_68_P24980375	chr7:16807208-16807254	NM_027883:151	Dhx34	INSIDE	1.706	2.067	963.48	1991.87	3.527	747.64	2637.04
A_68_P27551374	chr11:3232269-3232313	NM_178149:1557	Pik3ip1	INSIDE	1.706	2.224	832.12	1850.51	3.793	649.12	2462.26
A_68_P27968802	chr11:82684465-82684509	NM_001164570:-240	Rffl	PROMOTER	1.706	5.404	105512.20	570240.10	9.220	70913.33	653851.00

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31655789	chr18:42671379-42671423	NM_001039474:260	Tcerg1	INSIDE	1.706	7.326	13803.96	101132.70	12.500	9150.65	114384.80
A_68_P30476395	chr15:98606917-98606961	NM_011718:1643	Wnt10b	INSIDE	1.706	9.467	3105.78	29401.01	16.152	2449.64	39567.60
A_68_P23189066	chr4:106851077-106851121	NM_025617:-127	2210012G02Rik	DIVERGENT_PROMOTER	1.705	3.272	1742.72	5701.96	5.579	1469.17	8196.62
A_68_P24158559	chr5:144670369-144670413	NM_001172146:318	Aimp2	INSIDE	1.705	4.816	2415.13	11630.91	8.213	2055.23	16879.15
A_68_P23612479	chr5:37633037-37633081	NM_001136058:-260	Crmp1	PROMOTER	1.705	4.128	1558.86	6434.45	7.038	1230.62	8661.63
A_68_P28185591	chr11:120470102-120470146	NM_153288:334	Npb	INSIDE	1.705	2.681	3291.21	8822.68	4.571	2345.49	10720.74
A_68_P25091297	chr7:52384491-52384535	NM_009438:-407	Rpl13a	PROMOTER	1.705	6.002	1607.98	9650.27	10.230	1214.67	12426.62
A_68_P29455867	chr14:22804205-22804249	NM_145459:4597	Zfp503	INSIDE	1.705	2.108	6999.60	14757.56	3.594	5362.43	19273.32
A_68_P27835628	chr11:59041341-59041385	NM_001130408:302	Arf1	INSIDE	1.704	4.375	592.46	2591.78	7.456	507.66	3785.08
A_68_P20834309	chr1:174562662-174562706	NM_026725:421	Dusp23	INSIDE	1.704	4.278	19244.57	82328.57	7.290	13306.05	97004.34
A_68_P21826983	chr2:165818573-165818617	NM_008679:458	Ncoa3	INSIDE	1.704	7.206	5906.37	42563.88	12.282	4278.32	52547.31
A_68_P27898381	chr11:69809079-69809123	NM_030064:-172	Phf23	PROMOTER	1.704	1.792	4096.91	7341.58	3.054	2920.50	8919.54
A_68_P22388656	chr3:103718191-103718235	NM_172684:170	Rsbn1	INSIDE	1.704	3.997	845.40	3378.85	6.812	691.87	4712.77
A_68_P30489270	chr15:100877044-100877088	NM_011323:110365	Scn8a	DOWNSTREAM	1.704	1.428	2703.94	3861.00	2.433	2254.44	5485.81
A_68_P23447092	chr5:3802834-3802878	NM_001003909:253	Ankib1	INSIDE	1.703	3.584	749.53	2686.40	6.105	672.66	4106.67
A_68_P24423143	chr6:47403815-47403859	NM_012042:-486	Cul1	PROMOTER	1.703	5.922	1174.27	6954.62	10.083	914.15	9217.76
A_68_P21489528	chr2:104334070-104334114	NM_001145824:554	Hipk3	INSIDE	1.703	1.668	1201.67	2004.36	2.840	1086.32	3085.18
A_68_P30127809	chr15:34236397-34236441	NM_016762:-17	Matn2	PROMOTER	1.703	2.565	3731.02	9571.39	4.369	2799.86	12232.50
A_68_P31120336	chr17:28217206-28217250	NM_013687:301	Tcp11	INSIDE	1.703	8.975	36936.59	331494.10	15.286	22975.57	351212.70
A_68_P25360010	chr7:106289656-106289700	NM_178635:-24	Uvrag	PROMOTER	1.703	2.507	1624.33	4071.82	4.270	1259.73	5378.94
A_68_P27338392	chr10:90291975-90292019	NM_001177396:252561	Anks1b	INSIDE	1.702	6.325	1696.69	10730.82	10.766	1448.83	15598.30
A_68_P26014555	chr8:85856129-85856173	NM_001170691:235	Elmod2	INSIDE	1.702	4.294	2829.27	12149.53	7.307	2308.53	16868.67
A_68_P21257003	chr2:60047554-60047598	NM_020575:-416	Marchf7	PROMOTER	1.702	2.127	1773.27	3772.14	3.621	1423.23	5153.13
A_68_P27794924	chr11:51433455-51433500	NM_026631:203	Nhp2	INSIDE	1.702	3.715	4250.56	15790.13	6.324	3209.74	20297.16
A_68_P28873011	chr13:21560407-21560451	NM_025719:-58	Nkapl	PROMOTER	1.702	5.623	2171.94	12211.78	9.572	1787.51	17109.48
A_68_P25029775	chr7:30857776-30857820	NM_177889:44	Zfp82	INSIDE	1.702	2.524	1477.15	3728.99	4.296	1209.50	5196.36
A_68_P32846303	chr1:78485277-78485321	NM_011811:123	Farsb	INSIDE	1.701	2.498	580.73	1450.60	4.249	463.22	1968.35
A_68_P30849196	chr16:70314241-70314285	NM_028803:-69	Gbe1	PROMOTER	1.701	2.303	2485.26	5724.21	3.918	1985.75	7780.62
A_68_P22081218	chr3:40549756-40549800	NM_011020:244	Hspa4l	INSIDE	1.701	3.647	627.09	2287.30	6.203	700.15	4342.90
A_68_P26065137	chr8:94881817-94881861	NM_018826:144	Irx5	INSIDE	1.701	3.067	1410.84	4326.52	5.216	1114.31	5812.43
A_68_P29453037	chr14:22320470-22320514	NM_017479:1486	Myst4	INSIDE	1.701	8.500	7052.63	59950.60	14.457	5362.66	77527.39
A_68_P28137828	chr11:112643707-112643751	NM_011448:205	Sox9	INSIDE	1.701	3.547	3362.01	11926.44	6.035	2633.99	15895.53
A_68_P22931104	chr4:54958261-54958305	NM_172867:-2534	Zfp462	PROMOTER	1.701	2.761	1914.64	5286.90	4.698	1621.76	7619.02
A_68_P28081267	chr11:102623133-102623177	NM_001110778:402	Adam11	INSIDE	1.700	2.010	597.97	1201.94	3.417	526.77	1799.90
A_68_P25047313	chr7:35841354-35841398	NM_009884:209	Cebpg	INSIDE	1.700	1.809	3138.06	5676.12	3.075	2564.46	7886.72
A_68_P23523151	chr5:20387300-20387344	NM_172992:620	Phtf2	INSIDE	1.700	2.310	1113.80	2573.14	3.927	1022.76	4015.91
A_68_P28061204	chr11:99091669-99091713	NM_020618:641	Smarce1	INSIDE	1.700	1.808	1456.70	2633.66	3.073	1302.10	4000.92
A_68_P22752472	chr4:15872547-15872591	NM_026172:86	Decr1	INSIDE	1.699	5.267	2508.55	13212.65	8.947	2094.87	18743.45
A_68_P24218861	chr6:6829299-6829343	NM_010056:2748	Dlx5	INSIDE	1.699	2.436	1752.76	4269.76	4.138	1353.69	5601.47
A_68_P27697249	chr11:33743483-33743527	NM_001190885:81	Kcnip1	INSIDE	1.699	5.080	5765.99	29288.62	8.631	4620.64	39880.89
A_68_P27449326	chr10:110943860-110943904	NM_009344:541	Phlda1	INSIDE	1.699	4.686	709.78	3326.28	7.963	558.04	4443.61
A_68_P31934221	chr19:6363781-6363825	NM_001110791:113	Sf1	INSIDE	1.699	2.366	508.77	1203.74	4.020	393.59	1582.14
A_68_P25588514	chr7:148577796-148577840	NM_011528:-240	Taldo1	PROMOTER	1.699	1.899	1080.94	2052.65	3.227	874.05	2820.31
A_68_P20457301	chr1:95651221-95651265	NM_025920:173	Thap4	INSIDE	1.699	10.560	1017.56	10745.42	17.936	928.45	16652.85
A_68_P21826276	chr2:165671382-165671427	NM_027230:38784	Zmynd8	INSIDE	1.699	7.060	678.38	4789.61	11.993	547.10	6561.33
A_68_P32364063	chrX:45698568-45698612	NM_178782:4056	Bcorl1	INSIDE	1.698	3.139	2990.20	9385.67	5.330	1496.39	7975.42
A_68_P25954148	chr8:73321826-73321870	NM_199308:-5516	Mast3	PROMOTER	1.698	3.752	5167.04	19388.07	6.371	3777.88	24067.35
A_68_P32227000	chr19:60832730-60832774	NM_178421:863	Nanos1	INSIDE	1.698	1.374	2438.63	3350.63	2.333	1862.02	4344.11
A_68_P32766772	chrX:153930279-153930323	NM_009214:-322	Sms	PROMOTER	1.698	4.058	1323.76	5372.22	6.890	777.52	5357.23
A_68_P32552603	chrX:96133526-96133570	NM_207633:429	Yipf6	INSIDE	1.698	2.647	821.91	2175.68	4.496	459.10	2064.03
A_68_P25657178	chr8:11728695-11728739	NM_001113517:612	Arhgef7	INSIDE	1.697	4.997	1742.71	8709.00	8.478	1385.60	11747.66

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P21516743	chr2:109533914-109533958	NM_001048142:217	Bdnf	INSIDE	1.697	3.450	2201.21	7593.39	5.853	1533.04	8973.33
A_68_P30363892	chr15:78858298-78858342	NM_008197:-321	H1f0	PROMOTER	1.697	1.440	972.76	1400.49	2.443	844.95	2064.48
A_68_P21417961	chr2:90420785-90420829	NM_008982:-2	Ptprj	PROMOTER	1.697	5.256	745.42	3917.71	8.919	603.84	5385.76
A_68_P23405733	chr4:149745839-149745883	NM_001085492:89836	Rere	INSIDE	1.697	2.122	4707.06	9988.62	3.601	3562.93	12828.77
A_68_P24452215	chr6:52664021-52664065	NM_025816:320	Tax1bp1	INSIDE	1.697	6.629	2894.54	19187.84	11.248	2434.57	27383.92
A_68_P23591177	chr5:34124884-34124928	NM_019694:447	Letm1	INSIDE	1.696	3.111	1436.53	4468.72	5.276	1267.90	6689.45
A_68_P31926196	chr19:4989991-4990035	NM_153553:-41	Npas4	PROMOTER	1.696	2.125	311.58	662.19	3.605	264.17	952.35
A_68_P23617871	chr5:38550739-38550783	NM_010942:-54	Nsg1	PROMOTER	1.696	3.491	4284.39	14957.57	5.920	3403.27	20146.35
A_68_P21130445	chr2:34769374-34769418	NM_028716:100	Phf19	INSIDE	1.696	2.328	393.02	914.86	3.947	279.14	1101.68
A_68_P30366260	chr15:79233510-79233554	NM_172608:201	Tmem184b	INSIDE	1.696	2.289	1282.09	2934.90	3.882	1107.15	4297.46
A_68_P21105309	chr2:30657215-30657259	NM_198000:-9	1700001O22Rik	PROMOTER	1.695	3.081	983.14	3028.58	5.223	817.28	4268.44
A_68_P20153982	chr1:37486790-37486834	NM_198006:136	6330578E17Rik	INSIDE	1.695	2.028	3468.44	7034.36	3.437	2727.80	9375.07
A_68_P31950789	chr19:10531506-10531550	NM_001111140:409	Lrrc10b	INSIDE	1.695	1.584	591.01	936.18	2.684	514.45	1380.87
A_68_P21777851	chr2:157386103-157386147	NM_010923:279	Nnat	INSIDE	1.695	4.656	5260.47	24494.02	7.893	3548.90	28010.42
A_68_P23696525	chr5:53132855-53132899	NM_025951:64	Pi4k2b	INSIDE	1.695	5.578	1428.36	7967.54	9.456	1312.72	12413.29
A_68_P30589177	chr16:20718065-20718109	NM_145632:188	Polr2h	INSIDE	1.695	2.321	1698.55	3942.10	3.934	1393.67	5482.07
A_68_P23321241	chr4:133684793-133684837	NM_080559:-146	Sh3bgrl3	PROMOTER	1.695	3.600	2045.37	7362.38	6.101	1544.79	9425.19
A_68_P24118628	chr5:136410394-136410438	NM_018871:95	Ywhag	INSIDE	1.695	1.624	1284.33	2086.11	2.752	987.55	2718.20
A_68_P24513202	chr6:65621890-65621934	NM_172399:308	A930038C07Rik	INSIDE	1.694	3.364	496.39	1669.62	5.697	464.53	2646.23
A_68_P28731662	chr12:110290760-110290805	NM_001163175:15645	Begain	INSIDE	1.694	2.853	1011.07	2884.77	4.833	847.23	4094.86
A_68_P27278225	chr10:79144473-79144517	NM_177613:-445	Cdc34	PROMOTER	1.694	2.650	4981.62	13200.69	4.488	3951.36	17732.59
A_68_P28457807	chr12:57713035-57713080	NM_008701:1214	Nkx2-9	INSIDE	1.694	3.538	580.12	2052.72	5.995	556.78	3338.12
A_68_P24066931	chr5:125922400-125922444	NM_029752:485	Bri3bp	INSIDE	1.693	1.474	678.49	1000.22	2.495	592.40	1478.08
A_68_P23892217	chr5:92512328-92512372	NM_001080797:-407	G3bp2	PROMOTER	1.693	3.722	2491.50	9273.63	6.300	1946.07	12259.70
A_68_P21834182	chr2:167015184-167015228	NM_008420:-907	Kcnb1	PROMOTER	1.693	5.632	3446.00	19408.40	9.534	2638.55	25156.65
A_68_P30292506	chr15:66409382-66409426	NM_001081409:271	Phf20l1	INSIDE	1.693	2.130	765.44	1630.54	3.606	674.77	2432.95
A_68_P31087861	chr17:22058135-22058179	NM_001199048:41275	Zfp942	DOWNSTREAM	1.693	6.043	8521.82	51496.41	10.228	6647.56	67992.19
A_68_P28513315	chr12:70299066-70299110	NM_027269:328	1110034A24Rik	INSIDE	1.692	2.946	4125.79	12154.63	4.984	3535.00	17617.39
A_68_P30338802	chr15:74503171-74503215	NM_018790:-192	Arc	PROMOTER	1.692	3.131	5011.73	15690.22	5.298	3499.47	18539.99
A_68_P29040998	chr13:53024981-53025025	NM_016709:44	Auh	INSIDE	1.692	3.051	17814.71	54352.38	5.163	14317.06	73919.36
A_68_P28059222	chr11:98768831-98768880	NM_001025779:-347	Cdc6	PROMOTER	1.692	7.625	1315.70	10031.63	12.899	995.61	12841.84
A_68_P28153287	chr11:115264936-115264980	NM_026729:-121	Ict1	PROMOTER	1.692	2.679	1149.83	3080.74	4.535	929.72	4216.00
A_68_P23394435	chr4:147822699-147822743	NM_020009:30	Mtor	INSIDE	1.692	5.778	2393.80	13830.38	9.777	1997.31	19527.03
A_68_P30018904	chr15:11836154-11836198	NM_001039181:-747	Npr3	PROMOTER	1.692	2.096	1637.38	3432.46	3.547	1416.00	5023.16
A_68_P26165552	chr8:113443992-113444036	NM_009179:250	St3gal2	INSIDE	1.692	4.347	2103.08	9142.78	7.357	1692.26	12450.05
A_68_P28595535	chr12:85292140-85292184	NM_023633:605	2410016O06Rik	INSIDE	1.691	3.618	1248.07	4515.38	6.118	1021.70	6251.02
A_68_P24371747	chr6:37249971-37250015	NM_001081206:-16	Dgki	PROMOTER	1.691	3.057	2279.23	6968.62	5.169	1966.19	10162.98
A_68_P31253727	chr17:56219020-56219064	NM_008233:-37	Hdgfrp2	DIVERGENT_PROMOTER	1.691	2.480	1095.39	2716.84	4.194	842.04	3531.18
A_68_P25088095	chr7:51804301-51804346	NM_011131:-138	Pold1	PROMOTER	1.691	2.746	3343.13	9180.62	4.645	2543.73	11815.50
A_68_P28768143	chr12:117724447-117724491	NM_011215:276	Ptprn2	INSIDE	1.691	7.523	3494.12	26285.46	12.721	2807.79	35716.92
A_68_P27542729	chr10:128133023-128133067	NM_177411:280	Rab5b	INSIDE	1.691	2.472	2685.10	6638.46	4.180	2268.41	9481.84
A_68_P23407530	chr4:150026271-150026315	NM_173774:-9	Slc45a1	PROMOTER	1.691	6.326	669.12	4233.06	10.699	664.88	7113.70
A_68_P24759109	chr6:113327446-113327490	NM_133932:46	Tada3	INSIDE	1.691	3.894	1254.60	4885.71	6.584	1005.79	6621.83
A_68_P25798746	chr8:40068990-40069034	NM_030254:92	Tusc3	INSIDE	1.691	3.748	1215.15	4554.28	6.337	912.00	5779.74
A_68_P25589538	chr7:148725824-148725868	NM_001142681:-90	Chid1	PROMOTER	1.690	2.157	1913.62	4128.24	3.645	1568.84	5718.28
A_68_P23976347	chr5:109986035-109986079	NM_001164735:1956	Crlf2	INSIDE	1.690	6.297	6501.58	40937.80	10.638	4205.31	44737.50
A_68_P23590170	chr5:33972447-33972492	NM_178390:-185	Fam53a	PROMOTER	1.690	4.543	10365.60	47091.67	7.678	7189.64	55203.47
A_68_P30497696	chr15:102236237-102236289	NM_013672:-484	Sp1	PROMOTER	1.690	2.365	620.64	1467.90	3.996	432.04	1726.52
A_68_P20162793	chr1:38954859-38954904	NM_145142:124	Chst10	INSIDE	1.689	7.615	3082.84	23475.55	12.859	2404.60	30921.32
A_68_P29055348	chr13:55589381-55589425	NM_001177371:35	Dbn1	INSIDE	1.689	2.635	18468.36	48663.72	4.451	14895.89	66305.82
A_68_P21107218	chr2:30997212-30997256	NM_001038700:294	Fnbp1	INSIDE	1.689	2.193	906.60	1988.37	3.704	750.28	2778.80

						Sham group			TiO$_2$-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26077217	chr8:96910495-96910539	NM_022331:117	Herpud1	INSIDE	1.689	5.907	2741.31	16193.24	9.979	2088.27	20837.91
A_68_P29604760	chr14:52723420-52723464	NM_001170981:261	Hnrnpc	INSIDE	1.689	2.918	2786.63	8130.06	4.928	2129.02	10490.78
A_68_P26258415	chr8:129116306-129116350	NM_001164598:1008	Irf2bp2	INSIDE	1.689	2.066	5891.25	12169.15	3.488	4892.94	17068.30
A_68_P28049252	chr11:97049849-97049893	NM_008379:-664	Kpnb1	PROMOTER	1.689	2.834	861.80	2442.52	4.787	836.84	4005.87
A_68_P24027251	chr5:119010546-119010590	NM_172424:-159	Med13l	PROMOTER	1.689	4.857	1353.13	6571.65	8.204	1178.58	9668.76
A_68_P27841048	chr11:59954437-59954481	NM_001037764:875	Rai1	INSIDE	1.689	8.399	414.52	3481.42	14.186	380.45	5397.20
A_68_P21911518	chr2:181326975-181327019	NM_001164597:170	Znf512b	INSIDE	1.689	8.697	1229.90	10697.01	14.691	829.14	12180.90
A_68_P25108786	chr7:56137106-56137150	NM_001013368:-717	E2f8	PROMOTER	1.688	4.136	2662.40	11010.37	6.982	2311.18	16136.32
A_68_P25951936	chr8:72976257-72976301	NM_001122830:24564	Klhl26	INSIDE	1.688	2.504	251.71	630.21	4.226	258.31	1091.58
A_68_P27922756	chr11:74651953-74651997	NM_010813:7549	Mnt	INSIDE	1.688	2.764	2511.91	6941.73	4.665	2144.68	10004.52
A_68_P24592748	chr6:83267406-83267450	NM_008638:170	Mthfd2	INSIDE	1.688	1.747	2418.50	4225.33	2.950	1884.64	5558.99
A_68_P31831023	chr18:74602569-74602613	NM_201600:318	Myo5b	INSIDE	1.688	3.289	454.80	1495.78	5.552	442.03	2454.05
A_68_P27503014	chr10:120787968-120788012	ENSMUST00000078515:7663		DOWNSTREAM	1.688	3.951	4977.57	19668.80	6.670	3764.39	25109.76
A_68_P23408691	chr4:150229048-150229092	NM_133753:-129	Errfi1	PROMOTER	1.687	3.514	1955.79	6873.54	5.929	1754.32	10401.00
A_68_P20897125	chr1:186551788-186551832	NM_008250:4562	Hlx	INSIDE	1.687	2.130	1138.59	2425.27	3.593	783.07	2813.61
A_68_P30495553	chr15:101858609-101858653	NM_010664:-16	Krt18	PROMOTER	1.687	2.231	1396.41	3114.85	3.763	1205.16	4535.54
A_68_P24623660	chr6:88674554-88674598	NM_001166250:-121	Mgll	PROMOTER	1.687	7.609	2563.93	19509.59	12.836	2246.95	28842.34
A_68_P32579464	chrX:102347631-102347675	AK136781:-2542		PROMOTER	1.687	3.600	31139.15	112101.40	6.072	23137.23	140486.60
A_68_P27085191	chr10:40402970-40403014	NM_177793:-95	9030224M15Rik	PROMOTER	1.686	2.249	1059.70	2383.52	3.792	947.30	3592.40
A_68_P28079629	chr11:102308671-102308715	NM_199200:285	Fam171a2	INSIDE	1.686	1.895	1504.43	2851.23	3.195	1335.07	4265.03
A_68_P31937108	chr19:7054737-7054781	NM_008020:172	Fkbp2	INSIDE	1.686	3.435	4409.51	15146.83	5.790	3177.15	18395.36
A_68_P31938321	chr19:7239801-7239845	NM_134147:108565	Macrod1	INSIDE	1.686	7.484	804.27	6019.42	12.615	664.54	8383.14
A_68_P27931783	chr11:76212254-76212298	NM_008750:367	Nxn	INSIDE	1.686	2.497	957.35	2390.08	4.210	767.91	3232.83
A_68_P31065956	chr17:15635037-15635081	NM_011185:182	Psmb1	INSIDE	1.686	3.282	3320.49	10897.30	5.535	2703.66	14963.44
A_68_P22063513	chr3:37319180-37319224	NM_001163511:1	Spata5	INSIDE	1.686	1.914	702.42	1344.19	3.226	643.62	2076.33
A_68_P28601528	chr12:86337027-86337071	NM_178363:-222	Ylpm1	PROMOTER	1.686	2.102	574.60	1208.09	3.545	463.35	1642.77
A_68_P25949121	chr8:72498323-72498367	NM_001113346:-62	Gatad2a	PROMOTER	1.685	5.348	4294.38	22967.53	9.012	3393.33	30579.31
A_68_P22378540	chr3:101815556-101815600	NM_178777:1511	Nhlh2	INSIDE	1.685	2.047	1560.93	3195.92	3.450	1276.07	4402.83
A_68_P27835010	chr11:58947926-58947970	NM_001171512:1929	Obscn	INSIDE	1.685	5.288	2672.68	14132.77	8.908	1825.71	16262.78
A_68_P30486488	chr15:100408907-100408951	NM_010127:7868	Pou6f1	INSIDE	1.685	3.988	537.02	2141.41	6.718	406.10	2728.33
A_68_P23599458	chr5:35621995-35622039	NM_007418:802	Adra2c	INSIDE	1.684	1.754	1240.19	2175.88	2.955	1041.02	3076.60
A_68_P26022557	chr8:87427077-87427121	NM_010635:1272	Klf1	INSIDE	1.684	1.831	1470.19	2692.40	3.084	1256.92	3876.80
A_68_P20029518	chr1:10983714-10983758	NM_029525:191	Prex2	INSIDE	1.684	7.473	2583.25	19305.26	12.589	1991.24	25067.06
A_68_P25587467	chr7:148401624-148401668	NM_025886:-112	Rassf7	DIVERGENT_PROMOTER	1.684	3.437	3882.06	13343.77	5.788	2929.80	16958.03
A_68_P26878665	chr9:120486576-120486620	NM_025974:5965	Rpl14	DOWNSTREAM	1.684	1.848	1419.03	2622.10	3.112	1187.42	3695.48
A_68_P30486834	chr15:100467426-100467470	NM_001033872:-152	Smagp	PROMOTER	1.684	1.671	1685.07	2816.45	2.815	1373.73	3866.96
A_68_P32217704	chr19:59246215-59246259	NM_009501:-1717	Vax1	PROMOTER	1.684	2.583	3160.67	8165.50	4.349	2353.74	10237.25
A_68_P25952317	chr8:73030680-73030724	NM_025577:-64	2810428I15Rik	PROMOTER	1.683	3.799	2054.35	7803.78	6.392	1708.79	10922.38
A_68_P32260277	chrX:11657663-11657707	NM_029510:-5	Bcor	PROMOTER	1.683	3.273	1448.95	4742.62	5.508	876.58	4828.15
A_68_P30655034	chr16:32877951-32877995	NM_001159349:103	Fyttd1	INSIDE	1.683	2.031	1813.46	3682.82	3.417	1446.40	4943.06
A_68_P27019249	chr10:26095302-26095346	NM_172787:-333	L3mbtl3	PROMOTER	1.683	2.585	3469.39	8967.44	4.350	2605.96	11334.74
A_68_P31938323	chr19:7240213-7240257	NM_134147:108977	Macrod1	INSIDE	1.683	3.757	3541.01	13303.16	6.324	2898.79	18332.07
A_68_P25458299	chr7:125591289-125591333	NM_138649:-4244	Syt17	PROMOTER	1.683	5.072	2430.45	12326.97	8.537	2032.42	17351.21
A_68_P31713387	A_68_P31713387			Unknown	1.683	3.053	751.00	2292.45	5.137	499.62	2566.44
A_68_P32467861	chrX:71638358-71638402	NM_025473:98	Fam3a	INSIDE	1.682	4.438	2419.47	10737.62	7.463	1406.81	10498.39
A_68_P28187039	chr11:120686317-120686365	NM_007988:-479	Fasn	PROMOTER	1.682	4.348	211.73	920.69	7.315	146.38	1070.69
A_68_P23955154	chr5:105844706-105844750	NM_001033550:-65	Lrrc8b	PROMOTER	1.682	3.890	293.53	1141.87	6.542	220.20	1440.47
A_68_P26015636	chr8:86118488-86118532	NM_027179:-120	Tecr	PROMOTER	1.682	3.147	1544.48	4861.07	5.293	1080.67	5720.53
A_68_P28157432	chr11:115970917-115970961	NM_001205081:611	Trim47	INSIDE	1.682	5.953	1398.78	8326.68	10.014	1042.65	10441.36
A_68_P22702205	chr4:5571555-5571599	NM_173426:251	Fam110b	INSIDE	1.681	6.974	1660.64	11580.84	11.726	1443.83	16930.61
A_68_P21784239	chr2:158492898-158492942	NM_001159662:50	Ppp1r16b	INSIDE	1.681	3.141	534.12	1677.59	5.279	476.36	2514.85

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27177053	chr10:60293340-60293384	NM_029770:967	Unc5b	INSIDE	1.681	2.249	1672.25	3760.27	3.780	1433.56	5418.84
A_68_P27907301	chr11:71564787-71564831	NM_177618:604	Wscd1	INSIDE	1.681	2.114	1199.61	2536.24	3.555	939.08	3338.21
A_68_P26600189	chr9:67480966-67481010			Unknown	1.681	1.691	3911.43	6613.30	2.842	3124.26	8879.43
A_68_P29643102	chr14:60796162-60796206	ENSMUST00000140924:192		INSIDE	1.681	1.602	871.83	1396.31	2.692	731.71	1969.76
A_68_P27855082	chr11:62461774-62461819	NM_198861:229	BC046404	INSIDE	1.680	3.524	546.37	1925.28	5.918	463.03	2740.32
A_68_P30500966	chr15:102785392-102785436	NM_001024842:458	Hoxc11	INSIDE	1.680	1.528	651.42	995.66	2.568	617.42	1585.58
A_68_P28803336	chr13:6648044-6648088	NM_019703:-96	Pfkp	PROMOTER	1.680	2.512	1278.91	3213.24	4.221	960.08	4052.59
A_68_P25375611	chr7:108970306-108970350	NM_008887:3502	Phox2a	INSIDE	1.680	2.025	711.87	1441.29	3.402	593.26	2018.49
A_68_P26787844	chr9:103663476-103663520	NM_178638:669	Tmem108	INSIDE	1.680	6.287	1990.88	12516.72	10.564	1533.51	16200.24
A_68_P22570418	chr3:138405498-138405542	NM_019571:362	Tspan5	INSIDE	1.680	4.376	1624.13	7106.38	7.351	1326.85	9753.60
A_68_P25219571	chr7:78850463-78850507			Unknown	1.680	1.438	1733.56	2493.05	2.415	1453.41	3510.59
A_68_P21109230	chr2:31315614-31315658	ENSMUST00000142448:13382		INSIDE	1.680	4.368	3026.10	13217.90	7.338	2593.91	19033.59
A_68_P24057001	chr5:124133506-124133550	NM_019765:772	Clip1	INSIDE	1.679	2.030	4945.46	10040.83	3.408	3721.90	12684.82
A_68_P30585937	chr16:20098035-20098079	NM_029436:430	Klhl24	INSIDE	1.679	2.574	1667.15	4291.61	4.323	1290.36	5578.07
A_68_P22530159	chr3:130813231-130813275	NM_010703:-136	Lef1	PROMOTER	1.679	2.180	900.09	1962.64	3.661	805.09	2947.17
A_68_P28875600	chr13:22073387-22073431	NM_001162929:346	Pom121l2	INSIDE	1.679	2.064	2503.61	5166.48	3.465	2055.02	7119.94
A_68_P23978771	chr5:110715204-110715248	NM_008993:-39	Pxmp2	DIVERGENT_PROMOTER	1.679	2.132	1477.40	3149.50	3.579	1219.87	4365.70
A_68_P31420286	chr17:87362969-87363013	NM_145491:540	Rhoq	INSIDE	1.679	3.749	3149.75	11807.75	6.296	2640.34	16622.98
A_68_P21752666	chr2:152880620-152880664	NM_001011732:23055	Xkr7	INSIDE	1.679	4.032	1917.47	7731.35	6.769	1550.20	10493.70
A_68_P32369653	chrX:47014094-47014138	ENSMUST00000121891:-20		PROMOTER	1.679	3.462	1160.79	4018.34	5.812	565.03	3283.98
A_68_P22314836	chr3:88425692-88425736	NM_001198912:399	Arhgef2	INSIDE	1.678	6.619	2870.12	18996.50	11.103	2409.48	26752.56
A_68_P26134609	chr8:108089863-108089907	NM_013477:56	Atp6v0d1	INSIDE	1.678	1.831	3683.70	6745.62	3.072	2918.43	8965.38
A_68_P26019650	chr8:86938371-86938415	NM_007578:-870	Cacna1a	PROMOTER	1.678	2.045	684.93	1400.45	3.431	614.58	2108.74
A_68_P29511369	chr14:32149798-32149842	NM_009796:-89	Capn7	PROMOTER	1.678	1.996	1279.78	2554.88	3.350	1041.19	3487.70
A_68_P27845567	chr11:60745252-60745296	NR_027800:95	Gm16516	INSIDE	1.678	3.036	937.83	2847.45	5.094	736.27	3750.27
A_68_P31425152	chr17:88197017-88197061	NM_199251:296	Kcnk12	INSIDE	1.678	3.655	1476.38	5396.14	6.132	1317.96	8082.18
A_68_P20634033	chr1:136457792-136457836	NM_152895:1060	Kdm5b	INSIDE	1.678	3.188	3541.18	11290.03	5.350	2979.49	15940.59
A_68_P20453282	chr1:94998673-94998717	NM_001110315:-252	Kif1a	PROMOTER	1.678	2.859	3722.33	10641.12	4.798	2631.13	12622.95
A_68_P27629548	chr11:19921114-19921161	NM_033523:96693	Spred2	INSIDE	1.678	2.842	623.29	1771.16	4.768	471.80	2249.64
A_68_P26974633	chr10:18038772-18038816			Unknown	1.678	3.825	2132.84	8158.55	6.421	1708.52	10969.63
A_68_P23154895	chr4:101091776-101091820	NM_001177602:-95	Ak4	PROMOTER	1.677	3.409	2375.71	8097.86	5.716	1900.31	10862.63
A_68_P23881743	chr5:90652818-90652862	NM_001033310:181	Cox18	INSIDE	1.677	4.340	544.98	2365.02	7.278	501.88	3652.77
A_68_P32119294	chr19:42222686-42222730	NM_183195:830	Marveld1	INSIDE	1.677	1.867	2718.81	5074.92	3.130	2118.62	6630.74
A_68_P25957541	chr8:74093810-74093856	NM_011977:1007	Slc27a1	INSIDE	1.677	1.544	2369.95	3658.60	2.589	1777.86	4603.28
A_68_P28447129	chr12:55414382-55414426			Unknown	1.677	5.392	728.27	3926.73	9.043	644.52	5828.41
A_68_P28576811	chr12:81744792-81744836	NM_007951:34	Erh	INSIDE	1.676	3.329	3732.87	12426.91	5.578	2902.64	16192.26
A_68_P28728718	chr12:109792810-109792854	NM_001163394:-97	Evl	PROMOTER	1.676	3.664	11008.12	40332.18	6.141	7496.69	46040.40
A_68_P23339951	chr4:137024980-137025024	NM_008305:285	Hspg2	INSIDE	1.676	1.544	880.05	1359.16	2.588	737.14	1907.69
A_68_P29453036	chr14:22320298-22320342	NM_017479:1314	Myst4	INSIDE	1.676	3.472	1367.44	4747.66	5.820	1163.03	6768.46
A_68_P25578920	chr7:146770604-146770648	NR_027857:-1930	Nkx6-2	PROMOTER	1.676	13.760	1343.65	18488.62	23.064	1050.68	24232.72
A_68_P27362366	chr10:94407709-94407753	NM_018797:-518	Plxnc1	PROMOTER	1.676	12.375	270.07	3342.19	20.744	254.69	5283.15
A_68_P21110386	chr2:31495757-31495801	NM_001123362:222	Prdm12	INSIDE	1.676	3.384	3165.24	10710.31	5.671	2441.02	13843.20
A_68_P31054932	chr17:13200778-13200822	NM_013671:96	Sod2	INSIDE	1.676	3.293	1214.17	3997.88	5.520	988.75	5457.47
A_68_P23982396	chr5:111309011-111309055	NM_024477:211	Ttc28	INSIDE	1.676	4.893	6002.93	29374.08	8.200	4758.82	39022.67
A_68_P25023459	A_68_P25023459			Unknown	1.676	3.074	1800.55	5535.34	5.153	1467.75	7563.92
A_68_P26538539	chr9:56644557-56644601	AK155716:4490		DOWNSTREAM	1.676	2.512	4014.41	10083.20	4.210	3008.83	12668.33
A_68_P22342541	chr3:94965423-94965467	NM_011351:-2851	Sema6c	PROMOTER	1.675	3.265	2048.94	6690.65	5.471	1637.88	8960.23
A_68_P30574556	chr16:17576756-17576800	NM_144852:-14	Slc7a4	PROMOTER	1.675	2.076	1704.75	3539.73	3.478	1349.50	4693.46
A_68_P24880087	chr6:137683557-137683601	NM_011499:-24	Strap	PROMOTER	1.675	4.583	993.38	4552.59	7.675	898.68	6897.24
A_68_P22475542	chr3:120966000-120966044	NM_178936:212	Tmem56	INSIDE	1.675	2.106	842.69	1774.56	3.527	788.56	2781.43
A_68_P32328720	chrX:35988386-35988430	NM_021550:-88	C1galt1c1	PROMOTER	1.674	1.782	1695.13	3021.24	2.983	981.43	2927.47

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P23362371	chr4:140695718-140695762	NM_001025608:-29	D4Ertd22e	DIVERGENT_PROMOTER	1.674	1.754	970.90	1703.27	2.937	788.18	2314.72
A_68_P22081210	chr3:40548895-40548939	NM_011020:-618	Hspa4l	PROMOTER	1.674	3.368	1544.20	5200.55	5.638	1142.24	6439.66
A_68_P25088126	chr7:51807778-51807822	NM_009473:1493	Nr1h2	INSIDE	1.674	12.326	8310.29	102431.80	20.637	5463.46	112750.90
A_68_P23318161	chr4:133101757-133101801	NM_010948:164	Nudc	INSIDE	1.674	6.262	3142.55	19678.21	10.484	2430.84	25484.19
A_68_P24039106	chr5:120953388-120953432	NM_023625:222	Plbd2	INSIDE	1.674	3.995	959.96	3834.81	6.686	724.31	4842.55
A_68_P24864240	chr6:134871160-134871204	NM_009875:764	Cdkn1b	INSIDE	1.673	2.662	3361.10	8948.92	4.453	2603.18	11592.14
A_68_P28947125	chr13:36209443-36209487	NM_001039189:185	Fars2	INSIDE	1.673	3.957	2648.53	10479.59	6.621	2399.06	15884.25
A_68_P30884140	chr16:76372608-76372652	NM_173440:664	Nrip1	INSIDE	1.673	1.856	339.43	630.12	3.106	264.27	820.80
A_68_P31918148	chr19:3575782-3575826	NM_001164159:-55	Ppp6r3	PROMOTER	1.673	1.972	7854.17	15489.25	3.299	5282.36	17424.43
A_68_P21890548	chr2:178142227-178142271	NM_177191:115	Sycp2	INSIDE	1.673	4.488	7874.68	35339.82	7.508	6281.03	47156.69
A_68_P24810492	chr6:122751807-122751851	ENSMUST00000165884:-170		PROMOTER	1.673	2.515	1274.24	3204.41	4.207	950.85	3999.78
A_68_P25592704	chr7:149246956-149247000	NM_028308:-39	2700078K21Rik	PROMOTER	1.672	3.416	1686.03	5759.23	5.712	1471.01	8402.10
A_68_P23880193	chr5:90312354-90312398	NM_001081401:-17	Adamts3	PROMOTER	1.672	1.889	2641.21	4989.44	3.159	2203.61	6960.59
A_68_P24004993	chr5:115061259-115061303	NM_001004180:43021	BC057022	INSIDE	1.672	4.702	9280.21	43633.32	7.863	6289.56	49452.98
A_68_P29571979	chr14:46277367-46277411	NM_001039106:430	Ddhd1	INSIDE	1.672	3.868	8539.33	33027.56	6.465	7021.19	45391.26
A_68_P28198379	chr12:4038471-4038515	NM_001082483:423	Efr3b	INSIDE	1.672	4.411	3726.36	16435.80	7.373	2986.38	22017.64
A_68_P25176077	chr7:71432423-71432467	NM_172742:-111	Mtmr10	PROMOTER	1.672	1.737	383.89	666.99	2.905	368.33	1070.00
A_68_P27280126	chr10:79440000-79440044	NM_001003949:7053	ORF61	INSIDE	1.672	6.151	2393.85	14723.85	10.284	1638.63	16851.02
A_68_P26038373	chr8:90485269-90485313	NM_033327:-1796	Zfp423	PROMOTER	1.672	9.737	873.67	8506.77	16.277	734.07	11948.65
A_68_P27903827	chr11:70817840-70817884	NM_178367:72	Dhx33	INSIDE	1.671	2.399	725.62	1740.90	4.009	589.10	2361.84
A_68_P28334080	chr12:32634604-32634648	NM_153198:774	Hbp1	INSIDE	1.671	4.411	447.47	1973.84	7.371	388.89	2866.41
A_68_P24592782	chr6:83275935-83275979	NM_145571:-76	Mobkl1b	DIVERGENT_PROMOTER	1.671	2.406	1230.29	2959.67	4.021	999.48	4018.65
A_68_P33005865	A_68_P33005865			Unknown	1.671	5.393	410.63	2214.72	9.013	385.94	3478.49
A_68_P23593951	chr5:34712334-34712378	ENSMUST00000042234:-705		PROMOTER	1.671	1.855	3498.72	6491.48	3.100	2620.62	8123.74
A_68_P31341460	chr17:72953599-72953644	NM_007439:26	Alk	INSIDE	1.670	1.974	746.72	1473.91	3.296	648.62	2137.91
A_68_P24980722	chr7:16885176-16885220	NM_133234:-9733	Bbc3	PROMOTER	1.670	1.553	819.54	1272.83	2.594	910.99	2363.33
A_68_P29773624	chr14:84843322-84843371	NM_001013753:-23	Pcdh17	PROMOTER	1.670	2.058	854.99	1759.49	3.436	615.33	2114.28
A_68_P22484168	chr3:122432681-122432725	NM_153422:627	Pde5a	INSIDE	1.670	4.891	2019.15	9875.76	8.168	1558.90	12732.31
A_68_P24114960	chr5:135625731-135625775	NM_013763:172	Tbl2	INSIDE	1.670	3.290	1092.96	3595.91	5.494	907.58	4986.45
A_68_P28119631	chr11:109473059-109473103	NM_145940:-377	Wipi1	PROMOTER	1.670	3.869	13921.71	53858.78	6.460	10681.12	68996.43
A_68_P25051309	chr7:36588072-36588116	NM_177739:-86	Zfp507	PROMOTER	1.670	3.097	459.55	1423.12	5.172	360.31	1863.39
A_68_P29672919	chr14:65962555-65962599	AK028094:17409		DOWNSTREAM	1.670	3.682	6108.28	22488.65	6.147	4492.65	27616.55
A_68_P20972053	chr2:5058960-5059004	NM_028804:161	Ccdc3	INSIDE	1.669	4.180	648.95	2712.90	6.979	534.03	3726.86
A_68_P23250457	chr4:119959679-119959723	NM_194060:166	Foxo6	INSIDE	1.669	2.359	676.94	1597.15	3.937	600.87	2365.41
A_68_P32625282	chrX:117040767-117040811	NM_053114:-16	Pabpc5	PROMOTER	1.669	4.541	2248.43	10209.47	7.577	1645.15	12464.63
A_68_P28875767	chr13:22097925-22097969	NM_019429:3664	Prss16	INSIDE	1.669	3.391	1172.37	3975.96	5.660	929.50	5260.78
A_68_P23576447	chr5:31395717-31395761	NM_011773:162	Slc30a3	INSIDE	1.669	3.772	1644.43	6202.22	6.295	1250.89	7873.75
A_68_P27952852	chr11:79967507-79967551	NM_172133:-135	Adap2	PROMOTER	1.668	4.869	1002.22	4879.41	8.122	801.83	6512.36
A_68_P24167580	chr5:147072895-147072939	NM_153599:29666	Cdk8	INSIDE	1.668	2.767	354.85	982.03	4.616	296.88	1370.38
A_68_P20391718	chr1:82287606-82287650	NM_010570:386	Irs1	INSIDE	1.668	4.812	2917.59	14038.80	8.028	2754.29	22111.30
A_68_P28004910	chr11:89163525-89163569	NM_008711:327	Nog	INSIDE	1.668	1.556	2076.56	3230.68	2.595	1813.25	4705.13
A_68_P24951673	chr7:4981991-4982035	NM_001033383:10035	Zfp865	INSIDE	1.668	3.797	2167.70	8231.60	6.333	1920.71	12163.49
A_68_P33005883	A_68_P33005883			Unknown	1.668	6.752	372.39	2514.24	11.259	306.52	3451.06
A_68_P30969546	chr16:92498878-92498922	NM_172469:509	Clic6	INSIDE	1.667	6.182	3756.63	23221.76	10.303	2929.22	30179.61
A_68_P30113003	chr15:31154105-31154149	NM_146057:-13	Dap	PROMOTER	1.667	3.313	3856.43	12776.00	5.524	3116.01	17212.56
A_68_P24052812	chr5:123350466-123350510	NM_013910:-129	Kdm2b	PROMOTER	1.667	3.445	921.33	3173.67	5.744	809.91	4651.76
A_68_P28936013	chr13:34094245-34094289	NR_028309:352	Serpinb6a	INSIDE	1.667	2.063	1185.68	2445.85	3.438	1038.65	3571.02
A_68_P31412116	chr17:86087149-86087193	NM_011380:424	Six2	INSIDE	1.667	2.596	711.32	1846.23	4.328	623.31	2697.39
A_68_P29703989	chr14:71289781-71289825	NM_008115:-134	Gfra2	PROMOTER	1.666	6.103	2103.42	12836.84	10.165	1664.63	16920.80
A_68_P21077785	chr2:26171010-26171055	NM_001199146:-20	Gpsm1	PROMOTER	1.666	9.846	2502.21	24637.89	16.405	2243.11	36797.72
A_68_P32140499	chr19:45857773-45857817	NM_023799:-13	Mgea5	PROMOTER	1.666	6.837	801.80	5481.57	11.390	704.42	8023.62

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25050056	chr7:36369864-36369908	NM_145840:715	Rgs9bp	INSIDE	1.666	3.717	1154.63	4292.02	6.192	1035.92	6414.88
A_68_P28307270	chr12:28028339-28028383	NM_009234:-777	Sox11	PROMOTER	1.666	2.492	5072.19	12642.29	4.152	3722.72	15456.05
A_68_P27966238	chr11:82248332-82248376	NM_023438:45953	Tmem132e	INSIDE	1.666	6.280	392.39	2464.03	10.459	334.54	3499.15
A_68_P26134000	chr8:107995392-107995436	NM_026481:-92	Tppp3	PROMOTER	1.666	4.999	3639.91	18195.52	8.330	2948.59	24560.81
A_68_P28973959	chr13:40799401-40799445	ENSMUST00000069457:49		INSIDE	1.666	2.489	2892.03	7197.48	4.146	2339.63	9699.25
A_68_P33007795	chr4_random:128995-129039	NM_001033326:19215	Dhrsx	INSIDE	1.665	7.586	4871.29	36951.56	12.632	3359.62	42438.83
A_68_P22569284	chr3:138189919-138189963	NM_007917:786	Eif4e	INSIDE	1.665	4.216	1266.57	5340.30	7.018	1103.37	7743.61
A_68_P20875118	chr1:182262286-182262330	NR_003623:-1628	Gm5069	PROMOTER	1.665	2.628	2153.41	5658.70	4.375	1699.26	7433.81
A_68_P25652449	chr8:11008424-11008468	NM_001081212:-16	Irs2	PROMOTER	1.665	3.958	982.97	3891.03	6.591	988.57	6515.77
A_68_P23591267	A_68_P23591267			Unknown	1.665	4.040	288.57	1165.95	6.729	219.26	1475.35
A_68_P24636070	chr6:90938255-90938299			Unknown	1.665	1.851	336.69	623.25	3.082	268.57	827.71
A_68_P26749720	chr9:96790099-96790143	NM_153420:-279	Acpl2	PROMOTER	1.664	3.871	732.83	2837.06	6.444	609.12	3924.89
A_68_P27365819	chr10:95026630-95026674	NR_037212:-4697	Mir3058	PROMOTER	1.664	4.466	7057.96	31523.23	7.434	6155.54	45758.67
A_68_P32117861	chr19:41986212-41986256	NM_023418:-126	Pgam1	PROMOTER	1.664	2.604	2189.77	5702.93	4.335	1832.91	7945.02
A_68_P28137825	chr11:112643344-112643388	NM_011448:-157	Sox9	PROMOTER	1.664	1.701	4828.16	8213.36	2.830	3355.10	9494.71
A_68_P25042532	chr7:34953588-34953632	NM_016682:-62	Uba2	PROMOTER	1.664	13.458	665.13	8951.22	22.398	588.62	13184.03
A_68_P25005234	chr7:25292077-25292122	NM_146183:-6	Zfp428	PROMOTER	1.664	1.725	2355.04	4063.24	2.871	1775.29	5097.13
A_68_P22217916	chr3:68673757-68673801	NM_001167996:271	1110032F04Rik	INSIDE	1.663	3.292	653.04	2149.81	5.475	646.53	3539.97
A_68_P24797816	chr6:120244799-120244843	NM_198884:-243	B4galnt3	PROMOTER	1.663	4.357	3431.01	14947.66	7.245	2671.21	19353.42
A_68_P29488024	chr14:28435732-28435776	NM_177814:127	Erc2	INSIDE	1.663	4.562	1555.19	7095.31	7.589	1247.87	9469.50
A_68_P29723690	chr14:75131937-75131981	NM_016903:-193	Esd	PROMOTER	1.663	4.245	5108.14	21683.61	7.059	3639.86	25692.86
A_68_P24326454	chr6:29383341-29383385	NM_001081185:210	Flnc	INSIDE	1.663	1.445	6320.78	9136.28	2.403	4721.24	11346.29
A_68_P25174396	chr7:71082541-71082585	NM_021366:1239	Klf13	INSIDE	1.663	5.204	13884.08	72255.25	8.652	11746.07	101631.50
A_68_P30345384	chr15:75829239-75829283	NM_177922:5062	Mapk15	INSIDE	1.663	2.283	1737.25	3965.36	3.796	1347.49	5115.13
A_68_P29062977	chr13:56805003-56805048	NM_001164042:-3	Smad5	PROMOTER	1.663	6.202	2821.79	17499.50	10.311	2385.19	24592.75
A_68_P32467744	chrX:71613927-71613971	NM_145405:-82	Ubl4	PROMOTER	1.663	3.501	1792.31	6275.29	5.822	1302.37	7581.90
A_68_P24124212	chr5:137506063-137506107	NM_001039385:-80	Vgf	PROMOTER	1.663	2.955	535.21	1581.64	4.915	464.93	2285.03
A_68_P27287623	chr10:80599677-80599721	NM_010731:683	Zbtb7a	INSIDE	1.663	1.563	1306.00	2041.31	2.600	1135.28	2951.57
A_68_P21851410	chr2:169955855-169955909	NM_001033299:838	Zfp217	INSIDE	1.663	1.431	1120.11	1603.07	2.379	944.80	2248.13
A_68_P24430828	chr6:49023823-49023867	NM_029353:51	2410003K15Rik	INSIDE	1.662	2.935	2060.46	6047.62	4.877	1761.18	8589.71
A_68_P31114987	chr17:27341486-27341531	NM_146075:-125	Lemd2	PROMOTER	1.662	1.858	956.19	1776.83	3.088	785.44	2425.69
A_68_P27290094	chr10:80959100-80959144	NM_134009:-14	Ncln	PROMOTER	1.662	3.944	2154.24	8495.68	6.556	1834.97	12030.15
A_68_P27942685	chr11:78141893-78141937	NM_201406:-9	Pigs	PROMOTER	1.662	1.612	736.88	1187.49	2.678	654.41	1752.51
A_68_P31151050	chr17:34067192-34067236	NM_009059:376	Rgl2	INSIDE	1.662	1.844	5165.90	9526.14	3.065	3410.57	10453.66
A_68_P26579683	chr9:63870481-63870525	NM_008542:-636	Smad6	PROMOTER	1.662	2.949	2979.18	8784.45	4.901	2298.79	11266.06
A_68_P28048904	chr11:97000172-97000216	NM_198100:10832	Tbkbp1	INSIDE	1.662	4.015	955.93	3838.25	6.672	792.12	5284.78
A_68_P20345418	chr1:73954077-73954121	NM_027884:216923	Tns1	DOWNSTREAM	1.662	4.095	1102.23	4514.15	6.807	870.43	5925.32
A_68_P27938076	chr11:77328807-77328851	NM_026185:210	Abhd15	INSIDE	1.661	4.965	1329.88	6602.70	8.247	1178.66	9720.12
A_68_P21563665	chr2:118199048-118199092	NM_201367:85	Gpr176	INSIDE	1.661	2.525	975.61	2463.34	4.195	758.84	3183.08
A_68_P23997432	chr5:113739494-113739538	NM_172718:290	Sgsm1	INSIDE	1.661	4.145	4114.39	17054.40	6.886	3205.79	22073.60
A_68_P25377989	chr7:109416038-109416082	NM_009287:-277	Stim1	PROMOTER	1.661	5.566	1377.22	7666.18	9.247	1143.42	10572.66
A_68_P31326355	chr17:70318978-70319022	ENSMUST00000130971:240		INSIDE	1.661	1.412	1882.05	2656.86	2.345	1674.32	3925.97
A_68_P23961359	chr5:106887678-106887722	NM_001005477:-515	Barhl2	PROMOTER	1.660	2.219	607.95	1349.18	3.685	465.73	1716.21
A_68_P32364027	chrX:45694166-45694210	NM_178782:-346	Bcorl1	PROMOTER	1.660	4.598	1081.89	4974.40	7.632	723.01	5517.86
A_68_P24486168	chr6:59376435-59376479	NM_183183:-172	Gprin3	PROMOTER	1.660	2.105	1615.90	3401.38	3.494	1375.65	4807.21
A_68_P27065106	chr10:36226802-36226846	NM_001081208:212	Hs3st5	INSIDE	1.660	1.708	1289.14	2202.06	2.836	1048.96	2974.51
A_68_P30485948	chr15:100299486-100299530	NM_134093:44	Letmd1	INSIDE	1.660	2.013	1842.43	3709.41	3.343	1379.91	4612.61
A_68_P25031213	chr7:31145836-31145880	NM_175478:1933	Lrfn3	INSIDE	1.660	6.991	3361.08	23496.42	11.602	2447.42	28394.03
A_68_P25846165	chr8:49314031-49314075	NM_001145937:445992	Odz3	INSIDE	1.660	2.794	320.07	894.25	4.638	302.78	1404.39
A_68_P31420721	chr17:87424605-87424649	NM_008838:115	Pigf	INSIDE	1.660	2.008	871.61	1750.16	3.333	783.45	2610.98
A_68_P20083589	chr1:22540314-22540358	NM_001012623:272227	Rims1	INSIDE	1.660	1.572	1340.67	2107.75	2.610	1166.78	3045.41

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28862223	chr13:19487305-19487349	NM_024270:295	Stard3nl	INSIDE	1.660	1.728	1020.53	1763.43	2.869	858.88	2464.22
A_68_P23599469	chr5:35623311-35623355	NM_007418:2118	Adra2c	INSIDE	1.659	5.317	1510.31	8030.19	8.822	1307.97	11539.39
A_68_P20148721	chr1:36569446-36569490	NM_001039551:748	Cnnm3	INSIDE	1.659	5.939	2091.84	12424.11	9.855	1726.52	17014.04
A_68_P27285229	chr10:80217921-80217965	NM_199322:-8	Dot1l	PROMOTER	1.659	2.909	2296.28	6680.22	4.825	1829.74	8828.72
A_68_P30585939	chr16:20098297-20098341	NM_029436:692	Klhl24	INSIDE	1.659	2.204	1057.99	2331.82	3.656	989.42	3617.73
A_68_P22826133	chr4:33397493-33397537	NM_011884:229	Rngtt	INSIDE	1.659	2.930	1834.42	5374.19	4.859	1525.29	7411.58
A_68_P29648696	chr14:61791453-61791497	NM_172809:34181	Sacs	INSIDE	1.659	3.057	914.38	2795.69	5.073	777.56	3944.66
A_68_P28765899	chr12:117316302-117316346	NM_009511:129	Vipr2	INSIDE	1.659	1.819	1316.78	2395.76	3.018	1029.57	3107.40
A_68_P27995284	chr11:87452873-87452917	NM_001045527:22229	Hsf5	INSIDE	1.658	5.403	2219.32	11991.18	8.961	1829.83	16397.01
A_68_P24288408	chr6:21900000-21900044	NM_023626:408	Ing3	INSIDE	1.658	3.477	6884.72	23938.05	5.766	4668.75	26919.52
A_68_P21722727	chr2:147009567-147009611	NR_030769:-230	Nkx2-2as	PROMOTER	1.658	4.164	378.14	1574.57	6.904	306.78	2117.92
A_68_P30346619	chr15:76012289-76012333	NM_201394:13830	Plec	INSIDE	1.658	5.461	1257.05	6864.84	9.055	1034.03	9363.44
A_68_P30346599	chr15:76009927-76009971	NM_201394:16192	Plec	INSIDE	1.658	4.838	1926.06	9318.28	8.023	1489.19	11947.43
A_68_P22883653	chr4:45543529-45543573	NM_001033306:150	Shb	INSIDE	1.658	3.819	859.99	3284.17	6.333	816.57	5171.07
A_68_P22614372	chr3:146067861-146067905	NM_138744:232	Ssx2ip	INSIDE	1.658	6.185	795.13	4917.62	10.254	736.50	7552.35
A_68_P27846979	chr11:60988330-60988374	NM_001004143:209	Usp22	INSIDE	1.658	2.382	587.13	1398.64	3.949	512.90	2025.31
A_68_P23938671	chr5:102499208-102499252	NM_172882:-290	Wdfy3	PROMOTER	1.658	3.288	855.64	2813.62	5.451	689.08	3756.44
A_68_P29678557	chr14:66916156-66916200	NR_038077:-212	1700001G11Rik	PROMOTER	1.657	1.394	1033.06	1440.07	2.311	793.29	1832.91
A_68_P31108897	chr17:26337756-26337800	NM_008113:517	Arhgdig	INSIDE	1.657	6.939	5809.01	40307.93	11.500	4304.82	49505.05
A_68_P27476528	chr10:116018985-116019029	NM_001037846:-439	Cnot2	PROMOTER	1.657	3.208	4435.27	14229.05	5.315	3475.66	18474.40
A_68_P26590184	chr9:65757067-65757111	NM_173185:272	Csnk1g1	INSIDE	1.657	7.170	2904.33	20822.79	11.882	2120.45	25195.40
A_68_P22388169	chr3:103613288-103613332	NM_001025312:0	Dclre1b	INSIDE	1.657	8.165	1708.03	13946.79	13.526	1349.17	18249.39
A_68_P28976807	chr13:41315714-41315758	NM_019423:36	Elovl2	INSIDE	1.657	0.384	1063.81	408.94	0.637	991.98	632.02
A_68_P26394905	chr9:30234659-30234703	NM_028874:-233	Snx19	PROMOTER	1.657	1.766	790.61	1396.01	2.926	755.39	2210.60
A_68_P23320096	chr4:133467057-133467101	AK015234:372		INSIDE	1.657	1.740	1508.28	2624.10	2.883	1292.84	3727.63
A_68_P29102524	chr13:65361174-65361218	ENSMUST00000099425:350		INSIDE	1.657	3.466	742.09	2572.19	5.744	727.94	4181.38
A_68_P24084071	chr5:129106177-129106221	NR_015517:364	5930412G12Rik	INSIDE	1.656	2.695	2040.71	5500.05	4.464	1575.31	7032.18
A_68_P20796835	chr1:167775162-167775206	NM_001113391:56373	Cd247	INSIDE	1.656	3.749	1229.47	4609.55	6.210	1193.88	7414.07
A_68_P30478193	chr15:98924227-98924271	NM_176835:-5666	Dnajc22	DIVERGENT_PROMOTER	1.656	4.130	5541.49	22886.39	6.838	4719.82	32273.13
A_68_P28058704	chr11:98671394-98671438	NR_033551:-13	Gm12359	PROMOTER	1.656	3.705	8276.45	30660.92	6.135	6485.89	39792.04
A_68_P27840800	chr11:59918733-59918777	NM_009021:240	Rai1	INSIDE	1.656	3.280	677.65	2222.45	5.431	517.12	2808.25
A_68_P31208271	chr17:46811147-46811191	NM_144857:36	Rrp36	INSIDE	1.656	2.295	5152.14	11824.65	3.800	3977.79	15116.76
A_68_P24691294	chr6:100237868-100237912	NM_019743:-538	Rybp	PROMOTER	1.656	3.440	658.40	2264.60	5.697	567.63	3233.73
A_68_P25507562	chr7:134967999-134968043	NM_024414:25	Stx1b	INSIDE	1.656	2.692	6088.86	16388.52	4.459	4698.34	20947.61
A_68_P31982219	chr19:16855558-16855602	NM_173028:-163	Vps13a	PROMOTER	1.656	3.918	1634.12	6403.20	6.488	1341.32	8703.07
A_68_P31479231	chr18:7869684-7869728	NM_001146298:512	Wac	INSIDE	1.656	2.321	1157.71	2686.65	3.844	944.48	3630.44
A_68_P22903296	chr4:49072520-49072564	NM_178756:209	E130309F12Rik	INSIDE	1.655	1.726	2128.61	3672.93	2.856	1666.20	4758.16
A_68_P30596432	chr16:22162719-22162763	NM_183029:632	Igf2bp2	INSIDE	1.655	5.012	979.30	4907.86	8.295	862.69	7155.78
A_68_P28452657	chr12:56700590-56700634	NM_020287:709	Insm2	INSIDE	1.655	9.081	1368.34	12425.99	15.026	1009.74	15172.08
A_68_P21100497	chr2:29820983-29821027	NM_001076554:-75	Spna2	PROMOTER	1.655	1.873	8262.90	15476.18	3.100	6187.29	19181.71
A_68_P23742487	chr5:63157563-63157607	NM_178407:-168	Arap2	PROMOTER	1.654	4.428	1093.37	4841.67	7.324	873.88	6400.40
A_68_P26128337	chr8:106919324-106919368	NM_153582:250	Cmtm4	INSIDE	1.654	6.030	3389.72	20441.46	9.976	2593.04	25869.13
A_68_P22610589	chr3:145421770-145421814	NM_026993:137	Ddah1	INSIDE	1.654	3.326	2381.64	7920.16	5.501	1933.39	10634.74
A_68_P27041764	chr10:30562697-30562741	NM_013904:-129	Hey2	PROMOTER	1.654	2.910	517.85	1506.71	4.812	446.11	2146.52
A_68_P25953471	chr8:73223632-73223676	NM_010592:2017	Jund	INSIDE	1.654	4.674	1216.41	5685.67	7.731	1052.44	8136.16
A_68_P26920438	chr10:7445673-7445717	NM_011835:-103	Katna1	PROMOTER	1.654	1.716	3575.01	6133.04	2.837	2711.27	7691.58
A_68_P23334085	chr4:136025641-136025685	NM_024452:-13	Luzp1	PROMOTER	1.654	5.706	10787.59	61551.52	9.440	7883.57	74420.85
A_68_P28077571	chr11:101968496-101968540	NM_145435:572	Pyy	INSIDE	1.654	8.867	1245.68	11045.37	14.664	1014.87	14881.73
A_68_P28054168	chr11:97913868-97913912	NM_146028:886	Stac2	INSIDE	1.654	2.484	8806.47	21877.27	4.109	6437.64	26455.20
A_68_P25011349	chr7:26474463-26474507	NM_011577:2464	Tgfb1	INSIDE	1.654	4.639	1133.34	5257.87	7.675	964.32	7401.22
A_68_P20936911	chr1:193048707-193048751	ENSMUST00000139056:376		INSIDE	1.654	1.704	1637.26	2789.55	2.819	1242.74	3502.78

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28330749	chr12:32035950-32035994	NM_007861:330	Dld	INSIDE	1.653	4.600	1536.04	7066.43	7.607	1242.80	9453.52
A_68_P26350216	chr9:21855292-21855336	NM_010487:1153	Elavl3	INSIDE	1.653	2.648	559.24	1480.63	4.377	446.60	1954.97
A_68_P23896964	chr5:93370721-93370767	NM_001077596:43721	Shroom3	INSIDE	1.653	2.044	393.57	804.42	3.378	328.44	1109.39
A_68_P22236489	chr3:72861536-72861580	NM_198864:-693	Slitrk3	PROMOTER	1.653	2.647	8475.59	22433.80	4.376	6429.11	28135.05
A_68_P22185881	chr3:61963288-61963332			Unknown	1.653	6.500	1617.67	10514.98	10.745	1247.80	13407.95
A_68_P30387964	chr15:83197665-83197709	NR_027980:41	1700001L05Rik	INSIDE	1.652	4.523	7085.74	32046.29	7.470	5107.02	38149.22
A_68_P23342100	chr4:137351824-137351868	NM_007431:446	Alpl	INSIDE	1.652	2.796	617.01	1725.19	4.619	533.23	2463.21
A_68_P25712956	chr8:23916111-23916155	NM_001122820:-6	Ap3m2	PROMOTER	1.652	4.125	3610.71	14895.53	6.816	2789.42	19011.75
A_68_P31602497	chr18:32537058-32537102	NM_001083334:210	Bin1	INSIDE	1.652	1.753	1699.03	2977.56	2.895	1814.24	5252.63
A_68_P21748226	chr2:152053141-152053185	NM_007788:587	Csnk2a1	INSIDE	1.652	3.954	3066.05	12123.17	6.533	2172.35	14191.76
A_68_P29334871	chr13:113254322-113254366	NM_010560:67	Il6st	INSIDE	1.652	5.429	2889.77	15688.11	8.970	2431.44	21808.93
A_68_P31086236	chr17:21626256-21626300	NM_013843:327	Zfp53	INSIDE	1.652	1.868	1741.74	3253.80	3.086	1520.40	4691.44
A_68_P28743717	chr12:112615357-112615401	NM_183016:551	Cdc42bpb	INSIDE	1.651	11.373	1430.70	16271.87	18.774	1094.42	20546.89
A_68_P21425775	chr2:91815556-91815600	NM_011957:48749	Creb3l1	DOWNSTREAM	1.651	2.114	1190.64	2516.90	3.490	1000.79	3492.82
A_68_P28920307	chr13:31065636-31065680	NM_025588:258	Exoc2	INSIDE	1.651	1.876	3310.55	6212.09	3.098	2322.28	7193.72
A_68_P25678282	chr8:15027507-15027551	NM_029116:16504	Kbtbd11	INSIDE	1.651	3.122	764.09	2385.72	5.154	619.63	3193.55
A_68_P27898214	chr11:69779823-69779867	NM_016887:922	Cldn7	INSIDE	1.650	3.957	1568.10	6205.57	6.530	1333.22	8705.40
A_68_P28158619	chr11:116168104-116168148	NM_001162872:-74	Exoc7	PROMOTER	1.650	3.395	574.55	1950.42	5.602	532.83	2984.86
A_68_P30093918	chr15:27611330-27611374	NM_198301:-99	Fam105a	PROMOTER	1.650	2.064	569.45	1175.50	3.407	609.04	2074.72
A_68_P29248566	chr13:97695211-97695255	NM_001166065:589	Gcnt4	INSIDE	1.650	2.718	538.77	1464.12	4.484	429.38	1925.19
A_68_P21417960	chr2:90420716-90420760	NM_008982:66	Ptprj	INSIDE	1.650	4.856	1179.17	5726.52	8.015	976.27	7824.66
A_68_P24039805	chr5:121062634-121062678	NM_029096:-58	1110008J03Rik	DIVERGENT_PROMOTER	1.649	3.998	7528.67	30096.70	6.591	5424.59	35755.07
A_68_P22552055	chr3:135101078-135101122	NR_030689:529	4930539J05Rik	INSIDE	1.649	3.525	946.20	3335.59	5.813	843.84	4905.36
A_68_P30533736	chr16:8672646-8672705	NM_025821:-429	Carhsp1	PROMOTER	1.649	9.979	1344.51	13416.96	16.451	1050.57	17282.81
A_68_P25951144	chr8:72854849-72854893	NM_008107:1207	Gdf1	INSIDE	1.649	4.300	551.65	2372.07	7.090	441.95	3133.45
A_68_P24632571	chr6:90413720-90413764	NM_023184:1123	Klf15	INSIDE	1.649	4.076	1932.73	7877.24	6.721	1466.57	9856.49
A_68_P31150250	chr17:33855758-33855802	NM_145486:-165	Marchf2	PROMOTER	1.649	2.933	2568.68	7532.69	4.837	2197.27	10627.10
A_68_P20642551	chr1:137815771-137815815	NM_019645:-191	Pkp1	PROMOTER	1.649	2.439	2311.39	5636.91	4.021	1869.14	7515.51
A_68_P25458297	chr7:125591038-125591082	NM_138649:-3994	Syt17	PROMOTER	1.649	2.016	354.57	714.92	3.324	307.88	1023.45
A_68_P24358614	chr6:34860895-34860939	NM_001013366:-85	Wdr91	PROMOTER	1.649	1.524	6329.07	9643.26	2.512	4657.72	11699.40
A_68_P22222507	chr3:69525834-69525878	NM_133787:-120	Nmd3	PROMOTER	1.648	3.869	13203.19	51078.09	6.375	9180.51	58524.52
A_68_P25021894	chr7:29221444-29221488	NM_175021:-256	Samd4b	DIVERGENT_PROMOTER	1.648	4.085	2074.50	8475.26	6.732	1684.39	11340.10
A_68_P29514238	chr14:32643908-32643952	NM_001024604:-329	Ankrd28	PROMOTER	1.647	1.620	1147.20	1858.23	2.668	1038.20	2770.24
A_68_P25833746	chr8:47085665-47085709	NM_001039562:-482	Ankrd37	PROMOTER	1.647	2.622	3555.23	9320.60	4.318	2681.01	11575.77
A_68_P32463052	chrX:70748623-70748667	NM_177236:220	Atp2b3	INSIDE	1.647	2.172	401.11	871.38	3.578	214.89	768.83
A_68_P26659378	chr9:78243891-78243935	NM_001191044:329	Ddx43	INSIDE	1.647	3.794	1438.91	5459.07	6.249	1300.98	8129.60
A_68_P26802905	chr9:106270040-106270084	NM_153459:-900	Dusp7	PROMOTER	1.647	5.814	8987.36	52249.22	9.574	6248.62	59827.29
A_68_P23261233	chr4:122866390-122866434	NM_174998:5666	Hpcal4	INSIDE	1.647	2.404	598.81	1439.31	3.959	475.29	1881.44
A_68_P23269516	chr4:124335391-124335435	NM_011141:524	Pou3f1	INSIDE	1.647	4.999	1869.29	9344.93	8.232	1390.95	11450.48
A_68_P30250719	chr15:58720548-58720592	NM_175226:-213	Rnf139	PROMOTER	1.647	4.295	875.77	3761.37	7.074	754.23	5335.61
A_68_P29664626	chr14:64562881-64562925	NM_011446:360	Sox7	INSIDE	1.647	2.929	1685.38	4936.40	4.824	1370.78	6612.59
A_68_P23364697	chr4:141101930-141101974	NR_030695:-124	B330016D10Rik	DIVERGENT_PROMOTER	1.646	2.241	420.61	942.55	3.689	394.23	1454.27
A_68_P26543678	chr9:57612898-57612942	NM_007713:747	Clk3	INSIDE	1.646	2.204	5441.20	11992.11	3.627	4191.60	15201.53
A_68_P31862858	chr18:80389262-80389306	NM_199197:8074	Rbfa	INSIDE	1.646	1.852	375.68	695.88	3.049	324.99	990.77
A_68_P28082450	chr11:102809915-102809959	NM_011795:-2161	C1ql1	PROMOTER	1.645	1.681	2048.14	3443.75	2.766	1791.43	4955.48
A_68_P21315049	chr2:70499932-70499976	NM_027352:389	Gorasp2	INSIDE	1.645	3.840	509.53	1956.67	6.318	440.59	2783.49
A_68_P22518659	chr3:128907292-128907336	NM_001042502:-9540	Pitx2	PROMOTER	1.645	3.010	1668.95	5023.52	4.951	1335.15	6610.53
A_68_P28523569	chr12:72069499-72069543	NM_011184:-6089	Psma3	PROMOTER	1.645	2.378	192.91	458.66	3.912	164.85	644.90
A_68_P21071033	chr2:25127873-25127917	NM_023464:44	Ssna1	INSIDE	1.645	2.674	2235.25	5976.17	4.398	1902.58	8367.84
A_68_P31479228	chr18:7869362-7869406	NM_001146298:190	Wac	INSIDE	1.645	2.198	2696.63	5927.22	3.616	2065.93	7469.93
A_68_P29657349	A_68_P29657349			Unknown	1.645	3.129	1783.91	5581.20	5.148	1297.42	6679.07

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P30997386	chr16:97392403-97392447	NM_031174:-82	Dscam	PROMOTER	1.644	1.595	480.90	766.97	2.622	482.13	1264.18
A_68_P25609686	chr7:152047482-152047526	NM_010202:214	Fgf4	INSIDE	1.644	5.163	1113.15	5747.23	8.487	946.39	8032.38
A_68_P25091451	chr7:52409634-52409678	NM_029406:-111	Pih1d1	PROMOTER	1.644	2.322	1695.68	3936.97	3.817	1344.88	5133.11
A_68_P23318413	chr4:133155649-133155693	NM_018754:2413	Sfn	DOWNSTREAM	1.644	1.623	1136.06	1843.39	2.668	943.40	2516.70
A_68_P27942762	chr11:78157060-78157104	NM_011676:59	Unc119	INSIDE	1.644	4.324	5863.68	25357.28	7.109	4592.37	32645.92
A_68_P23249523	chr4:119821508-119821552			Unknown	1.644	2.927	1297.96	3798.79	4.811	1073.75	5165.37
A_68_P26170843	chr8:114434234-114434278	NM_019950:-157	Chst5	PROMOTER	1.643	2.517	1320.48	3323.84	4.136	1058.06	4375.93
A_68_P28058844	chr11:98698263-98698307	NM_001080925:186	Rapgefl1	INSIDE	1.643	2.311	1746.35	4035.94	3.797	1653.93	6279.52
A_68_P20821183	chr1:172145120-172145164	NM_010633:382	Uhmk1	INSIDE	1.643	1.951	1817.60	3545.33	3.204	1568.10	5024.87
A_68_P24992404	chr7:19857862-19857906	NM_009499:-681	Vasp	PROMOTER	1.643	1.942	3920.49	7612.56	3.190	3319.71	10591.52
A_68_P24063275	chr5:125343770-125343814	NM_001081750:718	Zfp664	INSIDE	1.643	3.056	2191.66	6698.03	5.021	1670.90	8389.72
A_68_P32265732	chrX:12859122-12859166	NM_010028:997	Ddx3x	INSIDE	1.642	2.048	627.54	1285.32	3.363	607.86	2043.95
A_68_P23323339	chr4:134091201-134091245	NM_029759:-2555	Fam54b	PROMOTER	1.642	2.789	1422.20	3966.22	4.578	1228.16	5622.49
A_68_P31857885	chr18:79306491-79306535	NM_053099:-382	Setbp1	PROMOTER	1.642	3.094	1006.69	3114.38	5.081	841.53	4275.84
A_68_P30436288	chr15:91403683-91403727	NM_001033633:-12	Slc2a13	PROMOTER	1.642	1.669	457.19	762.82	2.740	420.44	1152.03
A_68_P27942521	chr11:78115275-78115319	NM_017407:204	Spag5	INSIDE	1.642	5.783	1791.57	10361.45	9.494	1481.68	14067.16
A_68_P25017009	chr7:28160497-28160541	NM_001199235:19007	Spnb4	INSIDE	1.642	2.209	3530.92	7801.52	3.628	3013.58	10934.32
A_68_P30378284	chr15:81353498-81353542			Unknown	1.642	1.558	675.50	1052.36	2.557	654.93	1674.93
A_68_P23323199	chr4:134066870-134066914	NM_001081099:-21	2610002D18Rik	PROMOTER	1.641	3.069	2082.85	6392.84	5.036	1674.79	8433.89
A_68_P26080249	chr8:97441876-97441920	NM_001033533:100	Ccdc102a	INSIDE	1.641	1.764	2006.98	3540.67	2.895	1603.92	4644.14
A_68_P26350213	chr9:21855003-21855047	NM_010487:1443	Elavl3	INSIDE	1.641	3.509	2235.93	7845.85	5.757	1856.32	10686.97
A_68_P29713891	chr14:73109647-73109691	NM_207636:142	Fndc3a	INSIDE	1.641	3.333	1249.16	4163.45	5.469	1056.14	5776.46
A_68_P26762516	chr9:99040770-99040814	NM_029094:-162	Pik3cb	PROMOTER	1.641	2.485	1822.34	4528.06	4.078	1394.74	5688.22
A_68_P24020335	chr5:117838986-117839030	NM_028128:24	Rfc5	INSIDE	1.641	4.483	893.29	4004.39	7.355	861.69	6337.96
A_68_P28956729	chr13:37918014-37918058	NM_001177868:-744	Rreb1	PROMOTER	1.641	2.736	2349.87	6428.20	4.490	1779.07	7988.06
A_68_P30381701	chr15:81977690-81977734	NM_033218:14	Srebf2	INSIDE	1.641	2.567	7370.16	18917.36	4.213	5529.92	23299.25
A_68_P30601919	chr16:23225265-23225309	NM_145933:452	St6gal1	INSIDE	1.641	2.234	1424.73	3183.27	3.666	1177.58	4317.57
A_68_P21485725	chr2:103659783-103659827	ENSMUST00000167989:-171		PROMOTER	1.641	5.057	2260.32	11430.58	8.297	1657.10	13748.53
A_68_P27010234	chr10:24431792-24431836	NM_008813:94	Enpp1	INSIDE	1.640	6.266	2456.72	15393.62	10.275	2001.34	20564.38
A_68_P20939662	chr1:193541860-193541904	NM_172266:-20	Lpgat1	PROMOTER	1.640	2.460	919.65	2262.45	4.034	770.36	3107.48
A_68_P22568795	chr3:138105955-138105999	NM_007410:-151	Adh5	PROMOTER	1.639	2.652	6487.11	17202.67	4.345	5103.16	22173.81
A_68_P32538582	chrX:91612233-91612277	NM_026673:-194	Apoo	PROMOTER	1.639	2.182	678.97	1481.54	3.577	327.86	1172.65
A_68_P26630618	chr9:72833442-72833486	NM_001114328:107	Ccpg1	INSIDE	1.639	1.961	1956.95	3838.33	3.215	1718.91	5526.45
A_68_P30621546	chr16:26581967-26582011	NM_134103:198	Il1rap	INSIDE	1.639	5.035	2098.47	10565.95	8.251	1560.42	12874.40
A_68_P24132963	chr5:139469932-139469976	NM_008808:953	Pdgfa	INSIDE	1.639	2.663	4001.13	10655.82	4.365	3144.04	13724.14
A_68_P21909031	chr2:180921876-180921920	NM_025598:-149	Ppdpf	PROMOTER	1.639	1.741	1516.43	2640.73	2.853	1252.05	3572.49
A_68_P24086565	chr5:129526623-129526667	NM_009391:614	Ran	INSIDE	1.639	2.574	1550.69	3991.92	4.220	1358.16	5731.75
A_68_P29715887	chr14:73543290-73543334	NR_033185:721	Rcbtb2	INSIDE	1.639	1.870	715.43	1337.52	3.064	603.19	1848.33
A_68_P25232267	chr7:81158422-81158466	NM_009181:124	St8sia2	INSIDE	1.639	4.897	579.54	2837.93	8.027	450.86	3618.93
A_68_P22650336	chr3:152058904-152058948	NM_001080755:-47	Zzz3	PROMOTER	1.639	2.012	590.54	1188.06	3.298	679.08	2239.34
A_68_P21747321	chr2:151874396-151874440			Unknown	1.639	8.573	1419.06	12165.45	14.053	1112.80	15637.85
A_68_P20633260	chr1:136311773-136311817	NM_028320:-249	Adipor1	PROMOTER	1.638	1.899	1917.94	3642.07	3.110	1678.68	5221.19
A_68_P29187496	chr13:83860499-83860543	NR_015561:-7190	C130071C03Rik	PROMOTER	1.638	4.605	1216.96	5604.25	7.543	1022.94	7716.25
A_68_P27937736	chr11:77281473-77281517	NM_139128:4080	Coro6	INSIDE	1.638	1.704	1225.08	2087.69	2.791	1035.13	2889.33
A_68_P20146150	chr1:36125563-36125607	NM_015818:340	Hs6st1	INSIDE	1.638	4.027	2473.98	9963.62	6.599	2193.65	14474.81
A_68_P23156220	chr4:101320226-101320270	NM_175036:-139	Leprot	PROMOTER	1.638	1.858	6413.77	11913.85	3.042	4740.97	14421.47
A_68_P25261466	chr7:86650289-86650333	NR_029818:161	Mir9-3	DOWNSTREAM	1.638	2.324	2376.34	5523.69	3.807	2028.31	7722.67
A_68_P21494379	chr2:105239336-105239380	NM_009037:118	Rcn1	INSIDE	1.638	2.339	510.90	1194.90	3.831	450.73	1726.56
A_68_P21086006	chr2:27533318-27533362	NM_011305:620	Rxra	INSIDE	1.638	3.240	1257.40	4074.37	5.307	1004.52	5331.24
A_68_P23896971	chr5:93371578-93371622	NM_001077596:44577	Shroom3	INSIDE	1.638	2.786	519.73	1447.84	4.563	449.18	2049.51
A_68_P28615267	chr12:88640639-88640683	NM_011479:88520	Sptlc2	DOWNSTREAM	1.638	3.014	654.26	1971.91	4.938	576.68	2847.47

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28688783	chr12:103213937-103213981	NM_016856:-225	Cpsf2	PROMOTER	1.637	2.923	1412.05	4127.22	4.784	1184.21	5665.66
A_68_P30363898	chr15:78858851-78858898	NM_008197:233	H1f0	INSIDE	1.637	1.917	1289.33	2471.43	3.139	1051.84	3301.42
A_68_P31926197	chr19:4990111-4990155	NM_153553:-161	Npas4	PROMOTER	1.637	3.428	1185.76	4064.51	5.611	891.16	5000.01
A_68_P31438310	chr17:90855140-90855185	NM_020252:636980	Nrxn1	INSIDE	1.637	2.282	502.53	1146.56	3.734	388.45	1450.58
A_68_P25017511	chr7:28271855-28271899	NM_018820:-95	Sertad1	PROMOTER	1.637	3.640	3792.42	13803.19	5.956	2868.55	17086.23
A_68_P26239531	chr8:125898300-125898344	NM_001037877:588	Tcf25	INSIDE	1.637	4.492	13008.45	58440.41	7.353	8218.25	60426.39
A_68_P24162469	chr5:145529670-145529714	NM_001081362:32	Trrap	INSIDE	1.637	2.912	5153.75	15010.24	4.768	3947.39	18822.66
A_68_P32315765	chrX:33428989-33429033	NM_001009947:184	Dock11	INSIDE	1.636	4.768	664.47	3167.92	7.801	455.12	3550.48
A_68_P26214707	chr8:122082424-122082468	NM_001167910:215	Mbtps1	INSIDE	1.636	3.018	10827.35	32676.37	4.939	9094.19	44912.50
A_68_P31937159	chr19:7062178-7062222	NM_001185164:-59	Vegfb	PROMOTER	1.636	4.237	3920.15	16608.12	6.932	3142.11	21780.69
A_68_P25656690	chr8:11635804-11635848	NM_133971:-72	Ankrd10	PROMOTER	1.635	2.189	2794.43	6117.45	3.578	2349.68	8407.98
A_68_P20849149	chr1:177555403-177555447	NM_010209:342	Fh1	INSIDE	1.635	2.754	1911.22	5263.50	4.503	1609.59	7248.39
A_68_P26463576	chr9:43553455-43553499	NM_021424:818	Pvrl1	INSIDE	1.635	2.694	1269.60	3420.11	4.405	1012.01	4458.27
A_68_P27841688	chr11:60034191-60034235	NM_011480:-106	Srebf1	PROMOTER	1.635	1.775	1170.73	2077.55	2.902	1024.89	2974.20
A_68_P26883804	chr9:121403538-121403582	NM_031161:1247	Cck	INSIDE	1.634	3.579	904.53	3237.06	5.846	706.74	4131.75
A_68_P30378505	chr15:81416613-81416657	NM_177821:-9	Ep300	PROMOTER	1.634	2.357	831.78	1960.41	3.851	635.86	2448.47
A_68_P25496222	chr7:132850904-132850948	NM_207239:276	Gtf3c1	INSIDE	1.634	1.799	3778.37	6797.00	2.940	3048.35	8961.42
A_68_P27500776	chr10:120416131-120416176	NM_001081193:233	Lemd3	INSIDE	1.634	2.904	292.41	849.04	4.744	304.63	1445.30
A_68_P25019829	chr7:28834940-28834984	NM_011874:149	Psmc4	INSIDE	1.634	3.138	4381.20	13749.46	5.130	3217.72	16505.36
A_68_P30513218	chr16:5013781-5013827	NM_133185:-158	Rogdi	PROMOTER	1.634	3.783	2479.14	9378.26	6.183	1863.86	11524.08
A_68_P30497699	chr15:102236639-102236683	NM_013672:-86	Sp1	PROMOTER	1.634	2.607	1459.41	3804.34	4.259	1211.32	5158.72
A_68_P26817224	chr9:108838919-108838963	NM_025407:280	Uqcrc1	INSIDE	1.634	3.523	5287.92	18628.69	5.757	4049.89	23316.55
A_68_P28729933	chr12:110032849-110032893	NM_009537:1350	Yy1	INSIDE	1.634	2.528	1099.01	2778.47	4.132	930.27	3843.93
A_68_P25210201	chr7:77425441-77425485	AK148659:-817		PROMOTER	1.634	2.457	4533.42	11136.61	4.014	3412.47	13696.92
A_68_P24098740	chr5:132014030-132014074	NM_177047:1004161	Auts2	INSIDE	1.633	3.487	5752.28	20058.84	5.694	4561.64	25972.06
A_68_P24820864	chr6:125444507-125444551	NM_007657:245	Cd9	INSIDE	1.633	3.222	799.10	2574.41	5.262	716.17	3768.19
A_68_P20796287	chr1:167694031-167694075	NM_011804:142	Creg1	INSIDE	1.633	2.890	2035.65	5883.48	4.720	1667.89	7872.74
A_68_P26039225	chr8:90661714-90661758	NM_172757:-47	Heatr3	PROMOTER	1.633	2.504	2413.44	6042.63	4.088	2631.80	10757.83
A_68_P30963193	chr16:91485518-91485562	NM_010508:81	Ifnar1	INSIDE	1.633	1.748	1050.16	1835.82	2.855	791.62	2260.23
A_68_P20961517	chr2:3202117-3202161	NM_008708:579	Nmt2	INSIDE	1.633	1.432	1668.58	2389.46	2.338	1338.90	3130.71
A_68_P32672454	chrX:131076324-131076368	NM_013898:-178	Timm8a1	PROMOTER	1.633	3.393	810.91	2751.17	5.540	428.52	2374.03
A_68_P21836569	chr2:167457610-167457654	NM_023230:-127	Ube2v1	PROMOTER	1.633	3.680	822.83	3028.11	6.008	636.44	3824.00
A_68_P22766408	chr4:19636033-19636077	NM_177327:86	Wwp1	INSIDE	1.633	3.436	1455.50	5000.53	5.611	1334.52	7487.54
A_68_P24954457	chr7:6141163-6141207	NM_001146024:17070	Zfp444	INSIDE	1.633	2.299	250.55	575.91	3.754	227.18	852.87
A_68_P23591268	A_68_P23591268			Unknown	1.633	3.481	806.43	2807.22	5.686	553.20	3145.63
A_68_P33011727	A_68_P33011727			Unknown	1.633	2.385	193.78	462.11	3.894	160.14	623.51
A_68_P20914292	chr1:189431401-189431445	ENSMUST00000127489:-1247		PROMOTER	1.633	3.202	2279.69	7300.11	5.230	1679.29	8782.37
A_68_P27646748	chr11:23533451-23533495	NM_027860:159	0610010F05Rik	INSIDE	1.632	2.999	1129.84	3388.09	4.894	941.33	4606.87
A_68_P24050005	chr5:122821860-122821904	NM_026883:90	1500011H22Rik	INSIDE	1.632	2.350	644.45	1514.69	3.835	582.15	2232.74
A_68_P32373277	chrX:48194552-48194596	NM_133729:-38	2610018G03Rik	PROMOTER	1.632	3.797	920.52	3495.16	6.197	695.81	4311.93
A_68_P24759117	chr6:113328299-113328343	NM_001170485:214	Arpc4	INSIDE	1.632	11.956	3011.48	36006.38	19.517	2285.29	44602.84
A_68_P29009046	chr13:46764820-46764864	NM_001033192:-48	C78339	PROMOTER	1.632	1.658	654.49	1085.11	2.705	563.16	1523.44
A_68_P21421545	chr2:91095901-91095945	NM_030880:-1047	Pacsin3	PROMOTER	1.632	4.268	1205.71	5146.03	6.967	981.70	6839.83
A_68_P23749120	chr5:64484497-64484543	NM_025700:332	Pgm1	INSIDE	1.632	4.520	2595.29	11730.50	7.376	2168.53	15994.06
A_68_P27568397	chr11:6315971-6316015	NM_008907:120	Ppia	INSIDE	1.632	3.616	2360.54	8534.66	5.899	1898.06	11197.31
A_68_P24127508	chr5:138220341-138220385	NM_027242:217	2010007H12Rik	INSIDE	1.631	3.683	2150.37	7919.10	6.005	1663.78	9990.80
A_68_P27351975	chr10:92623318-92623362	NM_146239:-280	Cdk17	PROMOTER	1.631	5.287	5246.48	27740.47	8.626	4202.19	36248.87
A_68_P27543292	chr10:128242453-128242497	NM_028873:-257	Dnajc14	DIVERGENT_PROMOTER	1.631	2.164	846.84	1832.34	3.529	769.79	2716.63
A_68_P27924590	chr11:74982634-74982678	NM_001098203:-1002	Hic1	PROMOTER	1.631	2.257	1046.15	2361.43	3.682	817.05	3008.34
A_68_P26977750	chr10:18565037-18565081	NM_022032:182	Perp	INSIDE	1.631	6.079	2807.39	17066.31	9.913	2265.96	22463.50
A_68_P26918726	chr10:6979506-6979550	NM_133485:863	Ppp1r14c	INSIDE	1.631	3.344	2479.69	8292.48	5.454	1974.99	10772.07

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P23542998	chr5:24110558-24110602	NM_025891:-2760	Smarcd3	PROMOTER	1.631	8.477	7541.98	63933.24	13.824	5614.49	77617.03
A_68_P26153173	chr8:111324170-111324214	NM_007496:85649	Zfhx3	INSIDE	1.631	2.018	591.48	1193.66	3.292	440.15	1448.85
A_68_P23094811	chr4:88940707-88940751	NM_009877:-205	Cdkn2a	PROMOTER	1.630	1.577	574.53	906.09	2.571	449.85	1156.63
A_68_P25092923	chr7:52662436-52662480	NM_010596:1129	Kcna7	INSIDE	1.630	5.866	1061.24	6225.62	9.563	899.09	8597.98
A_68_P26811667	chr9:107803499-107803544	NM_028369:13062	Mon1a	INSIDE	1.630	6.893	1343.62	9261.42	11.234	1132.45	12721.99
A_68_P28961844	chr13:38727138-38727182	NM_139063:-182	Muted	PROMOTER	1.630	1.777	971.29	1726.20	2.897	765.87	2218.59
A_68_P29508104	chr14:31638725-31638769	NM_028839:-33	Tmem110	PROMOTER	1.630	7.519	1861.83	13998.85	12.256	1443.88	17696.25
A_68_P27912376	chr11:72420588-72420632	NM_025985:-152	Ube2g1	PROMOTER	1.630	3.721	980.28	3647.77	6.065	904.63	5486.35
A_68_P28190095	chr11:121215875-121215919	NM_025793:-135	Wdr45l	PROMOTER	1.630	9.024	2659.39	23999.48	14.714	1804.12	26545.49
A_68_P31469349	chr18:5591373-5591417	NM_011546:-494	Zeb1	PROMOTER	1.630	2.036	1186.01	2415.11	3.319	998.95	3315.18
A_68_P21105115	chr2:30627096-30627141			Unknown	1.630	2.805	2376.46	6665.33	4.572	1891.60	8648.49
A_68_P33008885	chr12:21117800-21117844	NM_001004364:206	Asap2	INSIDE	1.629	3.874	2797.09	10835.86	6.309	2307.57	14558.86
A_68_P28596932	chr12:85534521-85534565	NM_001163502:423	C130039O16Rik	INSIDE	1.629	4.959	3598.27	17843.45	8.078	2828.40	22847.40
A_68_P24423149	chr6:47404611-47404655	NM_012042:310	Cul1	INSIDE	1.629	10.303	2595.13	26738.51	16.788	1833.59	30782.91
A_68_P20910364	chr1:188791866-188791912	NM_033077:594	D1Pas1	INSIDE	1.629	6.821	1369.42	9340.44	11.108	1236.49	13735.20
A_68_P25498529	chr7:133225199-133225243	NM_001101488:705	Gsg1l	INSIDE	1.629	1.489	2851.67	4247.28	2.426	2298.74	5577.07
A_68_P21623006	chr2:128926947-128926991	NM_009086:237	Polr1b	INSIDE	1.629	1.389	1216.53	1689.37	2.262	1077.43	2436.99
A_68_P21773626	chr2:156665615-156665659	NM_173396:-176	Tgif2	PROMOTER	1.629	4.810	1506.49	7246.49	7.837	1272.30	9971.61
A_68_P22475538	chr3:120965447-120965491	NM_178936:766	Tmem56	INSIDE	1.629	3.110	1198.08	3726.36	5.068	1119.74	5674.32
A_68_P22860680	chr4:41082241-41082285	NM_026275:-791	Ube2r2	PROMOTER	1.629	1.364	2700.44	3684.57	2.222	2131.24	4735.93
A_68_P27830380	chr11:58136423-58136467	NM_178761:404	Zfp672	INSIDE	1.629	4.207	4136.22	17401.81	6.852	3392.02	23243.79
A_68_P20412463	chr1:88400704-88400748			Unknown	1.629	4.268	5210.04	22236.22	6.951	4080.44	28361.68
A_68_P26018418	chr8:86671979-86672023	NM_001163752:64	4930432K21Rik	INSIDE	1.628	2.483	2729.10	6776.31	4.043	2053.68	8303.57
A_68_P24330588	chr6:30124352-30124396	NR_038124:-2248	BB283400	DIVERGENT_PROMOTER	1.628	3.446	1069.53	3685.40	5.610	927.75	5204.62
A_68_P20422167	chr1:90102351-90102395	NM_008299:-49	Dnajb3	DIVERGENT_PROMOTER	1.628	6.145	1938.67	11913.38	10.006	1545.92	15468.64
A_68_P22410841	chr3:107948966-107949010	NM_010306:44	Gnai3	INSIDE	1.628	3.286	970.21	3187.70	5.350	788.34	4217.64
A_68_P24981713	chr7:17062092-17062136	NM_008718:15	Npas1	INSIDE	1.628	2.284	757.96	1731.04	3.718	644.47	2396.16
A_68_P23234756	chr4:117167070-117167114	NM_025739:2428	Rnf220	INSIDE	1.628	6.644	1123.56	7465.08	10.820	864.45	9353.10
A_68_P31187135	chr17:43153738-43153782	NM_178589:257	Tnfrsf21	INSIDE	1.628	4.557	2213.00	10085.59	7.421	1633.92	12124.77
A_68_P32565197	chrX:98892164-98892208	ENSMUST00000073812:-4997		PROMOTER	1.628	5.281	10261.67	54192.20	8.596	3845.96	33060.00
A_68_P25833742	chr8:47085366-47085410	NM_001039562:-184	Ankrd37	PROMOTER	1.627	1.854	2843.21	5270.09	3.016	2169.42	6542.60
A_68_P27183504	chr10:61441353-61441397	NM_007731:482	Col13a1	INSIDE	1.627	2.560	905.42	2317.85	4.164	745.87	3106.00
A_68_P25410984	chr7:117103504-117103548	NM_021494:410	Dennd5a	INSIDE	1.627	1.745	1202.04	2097.07	2.838	950.80	2698.44
A_68_P24429118	chr6:48692680-48692724	NM_008376:3657	Gimap1	INSIDE	1.627	6.458	1090.95	7045.70	10.506	940.90	9884.70
A_68_P30482201	chr15:99602827-99602871	NM_028015:98	Lass5	INSIDE	1.627	3.930	4100.43	16113.09	6.392	3087.66	19737.30
A_68_P21900919	chr2:179760085-179760129	NM_177727:415	Lsm14b	INSIDE	1.627	4.030	1686.18	6795.38	6.555	1408.10	9230.65
A_68_P32786683	chrX:158346162-158346206	NM_001081052:251538	Nhs	INSIDE	1.627	4.032	2483.51	10013.66	6.560	1267.66	8315.23
A_68_P28184543	chr11:120298753-120298797	NM_001195023:240	Nploc4	INSIDE	1.627	2.140	11825.52	25303.55	3.481	8744.97	30442.56
A_68_P27810583	chr11:54336349-54336393	NM_175258:22	Rapgef6	INSIDE	1.627	2.089	939.96	1963.23	3.398	789.84	2684.12
A_68_P22405709	chr3:107135696-107135740	NM_001045807:489	Rbm15	INSIDE	1.627	3.136	3799.14	11913.80	5.103	3192.75	16291.12
A_68_P27080342	chr10:39452039-39452083	NM_011264:95	Rev3l	INSIDE	1.627	2.038	1075.82	2192.25	3.315	865.77	2869.70
A_68_P31232583	chr17:51318678-51318722	NM_028162:-26	Tbc1d5	PROMOTER	1.627	2.670	1622.53	4332.51	4.344	1220.79	5303.73
A_68_P28182345	chr11:119959914-119959958	NM_183137:109	2410002I01Rik	INSIDE	1.626	1.880	1012.24	1902.83	3.057	758.19	2317.78
A_68_P30587818	chr16:20498949-20498993	NM_172265:81	Eif2b5	INSIDE	1.626	1.709	569.66	973.48	2.778	495.87	1377.71
A_68_P25099054	chr7:53683157-53683201	NM_001112739:31312	Kcnc1	INSIDE	1.626	7.224	2254.21	16284.40	11.748	1472.00	17293.73
A_68_P31106324	chr17:25934049-25934093	NM_133719:-80	Metrn	PROMOTER	1.626	2.274	1344.63	3058.13	3.697	1092.50	4039.16
A_68_P25009543	chr7:26082789-26082833	NM_008776:164	Pafah1b3	INSIDE	1.626	3.401	2594.91	8824.50	5.529	2029.01	11218.18
A_68_P23314345	chr4:132399162-132399206	NM_146154:-100	Ppp1r8	PROMOTER	1.626	4.182	1875.06	7842.09	6.801	1488.10	10121.29
A_68_P28875776	chr13:22098904-22098948	NM_019429:2684	Prss16	INSIDE	1.626	3.801	2569.89	9769.27	6.181	1796.94	11106.62
A_68_P28071137	chr11:100820628-100820677	NM_008986:11279	Ptrf	INSIDE	1.626	2.201	271.72	598.16	3.580	237.92	851.66
A_68_P25126430	chr7:59261254-59261298	NR_027704:-192	Svip	PROMOTER	1.626	3.084	7032.53	21687.90	5.015	5516.22	27665.59

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P22323188	chr3:89856392-89856436	NM_028475:-17	Ubap2l	PROMOTER	1.626	1.802	9446.78	17020.32	2.929	6798.45	19913.72
A_68_P24115158	chr5:135663906-135663950	NM_011714:736	Baz1b	INSIDE	1.625	4.863	843.16	4100.18	7.903	750.44	5930.37
A_68_P21840215	chr2:168055402-168055451	NM_010072:453	Dpm1	INSIDE	1.625	2.341	439.97	1029.83	3.804	363.32	1382.21
A_68_P29996481	chr15:7760813-7760857	NM_010275:-176	Gdnf	PROMOTER	1.625	3.802	1226.00	4661.44	6.177	960.25	5931.57
A_68_P26587299	chr9:65219825-65219869	NM_001111145:10980	Gm514	INSIDE	1.625	6.392	4269.15	27288.57	10.385	3395.63	35263.23
A_68_P29569514	chr14:45839639-45839683	NM_027518:269	Gpr137c	INSIDE	1.625	4.403	1455.02	6406.46	7.154	1082.09	7741.07
A_68_P27862275	chr11:63732951-63732995	NM_018805:2814	Hs3st3b1	INSIDE	1.625	4.099	641.44	2629.45	6.661	508.06	3384.07
A_68_P24024083	chr5:118478594-118478638	NM_021344:784	Tesc	INSIDE	1.625	4.891	4373.06	21388.98	7.949	3586.56	28509.15
A_68_P23429319	chr4:153514065-153514109	NM_011642:231	Trp73	INSIDE	1.625	4.438	1760.55	7813.59	7.211	1637.29	11805.84
A_68_P26875426	chr9:119883221-119883265	NM_153287:10534	Csrnp1	INSIDE	1.624	3.499	1072.24	3751.45	5.682	894.90	5084.44
A_68_P24156243	chr5:144131687-144131731	NM_133355:6122	Grid2ip	INSIDE	1.624	1.924	4737.74	9114.19	3.124	4028.32	12585.02
A_68_P26547037	chr9:58160685-58160729	NM_010729:313	Loxl1	INSIDE	1.624	3.568	794.13	2833.46	5.793	679.29	3935.25
A_68_P29360867	chr13:117813151-117813195	NM_001081009:1151	Parp8	INSIDE	1.624	2.720	1787.53	4862.28	4.418	1510.48	6672.61
A_68_P26766653	chr9:99775810-99775854	NM_011440:757	Sox14	INSIDE	1.624	2.131	357.97	762.89	3.461	336.16	1163.37
A_68_P21777116	chr2:157282885-157282929	NM_001025395:32878	Src	INSIDE	1.624	1.761	1431.74	2521.94	2.861	1201.96	3438.40
A_68_P23298057	chr4:129373770-129373814	NM_199305:290	Tmem39b	INSIDE	1.624	1.711	1592.30	2724.61	2.779	1302.78	3620.70
A_68_P26948857	chr10:12780907-12780951	FJ425893:619		INSIDE	1.624	2.131	456.21	972.32	3.462	445.93	1543.60
A_68_P32135373	chr19:45005375-45005419	NM_001081225:-212	Fam178a	PROMOTER	1.623	2.807	2918.14	8191.52	4.556	2514.21	11455.31
A_68_P23018909	chr4:73659645-73659689	NM_172869:160	Frmd3	INSIDE	1.623	1.485	899.52	1335.79	2.410	685.09	1650.77
A_68_P31834169	chr18:75121056-75121100	NM_010720:-161	Lipg	PROMOTER	1.623	1.568	2716.88	4259.32	2.544	2197.72	5591.66
A_68_P25285303	chr7:91032985-91033029	NM_030705:-155	Mesdc1	DIVERGENT_PROMOTER	1.623	2.693	480.29	1293.34	4.369	553.86	2419.97
A_68_P27564592	chr11:5607482-5607526	NM_026080:198	Mrps24	INSIDE	1.623	5.515	638.51	3521.43	8.951	525.42	4702.85
A_68_P31513737	chr18:14841164-14841208	NM_001161369:237	Ss18	INSIDE	1.623	5.982	1313.71	7859.24	9.711	1187.27	11529.15
A_68_P30140505	chr15:36723538-36723582	NM_011740:733	Ywhaz	INSIDE	1.623	2.586	1808.20	4675.67	4.198	1640.94	6888.50
A_68_P32410977	chrX:56820526-56820570	ENSMUST00000124402:101		INSIDE	1.623	3.590	723.06	2595.98	5.828	472.85	2755.59
A_68_P26631268	chr9:72951661-72951705	NM_025890:1478	2410004A20Rik	INSIDE	1.622	1.903	344.84	656.35	3.086	354.88	1095.29
A_68_P20293904	chr1:64737359-64737403	NR_038009:-147	2810408I11Rik	DIVERGENT_PROMOTER	1.622	1.860	1054.52	1961.20	3.017	834.70	2518.52
A_68_P21958957	chr3:14886237-14886281	NM_009801:-167	Car2	PROMOTER	1.622	2.677	743.86	1991.60	4.342	579.74	2517.33
A_68_P32567641	chrX:99384743-99384787	NM_009094:-1054	Rps4x	PROMOTER	1.622	2.279	620.42	1413.98	3.696	430.02	1589.15
A_68_P32750678	chrX:149204051-149204095	NM_172441:-68	Shroom2	PROMOTER	1.622	2.671	2098.76	5606.54	4.334	1352.04	5859.93
A_68_P25477108	chr7:129210764-129210808	NM_138589:75	Ubfd1	INSIDE	1.622	5.308	1922.64	10205.63	8.608	1580.94	13609.45
A_68_P24954292	chr7:6107153-6107197	NM_001013012:399	Zfp787	INSIDE	1.622	1.848	928.31	1715.63	2.997	1187.74	3560.21
A_68_P30931281	chr16:85803417-85803461	NM_009621:-78	Adamts1	PROMOTER	1.621	2.412	1529.85	3690.67	3.912	1277.02	4995.29
A_68_P22069519	chr3:38383514-38383558	NM_001167883:202	Ankrd50	INSIDE	1.621	3.267	2974.55	9716.58	5.297	2486.82	13171.62
A_68_P25772218	chr8:35171274-35171318	NM_011722:269	Dctn6	INSIDE	1.621	1.979	1786.21	3534.22	3.208	1530.23	4909.07
A_68_P23203786	chr4:109656795-109656839	NM_172296:6187	Dmrta2	DOWNSTREAM	1.621	8.757	7571.12	66301.58	14.193	5316.97	75464.36
A_68_P30720009	chr16:44173533-44173577	NM_001029889:45	Gm608	INSIDE	1.621	3.061	994.91	3045.29	4.961	793.75	3937.64
A_68_P28670941	chr12:99812671-99812719	NM_029911:3456	Kcnk10	INSIDE	1.621	2.562	1091.94	2797.22	4.153	868.16	3605.85
A_68_P28225274	chr12:8928368-8928412	NM_008640:278	Laptm4a	INSIDE	1.621	2.539	2628.18	6673.66	4.117	2032.54	8367.79
A_68_P20658349	chr1:140515986-140516030	NM_021605:265	Nek7	INSIDE	1.621	2.357	1442.96	3401.75	3.822	1214.75	4642.75
A_68_P32134209	chr19:44830746-44830790	NM_011037:-1115	Pax2	PROMOTER	1.621	2.469	5256.54	12977.15	4.002	3853.20	15420.81
A_68_P21431995	chr2:92855411-92855455	NM_001177536:30869	Prdm11	INSIDE	1.621	1.810	1126.49	2039.31	2.935	947.95	2782.42
A_68_P27925675	chr11:75162047-75162091	NM_001102611:134	Smyd4	INSIDE	1.621	1.499	641.77	962.31	2.431	578.57	1406.70
A_68_P31330059	chr17:71007053-71007097	NM_001128181:95988	Dlgap1	INSIDE	1.620	13.447	4003.88	53839.91	21.787	2580.13	56214.38
A_68_P25392118	chr7:112548478-112548522	NM_199009:25	Fam160a2	INSIDE	1.620	2.580	1482.11	3824.40	4.181	1279.22	5348.77
A_68_P27909076	chr11:71855740-71855784	NM_144526:-241	Fam64a	DIVERGENT_PROMOTER	1.620	3.912	2415.26	9447.36	6.336	2014.18	12761.04
A_68_P32507212	chrX:83022021-83022065	NM_008194:116	Gyk	INSIDE	1.620	5.178	30351.68	157156.00	8.389	20975.09	175956.90
A_68_P23602238	chr5:36022053-36022097	NM_030127:357	Htra3	INSIDE	1.620	5.000	2167.98	10840.38	8.098	1422.78	11521.52
A_68_P26983891	chr10:19653749-19653793	NM_008580:-561	Map3k5	PROMOTER	1.620	1.830	1693.83	3099.84	2.964	1458.46	4322.90
A_68_P23524104	chr5:20561279-20561323	NM_011203:315	Ptpn12	INSIDE	1.620	2.868	1128.95	3237.74	4.647	1044.95	4855.85
A_68_P27228619	chr10:69707994-69708038	NM_025807:-7	Slc16a9	PROMOTER	1.620	7.744	1500.53	11620.31	12.543	1322.87	16592.67

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31159487	chr17:35653700-35653744	NM_001163763:47	Tcf19	INSIDE	1.620	2.076	1916.59	3979.58	3.364	1478.90	4975.61
A_68_P27792052	chr11:50873003-50873047	NM_009329:266	Zfp354a	INSIDE	1.620	4.509	3530.93	15919.26	7.304	2608.28	19049.86
A_68_P32257887	chrX:11242111-11242155			Unknown	1.620	2.006	2657.86	5331.53	3.249	1402.51	4556.80
A_68_P21673356	chr2:138082901-138082945	NM_001025431:603	Btbd3	INSIDE	1.619	1.438	3011.91	4330.58	2.328	2338.35	5442.63
A_68_P21339006	chr2:74550322-74550366	NM_010468:295	Hoxd3	INSIDE	1.619	2.232	1636.44	3653.03	3.613	1498.00	5412.55
A_68_P30130469	chr15:34767206-34767250	NM_181317:93	Kcns2	INSIDE	1.619	2.579	2835.18	7311.52	4.174	2259.12	9429.48
A_68_P22028771	chr3:30407557-30407601	NM_021442:831	Mecom	INSIDE	1.619	1.748	767.78	1342.21	2.830	672.06	1901.65
A_68_P24337499	chr6:31349464-31349508	NM_013791:659	Mkln1	INSIDE	1.619	4.490	3001.53	13477.04	7.271	2353.24	17110.24
A_68_P28466190	chr12:59313609-59313653	NM_009216:840	Sstr1	INSIDE	1.619	5.454	1300.46	7092.60	8.829	990.04	8741.09
A_68_P28450734	chr12:56225622-56225666	NM_001100116:130	1700047I17Rik2	INSIDE	1.618	5.076	2323.24	11793.75	8.212	1827.50	15006.68
A_68_P31731124	chr18:56732842-56732886	NM_001127338:-271	Aldh7a1	PROMOTER	1.618	3.079	4363.12	13433.92	4.981	3711.04	18485.84
A_68_P27228310	chr10:69651858-69651902	NM_001111121:92012	Ccdc6	INSIDE	1.618	5.707	8650.37	49366.64	9.232	5818.45	53714.59
A_68_P23185134	chr4:106234075-106234119	NM_053272:454	Dhcr24	INSIDE	1.618	1.954	6180.72	12074.38	3.161	4658.67	14725.56
A_68_P25842954	chr8:48761152-48761196	NM_023503:-661	Ing2	PROMOTER	1.618	3.119	729.58	2275.67	5.047	620.16	3130.17
A_68_P32383986	chrX:50097843-50097887	NR_003188:-94	Kis2	PROMOTER	1.618	2.686	13355.12	35865.81	4.346	6244.36	27135.25
A_68_P29266707	chr13:100785592-100785636	NM_030026:-20	Mccc2	PROMOTER	1.618	1.916	809.86	1551.88	3.100	610.66	1893.18
A_68_P21587817	chr2:122564114-122564158	NM_019788:-104	Pldn	PROMOTER	1.618	4.136	1376.79	5694.31	6.692	1095.09	7328.83
A_68_P25669976	chr8:13677580-13677624	NM_009025:-15	Rasa3	PROMOTER	1.618	2.401	1590.19	3818.17	3.885	1295.35	5032.82
A_68_P22705223	chr4:6292852-6292896	NM_001098227:48	Sdcbp	INSIDE	1.618	2.569	3970.18	10197.67	4.156	3264.23	13567.49
A_68_P27929278	chr11:75780405-75780449			Unknown	1.618	2.631	267.46	703.76	4.257	283.23	1205.58
A_68_P21745337	chr2:151528077-151528121	NM_001160363:355	5430405G05Rik	INSIDE	1.617	12.534	2185.05	27386.41	20.261	1693.22	34306.73
A_68_P28449512	chr12:55963938-55963982	NM_007688:-96	Cfl2	PROMOTER	1.617	1.882	1457.03	2742.45	3.044	1200.81	3655.76
A_68_P23610086	chr5:37259995-37260039	NM_172994:208	Ppp2r2c	INSIDE	1.617	5.030	2473.74	12442.91	8.135	1955.76	15909.70
A_68_P21132202	chr2:35056385-35056429	NM_026697:234	Rab14	INSIDE	1.617	2.312	2909.12	6724.51	3.738	2509.32	9380.51
A_68_P26133052	chr8:107850532-107850576	NM_025486:291	Tmem208	INSIDE	1.617	2.535	7908.84	20050.59	4.099	6297.19	25813.56
A_68_P23059231	chr4:82505707-82505751	NM_026647:-163	Zdhhc21	PROMOTER	1.617	2.859	3478.55	9944.80	4.624	2488.71	11508.13
A_68_P26617701	chr9:70504626-70504670	NM_172772:333	Fam63b	INSIDE	1.616	4.671	1854.17	8661.53	7.548	1656.06	12499.60
A_68_P31930681	chr19:5758063-5758107	NM_008520:17181	Ltbp3	INSIDE	1.616	4.430	806.23	3571.76	7.160	691.28	4949.47
A_68_P27215083	chr10:67442230-67442274	NM_001081346:-93	Rtkn2	PROMOTER	1.616	3.542	8566.13	30338.77	5.723	5946.50	34030.73
A_68_P21890546	chr2:178142021-178142065	NM_177191:321	Sycp2	INSIDE	1.616	3.732	5809.31	21681.31	6.031	4181.96	25221.88
A_68_P27181843	chr10:61158699-61158743	NM_027912:459	Tysnd1	INSIDE	1.616	3.373	978.98	3301.84	5.452	761.99	4154.37
A_68_P32537531	chrX:91368428-91368472	NM_001044386:296	Zfx	INSIDE	1.616	5.107	1044.72	5335.77	8.253	681.29	5622.91
A_68_P24906444	chr6:142705194-142705238	NM_009908:11	Cmas	INSIDE	1.615	4.227	1261.52	5332.30	6.828	1003.63	6852.26
A_68_P25020574	chr7:28965243-28965287	NM_010092:752	Dyrk1b	INSIDE	1.615	3.240	2559.08	8290.75	5.233	2122.57	11107.96
A_68_P28083517	chr11:102994122-102994166	NM_001130516:-508	Hexim2	PROMOTER	1.615	3.255	2038.59	6635.67	5.256	1583.56	8323.43
A_68_P31381048	chr17:80461571-80461615	NM_144802:82	Hnrpll	INSIDE	1.615	1.950	1829.96	3569.05	3.150	1467.27	4621.90
A_68_P22028775	chr3:30408163-30408207	NM_021442:225	Mecom	INSIDE	1.615	3.398	2128.39	7231.49	5.487	1792.28	9834.61
A_68_P20188961	chr1:43503040-43503084	NM_010879:467	Nck2	INSIDE	1.615	2.269	1442.39	3273.18	3.665	1765.47	6470.17
A_68_P28178599	chr11:119410964-119411008	NM_008730:-1852	Nptx1	PROMOTER	1.615	1.911	1470.34	2810.36	3.087	1225.21	3782.05
A_68_P27357767	chr10:93610648-93610692	NM_011629:-5	Nr2c1	PROMOTER	1.615	3.242	3314.61	10746.06	5.237	2772.73	14520.12
A_68_P28697278	chr12:104627062-104627106	NM_001177841:193	Otub2	INSIDE	1.615	2.049	1442.32	2955.86	3.310	1280.20	4237.09
A_68_P31117689	chr17:27792526-27792570	NM_011861:-78	Pacsin1	PROMOTER	1.615	3.070	940.96	2889.02	4.959	739.85	3668.92
A_68_P30084544	chr15:25914715-25914759	NM_144523:616	Zfp622	INSIDE	1.615	2.547	2462.55	6272.56	4.112	2001.95	8232.98
A_68_P23366442	chr4:141430855-141430899	NM_025994:-41	Efhd2	PROMOTER	1.614	3.976	1143.10	4545.11	6.418	993.55	6376.66
A_68_P25460625	chr7:125999193-125999237	NM_001081446:-74	Iqck	DIVERGENT_PROMOTER	1.614	2.484	2719.29	6755.40	4.010	2190.94	8785.77
A_68_P21114609	chr2:32167955-32167999	NR_029811:-6003	Mir199b	PROMOTER	1.614	5.640	16942.30	95558.65	9.104	11346.08	103293.50
A_68_P21565317	chr2:118489132-118489176	NM_001033254:-158	Pak6	PROMOTER	1.614	1.728	1297.75	2242.70	2.790	1069.14	2982.74
A_68_P31632702	chr18:38371220-38371264	NM_029357:-1826	Pcdh1	PROMOTER	1.614	1.637	1732.59	2835.79	2.642	1331.45	3518.04
A_68_P27632484	chr11:20531833-20531877	NM_001038625:-125	Sertad2	PROMOTER	1.614	3.475	6104.15	21214.46	5.608	4460.01	25012.99
A_68_P22130348	chr3:51364282-51364326	NM_080793:441	Setd7	INSIDE	1.614	4.461	2334.51	10415.15	7.201	2072.84	14926.78
A_68_P31212432	chr17:47605282-47605326	NM_145489:31717	AI661453	INSIDE	1.613	1.960	621.47	1218.38	3.163	511.78	1618.89

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P29713894	chr14:73110055-73110099	NM_207636:-266	Fndc3a	PROMOTER	1.613	1.503	3401.65	5113.89	2.425	2664.88	6462.15
A_68_P30367927	chr15:79521233-79521289	NM_013818:-65	Gtpbp1	DIVERGENT_PROMOTER	1.613	3.259	2903.88	9462.94	5.255	2416.36	12697.28
A_68_P25730819	chr8:27229628-27229672	NM_207659:46	Hook3	INSIDE	1.613	2.939	1362.79	4005.67	4.742	1111.00	5268.23
A_68_P25010077	chr7:26164977-26165021	NM_001039507:10127	Lipe	INSIDE	1.613	3.417	2557.39	8738.93	5.511	1874.40	10329.97
A_68_P27787812	chr11:50105519-50105563	NM_175334:298	Maml1	INSIDE	1.613	3.738	461.82	1726.44	6.031	391.72	2362.56
A_68_P27280132	chr10:79440564-79440611	NM_001003949:6488	ORF61	INSIDE	1.613	3.420	396.18	1354.95	5.517	305.43	1685.10
A_68_P24173631	chr5:148241874-148241918	NM_028291:-259	Pan3	PROMOTER	1.613	2.699	3211.48	8667.31	4.355	2514.20	10948.12
A_68_P27631993	chr11:20443834-20443878	NM_021372:601	Sertad2	INSIDE	1.613	10.061	10624.97	106902.70	16.231	7456.42	121021.70
A_68_P24046730	chr5:122278610-122278654	NM_008507:8178	Sh2b3	INSIDE	1.613	4.679	832.36	3894.34	7.546	731.05	5516.12
A_68_P23311001	chr4:131830273-131830317	NM_025579:5	Taf12	INSIDE	1.613	11.344	3315.90	37616.64	18.297	2386.77	43669.74
A_68_P20350529	chr1:74838384-74838428	NM_009518:-186	Wnt10a	PROMOTER	1.613	4.124	4948.69	20405.98	6.653	3730.25	24816.45
A_68_P30499545	chr15:102577606-102577650			Unknown	1.613	2.317	1696.36	3931.06	3.738	1417.87	5299.73
A_68_P28889015	chr13:24892904-24892948	NM_024473:-599	BC005537	PROMOTER	1.612	2.710	573.41	1553.95	4.369	537.08	2346.26
A_68_P32364032	chrX:45694726-45694770	NM_178782:214	Bcorl1	INSIDE	1.612	2.508	1625.91	4078.50	4.044	1095.53	4430.73
A_68_P26536114	chr9:56265361-56265405	NM_172924:475	C230081A13Rik	INSIDE	1.612	3.543	2542.05	9007.74	5.713	1874.16	10706.98
A_68_P31065266	chr17:15513473-15513517	NM_007865:-707	Dll1	PROMOTER	1.612	5.376	1640.73	8821.10	8.668	1157.08	10028.99
A_68_P23927140	chr5:100408133-100408177	NM_001077265:-197	Hnrnpd	PROMOTER	1.612	1.778	1719.81	3057.63	2.866	1408.50	4036.58
A_68_P23326917	chr4:134708685-134708729	NM_019732:32147	Runx3	INSIDE	1.612	3.639	3739.75	13608.80	5.865	2960.41	17362.93
A_68_P27552432	chr11:3417267-3417311	NM_053267:2584	Selm	INSIDE	1.612	2.862	653.75	1870.73	4.613	526.96	2431.08
A_68_P31213521	chr17:47809690-47809734	NM_198421:42074	Usp49	INSIDE	1.612	2.789	2117.42	5904.90	4.496	1779.78	8002.52
A_68_P27926183	chr11:75267995-75268039	NM_138950:203	Wdr81	INSIDE	1.612	1.934	384.97	744.61	3.117	383.70	1196.10
A_68_P21103868	chr2:30400904-30400948	ENSMUST00000145413:10678		DOWNSTREAM	1.612	2.044	2240.78	4580.20	3.295	1770.68	5834.67
A_68_P20778066	chr1:164408081-164408125	NM_001038619:59	Dnm3	INSIDE	1.611	2.867	1051.30	3013.75	4.617	792.73	3660.19
A_68_P23966965	chr5:107867055-107867099	NM_027599:6509	Lpcat2b	DOWNSTREAM	1.611	5.020	584.64	2934.97	8.088	566.90	4585.04
A_68_P31781216	chr18:65590296-65590340	NM_172833:-332	Malt1	PROMOTER	1.611	4.275	3911.10	16718.62	6.885	2564.32	17654.60
A_68_P24329792	chr6:29998675-29998719	NM_001164230:709	Nrf1	INSIDE	1.611	1.694	1282.34	2172.15	2.730	1075.63	2936.14
A_68_P27993897	chr11:87172172-87172216	NM_177167:302	Ppm1e	INSIDE	1.611	3.684	1483.62	5465.32	5.934	1280.66	7599.66
A_68_P30580602	chr16:18586865-18586909	NM_011532:176	Tbx1	INSIDE	1.611	3.668	2181.79	8002.39	5.908	1820.13	10753.60
A_68_P27798408	chr11:52096304-52096348	NM_009331:-574	Tcf7	PROMOTER	1.611	1.663	2733.97	4546.98	2.679	2168.01	5807.09
A_68_P23584753	chr5:32913192-32913236	NM_001205132:-329	Yes1	PROMOTER	1.611	2.569	2853.62	7330.54	4.138	2033.11	8412.94
A_68_P24541220	chr6:72297774-72297818	NM_026696:486	0610030E20Rik	INSIDE	1.610	5.030	3501.90	17613.89	8.096	2811.14	22758.40
A_68_P27354277	chr10:93002683-93002727	NM_027908:74	Amdhd1	INSIDE	1.610	2.369	1000.49	2369.90	3.813	822.61	3136.64
A_68_P25951429	chr8:72897357-72897401	NM_016685:-68	Comp	PROMOTER	1.610	3.467	1420.43	4924.30	5.580	1152.70	6432.41
A_68_P23226835	chr4:115616658-115616702	NM_001025567:-4149	Dmbx1	PROMOTER	1.610	3.342	3326.32	11115.32	5.381	2563.60	13794.61
A_68_P29631109	chr14:58617905-58617949	NM_028643:173	Efha1	INSIDE	1.610	2.344	692.10	1622.39	3.773	615.13	2321.20
A_68_P21089590	chr2:28048879-28048923	NM_001038614:288	Olfm1	INSIDE	1.610	1.554	1325.05	2058.76	2.502	1162.53	2908.28
A_68_P31117688	chr17:27792442-27792486	NM_011861:-162	Pacsin1	PROMOTER	1.610	3.962	687.38	2723.32	6.378	565.99	3609.76
A_68_P23298636	chr4:129497126-129497170	NM_008974:-574	Ptp4a2	PROMOTER	1.610	1.810	1757.41	3181.61	2.915	1435.54	4185.16
A_68_P32975180	chr9:108393143-108393187	NM_027804:158	Usp19	INSIDE	1.610	2.831	1154.50	3268.25	4.559	1078.28	4915.64
A_68_P26129049	chr8:107064933-107064977	NM_053070:248	Car7	INSIDE	1.609	4.243	3692.17	15666.86	6.830	2946.61	20123.93
A_68_P21639427	chr2:132088879-132088923	NM_138651:-92	Cds2	DIVERGENT_PROMOTER	1.609	4.699	469.43	2205.66	7.559	401.49	3035.01
A_68_P26141979	chr8:109417535-109417579	NM_011574:17	Cirh1a	INSIDE	1.609	5.028	1394.45	7010.82	8.089	1220.21	9870.28
A_68_P32454735	chrX:68917753-68917797	NM_010340:833	Gpr50	INSIDE	1.609	2.705	1139.03	3080.77	4.352	599.11	2607.06
A_68_P23588236	chr5:33678555-33678599	NM_021500:356	Maea	INSIDE	1.609	5.083	3030.57	15404.30	8.177	2515.92	20572.74
A_68_P24117361	chr5:136164752-136164796	NM_008898:-309	Por	PROMOTER	1.609	5.202	3240.90	16858.04	8.370	2280.86	19090.59
A_68_P26805694	chr9:106789235-106789279	NM_175402:75	Rbm15b	INSIDE	1.609	4.059	394.04	1599.22	6.532	333.52	2178.54
A_68_P23158199	chr4:101760754-101760798	ENSMUST00000106911:629		INSIDE	1.609	4.814	2102.05	10119.75	7.746	2023.87	15677.45
A_68_P29050103	chr13:54666500-54666544	NM_133797:221	4833439L19Rik	INSIDE	1.608	6.099	2522.42	15383.10	9.808	1975.41	19375.44
A_68_P25724841	chr8:26127277-26127321	NM_007404:96	Adam9	INSIDE	1.608	2.741	2955.35	8101.89	4.408	2472.37	10898.08
A_68_P28329059	chr12:31758655-31758699	NM_027828:-156	Fam110c	PROMOTER	1.608	2.881	1404.76	4046.65	4.632	1230.34	5698.63
A_68_P20644877	chr1:138156885-138156929	NM_001101516:544	Gpr25	INSIDE	1.608	1.686	764.98	1289.80	2.712	648.05	1757.37

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25007878	chr7:25800603-25800647	NM_008168:56764	Grik5	INSIDE	1.608	4.820	2215.50	10677.62	7.749	1490.88	11552.75
A_68_P27182287	chr10:61246439-61246483	NM_207000:152	H2afy2	INSIDE	1.608	3.190	2241.58	7150.70	5.131	1689.84	8670.31
A_68_P25656224	chr8:11557705-11557749	NM_011919:1661	Ing1	INSIDE	1.608	5.077	2794.35	14186.40	8.162	2248.83	18355.30
A_68_P21137838	chr2:35960787-35960831	NM_001083126:-1228	Lhx6	PROMOTER	1.608	3.570	1602.64	5721.08	5.740	1283.41	7366.49
A_68_P21428205	chr2:92229093-92229137	NM_001202445:3726	Mapk8ip1	INSIDE	1.608	1.807	2330.81	4212.43	2.905	1815.98	5275.98
A_68_P27922751	chr11:74651412-74651456	NM_010813:7009	Mnt	INSIDE	1.608	4.731	2325.84	11002.83	7.608	1797.06	13671.47
A_68_P26816174	chr9:108594858-108594902	NM_008924:407	Prkar2a	INSIDE	1.608	2.779	1177.52	3272.61	4.468	955.42	4269.21
A_68_P30379756	chr15:81641379-81641423	NM_017376:-443	Tef	PROMOTER	1.608	3.952	12834.27	50717.44	6.355	10155.86	64536.56
A_68_P27446660	chr10:110446716-110446760	NM_172554:384	Zdhhc17	INSIDE	1.608	1.530	3567.01	5458.66	2.461	2850.16	7014.34
A_68_P25784087	chr8:37210103-37210147	NM_172911:52243	D8Ertd82e	INSIDE	1.607	4.243	5872.86	24917.49	6.816	4103.14	27967.73
A_68_P26659813	chr9:78328998-78329042	NM_010106:511	Eef1a1	INSIDE	1.607	1.741	1728.57	3008.93	2.798	1437.16	4021.22
A_68_P29034741	chr13:51941420-51941464	NM_011817:-601	Gadd45g	PROMOTER	1.607	4.308	2411.71	10388.75	6.924	1861.97	12891.70
A_68_P25471703	chr7:128178649-128178693	NM_021554:712	Mettl9	INSIDE	1.607	8.648	1551.29	13416.01	13.900	1343.46	18673.87
A_68_P23051091	chr4:81088361-81088405	NM_010820:327	Mpdz	INSIDE	1.607	3.445	10469.36	36066.76	5.537	8861.19	49066.76
A_68_P24618284	chr6:87761631-87761675	NM_133717:-1904	Rab43	PROMOTER	1.607	3.902	5101.09	19903.73	6.270	4202.66	26351.13
A_68_P23999965	chr5:114221529-114221573	NM_016926:108	Sart3	INSIDE	1.607	2.436	1029.35	2507.68	3.916	916.10	3587.48
A_68_P21635209	chr2:131317684-131317728	NM_001177833:109	Smox	INSIDE	1.607	7.670	1752.26	13439.82	12.323	1384.68	17062.93
A_68_P32050810	chr19:29122317-29122361	NM_021299:54	Ak3	INSIDE	1.606	6.341	972.54	6167.01	10.181	734.27	7475.93
A_68_P23299955	chr4:129724973-129725017	NM_028266:-89	Col16a1	PROMOTER	1.606	3.786	2438.22	9230.27	6.081	2043.77	12427.41
A_68_P29346593	chr13:115249654-115249698	NM_008046:-738	Fst	PROMOTER	1.606	2.498	3716.50	9282.35	4.010	2635.06	10566.83
A_68_P31672402	chr18:45719605-45719649	NM_080465:-181	Kcnn2	PROMOTER	1.606	3.625	3770.40	13666.74	5.820	3126.64	18196.65
A_68_P20620522	chr1:134195663-134195707	NM_144810:482	Klhdc8a	INSIDE	1.606	3.422	890.52	3047.47	5.495	786.43	4321.27
A_68_P21583618	chr2:121781814-121781858	NM_008545:-8	Mageb3	DIVERGENT_PROMOTER	1.606	1.769	3483.81	6162.50	2.841	2685.15	7628.37
A_68_P31415143	chr17:86567807-86567851	NM_011104:704	Prkce	INSIDE	1.606	2.633	1510.89	3977.79	4.228	1249.30	5282.05
A_68_P25195707	chr7:74904146-74904190	NM_183312:460	Synm	INSIDE	1.606	1.807	1191.57	2153.03	2.902	1015.20	2946.60
A_68_P29210184	chr13:89879184-89879228	NM_001081249:2911	Vcan	INSIDE	1.606	2.401	503.61	1209.38	3.856	446.94	1723.49
A_68_P24620345	chr6:88147159-88147203	NM_008090:-1477	Gata2	PROMOTER	1.605	1.930	784.07	1513.35	3.097	737.04	2282.76
A_68_P21957226	chr3:14534076-14534120	NM_001163579:311	Lrrcc1	INSIDE	1.605	3.448	2014.65	6946.97	5.533	1548.92	8570.49
A_68_P24428222	chr6:48547522-48547566	NM_001079901:3663	Repin1	INSIDE	1.605	2.155	589.84	1270.92	3.459	464.36	1606.02
A_68_P32601446	chrX:109008521-109008565			Unknown	1.605	2.464	449.98	1108.76	3.955	314.96	1245.81
A_68_P31620631	chr18:36033282-36033326			Unknown	1.605	3.000	1800.41	5401.85	4.815	1442.62	6946.38
A_68_P26166134	chr8:113551628-113551672	NM_001190800:20	Ddx19b	INSIDE	1.604	2.542	2363.69	6008.76	4.078	1826.18	7447.29
A_68_P31484539	chr18:9212402-9212446	NM_008058:-429	Fzd8	PROMOTER	1.604	2.193	2083.27	4569.12	3.518	1590.11	5594.11
A_68_P27285907	chr10:80317900-80317944	NM_025349:32	Lsm7	INSIDE	1.604	1.454	1032.35	1501.36	2.333	818.51	1909.53
A_68_P29668497	chr14:65206255-65206299	NR_029813:-3217	Mir124a-1	PROMOTER	1.604	3.902	7366.35	28747.14	6.258	4975.08	31133.68
A_68_P24135185	chr5:139847981-139848025	NR_029768:-2303	Mir339	DIVERGENT_PROMOTER	1.604	3.796	2433.75	9238.48	6.087	2046.61	12458.24
A_68_P26345770	chr9:20970026-20970070	NM_183408:-109	Pde4a	PROMOTER	1.604	5.969	970.27	5791.23	9.573	837.83	8020.49
A_68_P21149540	chr2:38499397-38499441	NM_011187:8	Psmb7	INSIDE	1.604	2.174	2497.94	5429.94	3.487	1906.18	6647.51
A_68_P23415826	chr4:151363053-151363098	NM_001145929:20	Thap3	INSIDE	1.604	1.650	491.30	810.45	2.646	399.61	1057.32
A_68_P26814405	chr9:108250089-108250133	NM_011678:-51	Usp4	PROMOTER	1.604	2.988	1313.14	3923.16	4.793	1096.62	5256.58
A_68_P30476410	chr15:98608643-98608687	NM_011718:-83	Wnt10b	PROMOTER	1.604	1.353	4751.71	6428.46	2.170	3765.60	8171.33
A_68_P21812641	chr2:163298061-163298105	NR_028122:-198	2310001K24Rik	PROMOTER	1.603	2.860	1751.00	5008.06	4.586	1461.56	6702.35
A_68_P21111049	chr2:31615339-31615383	NM_009594:-104	Abl1	PROMOTER	1.603	1.565	1024.47	1603.78	2.510	855.67	2147.89
A_68_P30026213	chr15:13102919-13102963	NM_007666:454	Cdh6	INSIDE	1.603	2.861	2518.02	7205.20	4.586	2042.09	9365.27
A_68_P32322121	chrX:34731184-34731228	NM_019443:27	Ndufa1	INSIDE	1.603	1.735	1435.26	2490.36	2.782	880.76	2449.86
A_68_P28538315	chr12:74685369-74685413	NM_008856:-637	Prkch	PROMOTER	1.603	4.059	997.12	4046.86	6.506	734.71	4779.80
A_68_P27222450	chr10:68675577-68675621	NM_001081347:194	Rhobtb1	INSIDE	1.603	3.581	5360.76	19199.15	5.739	4084.46	23442.44
A_68_P30976720	chr16:93603886-93603930	NM_145482:152	Setd4	INSIDE	1.603	4.985	4901.08	24430.88	7.990	3852.54	30782.88
A_68_P20872220	chr1:181733104-181733148	NM_026375:1020	Ahctf1	INSIDE	1.602	2.264	1393.41	3155.16	3.628	1213.64	4402.86
A_68_P27311154	chr10:85391524-85391568	NM_001163614:311	Ascl4	INSIDE	1.602	2.795	359.07	1003.47	4.477	296.83	1328.85
A_68_P23299678	chr4:129683985-129684029	NM_001199696:21685	Bai2	INSIDE	1.602	2.638	709.65	1872.38	4.226	588.49	2486.74

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P30567436	chr16:15887941-15887985	NM_007679:584	Cebpd	INSIDE	1.602	4.663	696.93	3249.69	7.469	603.47	4507.38
A_68_P20148715	chr1:36568684-36568728	NM_001039551:-14	Cnnm3	PROMOTER	1.602	2.142	3211.45	6880.19	3.431	2505.82	8597.79
A_68_P32463877	chrX:70882835-70882879	NM_029352:-1923	Dusp9	PROMOTER	1.602	2.572	789.86	2031.39	4.119	437.53	1802.33
A_68_P27083091	chr10:39977457-39977501	NM_026113:-7	Gtf3c6	PROMOTER	1.602	3.173	3397.42	10778.73	5.083	2673.04	13586.99
A_68_P24541702	chr6:72388860-72388904	NM_145569:670	Mat2a	INSIDE	1.602	2.735	1124.77	3076.39	4.383	983.64	4311.30
A_68_P27938848	chr11:77500486-77500530	NM_001024205:868	Nufip2	INSIDE	1.602	2.017	1984.94	4004.32	3.232	1657.94	5359.11
A_68_P24323855	chr6:28931080-28931124	ENSMUST00000164104:-531		PROMOTER	1.602	1.361	1615.01	2197.83	2.181	1235.55	2694.25
A_68_P29005211	chr13:46061364-46061408	NM_009124:-1041	Atxn1	PROMOTER	1.601	3.328	3978.55	13239.55	5.327	2945.77	15691.53
A_68_P22030511	chr3:30755072-30755116	NM_001134385:223	Gpr160	INSIDE	1.601	4.571	796.20	3639.25	7.317	677.92	4960.23
A_68_P30572653	chr16:17233627-17233671	NM_178922:-31	Hic2	PROMOTER	1.601	4.792	2127.46	10194.96	7.674	1775.80	13627.26
A_68_P26016967	chr8:86424037-86424081	NM_181039:62	Lphn1	INSIDE	1.601	3.211	2264.65	7272.80	5.141	2047.70	10527.10
A_68_P23264207	chr4:123341175-123341219	NM_001199136:20407	Macf1	INSIDE	1.601	2.225	1197.98	2665.43	3.563	1057.07	3766.45
A_68_P32777676	chrX:156426760-156426804	NM_001163085:418	Map3k15	INSIDE	1.601	3.482	3434.14	11957.67	5.574	2209.75	12316.96
A_68_P23316515	chr4:132797012-132797056	NM_016693:302	Map3k6	INSIDE	1.601	3.752	940.36	3528.30	6.005	814.28	4889.99
A_68_P23936340	chr5:102094274-102094318	NM_144955:-566	Nkx6-1	PROMOTER	1.601	2.012	1254.18	2523.11	3.222	1064.57	3429.80
A_68_P23398659	chr4:148473653-148473697	NM_019781:247	Pex14	INSIDE	1.601	3.023	1074.05	3246.82	4.840	773.96	3745.89
A_68_P23308582	chr4:131392468-131392512	NM_001083119:1703	Ptpru	INSIDE	1.601	2.243	2002.36	4491.97	3.592	1510.32	5425.13
A_68_P30394811	chr15:84276781-84276825	NM_001163145:725	1810041L15Rik	INSIDE	1.600	3.955	1864.88	7375.82	6.327	1441.31	9119.27
A_68_P26344263	chr9:20672999-20673043	NM_175687:-65	A230050P20Rik	PROMOTER	1.600	11.633	911.91	10608.40	18.613	684.93	12748.62
A_68_P26816895	chr9:108734927-108734971	NM_080437:6298	Celsr3	INSIDE	1.600	4.517	3492.77	15777.49	7.229	2474.22	17885.33
A_68_P26313788	chr9:13632555-13632599	NM_176836:406	Fam76b	INSIDE	1.600	1.733	1041.18	1804.15	2.773	816.41	2263.88
A_68_P29031120	chr13:51266739-51266783	NM_029173:367	Nxnl2	INSIDE	1.600	3.920	2615.10	10251.94	6.274	2115.39	13272.40
A_68_P21762360	chr2:154616838-154616882	NM_001139511:15	Raly	INSIDE	1.600	2.771	2007.08	5561.51	4.434	1712.11	7591.07
A_68_P26811550	chr9:107775126-107775170	NM_011251:2	Rbm6	INSIDE	1.600	4.161	612.46	2548.65	6.658	519.94	3461.97
A_68_P24691293	chr6:100237792-100237836	NM_019743:-462	Rybp	PROMOTER	1.600	3.966	2131.78	8453.78	6.345	1704.68	10815.92
A_68_P31868107	chr18:81182856-81182900	NM_178280:439	Sall3	INSIDE	1.600	3.902	3523.83	13749.52	6.244	2824.25	17633.53
A_68_P22872185	chr4:43536399-43536443	NM_009416:-160	Tpm2	PROMOTER	1.600	2.434	1937.75	4715.58	3.894	1520.65	5921.09
A_68_P23756659	chr5:65883667-65883711	NM_133697:386	1110003E01Rik	INSIDE	1.599	1.904	7260.24	13825.18	3.044	6186.80	18835.45
A_68_P20258663	chr1:58450520-58450564	NM_025824:563	Bzw1	INSIDE	1.599	3.266	2398.42	7833.03	5.223	2083.81	10883.14
A_68_P32576286	chrX:101396172-101396216	NM_001077354:262	C77370	INSIDE	1.599	4.081	7479.24	30522.25	6.527	6051.21	39497.18
A_68_P30010737	chr15:10399801-10399845	NM_030046:449	Dnajc21	INSIDE	1.599	4.759	1474.51	7017.39	7.611	1290.18	9819.95
A_68_P25023124	chr7:29478378-29478422	NM_001163702:238	Fbxo27	INSIDE	1.599	1.525	1881.91	2870.40	2.439	1510.43	3683.48
A_68_P23433055	chr4:154011802-154011846	NM_001177995:-842	Prdm16	PROMOTER	1.599	6.269	1955.43	12259.20	10.026	1598.27	16024.05
A_68_P23407012	chr4:149943746-149943790	NM_001085492:287744	Rere	INSIDE	1.599	1.670	531.33	887.33	2.670	426.21	1138.07
A_68_P22614971	chr3:146162605-146162649	NM_027617:91	Spata1	INSIDE	1.599	3.443	830.28	2858.85	5.504	725.21	3991.58
A_68_P23929552	chr5:100858837-100858881	NR_034038:-304	5430416N02Rik	PROMOTER	1.598	4.386	2091.10	9170.96	7.010	1771.53	12417.68
A_68_P23319354	chr4:133310209-133310253	NM_001080819:-704	Arid1a	PROMOTER	1.598	2.197	3613.68	7937.87	3.510	2699.47	9473.94
A_68_P30362677	chr15:78672776-78672820	NM_027219:-278	Cdc42ep1	PROMOTER	1.598	2.451	661.26	1620.50	3.915	598.40	2342.69
A_68_P30356227	chr15:77672647-77672691	NM_022410:-123	Myh9	PROMOTER	1.598	4.863	5861.69	28505.42	7.773	4607.92	35815.21
A_68_P30458578	chr15:95358757-95358801	NM_016743:359	Nell2	INSIDE	1.598	2.298	4531.86	10413.47	3.672	3655.64	13422.68
A_68_P27178875	chr10:60609327-60609371	NM_009163:1065	Sgpl1	INSIDE	1.598	1.769	2592.83	4587.47	2.828	2049.41	5795.72
A_68_P23072589	chr4:84851297-84851341	NM_019535:-41	Sh3gl2	PROMOTER	1.598	1.967	485.40	954.70	3.142	462.98	1454.73
A_68_P29418922	chr14:14794169-14794213	NM_025435:-451	Thoc7	PROMOTER	1.598	2.309	2178.68	5030.69	3.690	1673.07	6174.15
A_68_P22875967	chr4:44246168-44246212	ENSMUST00000123844:-5006		PROMOTER	1.598	5.630	5663.68	31884.31	8.996	4334.87	38996.60
A_68_P20877466	chr1:182655892-182655936	NM_133225:-259	Acbd3	PROMOTER	1.597	4.420	1550.19	6851.39	7.057	1414.09	9978.61
A_68_P23316365	chr4:132768551-132768595	NM_008154:-121	Gpr3	DIVERGENT_PROMOTER	1.597	4.311	3132.85	13506.40	6.884	2790.16	19208.65
A_68_P26228655	chr8:124277307-124277351	NM_020605:22870	Jph3	INSIDE	1.597	4.386	798.68	3502.79	7.004	595.82	4173.10
A_68_P31259695	chr17:57170806-57170850	NM_010613:102	Khsrp	INSIDE	1.597	4.699	2028.91	9532.99	7.505	1900.29	14262.48
A_68_P25727982	chr8:26707741-26707785	NM_173012:197	Letm2	INSIDE	1.597	5.315	1145.84	6090.24	8.487	988.09	8386.39
A_68_P31790832	chr18:67404825-67404869	NM_172630:638	Mppe1	INSIDE	1.597	2.013	1640.63	3302.46	3.214	1469.60	4723.63
A_68_P25007073	chr7:25669913-25669957	NM_023133:202	Rps19	INSIDE	1.597	3.412	1484.11	5063.19	5.450	1292.39	7043.04

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P32010020	chr19:22213374-22213418	NM_001035239:-210	Trpm3	PROMOTER	1.597	2.658	1036.70	2755.98	4.245	859.73	3649.29
A_68_P28731667	chr12:110291510-110291554	NM_001163175:14895	Begain	INSIDE	1.596	2.689	2110.52	5675.94	4.291	1760.86	7556.49
A_68_P22729559	chr4:11315357-11315401	NM_194055:-1448	Esrp1	PROMOTER	1.596	1.674	934.79	1565.25	2.673	741.88	1982.85
A_68_P28767111	chr12:117519591-117519635	NM_028731:-82	Esyt2	PROMOTER	1.596	2.903	1504.28	4366.28	4.632	1093.98	5067.52
A_68_P23145563	chr4:99324552-99324596	NM_010425:1585	Foxd3	INSIDE	1.596	1.997	1989.00	3971.76	3.187	1744.74	5559.83
A_68_P27560010	chr11:4749422-4749466	NM_010898:86	Nf2	INSIDE	1.596	2.351	3344.47	7862.57	3.752	2818.67	10576.64
A_68_P30568393	chr16:16213292-16213336	NM_026163:-123	Pkp2	PROMOTER	1.596	2.621	1302.42	3413.60	4.184	1066.08	4460.33
A_68_P21142183	chr2:37307736-37307780	NM_001033960:-15	Rabgap1	PROMOTER	1.596	5.228	3556.66	18595.17	8.346	2877.40	24014.49
A_68_P28685879	chr12:102321594-102321638	NM_001160214:296	Smek1	INSIDE	1.596	2.273	1733.74	3940.91	3.627	1557.98	5650.62
A_68_P28614745	chr12:88540669-88540713	NM_001033475:489	Tmed8	INSIDE	1.596	5.480	3474.84	19041.55	8.745	2597.15	22713.11
A_68_P20151305	chr1:36996651-36996695	NM_018872:-300	Tmem131	PROMOTER	1.596	2.608	1176.45	3067.66	4.162	972.02	4045.50
A_68_P21622816	chr2:128891587-128891631	NM_027192:-74	Ttl	PROMOTER	1.596	4.591	2434.91	11177.48	7.325	1775.89	13008.52
A_68_P26276227	chr9:4260687-4260731			Unknown	1.596	3.594	1726.01	6204.06	5.737	1444.73	8288.80
A_68_P31326351	chr17:70318541-70318585	ENSMUST00000060072:-23		PROMOTER	1.596	2.290	406.10	929.83	3.655	342.56	1252.03
A_68_P23817349	chr5:77087036-77087080	ENSMUST00000125922:313		INSIDE	1.596	3.109	1045.08	3248.75	4.961	938.76	4656.77
A_68_P31157711	chr17:35257720-35257764	NM_009975:650	Csnk2b	INSIDE	1.595	1.882	2747.60	5172.15	3.002	1920.74	5766.73
A_68_P22942456	chr4:56959870-56959914	NM_175518:409	D730040F13Rik	INSIDE	1.595	6.093	791.80	4824.54	9.717	707.64	6876.09
A_68_P20613818	chr1:133034787-133034831	NM_145508:3	Dyrk3	INSIDE	1.595	2.262	671.25	1518.37	3.608	591.10	2132.62
A_68_P27897958	chr11:69734258-69734302	NM_001166590:-148	Eif5a	PROMOTER	1.595	4.279	6778.16	29002.29	6.825	5191.36	35430.35
A_68_P32684282	chrX:133653782-133653826	NM_007957:1061	Esx1	INSIDE	1.595	3.270	3979.99	13014.37	5.216	2354.09	12279.98
A_68_P27281299	chr10:79613231-79613275	NM_021565:2218	Midn	INSIDE	1.595	1.942	729.15	1415.90	3.097	609.84	1888.57
A_68_P31112722	chr17:26978019-26978063	NM_008700:470	Nkx2-5	INSIDE	1.595	2.654	1733.03	4599.01	4.234	1351.92	5723.70
A_68_P23694283	chr5:52759912-52759956	NM_011435:4892	Sod3	INSIDE	1.595	4.202	2347.88	9864.82	6.699	1963.26	13152.84
A_68_P27985587	chr11:85651691-85651735	NM_009324:5596	Tbx2	INSIDE	1.595	1.611	1802.26	2903.35	2.570	1401.10	3600.16
A_68_P22948244	chr4:57969284-57969328	NM_011660:-23	Txn1	PROMOTER	1.595	3.002	664.99	1996.03	4.788	619.35	2965.60
A_68_P30476328	chr15:98593484-98593528	NM_007478:43	Arf3	INSIDE	1.594	2.018	3901.49	7874.01	3.216	3017.31	9704.51
A_68_P32573854	chrX:100810244-100810288	NR_028381:8827	B230206F22Rik	INSIDE	1.594	4.072	8298.88	33789.92	6.490	3713.15	24097.37
A_68_P25655858	chr8:11497803-11497847	NM_026995:257	Carkd	INSIDE	1.594	2.684	1919.84	5153.21	4.279	1524.74	6524.19
A_68_P28083428	chr11:102977758-102977802	NM_138753:142	Hexim1	INSIDE	1.594	1.775	3158.02	5605.34	2.830	2549.73	7215.73
A_68_P28397452	chr12:45429719-45429763	NM_001146031:-131	Nrcam	PROMOTER	1.594	3.036	974.16	2957.82	4.838	883.91	4276.75
A_68_P25411125	chr7:117129431-117129475	NM_153525:292	Tmem41b	INSIDE	1.594	2.631	4442.00	11687.76	4.195	3120.46	13091.02
A_68_P27589635	chr11:11013930-11013974	NM_177033:-66	Vwc2	PROMOTER	1.594	2.232	460.96	1029.09	3.559	447.80	1593.57
A_68_P21751445	chr2:152656855-152656899	NM_009743:542	Bcl2l1	INSIDE	1.593	2.403	439.51	1056.14	3.828	385.97	1477.30
A_68_P26971601	chr10:17443503-17443547	NM_010828:491	Cited2	INSIDE	1.593	1.437	1021.65	1468.46	2.290	866.24	1983.53
A_68_P23587982	chr5:33618039-33618083	NM_001198859:-407	Ctbp1	PROMOTER	1.593	2.427	696.54	1690.79	3.867	582.42	2252.40
A_68_P24171442	chr5:147840909-147840953	NM_080795:47218	Lnx2	INSIDE	1.593	2.871	522.01	1498.70	4.572	468.43	2141.74
A_68_P23577160	chr5:31522948-31522992	NM_008014:-52	Ppm1g	PROMOTER	1.593	5.580	2910.39	16240.42	8.892	2461.09	21883.42
A_68_P31759815	chr18:61946490-61946534	NM_178928:-196	Afap1l1	PROMOTER	1.592	1.383	1416.45	1959.53	2.203	1122.92	2473.79
A_68_P27835630	chr11:59041516-59041560	NM_001130408:126	Arf1	INSIDE	1.592	2.033	1722.66	3502.46	3.236	1427.13	4618.53
A_68_P32533249	chrX:90540139-90540183	NM_007492:8176	Arx	INSIDE	1.592	2.504	1322.93	3312.11	3.985	969.13	3861.84
A_68_P21704233	chr2:143740849-143740894	NM_019771:-195	Dstn	PROMOTER	1.592	3.379	3450.55	11659.34	5.380	2818.76	15163.67
A_68_P29259683	chr13:99585179-99585223	NM_172591:204	Fcho2	INSIDE	1.592	4.182	1087.69	4548.58	6.660	923.46	6149.83
A_68_P31922932	chr19:4396607-4396651	NM_001001984:449	Kdm2a	INSIDE	1.592	2.723	3295.26	8971.97	4.335	2770.30	12010.53
A_68_P28051873	chr11:97521768-97521812	NM_139311:-2935	Mllt6	PROMOTER	1.592	4.326	636.54	2753.65	6.886	596.03	4104.36
A_68_P30346592	chr15:76009110-76009154	NM_201394:17008	Plec	INSIDE	1.592	3.611	372.29	1344.43	5.748	317.36	1824.20
A_68_P27565811	chr11:5855744-5855788	NM_019661:6	Ykt6	INSIDE	1.592	1.660	494.53	820.84	2.643	392.71	1037.95
A_68_P22129179	chr3:51145355-51145399	ENSMUST00000135496:-796		PROMOTER	1.592	2.407	1351.50	3253.62	3.832	1112.68	4263.75
A_68_P26022004	chr8:87323463-87323507	NM_001081982:755	Nfix	INSIDE	1.591	1.494	801.96	1198.24	2.377	743.63	1767.40
A_68_P24643143	chr6:92042164-92042208	NM_011630:775	Nr2c2	INSIDE	1.591	2.293	1246.91	2859.03	3.649	1034.35	3774.36
A_68_P29057251	chr13:55927242-55927286	NM_011097:5522	Pitx1	INSIDE	1.591	2.076	628.89	1305.28	3.303	520.93	1720.60
A_68_P31067776	chr17:15968184-15968228	NM_178615:-4656	Rgmb	PROMOTER	1.591	2.104	1439.15	3027.84	3.347	1305.65	4370.41

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26533458	chr9:55785595-55785639	NM_001081341:306	Scaper	INSIDE	1.591	1.692	6215.45	10515.26	2.692	5095.27	13718.22
A_68_P24124227	chr5:137507750-137507794	NM_001039385:1608	Vgf	INSIDE	1.591	6.809	422.38	2876.05	10.831	459.61	4978.05
A_68_P30578495	chr16:18235059-18235103	NM_172151:149	Zdhhc8	INSIDE	1.591	2.521	1763.98	4446.77	4.011	1455.75	5839.54
A_68_P30347864	chr15:76199968-76200012	NM_021555:663	Fam203a	INSIDE	1.590	1.972	711.02	1402.24	3.137	582.35	1826.67
A_68_P32117383	chr19:41905096-41905140	NM_008043:659	Frat1	INSIDE	1.590	2.682	1948.71	5227.13	4.264	1756.91	7491.10
A_68_P30148784	chr15:38228806-38228850	NM_013692:1634	Klf10	INSIDE	1.590	2.565	2289.00	5871.06	4.079	1935.98	7897.38
A_68_P24434512	chr6:49772812-49772856	NM_023456:107	Npy	INSIDE	1.590	2.141	2840.99	6083.61	3.405	2464.85	8391.72
A_68_P33008139	A_68_P33008139			Unknown	1.590	3.923	9272.31	36375.59	6.238	6729.01	41976.06
A_68_P23467734	chr5:8367164-8367208	NM_001098225:895	Adam22	INSIDE	1.589	2.734	1717.39	4695.16	4.344	1279.99	5560.36
A_68_P20231549	chr1:53409460-53409504	NM_133728:61	Asnsd1	INSIDE	1.589	4.459	1548.31	6903.98	7.087	1276.77	9049.05
A_68_P30478144	chr15:98917975-98918019	NM_001024702:163	C1ql4	INSIDE	1.589	10.977	841.38	9235.98	17.442	720.72	12570.65
A_68_P20885895	chr1:184212870-184212914	NM_007853:-2	Degs1	PROMOTER	1.589	9.939	456.85	4540.71	15.794	377.16	5956.78
A_68_P27475787	chr10:115911149-115911205	NM_021452:-597	Kcnmb4	PROMOTER	1.589	2.152	256.78	552.55	3.418	188.17	643.27
A_68_P23985664	chr5:111847445-111847489	NM_001081235:281	Mn1	INSIDE	1.589	4.139	2050.83	8487.53	6.574	1625.04	10683.59
A_68_P27095676	chr10:42299357-42299401	NM_152229:4016	Nr2e1	INSIDE	1.589	5.157	3488.82	17991.60	8.195	2726.60	22344.39
A_68_P20005794	chr1:4482093-4482137	NM_011441:4380	Sox17	INSIDE	1.589	1.584	758.20	1201.34	2.517	626.08	1575.97
A_68_P26234573	chr8:125135855-125135899	NM_021502:351	Trappc2l	INSIDE	1.589	2.915	1854.83	5407.17	4.632	1334.71	6182.19
A_68_P31098616	chr17:24769435-24769479	NM_001039363:118	Tsc2	INSIDE	1.589	1.349	4463.30	6019.95	2.143	3751.78	8041.93
A_68_P21749221	chr2:152240295-152240339	NM_175126:464	Zcchc3	INSIDE	1.589	3.004	2569.64	7720.35	4.775	2282.28	10898.69
A_68_P24000795	chr5:114358894-114358938	NM_011779:-201	Coro1c	PROMOTER	1.588	2.186	1922.06	4201.58	3.471	1805.60	6267.42
A_68_P24783941	chr6:117857819-117857863	NM_001166427:-9471	Hnrnpf	PROMOTER	1.588	6.228	909.62	5664.78	9.888	695.15	6873.69
A_68_P23138267	chr4:98062517-98062561	NM_001005784:22	Inadl	INSIDE	1.588	4.487	849.63	3811.95	7.127	762.97	5437.57
A_68_P21078768	chr2:26301082-26301126	NM_153125:-368	Sec16a	PROMOTER	1.588	5.643	10762.58	60732.44	8.962	7729.46	69269.22
A_68_P29218720	chr13:91600319-91600363	NM_024186:-361	Ssbp2	PROMOTER	1.588	4.755	2770.98	13176.69	7.551	2307.64	17424.88
A_68_P25377988	chr7:109415960-109416004	NM_009287:-355	Stim1	PROMOTER	1.588	3.944	1503.95	5931.63	6.262	1256.37	7866.97
A_68_P21910960	chr2:181231996-181232040	NM_025482:61	Tpd52l2	INSIDE	1.588	2.405	810.93	1950.67	3.820	706.07	2696.99
A_68_P26974632	chr10:18038691-18038735			Unknown	1.588	2.681	1100.73	2951.11	4.258	938.92	3997.93
A_68_P26102845	chr8:101939884-101939928	NM_001039154:451	Cdh8	INSIDE	1.587	2.112	3141.75	6636.81	3.352	2242.95	7519.00
A_68_P29729812	chr14:76153932-76153976	NM_177381:346	Cog3	INSIDE	1.587	1.418	1256.41	1781.25	2.249	1056.18	2375.74
A_68_P32007552	chr19:21727793-21727837	NM_146096:16	Fam108b	INSIDE	1.587	4.598	476.18	2189.70	7.296	384.95	2808.78
A_68_P31930914	chr19:5803350-5803394	NR_002847:-701	Malat1	PROMOTER	1.587	2.239	2534.95	5676.06	3.553	1910.89	6790.18
A_68_P30346015	chr15:75921006-75921050	NM_144847:-585	Nrbp2	PROMOTER	1.587	2.955	3133.29	9260.38	4.690	2464.60	11559.95
A_68_P20585382	chr1:127457522-127457566	NM_028787:-48	Slc35f5	PROMOTER	1.587	3.073	987.60	3034.69	4.876	876.38	4272.84
A_68_P25588178	chr7:148514084-148514128	NR_024509:78	Tmem80	INSIDE	1.587	2.664	2355.48	6275.28	4.228	1974.60	8349.00
A_68_P25670894	chr8:13870055-13870099	NM_181854:436	Zfp828	INSIDE	1.587	1.726	1360.09	2347.50	2.740	1066.27	2921.49
A_68_P28745339	chr12:112908725-112908769	NM_021273:1803	Ckb	INSIDE	1.586	3.597	1932.40	6951.18	5.703	1796.13	10243.90
A_68_P21568184	chr2:118993532-118993576	NM_177157:31	Gchfr	INSIDE	1.586	3.148	2843.34	8949.78	4.993	2288.86	11428.31
A_68_P32181854	chr19:53403918-53403962	NM_001008543:-995	Mxi1	PROMOTER	1.586	2.159	1039.87	2244.67	3.423	842.54	2884.42
A_68_P27551118	chr11:3189560-3189605	NM_019574:-877	Patz1	PROMOTER	1.586	2.121	4010.21	8505.49	3.364	3196.90	10755.63
A_68_P26573393	chr9:62827843-62827887	NM_019663:822	Pias1	INSIDE	1.586	1.682	3374.87	5675.32	2.667	2383.82	6356.72
A_68_P20441527	chr1:93194765-93194809	NM_016717:-128	Scly	PROMOTER	1.586	4.107	3339.04	13712.54	6.514	2809.46	18299.80
A_68_P30572142	chr16:17131635-17131679	NM_022324:820	Sdf2l1	INSIDE	1.586	2.415	2158.71	5212.22	3.830	1737.14	6652.61
A_68_P26822089	chr9:110034498-110034542	NM_009211:-7	Smarcc1	PROMOTER	1.586	6.946	17001.44	118093.90	11.014	16425.11	180909.50
A_68_P23332899	chr4:135804076-135804120	NM_011542:227	Tcea3	INSIDE	1.586	2.093	1284.42	2687.88	3.319	1047.49	3476.56
A_68_P20156316	chr1:37922113-37922157	NM_207228:-210	Tsga10	DIVERGENT_PROMOTER	1.586	1.464	728.86	1066.79	2.321	599.54	1391.72
A_68_P28149093	chr11:114536801-114536845	NM_053273:41	Ttyh2	INSIDE	1.586	5.212	2080.39	10842.37	8.265	1728.79	14288.31
A_68_P24298747	chr6:23789611-23789655	NM_153163:-332	Cadps2	PROMOTER	1.585	1.887	2105.53	3972.97	2.991	1721.36	5148.84
A_68_P23363266	chr4:140864579-140864623	NM_010139:7446	Epha2	INSIDE	1.585	1.971	645.57	1272.51	3.125	472.81	1477.61
A_68_P29619799	chr14:56386649-56386693	NM_008519:1872	Ltb4r1	INSIDE	1.585	6.299	771.24	4857.79	9.981	638.62	6373.79
A_68_P31121837	chr17:28465985-28466029	NM_011287:591	Rpl10a	INSIDE	1.585	2.638	2942.12	7761.29	4.181	2365.40	9888.84
A_68_P21100496	chr2:29820843-29820887	NM_001076554:-215	Spna2	PROMOTER	1.585	2.106	2808.10	5914.80	3.338	2344.22	7824.94

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26165551	chr8:113443849-113443893	NM_009179:106	St3gal2	INSIDE	1.585	1.358	1611.73	2188.02	2.152	1539.91	3313.18
A_68_P25724844	chr8:26127584-26127628	NM_027194:-76	Tm2d2	DIVERGENT_PROMOTER	1.585	3.211	1452.58	4664.16	5.088	1112.65	5661.61
A_68_P22200394	chr3:65333128-65333172	NR_027955:186	4931440P22Rik	INSIDE	1.584	2.219	2078.16	4610.97	3.514	1826.35	6418.43
A_68_P22311242	chr3:87803722-87803766	NM_007529:534	Bcan	INSIDE	1.584	1.717	634.64	1089.84	2.719	548.77	1492.29
A_68_P31152235	chr17:34259132-34259176	NM_010238:-462	Brd2	PROMOTER	1.584	2.928	654.82	1917.42	4.640	523.46	2428.63
A_68_P20411731	chr1:88256083-88256127	NR_015507:-44	C130036L24Rik	DIVERGENT_PROMOTER	1.584	5.622	3907.23	21965.87	8.906	2878.08	25631.84
A_68_P21566994	chr2:118752369-118752413	NM_028117:158	Chst14	INSIDE	1.584	2.111	4274.41	9021.50	3.342	3244.99	10846.08
A_68_P29470478	chr14:25065176-25065220	NM_001163513:-56	Dlg5	PROMOTER	1.584	2.924	782.41	2287.43	4.630	663.38	3071.49
A_68_P30345428	chr15:75834117-75834161	NM_001168253:5790	Fam83h	INSIDE	1.584	8.887	2371.19	21072.30	14.073	1940.59	27309.55
A_68_P28656384	chr12:96934105-96934150	NM_201518:3692	Flrt2	INSIDE	1.584	2.959	1264.47	3741.34	4.687	1024.72	4803.15
A_68_P23403797	chr4:149383165-149383209	NM_173371:-54	H6pd	PROMOTER	1.584	6.988	3001.40	20974.56	11.069	2237.16	24763.46
A_68_P31621445	chr18:36177706-36177750	NM_001167891:179086	Nrg2	INSIDE	1.584	2.561	186.27	476.99	4.056	214.79	871.25
A_68_P26398232	chr9:30838076-30838120	NM_001115130:-130	Zbtb44	PROMOTER	1.584	5.966	5734.07	34207.50	9.452	4537.35	42885.20
A_68_P30371089	chr15:80086079-80086123	NM_009716:487	Atf4	INSIDE	1.583	3.049	1179.31	3596.02	4.827	964.24	4654.11
A_68_P30589274	chr16:20733484-20733528	NM_009893:307	Chrd	INSIDE	1.583	1.426	2944.10	4199.57	2.257	2340.81	5284.08
A_68_P29699037	chr14:70479901-70479945	NM_018781:2671	Egr3	INSIDE	1.583	4.276	1107.75	4736.44	6.769	861.94	5834.35
A_68_P22325451	chr3:90280267-90280311	NM_026374:166	Ilf2	INSIDE	1.583	4.404	4144.81	18254.36	6.971	3183.87	22195.81
A_68_P27787814	chr11:50105808-50105852	NM_175334:8	Maml1	INSIDE	1.583	2.825	2008.46	5672.99	4.471	1575.17	7043.18
A_68_P31556965	chr18:23962258-23962302	NM_153058:-190	Mapre2	PROMOTER	1.583	2.325	1721.23	4002.09	3.681	1225.12	4510.15
A_68_P22083003	chr3:40886734-40886778	NM_027558:212	Pgrmc2	INSIDE	1.583	4.991	30520.14	152321.60	7.899	21096.52	166634.90
A_68_P22658557	chr3:153388050-153388094	NM_011372:25	St6galnac3	INSIDE	1.583	2.667	3430.94	9151.06	4.222	2955.87	12479.41
A_68_P25503171	chr7:134093152-134093196	NM_001039645:-79	Asphd1	DIVERGENT_PROMOTER	1.582	1.818	2003.95	3643.79	2.877	1578.37	4540.81
A_68_P24449403	chr6:52196333-52196377	NM_010450:-588	Hoxa11	PROMOTER	1.582	2.100	1809.28	3799.64	3.323	1412.21	4692.87
A_68_P28751168	chr12:113838436-113838480	NM_198411:11464	Inf2	INSIDE	1.582	3.465	1310.26	4540.69	5.484	1032.55	5662.21
A_68_P28549425	chr12:76697618-76697662	NM_012024:-453	Ppp2r5e	PROMOTER	1.582	2.537	3045.09	7725.01	4.013	2503.22	10046.44
A_68_P28159701	chr11:116359924-116359968	NM_026364:-8286	Prpsap1	PROMOTER	1.582	2.957	3257.37	9633.54	4.679	2512.02	11752.83
A_68_P26044774	chr8:91565521-91565568	NM_021390:2517	Sall1	INSIDE	1.582	4.277	385.41	1648.29	6.766	343.98	2327.19
A_68_P26365989	chr9:25059719-25059763	NM_001205367:-299	Septin7	PROMOTER	1.582	3.061	4140.89	12675.54	4.843	3365.70	16299.80
A_68_P26587800	chr9:65308975-65309019	NM_138584:253	Spg21	INSIDE	1.582	4.852	7065.33	34279.80	7.673	4943.68	37934.16
A_68_P22650044	chr3:152009738-152009782	NM_001076676:316	Usp33	INSIDE	1.582	2.830	733.50	2075.90	4.476	652.95	2922.67
A_68_P30588338	chr16:20591336-20591380	NM_182636:1704	Vwa5b2	INSIDE	1.582	3.605	2568.88	9259.68	5.704	1877.16	10707.37
A_68_P24153997	chr5:143668325-143668369	NM_007393:57	Actb	INSIDE	1.581	2.044	1442.49	2948.69	3.232	1278.47	4131.59
A_68_P29113350	chr13:69138021-69138065	NM_153534:377	Adcy2	INSIDE	1.581	2.342	1347.48	3155.18	3.703	1119.72	4146.15
A_68_P21754297	chr2:153171289-153171333	NM_001039939:-564	Asxl1	PROMOTER	1.581	2.682	4922.89	13203.66	4.241	3681.23	15611.84
A_68_P23418114	chr4:151712427-151712471	NM_001081376:-311	Chd5	PROMOTER	1.581	2.138	1253.46	2679.94	3.379	968.47	3272.88
A_68_P25504835	chr7:134404064-134404108	NM_023203:95	Dctpp1	INSIDE	1.581	2.655	4740.09	12584.03	4.197	3408.48	14305.16
A_68_P31939393	chr19:7416055-7416099	NM_001080388:258	Mark2	INSIDE	1.581	2.657	5515.08	14651.84	4.199	4403.33	18491.38
A_68_P30568394	chr16:16213390-16213434	NM_026163:-25	Pkp2	PROMOTER	1.581	1.469	1701.74	2499.70	2.322	1438.16	3338.92
A_68_P32036088	chr19:26681356-26681400	NM_011416:1729	Smarca2	INSIDE	1.581	3.893	616.82	2401.14	6.156	548.04	3373.76
A_68_P24595943	chr6:83817210-83817254	ENSMUST00000113842:8189		DOWNSTREAM	1.581	1.572	847.83	1332.65	2.486	720.15	1790.19
A_68_P30382137	chr15:82043157-82043202	NM_001207021:66	AI848285	INSIDE	1.580	3.256	825.33	2687.65	5.144	638.50	3284.60
A_68_P21875562	chr2:174289603-174289647	NM_025983:-22	Atp5e	PROMOTER	1.580	3.191	1417.02	4521.49	5.041	1276.23	6434.07
A_68_P27649080	chr11:23979542-23979586	NM_001159290:-1130	Bcl11a	PROMOTER	1.580	1.559	1357.49	2115.82	2.463	1197.90	2950.60
A_68_P26816894	chr9:108734858-108734902	NM_080437:6230	Celsr3	INSIDE	1.580	3.081	4378.64	13489.38	4.868	3369.52	16404.32
A_68_P23345719	chr4:137990637-137990681	NM_026689:72	Mul1	INSIDE	1.580	2.436	2819.27	6866.86	3.849	2247.89	8653.07
A_68_P32462210	chrX:70599683-70599727	NM_001160229:11745	Zfp275	INSIDE	1.580	3.811	1027.01	3913.44	6.020	642.16	3866.00
A_68_P30356303	chr15:77688418-77688462			Unknown	1.580	1.913	1944.48	3720.65	3.023	1658.89	5014.82
A_68_P28458172	chr12:57782364-57782408	ENSMUST00000159874:-8518		PROMOTER	1.580	3.846	1132.52	4355.31	6.075	886.88	5387.73
A_68_P26342888	chr9:20348946-20348990	ENSMUST00000171046:111765		INSIDE	1.580	1.813	1457.75	2642.66	2.864	1294.14	3706.00
A_68_P30476596	chr15:98637471-98637515	NM_001013741:864	Ddn	INSIDE	1.579	3.302	1653.03	5459.03	5.215	1322.62	6897.74
A_68_P24804128	chr6:121362766-121362810	NM_001033354:60908	Iqsec3	INSIDE	1.579	3.200	3220.17	10305.15	5.052	2257.41	11404.89

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P24618420	chr6:87788600-87788644	NM_133934:131	Isy1	INSIDE	1.579	2.686	1150.74	3090.41	4.240	1002.82	4252.19
A_68_P28163660	chr11:117060956-117061000	NM_001113486:4	Septin9	INSIDE	1.579	3.981	1641.20	6532.99	6.285	1352.89	8503.57
A_68_P24954289	chr7:6106868-6106913	NM_001013012:683	Zfp787	INSIDE	1.579	3.682	2148.52	7910.72	5.812	1736.73	10094.57
A_68_P31145425	chr17:32533548-32533592	NR_029458:-6388	A530088E08Rik	PROMOTER	1.578	5.700	2471.14	14086.48	8.994	2301.26	20697.64
A_68_P26864197	chr9:117949927-117949971	NM_001048146:332	Azi2	INSIDE	1.578	4.258	401.44	1709.32	6.717	385.58	2590.10
A_68_P20472150	chr1:99557453-99557497	NM_133825:1121	D1Ertd622e	INSIDE	1.578	3.205	1890.17	6057.91	5.058	1626.71	8228.26
A_68_P30423478	chr15:88979773-88979817	NM_011161:242	Mapk11	INSIDE	1.578	2.423	2470.96	5987.54	3.823	2005.79	7668.84
A_68_P20352935	chr1:75248212-75248256	NM_008985:12549	Ptprn	INSIDE	1.578	2.927	2292.55	6709.62	4.618	1724.70	7964.70
A_68_P24018800	chr5:117566119-117566163	NM_001122666:-138	Suds3	DIVERGENT_PROMOTER	1.578	3.103	670.81	2081.47	4.896	648.91	3176.91
A_68_P28553589	chr12:77470150-77470194	NM_001172104:279	Zbtb25	INSIDE	1.578	2.047	870.21	1781.03	3.230	770.10	2487.54
A_68_P30243549	chr15:57526400-57526444	NM_199449:201	Zhx2	INSIDE	1.578	5.586	1314.57	7343.29	8.817	1022.93	9019.07
A_68_P27308088	chr10:84849580-84849624	NM_028709:44	Btbd11	INSIDE	1.577	2.863	487.57	1395.76	4.515	441.56	1993.86
A_68_P30895871	chr16:78377255-78377299	NM_009770:-246	Btg3	PROMOTER	1.577	3.362	738.15	2481.85	5.303	628.77	3334.18
A_68_P31373927	chr17:79234917-79234961	NM_181649:83	Ccdc75	INSIDE	1.577	2.673	2020.61	5401.30	4.216	1599.74	6744.32
A_68_P30542887	chr16:10545493-10545537	NM_001204229:83	Clec16a	INSIDE	1.577	3.144	1929.46	6067.15	4.960	1642.69	8147.72
A_68_P24850798	chr6:131338248-131338292	NM_011733:198	Csda	INSIDE	1.577	5.758	1846.89	10634.69	9.081	1644.68	14935.00
A_68_P24501242	chr6:63207663-63207707	NM_008167:834	Grid2	INSIDE	1.577	4.696	1727.57	8111.93	7.405	1561.71	11564.15
A_68_P31126967	chr17:29400949-29400993	NM_026845:-54	Ppil1	DIVERGENT_PROMOTER	1.577	1.945	970.15	1886.55	3.066	846.71	2596.06
A_68_P28237421	chr12:11273151-11273195	NM_025695:481	Smc6	INSIDE	1.577	2.663	948.41	2526.00	4.199	774.69	3253.12
A_68_P28074030	chr11:101327012-101327056	NM_012037:479	Vat1	INSIDE	1.577	3.290	3016.42	9925.08	5.188	2617.11	13577.53
A_68_P30578497	chr16:18235357-18235401	NM_172151:-149	Zdhhc8	PROMOTER	1.577	2.553	2395.00	6115.41	4.026	1963.17	7903.27
A_68_P28751328	chr12:113858149-113858193	NM_007421:-87	Adssl1	PROMOTER	1.576	1.860	1284.81	2389.37	2.931	1070.45	3137.30
A_68_P30588065	chr16:20535666-20535710	NM_009679:112	Ap2m1	INSIDE	1.576	4.216	3006.62	12676.79	6.643	2140.72	14221.37
A_68_P27998411	chr11:88007034-88007078	NM_001172099:23990	Cuedc1	INSIDE	1.576	1.634	744.42	1216.08	2.574	608.68	1566.62
A_68_P22803179	chr4:28740971-28741015	NM_001122889:698	Epha7	INSIDE	1.576	2.231	745.90	1664.05	3.515	564.62	1984.76
A_68_P21680284	chr2:139503094-139503138	NM_001126490:-797	Ism1	PROMOTER	1.576	2.196	1282.18	2816.30	3.462	995.39	3446.44
A_68_P23439858	chr4:155028864-155028908	NM_145124:14450	Mib2	INSIDE	1.576	1.782	3808.57	6788.31	2.808	2786.77	7826.64
A_68_P20412608	chr1:88424274-88424318	NM_008972:986	Ptma	INSIDE	1.576	1.716	777.56	1334.62	2.705	670.32	1813.35
A_68_P29639602	chr14:60244436-60244480	NM_145463:341	Shisa2	INSIDE	1.576	3.893	992.08	3861.92	6.133	779.98	4783.79
A_68_P21420490	chr2:90910289-90910333	NM_026721:68	Slc39a13	INSIDE	1.576	1.606	2381.15	3824.63	2.532	1770.20	4482.07
A_68_P31121999	chr17:28487626-28487670	NM_001098226:-103	Tead3	PROMOTER	1.576	1.906	4153.46	7917.25	3.004	3102.91	9321.84
A_68_P30560722	chr16:14159381-14159425	NM_001081154:-35	4921513D23Rik	DIVERGENT_PROMOTER	1.575	3.794	13836.62	52494.04	5.973	8244.00	49245.55
A_68_P27630023	chr11:20013151-20013195	NM_146243:-218	Actr2	PROMOTER	1.575	4.701	5876.49	27627.98	7.405	4547.82	33674.90
A_68_P21094161	chr2:28773677-28773726	NM_001164186:-1741	Barhl1	PROMOTER	1.575	1.669	957.36	1597.63	2.628	775.30	2037.63
A_68_P28962023	chr13:38751002-38751046	NM_025380:-127	Eef1e1	PROMOTER	1.575	2.491	3706.13	9230.73	3.922	2999.68	11764.15
A_68_P30080950	chr15:25344237-25344281	NR_027376:312	Gm5468	INSIDE	1.575	2.606	378.57	986.49	4.105	368.66	1513.46
A_68_P20905056	chr1:187941218-187941262	NM_146106:-51	Lyplal1	PROMOTER	1.575	3.364	1318.19	4435.03	5.298	1030.23	5457.80
A_68_P29664074	chr14:64479020-64479064	NM_028228:-106	Pinx1	PROMOTER	1.575	3.862	3348.45	12932.88	6.085	2482.57	15106.29
A_68_P30426169	chr15:89422304-89422348	NM_026817:28	Rabl2	INSIDE	1.575	3.008	939.82	2826.53	4.737	772.82	3660.98
A_68_P22963537	chr4:61947638-61947682	NM_025286:182	Slc31a2	INSIDE	1.575	2.257	4243.51	9576.03	3.553	3512.67	12481.00
A_68_P28160203	chr11:116442887-116442931	NM_173755:-147	Ube2o	PROMOTER	1.575	2.804	3375.46	9466.43	4.418	2808.59	12408.08
A_68_P26822984	chr9:110207818-110207862	NM_001081381:145	2610002I17Rik	INSIDE	1.574	2.186	1153.88	2522.94	3.441	942.26	3242.42
A_68_P28002763	chr11:88726023-88726068	NM_001042541:-145	Akap1	PROMOTER	1.574	3.521	843.99	2971.51	5.541	761.65	4220.24
A_68_P29009048	chr13:46764994-46765038	NM_001033192:126	C78339	INSIDE	1.574	2.856	1542.16	4404.73	4.497	1400.30	6296.65
A_68_P33005168	chr7:3366552-3366596	NM_133189:29890	Cacng7	DOWNSTREAM	1.574	3.885	3043.52	11824.58	6.115	2177.56	13315.37
A_68_P22019079	chr3:28680302-28680346	NM_177586:92	Eif5a2	INSIDE	1.574	5.981	1545.59	9243.98	9.412	1505.64	14171.48
A_68_P23362414	chr4:140703695-140703739	NM_172518:-120	Fbxo42	DIVERGENT_PROMOTER	1.574	1.696	1041.78	1767.35	2.670	914.58	2441.71
A_68_P25362933	chr7:106774200-106774244	NM_001195529:1391	Gm4980	INSIDE	1.574	1.983	2380.55	4720.30	3.121	1714.36	5350.31
A_68_P28515346	chr12:70683995-70684039	NM_001033236:-1	Mettl21d	PROMOTER	1.574	3.709	1807.51	6704.49	5.840	1491.54	8710.42
A_68_P30556205	chr16:13257041-13257085	NM_181860:-8109	Mkl2	PROMOTER	1.574	4.312	4838.93	20866.87	6.790	3944.61	26782.12
A_68_P30292508	chr15:66409642-66409686	NM_001081409:531	Phf20l1	INSIDE	1.574	2.490	1736.18	4323.53	3.921	1286.61	5044.53

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27534649	chr10:126648747-126648791	NM_054097:-90	Pip4k2c	PROMOTER	1.574	2.122	1956.33	4150.66	3.340	1693.26	5656.06
A_68_P28938191	chr13:34436110-34436154	NM_001033167:919	Slc22a23	INSIDE	1.574	3.253	3942.01	12824.17	5.122	2927.73	14995.06
A_68_P26887498	chr9:122026335-122026379	NM_001164572:-27	Snrk	PROMOTER	1.574	3.457	2955.78	10218.80	5.442	2375.99	12929.20
A_68_P28157433	chr11:115971055-115971099	NM_001205081:473	Trim47	INSIDE	1.574	7.514	4631.18	34796.67	11.828	3674.12	43458.28
A_68_P31625687	chr18:36919881-36919925	NM_026464:10	Wdr55	INSIDE	1.574	3.041	1928.33	5863.74	4.786	1532.31	7333.66
A_68_P27563479	chr11:5344842-5344886	NM_001080924:-14	Znrf3	PROMOTER	1.574	1.826	2713.11	4953.86	2.874	2271.20	6527.31
A_68_P23797912	chr5:73883055-73883099	NM_001190733:812	Dcun1d4	INSIDE	1.573	9.002	22377.90	201451.70	14.162	12948.66	183376.70
A_68_P20237360	chr1:54614625-54614669	NM_001163314:-120	Pgap1	PROMOTER	1.573	1.663	1951.68	3246.19	2.616	1243.26	3252.49
A_68_P28774236	chr12:118772882-118772926	NM_175930:17953	Rapgef5	INSIDE	1.573	1.763	672.93	1186.15	2.773	608.43	1687.13
A_68_P24040030	chr5:121099321-121099365	NM_013832:512	Rasal1	INSIDE	1.573	2.490	6047.64	15060.88	3.917	4697.18	18400.08
A_68_P23296214	chr4:129012152-129012196	NM_009030:440	Rbbp4	INSIDE	1.573	0.381	1028.53	392.14	0.600	1088.76	652.93
A_68_P30379760	chr15:81641863-81641907	NM_017376:41	Tef	INSIDE	1.573	2.878	884.23	2544.59	4.526	802.40	3631.53
A_68_P32488661	chrX:78315918-78315962	NM_138751:-42	Tmem47	PROMOTER	1.573	2.978	1549.11	4612.70	4.684	1104.22	5171.91
A_68_P23246908	chr4:119406642-119406686	ENSMUST00000123698:219		INSIDE	1.573	2.387	438.30	1046.35	3.756	363.98	1367.23
A_68_P22129174	chr3:51144832-51144876	ENSMUST00000135496:-274		PROMOTER	1.573	2.065	4796.61	9906.33	3.248	3599.83	11691.13
A_68_P27764455	chr11:45665845-45665889	NM_001045520:401	Clint1	INSIDE	1.572	1.508	1316.31	1985.46	2.371	1074.77	2547.83
A_68_P20462986	chr1:97210270-97210314	NM_026321:88	Fam174a	INSIDE	1.572	2.255	485.23	1094.27	3.546	465.92	1651.96
A_68_P25348908	chr7:104230293-104230337	NM_001162477:54	Gab2	INSIDE	1.572	2.820	412.83	1164.28	4.434	361.09	1600.99
A_68_P26656177	chr9:77602711-77602755	NM_010295:391	Gclc	INSIDE	1.572	0.426	1277.34	544.15	0.670	1078.63	722.15
A_68_P24476912	chr6:56747694-56747738	NM_145958:91	Kbtbd2	INSIDE	1.572	1.972	1031.50	2033.69	3.100	895.96	2777.48
A_68_P24818877	chr6:125081806-125081850	NM_138747:-72	Nop2	PROMOTER	1.572	2.177	640.40	1394.03	3.421	552.07	1888.75
A_68_P30650841	chr16:32078788-32078844	NM_177326:543	Pak2	INSIDE	1.572	5.599	463.67	2596.20	8.801	294.26	2589.67
A_68_P26133404	chr8:107898928-107898972	NM_001081333:-330	Plekhg4	PROMOTER	1.572	3.196	1633.40	5220.99	5.026	1335.87	6714.39
A_68_P25114625	chr7:57033846-57033890	NM_133740:141	Prmt3	INSIDE	1.572	1.486	840.46	1249.05	2.336	683.42	1596.68
A_68_P23703749	chr5:54390129-54390173	NM_001081103:389	Stim2	INSIDE	1.572	4.884	1311.45	6404.52	7.676	1102.18	8460.46
A_68_P32537532	chrX:91368506-91368550	NM_001044386:218	Zfx	INSIDE	1.572	4.782	3575.38	17099.25	7.520	2303.95	17325.96
A_68_P24066928	chr5:125921960-125922004	NM_029752:45	Bri3bp	INSIDE	1.571	1.735	1634.18	2835.85	2.727	1390.05	3790.44
A_68_P30822064	chr16:64851589-64851633	NM_178647:-300	Cggbp1	PROMOTER	1.571	1.499	3489.85	5231.78	2.355	2884.05	6790.67
A_68_P21904961	chr2:180332965-180333009	NM_009936:60	Col9a3	INSIDE	1.571	2.012	1222.98	2461.18	3.162	972.24	3074.01
A_68_P27282058	chr10:79727411-79727455	NM_001122604:-303	Dazap1	DIVERGENT_PROMOTER	1.571	1.727	1340.24	2314.13	2.713	1046.16	2838.21
A_68_P31135104	chr17:30749389-30749433	NM_001113560:194	Glo1	INSIDE	1.571	4.088	647.44	2646.58	6.422	564.46	3624.90
A_68_P27425024	chr10:106709059-106709103	NM_001033223:194	Lin7a	INSIDE	1.571	2.971	3596.44	10684.37	4.666	2802.49	13076.50
A_68_P21130446	chr2:34769487-34769531	NM_028716:-12	Phf19	PROMOTER	1.571	5.149	4230.44	21782.11	8.088	3388.78	27408.76
A_68_P25670554	chr8:13785750-13785794	NM_025924:158	Upf3a	INSIDE	1.571	3.934	1989.76	7828.20	6.182	1622.32	10028.85
A_68_P28613409	chr12:88331117-88331161	NM_001080943:-1512	Zdhhc22	PROMOTER	1.571	3.192	1058.11	3377.73	5.015	913.34	4579.94
A_68_P23467741	chr5:8368019-8368063	NM_001098225:41	Adam22	INSIDE	1.570	1.732	1004.19	1738.76	2.719	921.50	2505.13
A_68_P30990999	chr16:96304407-96304451	NM_145125:-393	Brwd1	PROMOTER	1.570	2.758	5273.40	14544.89	4.331	3882.58	16817.11
A_68_P28067423	chr11:100181873-100181917	NM_011508:585	Eif1	INSIDE	1.570	2.429	743.63	1806.49	3.813	565.99	2158.28
A_68_P27055250	chr10:33847341-33847385	NM_175449:416	Fam26f	INSIDE	1.570	3.541	2209.17	7822.10	5.557	1786.17	9926.43
A_68_P22892659	chr4:47105046-47105090	NM_172693:244	Galnt12	INSIDE	1.570	4.111	837.62	3443.52	6.453	723.30	4667.16
A_68_P27253670	chr10:74430232-74430276	NM_010311:279	Gnaz	INSIDE	1.570	1.802	1266.85	2282.44	2.829	1006.12	2846.54
A_68_P26885522	chr9:121686826-121686870	NM_028202:124	Kbtbd5	INSIDE	1.570	2.948	478.89	1411.61	4.628	485.79	2248.24
A_68_P24119778	chr5:136646540-136646584	NM_178751:-36	Orai2	PROMOTER	1.570	2.888	626.29	1808.83	4.534	612.18	2775.79
A_68_P26282992	chr9:6168448-6168492	NM_027924:-141	Pdgfd	PROMOTER	1.570	2.157	1141.79	2463.16	3.387	924.44	3131.10
A_68_P30346615	chr15:76011854-76011898	NM_201394:14264	Plec	INSIDE	1.570	4.794	1004.83	4816.70	7.527	812.41	6114.67
A_68_P28431157	chr12:52792863-52792907	NM_001172098:17	Strn3	INSIDE	1.570	1.974	635.80	1255.32	3.100	541.32	1678.28
A_68_P26894035	chr9:123169998-123170042	NM_001002267:-113	Tmem158	PROMOTER	1.570	5.235	1322.39	6923.00	8.219	1293.02	10627.22
A_68_P26295538	chr9:9239294-9239338	NM_027823:-303	Arhgap42	PROMOTER	1.569	3.162	3797.50	12008.35	4.961	2969.28	14729.70
A_68_P32111326	chr19:40905687-40905731	NM_172839:-60	Ccnj	PROMOTER	1.569	2.042	377.81	771.60	3.205	357.59	1146.05
A_68_P26940376	chr10:11063434-11063478	NM_010146:214	Epm2a	INSIDE	1.569	2.438	362.07	882.58	3.824	380.29	1454.08
A_68_P27289087	chr10:80820153-80820197	NM_028657:-140	F630110N24Rik	DIVERGENT_PROMOTER	1.569	2.472	1187.14	2934.50	3.880	956.23	3709.79

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P29448409	chr14:21514700-21514744	NM_028428:533	Fut11	INSIDE	1.569	1.750	974.29	1705.36	2.746	895.85	2460.26
A_68_P20997431	chr2:9796515-9796559	NM_008091:3691	Gata3	INSIDE	1.569	3.329	5427.34	18065.56	5.224	3876.76	20251.14
A_68_P26003887	chr8:83866396-83866440	ENSMUST00000172167:-36		PROMOTER	1.569	2.225	3413.89	7597.57	3.491	2846.17	9936.75
A_68_P20140952	chr1:34899643-34899687	NM_001160235:231	Fam168b	INSIDE	1.568	3.941	1156.93	4558.99	6.180	1041.76	6438.55
A_68_P25459669	chr7:125849289-125849333	NM_019580:-58	Gde1	DIVERGENT_PROMOTER	1.568	2.848	2463.48	7016.05	4.464	2041.48	9114.14
A_68_P20417070	chr1:89224090-89224134	NM_001110212:509	Gigyf2	INSIDE	1.568	2.784	842.92	2346.29	4.365	744.25	3248.54
A_68_P22404196	chr3:106904415-106904459	NM_008417:-48	Kcna2	PROMOTER	1.568	2.767	2265.93	6269.43	4.338	1842.84	7994.73
A_68_P25011324	chr7:26471878-26471922	NM_011577:-120	Tgfb1	PROMOTER	1.568	2.535	2686.22	6810.85	3.977	2203.33	8762.21
A_68_P27287712	chr10:80611089-80611133	NM_010731:12095	Zbtb7a	INSIDE	1.568	3.451	1624.44	5606.41	5.410	1331.74	7204.85
A_68_P25230180	chr7:80762845-80762889	AK158912:403		INSIDE	1.568	1.546	841.61	1301.17	2.425	793.56	1924.14
A_68_P23396096	chr4:148098703-148098747	ENSMUST00000139895:10913		DOWNSTREAM	1.568	2.054	3592.36	7376.99	3.220	3195.88	10289.84
A_68_P22820149	chr4:32327040-32327088	ENSMUST00000165661:-3643		PROMOTER	1.568	2.459	817.83	2011.16	3.856	654.28	2522.89
A_68_P24980793	chr7:16899189-16899233	NM_133234:4279	Bbc3	INSIDE	1.567	1.681	1963.70	3300.92	2.634	1626.81	4285.17
A_68_P23977812	chr5:110535984-110536028	NM_145147:1210	Gtpbp6	INSIDE	1.567	2.103	995.06	2092.77	3.295	788.22	2597.31
A_68_P26954150	chr10:13685112-13685158	NM_010437:-1050	Hivep2	PROMOTER	1.567	2.407	1916.49	4612.93	3.773	1407.57	5310.50
A_68_P20042287	chr1:13650338-13650382	NM_145381:230	Lactb2	INSIDE	1.567	5.127	2361.50	12108.17	8.035	1864.14	14978.65
A_68_P20897789	chr1:186669350-186669394	NM_133684:354	Mosc2	INSIDE	1.567	4.109	4824.79	19825.41	6.437	4411.19	28396.76
A_68_P24950760	chr7:4788206-4788250	NM_172737:8070	Shisa7	INSIDE	1.567	4.057	712.16	2889.21	6.357	591.98	3763.03
A_68_P20191548	chr1:43991025-43991069	NM_009418:195	Tpp2	INSIDE	1.567	4.232	826.31	3496.70	6.632	684.81	4541.32
A_68_P24025038	chr5:118620106-118620150	NM_007545:356	Hrk	INSIDE	1.566	2.149	1563.84	3361.45	3.366	1428.17	4806.89
A_68_P25503044	chr7:134072503-134072547	NM_172747:132	Kctd13	INSIDE	1.566	5.367	1536.35	8245.63	8.404	1331.12	11186.38
A_68_P30114898	chr15:31460199-31460243	NM_172606:572	Marchf6	INSIDE	1.566	1.520	2694.46	4094.33	2.380	2251.11	5357.45
A_68_P26400215	chr9:31193897-31193941	NM_172766:142	Nfrkb	INSIDE	1.566	3.163	6901.85	21828.89	4.954	5027.00	24903.77
A_68_P23544553	chr5:24414393-24414437	NM_001170555:-87	Prkag2	PROMOTER	1.566	3.308	1145.83	3790.78	5.181	1015.40	5261.24
A_68_P31106682	chr17:25981519-25981564	NM_145999:255	Rhot2	INSIDE	1.566	5.770	2491.85	14378.33	9.036	1778.26	16068.59
A_68_P26996375	chr10:21713739-21713783	NM_011361:-711	Sgk1	PROMOTER	1.566	3.211	605.84	1945.46	5.029	456.14	2293.94
A_68_P29937469	chr14:118633887-118633936	NM_177753:2341	Sox21	INSIDE	1.566	2.106	666.97	1404.33	3.298	548.73	1809.84
A_68_P24425595	A_68_P24425595			Unknown	1.566	4.863	796.97	3875.36	7.616	735.68	5602.61
A_68_P27644170	chr11:22968078-22968122	ENSMUST00000128996:103		INSIDE	1.566	3.114	326.32	1016.16	4.878	341.56	1666.04
A_68_P20893089	chr1:185857699-185857743	NM_028516:157	1700056E22Rik	INSIDE	1.565	3.564	2094.13	7462.54	5.577	1749.00	9754.76
A_68_P28513307	chr12:70298223-70298267	NR_033222:47	9330151L19Rik	INSIDE	1.565	5.402	2373.03	12819.39	8.457	1959.92	16574.74
A_68_P28743070	chr12:112513574-112513618	NM_033603:4275	Amn	INSIDE	1.565	2.620	686.38	1798.21	4.101	589.50	2417.74
A_68_P23295623	chr4:128900595-128900639	NM_001033189:25071	C77080	INSIDE	1.565	2.201	993.95	2187.89	3.445	861.28	2967.49
A_68_P23539566	chr5:23536151-23536195	NM_053090:329	Fam126a	INSIDE	1.565	4.054	2121.20	8598.55	6.346	1830.88	11618.57
A_68_P31484544	chr18:9212850-9212894	NM_008058:19	Fzd8	INSIDE	1.565	2.801	892.40	2499.57	4.384	806.66	3536.09
A_68_P27289029	chr10:80809838-80809882	NM_001163165:3311	Hmg20b	INSIDE	1.565	7.179	2823.24	20269.19	11.233	1862.01	20916.80
A_68_P21839351	chr2:167906222-167906266	NM_021409:-259	Pard6b	PROMOTER	1.565	6.818	1258.10	8577.99	10.671	1114.90	11897.11
A_68_P24979352	chr7:16638192-16638236	AK008102:4421		DOWNSTREAM	1.565	1.509	1254.00	1892.14	2.361	1022.36	2413.86
A_68_P28836964	chr13:14157071-14157115	NM_194262:1034	Arid4b	INSIDE	1.564	2.482	844.98	2096.93	3.880	657.33	2550.72
A_68_P29110678	chr13:68721295-68721339	NM_027123:192	Fastkd3	INSIDE	1.564	2.559	2112.04	5405.13	4.002	1553.20	6215.74
A_68_P32142001	chr19:46150433-46150477	NM_001039351:102	Nolc1	INSIDE	1.564	2.312	2268.24	5243.62	3.616	1941.60	7020.26
A_68_P29269012	chr13:101322550-101322594	NM_008756:-119	Ocln	PROMOTER	1.564	2.208	944.00	2084.61	3.455	1005.10	3472.29
A_68_P21417962	chr2:90420971-90421015	NM_008982:-188	Ptprj	PROMOTER	1.564	4.295	2423.28	10407.62	6.717	1930.35	12966.08
A_68_P28595365	chr12:85262189-85262233	ENSMUST00000085215:584		INSIDE	1.564	2.328	3510.08	8172.80	3.641	2840.92	10345.21
A_68_P28691640	chr12:103707382-103707426	NM_013747:-715	Golga5	PROMOTER	1.563	6.121	432.66	2648.22	9.568	300.97	2879.67
A_68_P23837522	chr5:81449591-81449635	NM_198702:-1005	Lphn3	PROMOTER	1.563	4.017	1797.47	7221.24	6.281	1431.07	8988.10
A_68_P21623003	chr2:128926712-128926756	NM_009086:3	Polr1b	INSIDE	1.563	1.939	2491.03	4831.30	3.031	1831.52	5550.56
A_68_P31757526	chr18:61558105-61558149	NM_133249:1959	Ppargc1b	INSIDE	1.563	2.958	4297.15	12709.21	4.622	3216.73	14868.65
A_68_P28963697	chr13:39052368-39052412	NM_001170430:16	Slc35b3	INSIDE	1.563	1.824	2096.03	3823.89	2.851	1602.74	4569.52
A_68_P30546005	chr16:11066391-11066435	NM_009223:22	Snn	INSIDE	1.563	1.775	1499.49	2661.18	2.774	1273.43	3531.86
A_68_P23222361	chr4:114597756-114597800	NM_015758:840	Foxe3	INSIDE	1.562	2.049	646.36	1324.62	3.200	520.65	1666.31

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28576082	chr12:81619771-81619815	NM_001081421:-184	Galntl1	PROMOTER	1.562	2.629	854.62	2246.53	4.105	779.49	3200.03
A_68_P31790105	chr18:67293085-67293129	NM_010307:-373	Gnal	PROMOTER	1.562	2.176	769.95	1675.10	3.399	684.73	2327.47
A_68_P23261232	chr4:122866227-122866271	NM_174998:5502	Hpcal4	INSIDE	1.562	3.900	3399.56	13256.62	6.092	2528.50	15404.63
A_68_P29702031	chr14:70953904-70953948	NM_021877:64	Hr	INSIDE	1.562	1.626	6204.00	10086.09	2.539	4768.71	12108.55
A_68_P28107247	chr11:107330576-107330620	NM_145823:1436	Pitpnc1	INSIDE	1.562	1.920	1761.15	3381.05	2.998	1368.08	4102.19
A_68_P24991219	chr7:19650979-19651023	NM_001159671:10965	Rsph6a	INSIDE	1.562	5.179	3800.91	19684.78	8.090	2925.80	23668.66
A_68_P25954806	chr8:73421106-73421150	NR_002901:-1373	Snora68	PROMOTER	1.562	1.778	2759.35	4907.28	2.777	2115.56	5875.71
A_68_P25504683	chr7:134376847-134376891	NM_146201:-88	Zfp553	DIVERGENT_PROMOTER	1.562	6.493	500.43	3249.53	10.143	454.10	4605.86
A_68_P26430110	chr9:37155994-37156038	NM_001081429:-39	Ccdc15	PROMOTER	1.561	6.025	3644.25	21958.08	9.405	2772.80	26079.27
A_68_P22695196	chr4:3866420-3866464	NM_001190322:382	Chchd7	INSIDE	1.561	3.322	1286.05	4272.59	5.187	980.84	5087.42
A_68_P28727385	chr12:109572280-109572324	NM_010010:-288	Cyp46a1	PROMOTER	1.561	2.654	4354.11	11554.80	4.141	3150.60	13047.81
A_68_P24636902	chr6:91066754-91066798	NM_018815:44	Nup210	INSIDE	1.561	4.842	904.94	4381.50	7.557	808.28	6107.96
A_68_P24770499	chr6:115312049-115312093	NM_001127330:832	Pparg	INSIDE	1.561	1.939	1450.39	2812.26	3.026	1089.63	3297.74
A_68_P26894026	chr9:123168701-123168745	NM_001002267:1185	Tmem158	INSIDE	1.561	2.872	2065.30	5931.81	4.485	1627.76	7300.04
A_68_P29964713	chr14:123381923-123381967	NM_028651:539	Tmtc4	INSIDE	1.561	5.108	1203.79	6149.55	7.972	922.30	7352.89
A_68_P31675568	chr18:46357840-46357884	NM_001170855:610	Trim36	INSIDE	1.561	2.855	486.55	1389.25	4.458	453.71	2022.68
A_68_P28082865	chr11:102878532-102878576	NM_026551:-93	Dcakd	PROMOTER	1.560	5.102	5424.26	27675.60	7.959	4348.58	34611.79
A_68_P28463190	chr12:58643591-58643635	NM_008259:3496	Foxa1	INSIDE	1.560	2.253	1457.12	3283.00	3.514	1177.59	4138.56
A_68_P29605899	chr14:52924704-52924752	NM_019721:71	Mettl3	INSIDE	1.560	3.087	740.61	2286.38	4.816	590.71	2845.04
A_68_P23541414	chr5:23889472-23889516	NM_008713:18858	Nos3	INSIDE	1.560	1.597	1009.38	1612.02	2.491	853.11	2125.19
A_68_P31420718	chr17:87424300-87424344	NM_008838:419	Pigf	INSIDE	1.560	1.566	712.72	1116.06	2.444	619.81	1514.57
A_68_P29143670	chr13:74147870-74147914	NM_182839:1026	Tppp	INSIDE	1.560	3.518	1149.79	4045.47	5.489	940.34	5161.41
A_68_P31257913	chr17:56856203-56856247	NM_178926:120	Vmac	INSIDE	1.560	1.548	592.48	917.36	2.415	522.90	1262.62
A_68_P24786877	chr6:118405159-118405203	NM_028335:344	Zfp248	INSIDE	1.560	2.221	2692.98	5980.02	3.464	2110.48	7311.15
A_68_P32565205	chrX:98893158-98893202	ENSMUST00000073812:-5991		PROMOTER	1.560	6.701	3873.46	25954.72	10.456	1949.34	20382.57
A_68_P20876216	chr1:182413344-182413388	NM_001081227:269	6330403A02Rik	INSIDE	1.559	1.478	4002.81	5914.28	2.304	3159.73	7278.97
A_68_P26486134	chr9:47339844-47339888	NM_001025600:1432	Cadm1	INSIDE	1.559	1.847	612.83	1132.05	2.880	470.46	1354.71
A_68_P28293506	chr12:25781121-25781165	NM_010496:-185	Id2	PROMOTER	1.559	2.315	4038.43	9349.15	3.609	3161.10	11406.85
A_68_P25954897	chr8:73438085-73438129	NM_173013:8234	Mtap1s	INSIDE	1.559	4.956	4668.80	23140.70	7.727	3349.62	25881.64
A_68_P23972071	chr5:108890061-108890105	NM_172716:-268	Pcgf3	PROMOTER	1.559	1.706	2087.61	3562.17	2.661	1779.09	4734.15
A_68_P22341205	chr3:94690730-94690774	NM_008945:128	Psmb4	INSIDE	1.559	2.185	1573.79	3438.45	3.406	1288.28	4387.92
A_68_P26932995	chr10:9620910-9620954	NM_001081344:-94	Stxbp5	PROMOTER	1.559	2.555	589.32	1505.86	3.985	591.01	2355.10
A_68_P23545743	chr5:24606691-24606735	NR_027851:-80	2900005J15Rik	DIVERGENT_PROMOTER	1.558	2.903	729.35	2117.61	4.523	624.82	2825.84
A_68_P28752038	chr12:113960892-113960936	NM_001024602:530	AW555464	INSIDE	1.558	2.278	1280.40	2916.80	3.548	1133.46	4021.72
A_68_P28041452	chr11:95775809-95775854	NM_008081:354	B4galnt2	INSIDE	1.558	4.699	3119.17	14657.35	7.323	2688.16	19685.59
A_68_P24222816	chr6:7794688-7794732	NM_052993:-513	C1galt1	PROMOTER	1.558	2.112	471.99	996.61	3.290	390.46	1284.47
A_68_P29651430	chr14:62305865-62305909	NR_028264:-4676	Dleu2	PROMOTER	1.558	4.143	1151.74	4771.58	6.455	932.74	6020.70
A_68_P24994096	chr7:20158742-20158786	NM_027189:-72	Gemin7	DIVERGENT_PROMOTER	1.558	1.518	990.39	1503.27	2.364	942.86	2229.39
A_68_P25587734	chr7:148445714-148445758	NM_001081118:31050	Phrf1	INSIDE	1.558	7.229	1689.14	12210.11	11.262	1175.85	13242.93
A_68_P26203094	chr8:120022462-120022506	NM_172285:294	Plcg2	INSIDE	1.558	2.890	674.71	1949.84	4.503	610.32	2748.25
A_68_P25086855	chr7:51591550-51591594	NM_001034115:25939	Shank1	INSIDE	1.558	3.042	2355.54	7164.91	4.738	1933.02	9158.01
A_68_P25844872	chr8:49076065-49076109	NM_133791:-181	Wwc2	PROMOTER	1.558	3.399	3388.99	11519.48	5.297	3233.27	17126.42
A_68_P20737714	chr1:157264468-157264512	NM_011273:84	Xpr1	INSIDE	1.558	3.906	11830.67	46212.57	6.084	9122.39	55504.65
A_68_P27274520	chr10:77945131-77945175	ENSMUST00000069431:5435		DOWNSTREAM	1.558	2.753	1617.45	4452.65	4.290	1515.23	6500.21
A_68_P28094671	chr11:105042686-105042730	NR_027956:39	1700052K11Rik	INSIDE	1.557	4.459	593.08	2644.78	6.941	610.23	4235.88
A_68_P24449862	chr6:52264017-52264061	NM_007966:547	Evx1	INSIDE	1.557	3.027	2102.31	6363.00	4.712	1730.99	8155.65
A_68_P32147197	chr19:47089479-47089523	NM_001164363:179	Nt5c2	INSIDE	1.557	5.384	1670.04	8991.04	8.381	1366.80	11454.95
A_68_P25524908	chr7:138009867-138009911	NM_133942:465	Plekha1	INSIDE	1.557	2.360	671.79	1585.13	3.673	567.60	2084.95
A_68_P23544551	chr5:24414128-24414172	NM_001170555:177	Prkag2	INSIDE	1.557	3.462	747.36	2587.60	5.389	642.16	3460.72
A_68_P27284238	chr10:80065633-80065677	NM_019575:28	Scamp4	INSIDE	1.557	3.207	2217.98	7114.18	4.993	1596.30	7969.72
A_68_P26289277	chr9:7763854-7763898	NM_133739:-200	Tmem123	PROMOTER	1.557	2.817	10958.54	30867.54	4.385	7497.56	32880.13

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P23297754	chr4:129318346-129318390	NM_001199695:-59	Txlna	PROMOTER	1.557	2.710	1619.38	4388.83	4.220	1351.27	5701.81
A_68_P24638863	chr6:91360911-91360955	NM_009527:431	Wnt7a	INSIDE	1.557	2.287	1572.05	3594.67	3.560	1198.48	4266.50
A_68_P31086417	chr17:21669593-21669637	NM_144515:-2888	Zfp52	PROMOTER	1.557	2.758	2058.15	5676.25	4.293	1665.77	7151.85
A_68_P32603677	chrX:109714158-109714202	NM_177747:46	Zfp711	INSIDE	1.557	2.212	329.82	729.70	3.444	225.13	775.44
A_68_P22312382	chr3:88004398-88004442	ENSMUST00000167043:-124		PROMOTER	1.557	2.729	3170.52	8651.45	4.248	2563.81	10891.21
A_68_P30608335	chr16:24393852-24393896	NR_037954:-133	1110054M08Rik	PROMOTER	1.556	4.325	927.24	4009.93	6.729	797.55	5366.96
A_68_P30423567	chr15:88991606-88991650	NM_001159521:12652	Plxnb2	INSIDE	1.556	5.958	10055.88	59914.80	9.268	6667.91	61798.74
A_68_P30330343	chr15:73253736-73253780	NM_007982:-137	Ptk2	PROMOTER	1.556	4.901	771.75	3782.28	7.628	660.37	5037.13
A_68_P23298639	chr4:129497779-129497823	NM_001164745:-151	Ptp4a2	PROMOTER	1.556	2.745	1814.44	4980.11	4.270	1507.66	6437.66
A_68_P28071133	chr11:100820100-100820144	NM_008986:11809	Ptrf	INSIDE	1.556	3.925	2274.88	8928.80	6.107	1679.27	10254.57
A_68_P22236487	chr3:72861315-72861359	NM_198864:-471	Slitrk3	PROMOTER	1.556	1.938	2102.13	4073.97	3.015	1678.91	5062.21
A_68_P24009031	chr5:115777029-115777073	NM_025573:-135	Srsf9	PROMOTER	1.556	4.084	2154.06	8797.49	6.357	1708.11	10857.85
A_68_P25056451	chr7:37481970-37482014	NM_172298:-1144	Tshz3	PROMOTER	1.556	2.088	1067.78	2229.64	3.249	934.35	3035.37
A_68_P31922246	chr19:4283254-4283298	NM_026720:-139	Ankrd13d	PROMOTER	1.555	3.090	3143.54	9713.27	4.806	2202.06	10583.65
A_68_P31867752	chr18:81130655-81130699	NM_001201569:121	Atp9b	INSIDE	1.555	3.281	3663.16	12018.74	5.101	3085.38	15738.90
A_68_P22941962	chr4:56877715-56877759	NM_018761:347	Ctnnal1	INSIDE	1.555	6.301	881.48	5553.93	9.797	740.94	7259.07
A_68_P29751456	chr14:79851782-79851826	NM_001034882:163	Gm5465	INSIDE	1.555	2.370	3615.36	8570.06	3.685	2881.89	10619.67
A_68_P23230189	chr4:116299784-116299829	NM_001081475:296	Nasp	INSIDE	1.555	1.757	1532.01	2691.16	2.732	1330.79	3635.84
A_68_P20040932	chr1:13363158-13363202	NM_001077695:984	Ncoa2	INSIDE	1.555	1.573	1015.20	1596.89	2.446	928.22	2270.58
A_68_P28174632	chr11:118769905-118769949	NM_001024931:960	Rbfox3	INSIDE	1.555	2.369	1467.31	3476.28	3.685	1339.73	4937.01
A_68_P22383504	chr3:102739949-102739993	NM_011516:53	Sycp1	INSIDE	1.555	3.031	522.26	1582.80	4.713	383.30	1806.57
A_68_P24951859	chr7:5012645-5012689	NM_001205231:-1078	U2af2	PROMOTER	1.555	1.754	3975.91	6972.82	2.727	2829.09	7714.78
A_68_P24979382	chr7:16646941-16646985			Unknown	1.555	4.452	3071.18	13673.68	6.922	2294.18	15879.60
A_68_P21755504	chr2:153354420-153354464	NM_001134300:1265	8430427H17Rik	INSIDE	1.554	4.392	2757.42	12109.24	6.824	2447.02	16699.70
A_68_P31157235	chr17:35183322-35183366	NM_013600:207	Msh5	INSIDE	1.554	1.393	1449.87	2019.11	2.164	1177.43	2547.74
A_68_P21073067	chr2:25430182-25430226	NM_029293:187	Phpt1	INSIDE	1.554	4.301	8690.48	37378.51	6.683	6210.23	41501.24
A_68_P23331577	chr4:135543069-135543113	NM_025411:69	1110049F12Rik	INSIDE	1.553	3.233	1282.56	4146.47	5.022	1113.13	5590.41
A_68_P22682769	chr3:157610620-157610664	NM_001013806:213	Ankrd13c	INSIDE	1.553	4.429	3140.67	13909.20	6.876	2744.75	18872.23
A_68_P24205541	chr6:4551256-4551300	NM_145398:213	Casd1	INSIDE	1.553	4.127	993.11	4098.52	6.408	828.17	5306.98
A_68_P27812111	chr11:54600916-54600960	NM_178626:267	Cdc42se2	INSIDE	1.553	2.021	2859.81	5779.07	3.138	2218.76	6963.45
A_68_P29142604	chr13:73984411-73984456	NM_028186:646	Nkd2	INSIDE	1.553	2.001	1418.80	2838.52	3.107	1209.81	3759.14
A_68_P21775093	chr2:156904079-156904123	NM_001164663:901	9830001H06Rik	INSIDE	1.552	3.069	1296.16	3978.46	4.764	1121.73	5344.35
A_68_P24423144	chr6:47403969-47404013	NM_012042:-332	Cul1	PROMOTER	1.552	7.853	739.60	5808.22	12.189	704.37	8585.29
A_68_P22128832	chr3:51080406-51080450	NM_023502:49481	Elf2	INSIDE	1.552	2.100	2655.74	5575.74	3.259	2102.07	6851.41
A_68_P25892520	chr8:60131247-60131291	NM_001167981:584	Galnt7	INSIDE	1.552	2.796	777.11	2172.51	4.339	632.87	2746.20
A_68_P22311352	chr3:87826975-87827019	NM_022031:4437	Hapln2	INSIDE	1.552	1.404	4589.08	6441.50	2.178	3396.94	7399.58
A_68_P22661977	chr3:153991290-153991334	NM_010713:2212	Lhx8	INSIDE	1.552	2.620	2433.89	6377.55	4.067	2210.04	8988.50
A_68_P28991174	chr13:43711396-43711440	NM_183204:253	Rnf182	INSIDE	1.552	4.911	1583.61	7776.79	7.619	1313.01	10004.08
A_68_P31598791	chr18:31769247-31769291	NM_026165:288	Slc25a46	INSIDE	1.552	3.700	928.88	3437.12	5.743	845.62	4856.30
A_68_P28332010	chr12:32244021-32244065	NM_011867:792	Slc26a4	INSIDE	1.552	2.591	663.55	1719.32	4.020	565.21	2272.30
A_68_P29745018	chr14:78707731-78707775	NM_011613:98	Tnfsf11	INSIDE	1.552	3.653	2008.53	7338.06	5.671	1580.84	8964.18
A_68_P30176277	chr15:43309087-43309131	NM_025736:334	Ttc35	INSIDE	1.552	2.774	2444.85	6782.67	4.306	2147.63	9247.83
A_68_P21311589	chr2:69735872-69735916	NM_001081548:592	Ubr3	INSIDE	1.552	2.467	2694.52	6646.05	3.829	2134.09	8170.82
A_68_P25268780	chr7:87947830-87947874	NM_016721:365	Iqgap1	INSIDE	1.551	1.594	2098.11	3343.77	2.473	1544.84	3819.74
A_68_P29222297	chr13:92901976-92902020	NM_009027:-549	Rasgrf2	PROMOTER	1.551	15.440	1145.93	17693.03	23.952	845.42	20249.63
A_68_P22883647	chr4:45542639-45542683	NM_001033306:1040	Shb	INSIDE	1.551	3.693	825.96	3050.21	5.728	737.06	4222.19
A_68_P32036079	chr19:26680265-26680310	NM_011416:638	Smarca2	INSIDE	1.551	1.658	1913.20	3172.21	2.571	1502.58	3863.03
A_68_P29672994	chr14:65977929-65977973	NM_199029:438	Zfp395	INSIDE	1.551	0.410	847.18	347.45	0.636	967.85	615.83
A_68_P24425393	chr6:47974535-47974579	NM_001081382:23557	Zfp777	INSIDE	1.551	3.239	550.43	1782.89	5.025	529.21	2659.20
A_68_P22454038	chr3:117062948-117062993	NM_177664:824	D3Bwg0562e	INSIDE	1.550	2.469	1291.03	3187.15	3.827	1048.07	4011.15
A_68_P30361565	chr15:78503546-78503590	NM_183141:44975	Elfn2	INSIDE	1.550	3.398	991.25	3368.41	5.267	733.37	3862.41

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25412180	chr7:117365261-117365305	NM_009302:66	Swap70	INSIDE	1.550	5.265	1061.01	5585.94	8.159	899.62	7339.83
A_68_P28167342	chr11:117671257-117671301	NM_009304:298	Syngr2	INSIDE	1.550	2.821	975.53	2752.34	4.374	772.61	3379.42
A_68_P23541913	chr5:23953475-23953519	NM_022418:168	Tmub1	INSIDE	1.550	2.442	1120.23	2736.03	3.785	956.45	3620.14
A_68_P22492339	chr3:124023918-124023962	NM_146140:-14	Tram1l1	PROMOTER	1.550	1.883	1710.74	3222.01	2.919	1366.00	3986.99
A_68_P31301686	A_68_P31301686			Unknown	1.550	2.978	386.38	1150.55	4.615	316.07	1458.75
A_68_P29055344	A_68_P29055344			Unknown	1.550	2.883	1046.86	3018.37	4.468	814.21	3637.95
A_68_P32143654	chr19:46469962-46470006	NM_016860:241	Actr1a	INSIDE	1.549	3.348	2979.00	9972.94	5.187	2460.95	12764.18
A_68_P30483162	chr15:99803108-99803152	NM_001024526:-80	Larp4	PROMOTER	1.549	1.794	1419.86	2547.83	2.780	1207.46	3356.65
A_68_P30990393	chr16:96212588-96212632	NM_019537:-100	Psmg1	PROMOTER	1.549	3.381	2069.66	6997.91	5.238	1779.04	9318.84
A_68_P23227949	chr4:115817024-115817068	NM_026547:175	1520402A15Rik	INSIDE	1.548	3.087	1615.03	4985.29	4.777	1317.12	6292.45
A_68_P27288890	chr10:80788199-80788243	NM_027381:4373	2510012J08Rik	INSIDE	1.548	5.347	2882.86	15415.59	8.279	2017.82	16705.88
A_68_P32260649	chrX:11714704-11714748	NM_001168321:22755	Bcor	INSIDE	1.548	1.375	1999.44	2748.78	2.128	960.24	2043.29
A_68_P27781640	chr11:48982878-48982922	NM_172793:17691	Btnl9	INSIDE	1.548	4.075	2307.06	9401.42	6.310	1769.63	11166.23
A_68_P30686262	chr16:38483294-38483338	NM_009855:24304	Cd80	INSIDE	1.548	3.799	3027.88	11502.80	5.880	2326.95	13681.60
A_68_P31252966	chr17:56095674-56095719	NM_015766:3651	Ebi3	INSIDE	1.548	3.023	2670.05	8070.77	4.679	1946.40	9107.33
A_68_P30452934	chr15:94374073-94374117	NM_029926:4	Irak4	INSIDE	1.548	2.034	1421.64	2891.15	3.149	1041.72	3279.94
A_68_P27011028	chr10:24589929-24589973	NM_001166416:159	Med23	INSIDE	1.548	4.361	469.79	2048.95	6.752	420.87	2841.82
A_68_P23439842	chr4:155027173-155027217	NM_011985:299	Mmp23	INSIDE	1.548	1.467	1762.94	2585.39	2.270	1420.78	3224.59
A_68_P25585272	chr7:148043313-148043357	NM_053194:39	Ric8	INSIDE	1.548	1.798	1175.98	2113.99	2.783	980.39	2728.28
A_68_P21748557	chr2:152119766-152119810	NM_024196:181	Tbc1d20	INSIDE	1.548	5.502	3289.69	18098.61	8.515	2765.79	23551.72
A_68_P31744348	chr18:58995914-58995958	NM_175506:-481	Adamts19	PROMOTER	1.547	1.578	2334.17	3684.29	2.442	2112.33	5158.87
A_68_P20947409	chr1:194956122-194956166	NM_145415:301	Diexf	INSIDE	1.547	1.635	441.40	721.86	2.530	342.33	866.11
A_68_P29713887	chr14:73109166-73109210	NM_207636:622	Fndc3a	INSIDE	1.547	1.720	371.99	639.79	2.661	324.89	864.39
A_68_P29700471	chr14:70689220-70689264	NM_008915:14	Ppp3cc	INSIDE	1.547	2.361	288.34	680.82	3.653	268.34	980.17
A_68_P21491162	chr2:104689920-104689964	NM_178695:65	Prrg4	INSIDE	1.547	2.682	1472.56	3950.02	4.149	1224.68	5081.32
A_68_P30642387	chr16:30550318-30550362	NM_172614:324	Tmem44	INSIDE	1.547	1.662	2144.39	3563.03	2.571	1758.73	4521.84
A_68_P21084621	chr2:27281926-27281970	NM_009500:397	Vav2	INSIDE	1.547	2.812	1136.36	3195.93	4.352	994.41	4327.32
A_68_P30133051	chr15:35301203-35301247	NM_177151:-76	Vps13b	PROMOTER	1.547	3.342	818.23	2734.90	5.169	728.49	3765.74
A_68_P32573118	chrX:100677473-100677517	NR_001463:1078	Xist	INSIDE	1.547	3.534	3844.65	13587.88	5.467	1405.29	7682.44
A_68_P30150543	chr15:38591462-38591506	NM_025494:-174	Atp6v1c1	PROMOTER	1.546	2.549	521.34	1328.89	3.940	401.56	1582.16
A_68_P31676224	chr18:46471665-46471709	NM_001160399:-104	Ccdc112	PROMOTER	1.546	5.163	5877.27	30343.65	7.984	4145.92	33101.35
A_68_P31741000	chr18:58369346-58369390	NM_010181:212	Fbn2	INSIDE	1.546	5.117	3637.60	18612.62	7.912	2582.50	20433.97
A_68_P25957808	chr8:74135004-74135048	NM_146211:104	Glt25d1	INSIDE	1.546	2.720	1477.88	4019.96	4.206	1203.59	5061.77
A_68_P31117120	chr17:27694784-27694828	NM_001166476:1209	Hmga1-rs1	INSIDE	1.546	1.715	1484.34	2545.31	2.651	1267.24	3358.95
A_68_P24535483	chr6:71221618-71221662	NM_145568:-372	Krcc1	DIVERGENT_PROMOTER	1.546	7.603	684.67	5205.32	11.755	621.59	7307.05
A_68_P24656000	chr6:94233185-94233229	NM_001029850:692	Magi1	INSIDE	1.546	1.641	4535.04	7442.85	2.537	3708.37	9406.35
A_68_P31095624	chr17:24278101-24278145	NM_001080773:434	Pdpk1	INSIDE	1.546	2.407	3121.36	7513.71	3.722	2605.17	9697.66
A_68_P27804984	chr11:53292506-53292550	NM_183173:1169	Ankrd43	INSIDE	1.545	2.755	606.94	1672.19	4.257	522.39	2223.93
A_68_P24052105	chr5:123213863-123213907	NM_001199676:15535	Camkk2	INSIDE	1.545	8.285	1777.03	14721.93	12.803	1302.84	16679.92
A_68_P29992340	chr15:7079603-7079647	NM_001113386:53	Lifr	INSIDE	1.545	2.541	797.88	2027.27	3.925	630.42	2474.26
A_68_P31708189	chr18:52688590-52688634	NM_010728:750	Lox	INSIDE	1.545	1.456	1093.75	1592.08	2.249	860.22	1934.74
A_68_P25992691	chr8:81636666-81636710	NM_178267:84353	Zfp827	INSIDE	1.545	9.692	5183.46	50237.54	14.970	3215.13	48129.18
A_68_P22129414	chr3:51200267-51200311	NM_026358:181	4930583H14Rik	INSIDE	1.544	6.105	1129.35	6894.20	9.424	898.09	8463.53
A_68_P24942894	chr6:148893997-148894041	NM_019643:936	Fam60a	INSIDE	1.544	4.314	2874.14	12399.49	6.660	2592.69	17268.14
A_68_P25049946	chr7:36340772-36340816	NM_033080:153	Nudt19	INSIDE	1.544	3.580	1871.68	6700.77	5.526	1707.74	9437.16
A_68_P23527584	chr5:21243055-21243099	NM_028431:99	Pmpcb	INSIDE	1.544	3.765	910.72	3429.27	5.814	810.88	4714.20
A_68_P27614514	chr11:17059211-17059255	NM_024459:-68	Ppp3r1	PROMOTER	1.544	2.576	1662.81	4284.09	3.979	1513.69	6022.63
A_68_P21740964	chr2:150612823-150612867	NM_153781:313	Pygb	INSIDE	1.544	4.723	1686.40	7964.35	7.293	1405.35	10248.92
A_68_P30669634	chr16:35363730-35363774	NM_133704:252	Sec22a	INSIDE	1.544	2.387	1288.67	3075.84	3.686	1150.47	4240.27
A_68_P28739967	chr12:111976055-111976099	NM_027149:-82	Wdr20a	PROMOTER	1.544	3.066	1411.64	4327.86	4.735	1260.98	5970.71
A_68_P32151692	chr19:47806456-47806500	NM_026377:233	6330577E15Rik	INSIDE	1.543	4.098	11852.91	48570.74	6.323	7969.21	50392.81

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P24357881	chr6:34730747-34730791	NM_178630:337	Agbl3	INSIDE	1.543	3.147	427.26	1344.79	4.855	354.26	1720.04
A_68_P25957034	chr8:74004823-74004867	NM_001164679:5122	Ano8	INSIDE	1.543	4.355	2896.34	12613.58	6.719	2375.92	15964.47
A_68_P28175458	chr11:118903402-118903447	NM_013926:-1197	Cbx8	PROMOTER	1.543	2.606	1629.10	4245.70	4.020	1283.32	5159.52
A_68_P27080340	chr10:39451597-39451641	NR_038037:195	E130307A14Rik	INSIDE	1.543	1.585	1856.03	2942.01	2.446	1386.50	3391.38
A_68_P26940374	chr10:11063250-11063294	NM_010146:30	Epm2a	INSIDE	1.543	2.782	270.82	753.53	4.294	282.19	1211.60
A_68_P26587421	chr9:65238821-65238865	NM_028974:617	Kbtbd13	INSIDE	1.543	3.366	640.77	2157.15	5.196	558.74	2903.16
A_68_P23801768	chr5:74591245-74591289	NM_026878:-84	Rasl11b	PROMOTER	1.543	4.567	3818.49	17438.72	7.045	3002.06	21150.25
A_68_P25195705	chr7:74903906-74903950	NM_183312:700	Synm	INSIDE	1.543	2.131	1661.38	3540.87	3.288	1378.62	4533.34
A_68_P29964714	chr14:123382020-123382064	NM_028651:441	Tmtc4	INSIDE	1.543	3.639	289.34	1053.04	5.616	247.28	1388.75
A_68_P32340725	chrX:39421489-39421533	NM_009688:498	Xiap	INSIDE	1.543	3.144	351.26	1104.43	4.851	150.06	727.98
A_68_P24688740	chr6:99828403-99828447	ENSMUST00000121046:-96		PROMOTER	1.543	3.656	1559.34	5700.35	5.642	1234.95	6967.17
A_68_P21633051	chr2:130889050-130889094	NM_001163529:478	Adam33	INSIDE	1.542	2.455	602.88	1480.03	3.785	522.00	1975.90
A_68_P27539535	chr10:127533910-127533954	NM_054078:4094	Baz2a	INSIDE	1.542	1.931	1625.26	3138.52	2.978	1391.91	4145.42
A_68_P31524836	chr18:16965652-16965696	NM_007664:1884	Cdh2	INSIDE	1.542	5.347	1273.88	6811.52	8.243	1060.08	8737.75
A_68_P24048238	chr5:122499986-122500030	NM_007804:-2174	Cux2	PROMOTER	1.542	2.754	614.04	1691.04	4.248	530.72	2254.36
A_68_P27930554	chr11:76015406-76015450	NM_027773:-129	Fam57a	PROMOTER	1.542	2.236	2797.45	6253.97	3.446	2477.12	8536.80
A_68_P21339417	chr2:74601653-74601697	NM_010467:638	Hoxd1	INSIDE	1.542	2.014	1822.69	3670.23	3.104	1498.07	4650.35
A_68_P29448698	chr14:21553543-21553587	NM_010811:220	Ndst2	INSIDE	1.542	1.813	339.59	615.81	2.797	289.37	809.26
A_68_P29694905	chr14:69808678-69808722	NM_010921:-48	Nkx3-1	PROMOTER	1.542	6.019	1396.90	8407.55	9.278	1099.45	10200.87
A_68_P22180925	chr3:60806609-60806653	NM_008772:-86	P2ry1	PROMOTER	1.542	1.612	1581.70	2549.48	2.485	1392.53	3460.49
A_68_P25962147	chr8:75095836-75095880	NM_144534:-143	Tmem38a	DIVERGENT_PROMOTER	1.542	2.800	1226.51	3434.52	4.317	1052.87	4545.69
A_68_P26521623	chr9:53418301-53418345	NM_144784:133	Acat1	INSIDE	1.541	3.585	943.56	3382.47	5.525	828.27	4576.50
A_68_P26057102	chr8:93657583-93657627	NM_010241:1791	Aktip	INSIDE	1.541	3.702	3600.06	13328.11	5.705	2907.92	16588.87
A_68_P27558727	chr11:4537643-4537687	NM_029291:-131	Ascc2	DIVERGENT_PROMOTER	1.541	4.826	3891.78	18781.00	7.434	2991.62	22240.76
A_68_P24063264	chr5:125342497-125342541	NM_144819:73	Ccdc92	INSIDE	1.541	1.589	1082.41	1720.18	2.449	961.94	2355.74
A_68_P23295047	chr4:128798459-128798503	NM_010471:55	Hpca	INSIDE	1.541	1.416	875.12	1239.51	2.183	803.08	1753.03
A_68_P23301755	chr4:130219531-130219575	NM_001159603:279	Pum1	INSIDE	1.541	2.281	1424.00	3247.45	3.515	1128.39	3965.86
A_68_P22207824	chr3:66777458-66777502	NM_013665:8213	Shox2	INSIDE	1.541	1.628	3214.15	5233.73	2.510	2755.27	6914.40
A_68_P28184189	chr11:120239967-120240011	NM_027980:72	2310003H01Rik	INSIDE	1.540	3.421	542.84	1857.08	5.269	466.14	2456.01
A_68_P23368580	chr4:141795400-141795444	NM_001109685:-106	9030409G11Rik	PROMOTER	1.540	4.200	12506.51	52523.82	6.467	9077.38	58703.21
A_68_P28112958	chr11:108286558-108286602	NM_029606:1	Ccdc46	INSIDE	1.540	1.840	1341.81	2468.67	2.833	1139.15	3226.70
A_68_P21832544	chr2:166731558-166731602	NM_023565:-15	Cse1l	PROMOTER	1.540	2.158	2544.10	5490.79	3.323	1922.64	6388.29
A_68_P23585886	chr5:33206293-33206337	NM_177786:-55	Depdc5	DIVERGENT_PROMOTER	1.540	1.961	1701.05	3335.59	3.019	1486.86	4489.25
A_68_P21115865	chr2:32391002-32391046	NM_153560:146	Fam102a	INSIDE	1.540	2.078	1162.78	2416.42	3.200	965.79	3090.04
A_68_P21124370	chr2:33742800-33742844	NM_175184:644	Fam125b	INSIDE	1.540	2.933	4745.41	13920.28	4.516	3493.69	15778.51
A_68_P28184739	chr11:120329033-120329077	NM_001159328:106	Hgs	INSIDE	1.540	1.893	2172.26	4112.60	2.915	1783.07	5197.83
A_68_P32132967	chr19:44637357-44637401	NM_176958:35	Hif1an	INSIDE	1.540	3.012	677.07	2039.17	4.638	597.35	2770.71
A_68_P28997657	chr13:44826068-44826112	NM_001205044:-52	Jarid2	PROMOTER	1.540	2.474	2897.66	7168.55	3.810	2247.25	8561.24
A_68_P29618044	chr14:56110165-56110209	NM_001024645:257	Lrrc16b	INSIDE	1.540	2.286	3597.59	8222.54	3.520	3076.47	10829.15
A_68_P25581950	chr7:147234174-147234218	NM_010836:791	Msx3	INSIDE	1.540	2.192	1382.25	3030.30	3.376	1166.43	3937.96
A_68_P23439553	chr4:154976002-154976046	NM_177186:500	Slc35e2	INSIDE	1.540	2.236	771.25	1724.72	3.443	614.18	2114.67
A_68_P28344356	chr12:34642925-34642969	NM_011658:411	Twist1	INSIDE	1.540	1.644	423.44	696.13	2.532	392.98	995.14
A_68_P22695192	chr4:3865915-3865959	NM_001190323:-98	Chchd7	DIVERGENT_PROMOTER	1.539	2.922	3388.26	9901.35	4.496	2546.72	11450.11
A_68_P28525474	chr12:72410830-72410874	NM_001190466:-18	Dact1	PROMOTER	1.539	2.050	5746.86	11781.79	3.155	4667.44	14727.36
A_68_P27385041	chr10:98569996-98570040	NM_015737:-750	Galnt4	PROMOTER	1.539	1.907	370.06	705.59	2.935	285.70	838.51
A_68_P31150606	chr17:33954625-33954670	NM_030697:7180	Kank3	INSIDE	1.539	2.105	592.68	1247.40	3.239	549.54	1780.05
A_68_P22347470	chr3:95908249-95908293	NM_001025613:-179	Otud7b	PROMOTER	1.539	1.937	515.73	999.13	2.982	384.89	1147.91
A_68_P22246600	chr3:75360381-75360425	NM_019745:319	Pdcd10	INSIDE	1.539	2.256	8011.46	18072.48	3.472	5244.25	18209.34
A_68_P26142832	chr8:109571961-109572005	NM_026513:532	Pdf	INSIDE	1.539	2.131	1545.36	3293.12	3.279	1239.71	4064.46
A_68_P22680840	chr3:157229758-157229802	NM_011196:-75	Ptger3	PROMOTER	1.539	3.172	1382.86	4385.80	4.881	1383.01	6749.95
A_68_P28314231	chr12:29320191-29320235	NM_011300:606	Rps7	INSIDE	1.539	1.793	3656.30	6553.99	2.759	3029.59	8358.80

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P33007029	A_68_P33007029			Unknown	1.539	3.724	3393.02	12634.27	5.729	2908.95	16665.78
A_68_P20121782	chr1:30930313-30930357	ENSMUST00000046443:205		INSIDE	1.539	1.825	3153.60	5755.99	2.809	2895.33	8133.96
A_68_P26476281	chr9:45647027-45647071	NM_001145947:437	Bace1	INSIDE	1.538	3.408	1593.42	5430.55	5.240	1236.49	6479.45
A_68_P30349739	chr15:76487469-76487513	NM_019396:3001	Cyhr1	INSIDE	1.538	2.365	2055.01	4860.62	3.637	1485.47	5402.77
A_68_P27551860	chr11:3309041-3309085	NM_010718:176	Limk2	INSIDE	1.538	3.518	1658.89	5835.56	5.410	1398.92	7568.53
A_68_P32536210	chrX:91077357-91077401	NM_145630:56	Pdk3	INSIDE	1.538	3.659	1319.92	4829.75	5.629	988.31	5563.58
A_68_P23981859	chr5:111209498-111209542	NM_001025561:95	Pus1	INSIDE	1.538	2.394	3325.28	7960.55	3.681	2575.26	9480.36
A_68_P28741731	chr12:112278009-112278053	NM_198023:22	Rcor1	INSIDE	1.538	3.326	9572.13	31835.52	5.114	7748.35	39625.39
A_68_P26932993	chr10:9620586-9620630	NM_001081344:230	Stxbp5	INSIDE	1.538	17.246	1505.89	25970.25	26.529	1250.90	33185.50
A_68_P24304143	chr6:24905716-24905760	NM_177013:387	Tmem229a	INSIDE	1.538	2.687	1431.27	3845.77	4.133	1315.59	5436.84
A_68_P25411826	chr7:117266404-117266448	NM_009516:854	Wee1	INSIDE	1.538	2.467	904.96	2232.32	3.794	799.90	3034.79
A_68_P26252592	chr8:128094354-128094398	BC072593:-720		PROMOTER	1.538	8.899	274.41	2442.03	13.684	230.31	3151.62
A_68_P25834612	chr8:47248897-47248941	NM_025747:-5991	4933411K20Rik	PROMOTER	1.537	1.755	5189.64	9109.37	2.698	4110.67	11092.42
A_68_P29587993	chr14:49066241-49066285	NM_172600:236	6720456H20Rik	INSIDE	1.537	2.300	2572.13	5914.65	3.534	2101.71	7427.21
A_68_P28859761	chr13:19040366-19040410	NM_175007:149	Amph	INSIDE	1.537	2.967	5674.37	16838.28	4.562	4718.16	21522.00
A_68_P21266439	chr2:61649898-61649942	NM_009322:7411	Tbr1	INSIDE	1.537	2.571	364.72	937.82	3.952	383.31	1514.93
A_68_P31655791	chr18:42671723-42671767	NM_001039474:604	Tcerg1	INSIDE	1.537	1.628	1908.82	3108.31	2.502	1457.80	3647.64
A_68_P31982216	chr19:16855225-16855273	NM_173028:169	Vps13a	INSIDE	1.537	1.643	672.73	1105.45	2.526	541.01	1366.40
A_68_P29102522	chr13:65360990-65361034	ENSMUST00000099425:166		INSIDE	1.537	5.390	861.37	4642.76	8.282	759.18	6287.68
A_68_P23235081	chr4:117222839-117222883	NM_080469:-238	Eri3	PROMOTER	1.536	1.899	1162.81	2208.21	2.917	989.53	2886.33
A_68_P28576090	chr12:81620528-81620572	NM_001081421:574	Galntl1	INSIDE	1.536	2.152	4793.87	10316.28	3.306	3707.25	12255.35
A_68_P24112574	chr5:134790846-134790890	NM_001080746:-252	Gtf2i	PROMOTER	1.536	2.895	1190.75	3446.85	4.446	1021.12	4539.79
A_68_P25846166	chr8:49314139-49314183	NM_001145937:445884	Odz3	INSIDE	1.536	1.963	353.88	694.53	3.014	297.77	897.56
A_68_P26630339	chr9:72773100-72773144	NM_028116:-334	Pygo1	PROMOTER	1.536	1.416	2378.36	3368.63	2.176	2002.26	4356.21
A_68_P28726321	chr12:109416856-109416900	NM_028262:616	Setd3	INSIDE	1.536	2.422	1209.78	2930.42	3.721	910.50	3388.06
A_68_P23294938	chr4:128782726-128782770	NM_025452:-25	Tmem54	PROMOTER	1.536	4.533	3146.01	14260.84	6.964	2437.77	16975.62
A_68_P33012156	chr9_random:54584-54628	NR_027950:-86	4930526I15Rik	PROMOTER	1.535	1.664	567.58	944.36	2.554	454.38	1160.30
A_68_P27103323	chr10:43723779-43723823	NM_172393:852	Aim1	INSIDE	1.535	1.987	1204.32	2393.59	3.050	960.45	2929.32
A_68_P25637623	chr8:8661349-8661393	NM_010111:-597	Efnb2	PROMOTER	1.535	3.006	909.85	2734.56	4.615	760.62	3509.94
A_68_P32140182	chr19:45811402-45811446	NM_001166361:5950	Fgf8	INSIDE	1.535	5.312	3067.67	16296.33	8.155	2340.21	19085.57
A_68_P21764750	chr2:155102799-155102843	NM_025735:641	Map1lc3a	INSIDE	1.535	2.782	4218.66	11735.73	4.269	3229.90	13789.31
A_68_P28950790	chr13:36827018-36827062	NM_153529:-717	Nrn1	PROMOTER	1.535	1.902	4299.20	8179.08	2.920	3310.23	9664.48
A_68_P27280131	chr10:79440436-79440480	NM_001003949:6617	ORF61	INSIDE	1.535	3.448	2109.25	7272.62	5.293	1727.17	9141.30
A_68_P23972073	chr5:108890220-108890264	NM_172716:-108	Pcgf3	PROMOTER	1.535	1.619	1040.16	1683.50	2.484	873.42	2169.90
A_68_P23430798	chr4:153715842-153715886	NM_001177995:295118	Prdm16	INSIDE	1.535	6.877	4530.81	31157.62	10.557	3110.63	32839.81
A_68_P23801771	chr5:74591574-74591618	NM_026878:246	Rasl11b	INSIDE	1.535	2.669	1030.92	2751.48	4.097	893.49	3660.55
A_68_P31104792	chr17:25707704-25707748	NM_011447:-95	Sox8	DIVERGENT_PROMOTER	1.535	5.972	1910.27	11407.68	9.169	1274.07	11682.41
A_68_P31207579	chr17:46692454-46692498	NM_020493:635	Srf	INSIDE	1.535	2.991	2127.40	6364.07	4.593	1763.88	8101.18
A_68_P31921226	chr19:4125896-4125940	NM_001078649:-41	Tmem134	DIVERGENT_PROMOTER	1.535	1.599	2143.89	3428.02	2.454	1865.14	4577.64
A_68_P25951334	chr8:72877112-72877156	NM_001122829:38	Upf1	INSIDE	1.535	4.103	1615.14	6627.05	6.300	1315.38	8287.26
A_68_P27939271	chr11:77580034-77580078	ENSMUST00000108376:-181		PROMOTER	1.535	3.753	812.30	3048.39	5.762	671.76	3870.66
A_68_P20250405	chr1:57029997-57030046	NR_024325:1709	9130024F11Rik	INSIDE	1.534	1.803	368.62	664.80	2.767	298.59	826.23
A_68_P26530603	chr9:55174506-55174550	NM_172923:-227	AI118078	PROMOTER	1.534	3.931	1708.92	6717.38	6.028	1408.98	8493.67
A_68_P30357053	chr15:77825858-77825902	NM_007583:123830	Cacng2	INSIDE	1.534	3.795	7182.40	27260.62	5.824	5370.61	31279.25
A_68_P22715810	chr4:8617868-8617912	NM_001081417:-177	Chd7	PROMOTER	1.534	4.212	492.27	2073.62	6.460	414.93	2680.59
A_68_P23969232	chr5:108297963-108298007	NM_007964:6142	Evi5	INSIDE	1.534	3.333	2981.35	9936.38	5.114	2623.33	13416.10
A_68_P24038707	chr5:120886274-120886318	NM_008499:4402	Lhx5	INSIDE	1.534	5.622	734.69	4130.74	8.623	673.95	5811.19
A_68_P21633642	chr2:130997305-130997349	NM_027641:3220	Spef1	INSIDE	1.534	2.060	1345.19	2770.51	3.159	1104.99	3490.29
A_68_P28615783	chr12:88728757-88728801	NM_011479:402	Sptlc2	INSIDE	1.534	2.160	1028.58	2221.43	3.312	828.94	2745.68
A_68_P25459064	chr7:125728226-125728270	NM_172476:-48	Tmc7	PROMOTER	1.534	3.283	1856.92	6095.49	5.036	1642.42	8271.82
A_68_P20087498	chr1:23262935-23262979	ENSMUST00000097807:289		INSIDE	1.534	1.963	1047.48	2056.14	3.011	901.14	2713.14

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group Relative methylation (Cy5/Cy3)	Sham group Cy3 signal (Input)	Sham group Cy5 signal (MeDIP)	TiO_2-H group Relative methylation (Cy5/Cy3)	TiO_2-H group Cy3 signal (Input)	TiO_2-H group Cy5 signal (MeDIP)
A_68_P28104781	chr11:106889949-106889993	NM_001163473:434	1810010H24Rik	INSIDE	1.533	3.836	1002.22	3844.42	5.880	863.11	5074.98
A_68_P25276872	chr7:89483764-89483808	NM_001190374:-417	Adamtsl3	PROMOTER	1.533	7.631	1584.93	12094.30	11.695	1347.21	15755.90
A_68_P28752830	chr12:114067331-114067375	NM_028023:248	Cdca4	INSIDE	1.533	3.522	2449.67	8627.34	5.401	1964.09	10607.28
A_68_P27921508	chr11:74433189-74433233	NM_001013784:104	E130309D14Rik	INSIDE	1.533	3.394	3585.16	12167.32	5.202	3056.19	15899.69
A_68_P27921510	chr11:74433466-74433510	NM_001013784:382	E130309D14Rik	INSIDE	1.533	8.832	2611.07	23060.27	13.542	1959.59	26536.29
A_68_P28052725	chr11:97660923-97660967	NM_010688:-41	Lasp1	PROMOTER	1.533	5.253	3494.89	18360.31	8.055	2884.12	23231.12
A_68_P27937051	chr11:77161599-77161643	NM_177710:131694	Ssh2	INSIDE	1.533	4.004	1450.50	5807.99	6.140	1278.99	7852.84
A_68_P26530601	chr9:55174289-55174334	NM_172923:-444	AI118078	PROMOTER	1.532	4.214	1874.00	7897.77	6.456	1473.35	9512.37
A_68_P24428428	chr6:48579466-48579510	NR_027236:1323	AI854703	INSIDE	1.532	2.268	658.89	1494.33	3.475	601.02	2088.42
A_68_P21632194	chr2:130732229-130732273	NM_009730:19	Atrn	INSIDE	1.532	5.371	1345.00	7224.55	8.228	1081.03	8894.90
A_68_P26019095	chr8:86794255-86794299	NM_026350:-17	Ccdc130	PROMOTER	1.532	2.969	3007.20	8927.37	4.548	2405.15	10938.41
A_68_P31928777	chr19:5457059-5457103	NM_198616:469	Ccdc85b	INSIDE	1.532	2.179	1183.56	2579.21	3.338	1028.36	3432.85
A_68_P22355191	chr3:97414110-97414154	NM_026539:-19	Chd1l	PROMOTER	1.532	4.639	481.16	2232.03	7.109	455.84	3240.45
A_68_P31258211	chr17:56901482-56901526	NM_144858:-2669	Dus3l	DIVERGENT_PROMOTER	1.532	1.538	1244.70	1913.87	2.355	1027.37	2419.82
A_68_P20644035	chr1:138028029-138028073	NM_001039472:73	Kif21b	INSIDE	1.532	1.639	677.67	1110.85	2.512	547.07	1374.03
A_68_P26345157	chr9:20837581-20837625	NR_035438:-830	Mir1900	PROMOTER	1.532	2.271	1080.63	2454.17	3.479	904.14	3145.28
A_68_P26873355	chr9:119487746-119487790	NM_021544:366	Scn5a	INSIDE	1.532	1.767	1439.43	2543.43	2.708	1209.86	3275.78
A_68_P27325555	chr10:87922666-87922710	NM_011517:357	Sycp3	INSIDE	1.532	7.924	5644.23	44726.54	12.140	3909.36	47458.33
A_68_P24591236	chr6:83018754-83018798	NM_009392:1443	Tlx2	INSIDE	1.532	2.775	421.84	1170.68	4.251	650.07	2763.26
A_68_P25504790	chr7:134397531-134397575	NM_177362:9513	Zfp771	INSIDE	1.532	1.867	1286.01	2400.51	2.860	1137.32	3252.78
A_68_P23880196	chr5:90312755-90312799	NM_001081401:-417	Adamts3	PROMOTER	1.531	3.069	1012.76	3108.29	4.698	777.44	3652.78
A_68_P26469460	chr9:44575399-44575447	NM_145985:469	Arcn1	INSIDE	1.531	7.501	660.54	4954.98	11.486	401.09	4606.84
A_68_P28727039	chr12:109513784-109513828	NM_001159910:-179	Ccdc85c	PROMOTER	1.531	3.067	3029.72	9291.40	4.694	2394.92	11242.71
A_68_P23573354	chr5:30890939-30890983	NM_010608:418	Kcnk3	INSIDE	1.531	6.699	1037.65	6951.16	10.254	713.64	7317.35
A_68_P26537272	chr9:56468941-56468985	NM_181074:64098	Lingo1	INSIDE	1.531	4.659	605.59	2821.38	7.135	486.37	3470.21
A_68_P27354860	chr10:93103568-93103612	NM_021320:-203	Ntn4	PROMOTER	1.531	1.740	1786.47	3107.84	2.664	1503.59	4005.25
A_68_P28738217	chr12:111684829-111684873	NM_001135001:-538	Ppp2r5c	PROMOTER	1.531	2.468	2455.41	6061.07	3.780	1822.54	6888.58
A_68_P22944675	chr4:57313204-57313248	NM_011207:1483	Ptpn3	INSIDE	1.531	4.074	349.23	1422.69	6.235	481.41	3001.86
A_68_P27798065	chr11:52045603-52045647	NM_011543:128	Skp1a	INSIDE	1.531	2.037	756.45	1540.63	3.117	659.84	2056.86
A_68_P30363492	chr15:78798174-78798218	NM_001039155:20043	Triobp	INSIDE	1.531	4.304	3043.35	13098.90	6.588	2143.46	14121.76
A_68_P25670559	chr8:13786249-13786293	NM_025924:656	Upf3a	INSIDE	1.531	1.530	2669.49	4083.41	2.342	2133.74	4998.14
A_68_P22394252	chr3:104770874-104770918	NM_009520:-6269	Wnt2b	PROMOTER	1.531	2.252	1357.05	3055.94	3.448	1114.67	3843.22
A_68_P24086494	A_68_P24086494			Unknown	1.531	2.899	569.27	1650.39	4.439	505.79	2244.97
A_68_P25352334	chr7:104936888-104936932	ENSMUST00000172423:-140		PROMOTER	1.531	1.373	1404.07	1927.65	2.103	1176.25	2473.09
A_68_P31679073	chr18:47009821-47009865	NM_029008:150	4833403I15Rik	INSIDE	1.530	1.493	1261.63	1883.79	2.284	1016.66	2322.55
A_68_P23961301	chr5:106881112-106881156	NM_001005477:6051	Barhl2	DOWNSTREAM	1.530	4.458	1187.26	5292.41	6.821	1025.21	6992.74
A_68_P32395905	chrX:53709083-53709127	NM_172779:1089	Ddx26b	INSIDE	1.530	1.452	5384.84	7816.63	2.221	2264.74	5029.57
A_68_P20863428	chr1:180267506-180267550	NM_016805:387	Hnrnpu	INSIDE	1.530	1.492	616.38	919.53	2.283	550.33	1256.38
A_68_P25144266	chr7:63217700-63217744	NM_023647:98	Nipa2	INSIDE	1.530	1.692	1197.66	2026.59	2.589	1035.15	2680.06
A_68_P20259227	chr1:58561519-58561563	NM_001025378:-3280	Orc2	PROMOTER	1.530	2.177	586.53	1276.70	3.330	452.39	1506.25
A_68_P22886521	chr4:46051942-46051986	NM_021883:-129	Tmod1	PROMOTER	1.530	2.741	2565.11	7031.71	4.195	2101.39	8815.76
A_68_P29308210	chr13:108681440-108681484	NM_145456:-1204	Zswim6	PROMOTER	1.530	3.652	1260.57	4603.49	5.589	1054.22	5891.68
A_68_P24086560	A_68_P24086560			Unknown	1.530	4.553	524.04	2385.92	6.964	363.09	2528.68
A_68_P25021007	chr7:29079751-29079795	NM_007866:7032	Dll3	INSIDE	1.529	4.149	1259.27	5225.23	6.346	1111.25	7052.15
A_68_P27253669	chr10:74430095-74430139	NM_010311:141	Gnaz	INSIDE	1.529	2.357	789.78	1861.25	3.603	726.43	2617.05
A_68_P26812405	chr9:107905152-107905196	NM_013785:196	Ip6k1	INSIDE	1.529	3.185	897.89	2859.76	4.869	759.91	3700.20
A_68_P30478815	chr15:99054306-99054350	NM_010601:-1078	Kcnh3	PROMOTER	1.529	2.143	1207.57	2587.92	3.278	1052.83	3450.90
A_68_P28583196	chr12:82961089-82961133	NM_018814:94	Pcnx	INSIDE	1.529	2.203	1583.96	3489.16	3.368	1330.25	4480.48
A_68_P21098343	chr2:29475430-29475474	NM_001039086:213	Rapgef1	INSIDE	1.529	1.667	532.10	886.98	2.548	499.46	1272.59
A_68_P23749454	chr5:64551417-64551461	NM_019636:-11	Tbc1d1	PROMOTER	1.529	1.732	1641.37	2843.35	2.650	1396.68	3700.54
A_68_P26713768	chr9:89599588-89599632	NM_025360:271	Tmed3	INSIDE	1.529	1.959	612.80	1200.66	2.995	523.72	1568.54

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P29286853	chr13:104564644-104564688	ENSMUST00000109322:-127		PROMOTER	1.529	2.288	823.90	1884.69	3.498	732.31	2561.91
A_68_P21809324	chr2:162734117-162734161	ENSMUST00000122376:479		INSIDE	1.529	4.797	1120.76	5376.75	7.337	932.71	6843.66
A_68_P23562830	chr5:28784867-28784911	NR_015562:-8635	9530036O11Rik	PROMOTER	1.528	3.034	425.37	1290.71	4.636	458.45	2125.45
A_68_P31150132	chr17:33822462-33822506	NM_001109913:-81	Hnrnpm	PROMOTER	1.528	3.972	1968.27	7818.47	6.071	1520.49	9230.34
A_68_P20788410	chr1:166237694-166237738	NM_178071:-89	Nme7	DIVERGENT_PROMOTER	1.528	3.811	729.52	2780.46	5.824	566.98	3302.24
A_68_P23176709	chr4:104782027-104782071	NM_178143:455	Prkaa2	INSIDE	1.528	1.581	4004.06	6331.55	2.416	3082.03	7445.24
A_68_P23223131	chr4:114729380-114729424	NM_011527:-2729	Tal1	PROMOTER	1.528	1.748	4063.28	7104.22	2.671	3092.87	8261.82
A_68_P20936016	chr1:192886793-192886837	NM_001163421:-3	Tatdn3	DIVERGENT_PROMOTER	1.528	2.584	13552.33	35014.66	3.948	11020.49	43506.03
A_68_P21121774	chr2:33323833-33323877	NM_001025594:198	Zbtb43	INSIDE	1.528	2.141	1900.30	4068.74	3.271	1754.03	5738.29
A_68_P32288518	chrX:20002618-20002662	ENSMUST00000115384:-173		PROMOTER	1.528	3.462	1052.72	3644.25	5.289	598.35	3164.43
A_68_P25597935	chr7:150155005-150155050	NM_008554:142	Ascl2	INSIDE	1.527	1.424	1230.80	1753.04	2.175	972.17	2114.90
A_68_P26317084	chr9:14185441-14185485	NM_028013:224	Endod1	INSIDE	1.527	1.671	826.93	1381.89	2.551	778.11	1985.00
A_68_P28158070	chr11:116083313-116083358	NM_025276:16070	Evpl	INSIDE	1.527	6.358	2493.61	15855.54	9.710	1964.19	19072.41
A_68_P31371532	chr17:78817452-78817496	NM_199448:-31	Fez2	PROMOTER	1.527	5.391	8891.70	47938.00	8.235	6744.37	55539.39
A_68_P24951566	chr7:4966239-4966283	NM_011813:-405	Fiz1	PROMOTER	1.527	1.489	2233.90	3326.98	2.274	1677.08	3813.57
A_68_P20553865	chr1:120734246-120734290	NM_001081125:215928	Gli2	INSIDE	1.527	2.576	834.66	2150.49	3.933	708.23	2785.64
A_68_P28067969	chr11:100275377-100275421	NM_176830:735	Leprel4	INSIDE	1.527	2.451	999.41	2449.55	3.742	782.26	2927.01
A_68_P25962045	chr8:75071657-75071701	NM_027485:531	Med26	INSIDE	1.527	2.995	3341.21	10006.22	4.572	2633.69	12040.27
A_68_P31425843	chr17:88374364-88374408	NM_010830:-3	Msh6	PROMOTER	1.527	1.680	584.04	981.29	2.566	572.71	1469.51
A_68_P22540268	chr3:132612964-132613008	NM_001029836:269	Npnt	INSIDE	1.527	2.202	1452.72	3198.70	3.362	1305.20	4387.93
A_68_P22825736	chr4:33296596-33296640	NM_177774:653	Srsf12	INSIDE	1.527	3.172	5337.83	16931.31	4.845	3663.72	17751.12
A_68_P23749879	chr5:64621748-64621793	NM_019636:70321	Tbc1d1	INSIDE	1.527	3.790	7787.71	29513.45	5.786	6371.74	36869.30
A_68_P28053990	chr11:97883852-97883896	NM_001159320:-4188	Cacnb1	PROMOTER	1.526	1.645	2003.46	3296.48	2.511	1678.37	4215.21
A_68_P29651385	chr14:62300358-62300402	NR_028264:830	Dleu2	INSIDE	1.526	3.449	4014.63	13847.19	5.263	3245.48	17082.07
A_68_P20826000	chr1:172995096-172995140	NM_010188:-5584	Fcgr3	PROMOTER	1.526	2.291	17110.18	39195.13	3.495	12593.44	44016.75
A_68_P21258086	chr2:60221286-60221330	NM_013825:-20	Ly75	PROMOTER	1.526	2.902	3297.93	9570.93	4.427	2671.37	11827.18
A_68_P22752523	chr4:15885168-15885212	NM_013752:77	Nbn	INSIDE	1.526	2.495	486.75	1214.43	3.808	417.33	1589.30
A_68_P26021284	chr8:87230641-87230685	NM_001081981:67606	Nfix	DOWNSTREAM	1.526	5.117	5399.70	27630.41	7.807	4219.66	32941.71
A_68_P30961954	chr16:91271188-91271232	NM_016968:1197	Olig1	INSIDE	1.526	1.925	2176.75	4190.72	2.937	1710.79	5024.60
A_68_P26477292	chr9:45821526-45821572	NM_027498:646	Sik3	INSIDE	1.526	3.393	1087.02	3688.45	5.178	884.56	4579.83
A_68_P29062337	chr13:56710941-56710985	NM_009369:-1	Tgfbi	PROMOTER	1.526	3.737	5366.24	20054.80	5.704	4386.93	25022.32
A_68_P24136157	chr5:140020297-140020341	NM_013702:467	Uncx	INSIDE	1.526	3.136	2512.84	7880.53	4.786	2233.60	10689.77
A_68_P32410980	chrX:56820824-56820868	ENSMUST00000124402:-197		PROMOTER	1.526	2.019	554.33	1119.11	3.080	325.16	1001.56
A_68_P24189032	chr5:150921298-150921342	ENSMUST00000165030:79		INSIDE	1.526	1.614	1184.67	1911.70	2.462	1095.03	2696.21
A_68_P23339473	chr4:136913085-136913129	NM_009861:546	Cdc42	INSIDE	1.525	1.562	644.29	1006.07	2.381	953.81	2270.72
A_68_P30378507	chr15:81416859-81416903	NM_177821:237	Ep300	INSIDE	1.525	1.529	2839.79	4341.31	2.331	2245.83	5234.89
A_68_P30364007	chr15:78873556-78873600	NM_015738:1264	Galr3	INSIDE	1.525	1.580	1550.00	2449.54	2.410	1295.18	3121.49
A_68_P21270819	chr2:62502267-62502311	NM_145523:-95	Gca	PROMOTER	1.525	1.673	2277.55	3809.24	2.551	1855.99	4734.25
A_68_P23927386	chr5:100468112-100468156	NM_016690:107	Hnrpdl	INSIDE	1.525	1.347	2453.41	3303.61	2.053	2090.79	4292.30
A_68_P21078500	chr2:26264786-26264830	NM_033134:-100	Inpp5e	PROMOTER	1.525	2.628	4230.13	11117.76	4.007	3630.11	14546.65
A_68_P30980968	chr16:94592282-94592326	NM_001159618:-147	Pigp	PROMOTER	1.525	3.774	2425.87	9154.33	5.756	2179.99	12547.77
A_68_P20638994	chr1:137271658-137271702	NM_175259:-40	Shisa4	PROMOTER	1.525	1.713	767.81	1315.14	2.612	633.58	1654.92
A_68_P23294939	chr4:128782828-128782872	NM_025452:77	Tmem54	INSIDE	1.525	2.730	3022.03	8250.80	4.163	2406.60	10019.09
A_68_P32700067	chrX:137134400-137134444	NM_001077364:639	Tsc22d3	INSIDE	1.525	2.951	4716.72	13920.73	4.500	2959.65	13317.83
A_68_P21770588	chr2:156137716-156137760	NM_027585:-470	4921517L17Rik	PROMOTER	1.524	2.899	1622.43	4703.88	4.418	1472.90	6507.65
A_68_P30588038	chr16:20531403-20531447	NM_007889:14288	Dvl3	INSIDE	1.524	3.268	6445.03	21060.16	4.980	4893.53	24368.66
A_68_P31937111	chr19:7054987-7055031	NM_001166368:-57	Fkbp2	PROMOTER	1.524	1.910	1073.69	2050.39	2.910	831.21	2418.70
A_68_P26644020	chr9:75289818-75289862	NM_001039522:510	Leo1	INSIDE	1.524	2.105	470.35	990.02	3.207	362.79	1163.57
A_68_P30571313	chr16:16983889-16983933	NM_001038663:436	Mapk1	INSIDE	1.524	2.580	3619.05	9335.38	3.932	2928.64	11514.79
A_68_P31640485	chr18:39650185-39650229	NM_008173:-3307	Nr3c1	PROMOTER	1.524	2.039	5516.93	11249.55	3.107	4451.15	13830.80
A_68_P31302584	chr17:66121929-66121973	NM_133685:142	Rab31	INSIDE	1.524	5.368	2447.72	13138.28	8.182	2211.95	18098.76

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31120939	chr17:28314640-28314684	NM_172617:300	Zfp523	INSIDE	1.524	2.620	5376.46	14087.07	3.993	3975.25	15871.32
A_68_P31090923	chr17:23013560-23013604	NM_001110254:-9481	Zfp945	PROMOTER	1.524	3.867	1295.52	5010.37	5.892	1139.64	6715.07
A_68_P30591825	chr16:21333336-21333380	AK018285:71		INSIDE	1.524	1.848	1711.65	3162.98	2.817	1599.45	4505.55
A_68_P31127961	chr17:29574415-29574459	AK153778:-2035		PROMOTER	1.524	2.268	647.74	1469.09	3.456	595.62	2058.33
A_68_P23264561	chr4:123427058-123427102	NM_023423:462	Akirin1	INSIDE	1.523	1.873	844.93	1582.79	2.854	666.74	1902.56
A_68_P20258850	chr1:58480309-58480353	NM_001042634:602	Clk1	INSIDE	1.523	1.658	1405.07	2330.06	2.526	1048.58	2648.61
A_68_P30743456	chr16:48994162-48994206	NM_001110017:41	Dzip3	INSIDE	1.523	3.027	2735.09	8279.27	4.610	2240.86	10331.14
A_68_P23280028	chr4:126106770-126106814	NM_153402:-6	Eif2c3	PROMOTER	1.523	3.112	1596.04	4967.57	4.742	1337.85	6343.42
A_68_P26891190	chr9:122656383-122656427	NM_001199736:-59	Gm9524	PROMOTER	1.523	7.913	889.69	7039.99	12.054	658.89	7942.60
A_68_P29330804	chr13:112598387-112598431	NM_011945:783	Map3k1	INSIDE	1.523	2.477	2532.55	6272.51	3.773	2203.81	8314.87
A_68_P31668416	chr18:44821733-44821777	NM_001085374:166	Mcc	INSIDE	1.523	3.694	1617.21	5974.76	5.627	1172.44	6597.50
A_68_P26026035	chr8:88224110-88224154	NM_001081324:-9224	Neto2	PROMOTER	1.523	1.881	423.11	795.66	2.864	418.85	1199.59
A_68_P25144564	chr7:63274831-63274875	NM_153578:91	Nipa1	INSIDE	1.523	5.769	4245.98	24493.11	8.786	3181.43	27952.98
A_68_P25524905	chr7:138009499-138009543	NM_133942:97	Plekha1	INSIDE	1.523	3.165	4756.44	15053.68	4.820	3968.99	19129.86
A_68_P27974634	chr11:83777899-83777943	NM_001115009:-9	Synrg	PROMOTER	1.523	2.208	376.20	830.79	3.364	416.91	1402.61
A_68_P23381898	chr4:144784634-144784678	NM_001128198:-4161	Vps13d	PROMOTER	1.523	2.268	1021.53	2316.37	3.453	893.16	3083.71
A_68_P31335313	chr17:71965569-71965613	NM_175639:36	Wdr43	INSIDE	1.523	1.559	551.97	860.51	2.374	500.10	1187.19
A_68_P26038355	chr8:90482696-90482740	NM_033327:776	Zfp423	INSIDE	1.523	2.485	1179.34	2930.14	3.784	1066.12	4034.58
A_68_P32573868	chrX:100812194-100812238	NR_028381:6877	B230206F22Rik	INSIDE	1.522	1.930	590.26	1139.31	2.937	464.53	1364.45
A_68_P28109104	chr11:107655957-107656001	NM_019431:-200	Cacng4	PROMOTER	1.522	5.935	2073.53	12305.65	9.033	1748.37	15792.28
A_68_P24791602	chr6:119125266-119125312	NM_001033379:18	Dcp1b	INSIDE	1.522	6.481	3512.61	22766.90	9.865	2669.19	26332.06
A_68_P27997247	chr11:87800951-87800995	NM_001168472:-885	Dynll2	PROMOTER	1.522	2.430	1692.09	4111.94	3.698	1379.73	5101.95
A_68_P27827804	chr11:57650530-57650574	NM_008213:-4903	Hand1	PROMOTER	1.522	2.081	2280.25	4744.95	3.166	1619.94	5128.94
A_68_P26648623	chr9:76171335-76171379	NM_198962:29	Hcrtr2	INSIDE	1.522	2.097	1253.70	2629.01	3.192	1031.47	3292.40
A_68_P25953853	chr8:73284695-73284739	NM_183170:104	Mpv17l2	INSIDE	1.522	3.011	1073.38	3231.59	4.583	912.14	4180.48
A_68_P29162295	chr13:78338732-78338776	NM_010151:-511	Nr2f1	PROMOTER	1.522	2.715	1410.20	3828.32	4.131	1237.84	5113.65
A_68_P23415887	chr4:151369933-151369977	NM_172705:334	Phf13	INSIDE	1.522	2.338	8895.10	20795.78	3.559	7091.16	25238.78
A_68_P21091625	chr2:28389284-28389328	NM_001145835:323	Ralgds	INSIDE	1.522	1.960	879.08	1722.93	2.982	703.10	2096.69
A_68_P21747609	chr2:151919690-151919734	NM_001160410:12448	Scrt2	INSIDE	1.522	7.979	1606.17	12814.85	12.144	1057.18	12838.79
A_68_P29507580	chr14:31529106-31529150	NM_001166532:328	Sfmbt1	INSIDE	1.522	4.440	1023.75	4545.37	6.758	860.17	5813.21
A_68_P23594804	chr5:34868325-34868369	NM_011893:-86	Sh3bp2	PROMOTER	1.522	3.182	1059.93	3372.88	4.843	1020.92	4944.01
A_68_P21840492	chr2:168106455-168106499	ENSMUST00000109191:156		INSIDE	1.522	3.036	1075.46	3265.51	4.621	990.43	4576.44
A_68_P27942253	chr11:78075063-78075107	NM_001002004:-171	2610507B11Rik	PROMOTER	1.521	5.560	2221.97	12353.43	8.457	2054.15	17372.83
A_68_P26741563	chr9:95306199-95306243	NM_018763:1469	Chst2	INSIDE	1.521	1.952	1403.78	2740.04	2.970	1182.30	3511.08
A_68_P22968875	chr4:62875286-62875330	NM_025685:-1137	Col27a1	PROMOTER	1.521	1.878	674.44	1266.91	2.857	542.61	1550.01
A_68_P30555522	chr16:13110157-13110201	NM_015769:350	Ercc4	INSIDE	1.521	2.963	2035.68	6031.25	4.507	1728.16	7789.45
A_68_P25528898	chr7:138685827-138685871	NM_008257:-628	Hmx3	PROMOTER	1.521	3.334	310.68	1035.88	5.071	297.74	1509.99
A_68_P29048046	chr13:54287380-54287425	NM_008286:-95	Hrh2	PROMOTER	1.521	2.939	1503.11	4418.07	4.470	943.46	4217.09
A_68_P25837693	chr8:47826718-47826762	NM_008391:1642	Irf2	INSIDE	1.521	3.072	367.43	1128.61	4.671	336.01	1569.53
A_68_P27512349	chr10:122513403-122513447	NM_001163024:137	Mon2	INSIDE	1.521	3.284	2131.92	7000.31	4.995	1977.70	9878.64
A_68_P22616951	chr3:146475944-146475988	NM_011100:-56	Prkacb	PROMOTER	1.521	2.762	2101.38	5803.43	4.202	1851.47	7779.21
A_68_P26138372	chr8:108734689-108734733	NM_001007567:123	Slc7a6os	INSIDE	1.521	2.938	1210.21	3555.44	4.469	1091.81	4879.33
A_68_P30255510	chr15:59479785-59479829	NM_144549:-402	Trib1	PROMOTER	1.521	2.815	1344.26	3784.38	4.282	1178.22	5044.74
A_68_P28185441	chr11:120442461-120442505	NM_133796:452	Arhgdia	INSIDE	1.520	1.757	2949.75	5183.66	2.671	2275.76	6078.96
A_68_P22288626	chr3:83844024-83844068	NM_172681:37	D930015E06Rik	INSIDE	1.520	3.459	496.73	1718.18	5.259	409.31	2152.57
A_68_P21819501	chr2:164571271-164571315	NM_133763:-222	Dnttip1	DIVERGENT_PROMOTER	1.520	2.327	7413.05	17246.82	3.535	5386.08	19041.21
A_68_P21556816	chr2:117075560-117075604	NM_026620:108	Fam98b	INSIDE	1.520	2.828	1580.47	4470.05	4.299	1399.84	6017.61
A_68_P25261383	chr7:86640870-86640922	NR_029818:-9253	Mir9-3	PROMOTER	1.520	4.997	818.01	4087.90	7.595	655.17	4976.12
A_68_P29228002	chr13:93962021-93962065	NM_133905:196	Papd4	INSIDE	1.520	4.177	1394.45	5824.97	6.349	1073.14	6813.49
A_68_P27898394	chr11:69810400-69810444	NM_030064:1150	Phf23	INSIDE	1.520	2.800	6398.65	17918.06	4.255	4222.08	17965.36
A_68_P26135404	chr8:108218075-108218119	NM_001033320:3291	Rltpr	INSIDE	1.520	1.873	10467.60	19607.79	2.848	8262.30	23530.51

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28938196	chr13:34436655-34436699	NM_001033167:375	Slc22a23	INSIDE	1.520	1.966	319.47	628.20	2.988	317.30	948.12
A_68_P23416421	chr4:151460684-151460728	ENSMUST00000118648:-260		PROMOTER	1.520	7.398	551.53	4080.29	11.246	515.12	5792.83
A_68_P23345840	chr4:138010011-138010055	NM_025451:-1030	Camk2n1	PROMOTER	1.519	2.325	1032.72	2401.05	3.531	867.53	3063.29
A_68_P26127993	chr8:106865035-106865079	NM_024217:563	Cmtm3	INSIDE	1.519	1.997	1888.06	3770.79	3.034	1463.37	4439.83
A_68_P23299954	chr4:129724880-129724924	NM_028266:-181	Col16a1	PROMOTER	1.519	3.754	598.62	2247.47	5.703	528.13	3011.74
A_68_P23318268	chr4:133130953-133130997	NM_172876:315	Gpatch3	INSIDE	1.519	3.239	1150.61	3726.47	4.921	1036.16	5098.82
A_68_P25301151	chr7:95278746-95278790	NM_001081414:546091	Grm5	INSIDE	1.519	2.111	1277.37	2695.95	3.206	1012.31	3245.16
A_68_P27995147	chr11:87430388-87430432	NM_001045527:-255	Hsf5	PROMOTER	1.519	4.025	862.35	3470.63	6.115	735.11	4494.96
A_68_P22397067	chr3:105255865-105255909	NM_019931:-5847	Kcnd3	PROMOTER	1.519	2.065	1408.52	2909.25	3.138	1170.27	3672.79
A_68_P25092719	chr7:52625927-52625971	NM_011698:-14	Lin7b	PROMOTER	1.519	2.163	3110.79	6728.46	3.285	2368.96	7782.17
A_68_P26949005	chr10:12810608-12810652	NM_009538:37	Plagl1	INSIDE	1.519	8.094	996.87	8068.42	12.295	851.53	10469.14
A_68_P25672219	chr8:14090321-14090365	NM_001034862:-15	Erich1	DIVERGENT_PROMOTER	1.518	2.067	1232.12	2546.24	3.138	955.63	2998.66
A_68_P28089851	chr11:104093898-104093942	NM_001038609:1171	Mapt	INSIDE	1.518	3.201	2664.13	8526.89	4.858	2303.11	11189.67
A_68_P28445674	chr12:55169509-55169553	NM_013780:819867	Npas3	INSIDE	1.518	3.022	1322.00	3995.28	4.587	1122.49	5148.47
A_68_P24114435	chr5:135518130-135518174	NM_016801:18711	Stx1a	INSIDE	1.518	10.296	11814.23	121639.30	15.628	7533.59	117737.10
A_68_P24151265	chr5:142843572-142843616			Unknown	1.518	1.665	1769.80	2946.27	2.527	1501.31	3794.47
A_68_P24182785	chr5:149826986-149827030	ENSMUST00000133243:381		INSIDE	1.518	3.325	7588.27	25228.93	5.047	4600.37	23216.64
A_68_P30357863	chr15:77950040-77950084	NM_007583:-352	Cacng2	PROMOTER	1.517	2.852	1563.96	4460.78	4.328	1372.23	5939.16
A_68_P21122760	chr2:33496334-33496378	NM_010725:-325	Lmx1b	PROMOTER	1.517	2.550	1335.58	3406.27	3.870	1103.55	4270.81
A_68_P24337493	chr6:31348815-31348859	NM_013791:9	Mkln1	INSIDE	1.517	7.206	1344.21	9686.86	10.934	1148.97	12562.71
A_68_P31759277	chr18:61867112-61867156	NM_172832:155	Pcyox1l	INSIDE	1.517	2.206	3676.05	8109.10	3.347	2825.32	9456.43
A_68_P27896916	chr11:69572824-69572871	NM_009089:-1122	Polr2a	PROMOTER	1.517	1.649	653.89	1078.34	2.502	517.68	1295.20
A_68_P29648697	chr14:61791606-61791650	NM_172809:34335	Sacs	INSIDE	1.517	1.545	1833.51	2833.14	2.345	1362.27	3193.90
A_68_P29033511	chr13:51746883-51746927	NM_029279:-178	Secisbp2	PROMOTER	1.517	2.454	3102.77	7613.38	3.723	2647.15	9854.78
A_68_P29218723	chr13:91600897-91600941	NM_024186:217	Ssbp2	INSIDE	1.517	4.122	4099.33	16896.23	6.251	3046.95	19047.37
A_68_P27187531	chr10:62188832-62188876	NM_001033260:-7	Stox1	PROMOTER	1.517	3.109	1793.62	5576.70	4.717	1443.07	6807.33
A_68_P29244723	chr13:96902535-96902579	NM_029210:-24	Sv2c	PROMOTER	1.517	1.877	1202.09	2255.91	2.847	970.77	2764.28
A_68_P28520555	chr12:71554358-71554402	NM_028339:240	Tmx1	INSIDE	1.517	1.462	1187.01	1735.79	2.218	1077.70	2390.47
A_68_P22321608	chr3:89577074-89577118	NM_027315:-434	Ube2q1	DIVERGENT_PROMOTER	1.517	1.749	2102.20	3677.00	2.653	1641.16	4353.86
A_68_P26350328	A_68_P26350328			Unknown	1.517	2.943	449.87	1324.02	4.464	345.01	1540.05
A_68_P27288853	chr10:80783632-80783676	NM_027381:-193	2510012J08Rik	PROMOTER	1.516	1.546	1103.03	1705.68	2.344	891.15	2088.80
A_68_P23467742	chr5:8368117-8368161	NM_001098225:-57	Adam22	PROMOTER	1.516	2.463	690.62	1701.06	3.735	631.65	2359.29
A_68_P30350779	chr15:76647508-76647552	NM_001168288:1070	Arhgap39	INSIDE	1.516	2.606	1450.37	3779.73	3.952	1090.58	4309.65
A_68_P29338038	chr13:113778161-113778205	NM_001081062:173	Ccno	INSIDE	1.516	1.461	3379.73	4937.96	2.215	2794.94	6190.79
A_68_P31376862	chr17:79755142-79755186	NM_026514:-733	Cdc42ep3	PROMOTER	1.516	1.712	474.69	812.66	2.596	415.37	1078.28
A_68_P27910787	chr11:72128038-72128082	NM_001099688:115	Fbxo39	INSIDE	1.516	3.848	1223.64	4709.14	5.834	1038.74	6060.44
A_68_P30148791	chr15:38229661-38229705	NM_013692:780	Klf10	INSIDE	1.516	5.717	1731.12	9896.19	8.669	1387.82	12030.48
A_68_P23539922	chr5:23606508-23606552	NM_001161800:123	Klhl7	INSIDE	1.516	1.684	880.42	1482.98	2.553	695.55	1775.95
A_68_P25086960	chr7:51607818-51607862	NM_001034115:42207	Shank1	INSIDE	1.516	5.044	7768.35	39184.21	7.649	5667.39	43348.23
A_68_P28635993	chr12:92886575-92886620	NM_175367:138279	Ston2	INSIDE	1.516	2.163	294.02	636.00	3.280	230.66	756.53
A_68_P30980679	chr16:94534837-94534881	ENSMUST00000163193:312		INSIDE	1.516	4.109	565.54	2323.63	6.228	554.91	3456.16
A_68_P31126996	chr17:29406043-29406087	NM_030561:332	BC004004	INSIDE	1.515	3.081	2100.11	6469.43	4.666	1938.91	9046.55
A_68_P28694110	chr12:104116592-104116636	NM_172806:2	Btbd7	INSIDE	1.515	1.901	366.82	697.42	2.881	341.52	984.04
A_68_P27784449	chr11:49525483-49525527	NM_212484:708	Cnot6	INSIDE	1.515	4.727	1217.49	5755.20	7.160	1081.63	7744.99
A_68_P26128587	chr8:106966661-106966705	NM_001013380:265	Dync1li2	INSIDE	1.515	3.010	3069.91	9241.24	4.561	2459.41	11216.76
A_68_P26001982	chr8:83403879-83403923	NM_021356:478	Gab1	INSIDE	1.515	4.546	3277.91	14899.97	6.888	2505.41	17257.68
A_68_P25274814	chr7:89079181-89079225	NM_013886:143	Hdgfrp3	INSIDE	1.515	3.405	2741.20	9335.16	5.161	2297.83	11858.66
A_68_P30639681	chr16:30070804-30070848	NM_008235:5384	Hes1	DOWNSTREAM	1.515	1.520	4721.65	7178.51	2.303	3831.89	8826.15
A_68_P25528895	chr7:138685558-138685602	NM_008257:-896	Hmx3	PROMOTER	1.515	2.685	721.58	1937.75	4.069	630.15	2564.25
A_68_P28886522	chr13:24373081-24373125	NM_026825:-443	Lrrc16a	PROMOTER	1.515	5.019	1735.70	8711.35	7.604	1462.36	11119.99
A_68_P24792500	chr6:119280593-119280637	NM_001172207:-1392	Lrtm2	PROMOTER	1.515	2.033	2029.62	4125.92	3.080	1634.56	5034.32

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P30020394	chr15:12134922-12134966	NM_172958:96	Mtmr12	INSIDE	1.515	2.637	924.58	2437.87	3.993	797.05	3182.95
A_68_P30139527	chr15:36538715-36538759	NM_008774:-8	Pabpc1	PROMOTER	1.515	1.917	3127.60	5996.12	2.904	2496.02	7248.76
A_68_P22355467	chr3:97462102-97462146	NM_182997:-10	Prkab2	PROMOTER	1.515	4.803	8266.35	39707.11	7.277	6308.41	45903.36
A_68_P26229674	chr8:124431610-124431654	NM_011404:-46	Slc7a5	DIVERGENT_PROMOTER	1.515	2.080	3412.27	7097.53	3.152	2669.32	8414.32
A_68_P31351023	chr17:74738587-74738631	NM_001162870:282	Spast	INSIDE	1.515	3.242	614.24	1991.24	4.912	530.71	2606.66
A_68_P28161643	chr11:116713965-116714009	NM_011358:422	Srsf2	INSIDE	1.515	2.553	535.98	1368.48	3.867	467.60	1808.41
A_68_P20935551	chr1:192803342-192803386	NR_027352:-189	Vash2	PROMOTER	1.515	2.830	1064.05	3011.52	4.287	847.11	3631.88
A_68_P32186048	chr19:54119950-54119994	NM_007417:301	Adra2a	INSIDE	1.514	1.870	1207.84	2258.19	2.830	1019.30	2884.49
A_68_P31524834	chr18:16965463-16965507	NM_007664:2074	Cdh2	INSIDE	1.514	1.442	5317.30	7667.13	2.183	4181.25	9127.82
A_68_P23222243	chr4:114580052-114580096	NM_008593:1429	Foxd2	INSIDE	1.514	3.361	1114.32	3744.93	5.088	999.09	5082.91
A_68_P27980051	chr11:84683596-84683640	NM_153144:622	Ggnbp2	INSIDE	1.514	2.029	3310.52	6716.55	3.072	2466.36	7576.01
A_68_P27977954	chr11:84333936-84333980	NM_008498:5078	Lhx1	INSIDE	1.514	2.640	571.16	1507.89	3.996	476.27	1903.32
A_68_P22601440	chr3:143867896-143867940	NM_001161769:-2558	Lmo4	PROMOTER	1.514	3.237	4765.00	15423.48	4.901	3566.87	17481.44
A_68_P24156969	chr5:144288624-144288668	NM_009007:215	Rac1	INSIDE	1.514	2.574	1631.45	4199.18	3.897	1284.55	5006.06
A_68_P31943158	chr19:8788397-8788441	NM_008577:-31	Slc3a2	PROMOTER	1.514	3.055	1784.84	5452.80	4.624	1356.57	6272.64
A_68_P25239159	chr7:82453955-82453999	NM_001109753:-704	Sv2b	PROMOTER	1.514	4.067	2346.69	9543.51	6.158	1944.04	11971.56
A_68_P23397204	chr4:148265329-148265373	NM_027195:86850	Casz1	INSIDE	1.513	1.413	1598.88	2258.72	2.138	1270.07	2715.47
A_68_P25392270	chr7:112574421-112574465	NM_007627:109	Cckbr	INSIDE	1.513	3.964	6148.54	24371.44	5.996	5077.69	30446.86
A_68_P31490815	chr18:10609631-10609677	NM_001081222:696	Esco1	INSIDE	1.513	2.126	827.03	1758.24	3.216	726.99	2338.32
A_68_P24620367	chr6:88149612-88149656	NM_008090:977	Gata2	INSIDE	1.513	1.864	2081.20	3879.08	2.820	1736.45	4897.60
A_68_P26220480	chr8:123011650-123011694	NM_198671:-1093	Gse1	PROMOTER	1.513	2.779	968.75	2692.41	4.206	807.18	3395.13
A_68_P21038125	chr2:17987169-17987213	NM_010804:10293	Mllt10	INSIDE	1.513	2.283	1455.18	3322.77	3.454	1218.79	4209.49
A_68_P30560744	chr16:14163261-14163305	NM_001114085:-85	Nde1	PROMOTER	1.513	1.741	1004.83	1749.37	2.633	774.54	2039.73
A_68_P31084402	chr17:21082837-21082881	NM_016891:441	Ppp2r1a	INSIDE	1.513	1.991	424.01	844.09	3.012	391.52	1179.10
A_68_P24445013	chr6:51542631-51542675	NM_001127348:48131	Snx10	DOWNSTREAM	1.513	1.619	5835.38	9446.43	2.449	4234.39	10370.79
A_68_P30401894	chr15:85456416-85456460			Unknown	1.513	4.687	777.98	3646.20	7.091	665.73	4720.50
A_68_P23699554	chr5:53658257-53658301	NM_001145433:-66	1810013D10Rik	PROMOTER	1.512	1.927	1747.30	3367.67	2.914	1494.68	4355.06
A_68_P24799551	chr6:120615439-120615483	NM_001128151:-978	Cecr2	PROMOTER	1.512	2.599	2655.71	6901.62	3.928	2199.66	8641.34
A_68_P32769550	chrX:154480805-154480849	NM_177751:216	Cnksr2	INSIDE	1.512	2.146	1326.45	2845.95	3.244	822.04	2667.04
A_68_P23309923	chr4:131604805-131604849	NM_001128606:167	Epb4.1	INSIDE	1.512	5.819	1030.57	5996.78	8.796	869.44	7647.47
A_68_P23345562	chr4:137952020-137952064	NM_001081672:331	Fam43b	INSIDE	1.512	2.773	891.39	2472.07	4.193	757.52	3175.97
A_68_P26221250	chr8:123112916-123112960	NM_178856:37	Gins2	INSIDE	1.512	1.444	2567.51	3706.97	2.182	2080.94	4541.31
A_68_P24947962	chr7:4098539-4098584	NM_172736:9904	Leng8	INSIDE	1.512	4.325	1465.62	6339.23	6.541	1229.91	8045.26
A_68_P28162003	chr11:116780529-116780573	NM_172948:374	Mgat5b	INSIDE	1.512	1.990	423.87	843.57	3.008	438.90	1320.33
A_68_P31207975	chr17:46766402-46766446	NM_175168:29	Ptk7	INSIDE	1.512	2.633	12220.97	32171.92	3.980	10248.26	40791.04
A_68_P32234202	chrX:5977172-5977216	NM_001040459:-68	Shroom4	PROMOTER	1.512	2.645	1691.44	4473.07	3.997	1083.40	4330.82
A_68_P23568207	chr5:29896110-29896154	NM_133907:351	Ube3c	INSIDE	1.512	2.739	1584.16	4339.25	4.140	1228.08	5084.59
A_68_P25034247	chr7:31740799-31740843	NM_011680:1002	Usf2	INSIDE	1.512	2.427	822.98	1997.11	3.670	742.19	2723.71
A_68_P32152243	chr19:47911627-47911671	NM_027559:203	Wdr96	INSIDE	1.512	1.971	1964.46	3872.11	2.981	1536.97	4581.51
A_68_P25364270	chr7:107007573-107007617	NM_001164258:-133	Xrra1	DIVERGENT_PROMOTER	1.512	3.183	829.70	2640.68	4.811	747.86	3598.25
A_68_P23820887	chr5:77738314-77738358	NM_019836:775	2610024G14Rik	INSIDE	1.511	2.988	773.65	2311.49	4.515	651.71	2942.33
A_68_P30931894	chr16:85900162-85900206	NM_011782:1186	Adamts5	INSIDE	1.511	4.290	1821.56	7814.98	6.483	1287.00	8343.12
A_68_P24138663	chr5:140449111-140449155	NM_175522:65236	Elfn1	INSIDE	1.511	1.973	1056.98	2085.69	2.981	1263.29	3766.04
A_68_P31382195	chr17:80689441-80689485	NM_194269:-89	Morn2	PROMOTER	1.511	5.017	1251.41	6278.01	7.579	1032.08	7821.99
A_68_P26016101	chr8:86222687-86222731	NM_001199593:-4748	Pkn1	PROMOTER	1.511	2.520	992.70	2501.25	3.806	882.85	3360.44
A_68_P25553143	chr7:142729512-142729556	NM_011212:28	Ptpre	INSIDE	1.511	3.674	958.74	3522.72	5.553	802.21	4454.28
A_68_P22715106	chr4:8463176-8463220	NM_021518:408	Rab2a	INSIDE	1.511	2.557	1306.31	3340.23	3.864	1128.70	4361.49
A_68_P24328146	chr6:29685667-29685711	NM_176996:192	Smo	INSIDE	1.511	4.847	1094.66	5305.59	7.325	874.54	6405.71
A_68_P23696773	chr5:53174399-53174443	NM_030185:115	Zcchc4	INSIDE	1.511	2.632	2596.84	6834.23	3.977	2118.43	8424.77
A_68_P24004682	chr5:115017652-115017696	NM_001004180:-585	BC057022	PROMOTER	1.510	2.639	1484.21	3916.52	3.985	1255.60	5003.35
A_68_P20872965	chr1:181889796-181889840	NM_001033285:-1401	Cdc42bpa	PROMOTER	1.510	1.895	2361.56	4474.53	2.861	1933.91	5532.09

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P20885892	chr1:184212460-184212504	NM_007853:408	Degs1	INSIDE	1.510	1.720	462.28	795.14	2.597	412.83	1072.19
A_68_P26132767	chr8:107813885-107813929	NM_177788:6092	Exoc3l	INSIDE	1.510	1.383	3404.14	4707.23	2.088	2623.45	5478.57
A_68_P26220858	chr8:123061951-123061995	NM_001145896:664	Gse1	INSIDE	1.510	3.980	1269.37	5052.43	6.011	964.46	5796.91
A_68_P31259625	chr17:57161925-57161969	NM_010613:8984	Khsrp	INSIDE	1.510	2.764	4307.69	11905.11	4.173	3401.95	14196.21
A_68_P24520694	chr6:67217359-67217403	NM_001113564:408	Serbp1	INSIDE	1.510	1.793	659.14	1181.96	2.707	523.12	1416.16
A_68_P23283131	chr4:126698502-126698546	NM_023603:-20	Sfpq	PROMOTER	1.510	10.628	252.76	2686.37	16.045	227.79	3654.84
A_68_P26540094	chr9:56924177-56924221	NM_001110350:16	Sin3a	INSIDE	1.510	1.692	1975.15	3341.37	2.555	1590.03	4062.80
A_68_P21748558	chr2:152119855-152119899	NM_024196:269	Tbc1d20	INSIDE	1.510	3.767	2842.08	10706.49	5.687	2383.82	13556.14
A_68_P25947840	chr8:72273755-72273799	NM_001200023:85	Zfp963	INSIDE	1.510	2.939	4922.90	14468.46	4.439	3866.13	17161.24
A_68_P21070248	chr2:25023708-25023752			Unknown	1.510	1.986	1032.55	2050.38	2.999	889.93	2668.77
A_68_P23062804	chr4:83171213-83171257	NM_001081012:-214	4930473A06Rik	PROMOTER	1.509	2.827	912.04	2578.63	4.268	849.60	3625.74
A_68_P27932872	chr11:76384849-76384893	NM_198895:6	Abr	INSIDE	1.509	1.675	3476.87	5823.44	2.528	2873.42	7262.84
A_68_P27176099	chr10:60150136-60150180	NM_023370:9080	Cdh23	INSIDE	1.509	2.178	935.31	2037.03	3.287	895.72	2944.61
A_68_P26102842	chr8:101939617-101939661	NM_001039154:719	Cdh8	INSIDE	1.509	4.432	1458.56	6464.77	6.686	1284.16	8586.35
A_68_P32070425	chr19:32560187-32560231	NM_010799:-50	Minpp1	PROMOTER	1.509	2.151	1498.34	3223.34	3.247	1254.33	4072.98
A_68_P25954894	chr8:73437692-73437736	NM_173013:7842	Mtap1s	INSIDE	1.509	2.762	422.18	1166.14	4.169	350.12	1459.49
A_68_P27168073	chr10:58785999-58786043	NM_011030:-23	P4ha1	PROMOTER	1.509	2.524	683.06	1724.28	3.809	537.46	2046.99
A_68_P28035927	chr11:94853399-94853443	NM_172261:895	Ppp1r9b	INSIDE	1.509	4.641	494.07	2292.84	7.001	468.52	3280.20
A_68_P31612299	chr18:34490607-34490651	NM_025527:-170	Srp19	PROMOTER	1.509	2.820	1687.65	4759.55	4.255	1369.71	5827.73
A_68_P20634933	chr1:136605811-136605855	NM_009307:62575	Syt2	INSIDE	1.509	2.023	1859.43	3762.50	3.053	1570.85	4795.85
A_68_P28871497	chr13:21271956-21272000	NM_009054:151	Trim27	INSIDE	1.509	1.526	771.34	1177.15	2.304	742.76	1710.95
A_68_P27287631	chr10:80600637-80600681	NM_010731:1643	Zbtb7a	INSIDE	1.509	2.562	2040.84	5227.85	3.864	1790.23	6917.92
A_68_P27914868	chr11:72861634-72861678	NM_025818:288	1200014J11Rik	INSIDE	1.508	2.998	3522.26	10560.49	4.520	2793.53	12627.23
A_68_P21419477	chr2:90729763-90729807	NM_026161:3842	C1qtnf4	INSIDE	1.508	2.241	777.41	1742.33	3.381	697.75	2358.80
A_68_P24757354	chr6:113026958-113027002	NR_027010:258	Gt(ROSA)26Sor	INSIDE	1.508	2.265	1639.14	3713.15	3.417	1379.95	4714.75
A_68_P27189032	chr10:62486795-62486839	NM_001079824:-219	Hnrnph3	DIVERGENT_PROMOTER	1.508	2.966	1117.74	3315.50	4.472	978.50	4376.19
A_68_P30925479	chr16:84774664-84774708	NM_023844:319	Jam2	INSIDE	1.508	3.443	838.56	2887.49	5.193	795.58	4131.20
A_68_P31251161	chr17:55585081-55585126	NM_172829:89	St6gal2	INSIDE	1.508	1.632	618.68	1009.67	2.461	567.75	1397.19
A_68_P26626137	chr9:71959791-71959835	NM_011544:-186	Tcf12	PROMOTER	1.508	4.049	2317.19	9381.37	6.106	2028.59	12386.53
A_68_P22630580	chr3:148653297-148653341	ENSMUST00000098518:-1038		PROMOTER	1.508	1.703	1888.29	3215.15	2.567	1552.98	3987.28
A_68_P27169799	chr10:59079055-59079099	NM_001033259:364	Ccdc109a	INSIDE	1.507	1.574	2053.34	3232.15	2.371	1593.85	3779.80
A_68_P31890103	chr18:84855123-84855167	NM_023149:-119	Cndp2	PROMOTER	1.507	2.250	7270.70	16356.27	3.391	5158.92	17494.56
A_68_P26542219	chr9:57369547-57369591	NM_007747:530	Cox5a	INSIDE	1.507	1.737	1447.75	2514.73	2.617	1202.89	3148.03
A_68_P31677413	chr18:46685542-46685586	NM_173423:61	Fem1c	INSIDE	1.507	1.993	1402.64	2795.91	3.005	1532.05	4603.56
A_68_P20184678	chr1:42755116-42755160	NM_008900:1148	Pou3f3	INSIDE	1.507	3.857	1035.60	3994.36	5.813	842.84	4899.23
A_68_P20632910	chr1:136241239-136241283	NM_001042485:17316	Tmem183a	DOWNSTREAM	1.507	1.589	1960.62	3116.15	2.395	1775.76	4253.73
A_68_P21094978	chr2:28910349-28910393	NM_001166705:216	1700101E01Rik	INSIDE	1.506	1.659	1643.86	2726.81	2.498	1408.24	3517.32
A_68_P26486127	chr9:47339193-47339237	NM_001025600:780	Cadm1	INSIDE	1.506	2.674	550.83	1472.74	4.026	421.57	1697.37
A_68_P29856055	chr14:102039383-102039427	NM_001033132:284	Commd6	INSIDE	1.506	3.406	2079.90	7084.80	5.129	1713.73	8790.10
A_68_P23415959	chr4:151383528-151383572	NM_001033352:551	Klhl21	INSIDE	1.506	1.829	351.42	642.62	2.754	315.28	868.14
A_68_P20352133	chr1:75121786-75121830	NM_029342:-8	Nhej1	PROMOTER	1.506	3.573	3084.75	11022.24	5.382	2114.11	11378.24
A_68_P21820253	chr2:164705104-164705148	NM_146129:259	Pcif1	INSIDE	1.506	2.676	1462.77	3914.74	4.030	1325.28	5340.69
A_68_P27288650	chr10:80755715-80755759	NM_001146687:20	Pip5k1c	INSIDE	1.506	2.439	1510.25	3683.36	3.672	1267.97	4656.54
A_68_P26596131	chr9:66794074-66794118	NM_026467:172	Rps27l	INSIDE	1.506	2.303	551.36	1269.99	3.468	380.12	1318.23
A_68_P25351157	chr7:104729030-104729074	NM_001081267:647	Rsf1	INSIDE	1.506	2.725	802.51	2186.66	4.104	732.60	3006.58
A_68_P25592703	chr7:149246867-149246911	NM_028308:51	2700078K21Rik	INSIDE	1.505	3.078	809.83	2492.47	4.632	861.56	3990.66
A_68_P30587610	chr16:20425965-20426009	NM_013790:481	Abcc5	INSIDE	1.505	2.189	1643.18	3597.22	3.294	1348.96	4443.74
A_68_P20231550	chr1:53409540-53409584	NM_133728:-19	Asnsd1	PROMOTER	1.505	3.087	1517.71	4684.89	4.647	1377.76	6402.13
A_68_P30333008	chr15:73670325-73670369	NM_001033365:-245	Gm628	PROMOTER	1.505	1.455	862.56	1255.19	2.189	759.49	1662.90
A_68_P25525511	chr7:138079707-138079751	NM_019564:12	Htra1	INSIDE	1.505	1.501	3874.53	5817.41	2.260	3128.33	7070.53
A_68_P28060084	chr11:98902871-98902915	NM_010517:319	Igfbp4	INSIDE	1.505	1.812	1193.02	2161.77	2.726	1051.81	2867.48

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P29616407	chr14:55733626-55733670	NM_177049:2124	Jph4	INSIDE	1.505	3.567	6810.59	24294.32	5.368	4485.51	24077.71
A_68_P30984747	chr16:95219135-95219179	NM_001025584:147	Kcnj6	INSIDE	1.505	6.088	1997.49	12160.32	9.160	1688.40	15466.36
A_68_P26068285	chr8:95379185-95379229	NM_173014:-42	Lpcat2	PROMOTER	1.505	6.893	3200.62	22061.99	10.374	2288.30	23738.41
A_68_P27891735	chr11:68666059-68666103	NM_023668:553	Ndel1	INSIDE	1.505	1.532	1208.31	1851.00	2.306	966.35	2228.04
A_68_P31323668	chr17:69733260-69733304	NM_009547:-35	Zfp161	PROMOTER	1.505	4.474	2569.08	11495.08	6.736	2114.62	14243.16
A_68_P32288519	chrX:20002775-20002819	ENSMUST00000115384:-17		PROMOTER	1.505	2.230	1112.18	2480.71	3.356	672.13	2255.95
A_68_P30345268	chr15:75812328-75812373	NM_001163518:365	2410075B13Rik	INSIDE	1.504	2.082	651.05	1355.76	3.133	588.82	1844.67
A_68_P32443538	chrX:66613886-66613930	NM_008032:403	Aff2	INSIDE	1.504	1.550	1876.72	2909.56	2.332	929.04	2166.58
A_68_P32576287	chrX:101396366-101396410	NM_001077354:68	C77370	INSIDE	1.504	4.104	553.75	2272.55	6.172	442.53	2731.40
A_68_P27813685	chr11:54911498-54911542	NM_010299:34	Gm2a	INSIDE	1.504	4.655	2755.36	12826.30	7.003	2025.41	14183.33
A_68_P27127187	chr10:49502783-49502839	NM_001111268:5750	Grik2	INSIDE	1.504	2.794	331.81	927.16	4.203	255.99	1075.91
A_68_P28152414	chr11:115126813-115126857	NM_010350:1723	Grin2c	INSIDE	1.504	1.820	7588.84	13811.37	2.738	5649.71	15466.21
A_68_P25971363	chr8:77517838-77517882	NM_178017:259	Hmgxb4	INSIDE	1.504	3.776	1144.27	4320.45	5.679	1081.27	6140.09
A_68_P29071664	chr13:58228883-58228927	NM_029872:1013	Hnrnpa0	INSIDE	1.504	3.383	2280.21	7714.19	5.090	1800.45	9163.93
A_68_P20646088	chr1:138363089-138363133	NM_001081258:-1424	Kif14	PROMOTER	1.504	5.511	2003.58	11041.10	8.290	1645.78	13643.44
A_68_P25922763	chr8:66684161-66684205	NM_009390:608	Tll1	INSIDE	1.504	2.938	650.04	1910.15	4.418	499.30	2205.96
A_68_P30593950	chr16:21694881-21694925	NM_001001881:-164	2510009E07Rik	PROMOTER	1.503	0.434	1506.73	654.64	0.653	1233.71	805.79
A_68_P26569977	chr9:62192249-62192293	NM_009672:3121	Anp32a	INSIDE	1.503	1.406	1688.30	2373.21	2.113	1514.34	3199.71
A_68_P27643047	chr11:22758992-22759036	NM_016888:721	B3gnt2	INSIDE	1.503	2.345	1392.02	3264.16	3.524	1171.12	4127.43
A_68_P21646236	chr2:133380456-133380500	NM_007553:1544	Bmp2	INSIDE	1.503	3.428	1928.92	6612.98	5.151	1538.58	7925.62
A_68_P20778063	chr1:164407783-164407827	NM_001038619:357	Dnm3	INSIDE	1.503	2.197	2396.10	5263.29	3.302	1800.71	5945.11
A_68_P23300612	chr4:129816147-129816191	NM_001163027:-373	Hcrtr1	PROMOTER	1.503	1.713	3407.08	5835.44	2.575	2819.48	7260.01
A_68_P28518531	chr12:71213190-71213234	NM_008697:-300	Nin	PROMOTER	1.503	3.023	1996.26	6034.16	4.544	1812.79	8237.10
A_68_P27287763	chr10:80617060-80617104	NM_021501:13383	Pias4	INSIDE	1.503	3.958	1158.08	4583.60	5.950	877.19	5219.09
A_68_P28566640	chr12:80013209-80013253	NM_013738:-5305	Plek2	PROMOTER	1.503	1.504	2873.07	4322.23	2.261	2125.31	4805.89
A_68_P21745020	chr2:151457975-151458019	NM_198214:273	Snph	INSIDE	1.503	4.184	431.24	1804.12	6.287	374.44	2354.14
A_68_P25777211	chr8:36028290-36028334	NM_175091:432	Tnks	INSIDE	1.503	3.928	823.33	3233.88	5.903	639.69	3775.94
A_68_P21936419	chr3:9251754-9251798	NM_177660:1210	Zbtb10	INSIDE	1.503	2.892	5521.23	15969.96	4.346	4422.08	19220.12
A_68_P22880598	chr4:45025167-45025211	NM_001163283:96	Zbtb5	INSIDE	1.503	4.230	645.60	2730.70	6.358	540.93	3439.40
A_68_P26218677	chr8:122752875-122752919	ENSMUST00000127664:318156		INSIDE	1.503	7.820	1854.22	14499.10	11.750	1420.25	16687.41
A_68_P24135766	chr5:139936328-139936372	NM_028469:138	3110082I17Rik	INSIDE	1.502	1.936	4745.40	9185.42	2.908	3667.44	10663.21
A_68_P30599077	chr16:22657267-22657311	NM_138650:16	Dgkg	INSIDE	1.502	1.609	1659.05	2669.27	2.416	1302.66	3147.24
A_68_P28553818	chr12:77505144-77505188	NM_008301:-190	Hspa2	PROMOTER	1.502	3.614	2028.44	7330.59	5.430	1623.90	8817.36
A_68_P28036074	chr11:94871790-94871834	NM_146025:620	Samd14	INSIDE	1.502	2.501	2221.81	5557.73	3.757	1714.51	6441.51
A_68_P31931517	chr19:5894108-5894152	NM_198634:-23	Tigd3	PROMOTER	1.502	1.820	1100.87	2003.78	2.734	879.37	2403.95
A_68_P30255512	chr15:59479961-59480005	NM_144549:-226	Trib1	PROMOTER	1.502	2.370	2851.21	6758.58	3.560	2415.27	8599.13
A_68_P28931383	chr13:32894479-32894523	NM_030215:602	Wrnip1	INSIDE	1.502	3.982	1699.99	6769.26	5.980	1708.82	10218.32
A_68_P29063253	chr13:56854488-56854532	AK131829:678		INSIDE	1.502	4.787	2312.37	11068.22	7.188	1936.18	13917.98
A_68_P21094081	chr2:28764046-28764090	NM_019446:7873	Barhl1	INSIDE	1.501	2.176	1638.99	3567.19	3.267	1373.26	4487.10
A_68_P27476525	chr10:116018687-116018731	NM_001037846:-141	Cnot2	PROMOTER	1.501	2.634	907.22	2389.64	3.952	776.04	3067.27
A_68_P21202301	chr2:49307033-49307077	NM_172663:49	Epc2	INSIDE	1.501	2.387	1763.84	4209.42	3.583	1485.53	5322.72
A_68_P23525900	chr5:20931065-20931109	NM_177869:366	Fam185a	INSIDE	1.501	1.522	1176.74	1790.95	2.284	1000.93	2286.17
A_68_P23295046	chr4:128798355-128798400	NM_010471:158	Hpca	INSIDE	1.501	5.295	891.80	4722.32	7.947	799.18	6350.88
A_68_P27927426	chr11:75469605-75469649	NM_001080775:110	Myo1c	INSIDE	1.501	3.042	780.85	2375.39	4.567	661.02	3019.16
A_68_P27678665	chr11:30167644-30167688	ENSMUST00000146985:203		INSIDE	1.501	7.255	3141.26	22790.57	10.889	2975.88	32405.32
A_68_P22148834	chr3:54437446-54437490	ENSMUST00000172420:2108		INSIDE	1.501	4.213	925.25	3898.13	6.324	727.00	4597.46
A_68_P20584830	chr1:127331799-127331843	NM_001205385:484	Actr3	INSIDE	1.500	2.916	7966.52	23227.85	4.375	6005.45	26271.98
A_68_P23447646	chr5:3928274-3928318	NM_194462:111	Akap9	INSIDE	1.500	2.272	1022.53	2322.79	3.408	789.77	2691.39
A_68_P24186507	chr5:150480724-150480768	NM_001081204:-85	B3galtl	PROMOTER	1.500	1.836	485.61	891.45	2.753	476.66	1312.40
A_68_P31097616	chr17:24625344-24625388	NM_027937:-361	Caskin1	DIVERGENT_PROMOTER	1.500	1.672	796.20	1330.91	2.508	669.03	1677.63
A_68_P23571444	chr5:30559486-30559531	NM_027652:351	Ept1	INSIDE	1.500	1.791	1159.99	2077.24	2.686	1065.22	2860.95

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P32823846	chrX:166435801-166435845	NM_183151:118269	Mid1	DOWNSTREAM	1.500	1.929	3218.86	6210.66	2.895	3388.99	9809.69
A_68_P21152640	chr2:39046217-39046261	NM_178778:12	Scai	INSIDE	1.500	2.913	813.18	2369.11	4.370	698.70	3053.46
A_68_P24141204	chr5:140865179-140865223	NM_172277:1	Snx8	INSIDE	1.500	1.386	1327.27	1839.93	2.079	1159.03	2409.47
A_68_P27835858	chr11:59077515-59077559	NM_009522:26717	Wnt3a	INSIDE	1.500	2.344	2131.54	4997.33	3.518	1898.80	6679.52
A_68_P26350251	chr9:21860554-21860598	NM_177318:15213	Zfp653	INSIDE	1.500	2.831	1323.23	3746.33	4.247	1055.78	4483.80
A_68_P32977632	A_68_P32977632			Unknown	1.500	4.971	1611.43	8011.05	7.456	1167.80	8707.48
A_68_P30402200	chr15:85501825-85501869	AK038224:-5325		PROMOTER	1.500	3.951	537.13	2122.34	5.926	487.27	2887.43
A_68_P25486797	chr7:131127028-131127072	ENSMUST00000106437:668		INSIDE	1.500	1.926	661.20	1273.48	2.889	547.21	1580.74
A_68_P32410978	chrX:56820599-56820643	ENSMUST00000124402:29		INSIDE	1.500	3.436	446.12	1532.94	5.153	273.20	1407.78
A_68_P22540995	chr3:132754697-132754741	NM_026231:-14	Gstcd	DIVERGENT_PROMOTER	1.499	2.324	672.14	1561.92	3.483	565.10	1968.07
A_68_P27922692	chr11:74644684-74644728	NM_010813:281	Mnt	INSIDE	1.499	2.830	1929.46	5460.65	4.243	1709.52	7252.82
A_68_P29977213	chr15:3976841-3976885	NM_024188:435	Oxct1	INSIDE	1.499	3.650	544.74	1988.15	5.470	451.02	2467.31
A_68_P28194540	chr12:3309680-3309724	NM_016676:267	Rab10	INSIDE	1.499	4.003	1635.64	6547.04	6.001	1438.90	8635.07
A_68_P23283135	chr4:126699373-126699417	NM_023603:850	Sfpq	INSIDE	1.499	8.155	8727.66	71176.42	12.221	6037.34	73783.94
A_68_P28938194	chr13:34436403-34436447	NM_001033167:627	Slc22a23	INSIDE	1.499	1.665	1049.25	1747.35	2.496	979.35	2444.71
A_68_P30387965	chr15:83197791-83197835	NR_027980:-85	1700001L05Rik	PROMOTER	1.498	3.254	10728.36	34910.23	4.876	7471.87	36432.60
A_68_P21436146	chr2:93482709-93482753	NM_007442:140	Alx4	INSIDE	1.498	3.971	1582.58	6284.85	5.950	1249.96	7437.44
A_68_P21630555	chr2:130406725-130406769	NM_009732:1531	Avp	INSIDE	1.498	1.378	5629.21	7758.02	2.064	4446.85	9178.68
A_68_P31921521	chr19:4169457-4169501	NM_134148:6001	Carns1	INSIDE	1.498	1.811	5127.86	9285.25	2.712	3896.91	10569.98
A_68_P28098603	chr11:105805256-105805300	NM_007805:183	Cyb561	INSIDE	1.498	3.582	1476.04	5286.87	5.364	1148.77	6161.80
A_68_P25554390	chr7:142907763-142907807	NM_001081117:278	Mki67	INSIDE	1.498	1.812	1042.27	1888.86	2.715	958.07	2601.06
A_68_P29753346	chr14:80170179-80170223	NM_001042726:919	Pcdh8	INSIDE	1.498	1.635	727.63	1189.84	2.450	621.18	1521.77
A_68_P22889129	chr4:46520101-46520145	NM_029077:28894	Trim14	INSIDE	1.498	2.217	1000.12	2216.93	3.321	989.66	3286.24
A_68_P26601300	chr9:67688155-67688199	NM_177184:-26	Vps13c	DIVERGENT_PROMOTER	1.498	5.144	3237.18	16652.92	7.705	2570.25	19803.03
A_68_P28596933	chr12:85534608-85534652	NM_001163502:335	C130039O16Rik	INSIDE	1.497	5.387	1169.98	6302.50	8.063	1274.29	10274.97
A_68_P26762950	chr9:99144040-99144084	NM_023873:176	Cep70	INSIDE	1.497	6.111	1295.82	7919.20	9.151	1096.40	10033.53
A_68_P20794600	chr1:167390414-167390458	NM_028759:158	Dcaf6	INSIDE	1.497	2.139	2568.30	5493.40	3.201	2066.97	6616.97
A_68_P29751618	chr14:79880592-79880636	NM_007920:-386	Elf1	PROMOTER	1.497	2.751	378.29	1040.82	4.118	390.19	1606.65
A_68_P30363895	chr15:78858579-78858623	NM_008197:-41	H1f0	PROMOTER	1.497	2.021	385.83	779.59	3.024	312.88	946.11
A_68_P31936765	chr19:7008355-7008399	NM_008431:629	Kcnk4	INSIDE	1.497	1.604	5143.15	8248.42	2.400	3717.11	8922.84
A_68_P21101981	chr2:30093673-30093717	NM_177725:406	Lrrc8a	INSIDE	1.497	1.509	1338.03	2019.61	2.260	1058.68	2392.53
A_68_P30252145	chr15:58913581-58913625	NM_001146180:-21	Mtss1	PROMOTER	1.497	3.797	3359.57	12755.92	5.685	2750.82	15637.27
A_68_P26744225	chr9:95745638-95745682	NM_001033210:38	Pls1	INSIDE	1.497	2.484	3334.46	8281.80	3.717	2629.21	9772.42
A_68_P24152262	chr5:143027306-143027350	NM_178702:-297	Radil	PROMOTER	1.497	1.658	2003.76	3323.21	2.483	1539.05	3821.45
A_68_P28051255	chr11:97407967-97408011	NM_018873:28452	Srcin1	INSIDE	1.497	3.347	1094.35	3663.05	5.011	871.73	4368.59
A_68_P27981398	chr11:84953893-84953937	NM_001029934:-457	Usp32	PROMOTER	1.497	2.203	743.47	1638.01	3.298	590.65	1948.14
A_68_P26801603	chr9:106073078-106073122	NM_029896:-159	Wdr82	PROMOTER	1.497	2.599	798.22	2074.18	3.889	757.80	2947.20
A_68_P27797797	chr11:51981491-51981535	ENSMUST00000155549:101504		INSIDE	1.497	2.585	570.77	1475.40	3.870	508.48	1967.72
A_68_P24671353	chr6:97098869-97098913	NM_175313:-13	A130022J15Rik	PROMOTER	1.496	2.483	1343.44	3335.11	3.713	1158.58	4302.05
A_68_P20804630	chr1:169280208-169280252	NM_019993:109	Aldh9a1	INSIDE	1.496	2.695	2883.49	7770.36	4.031	2382.36	9604.02
A_68_P24098215	chr5:131915714-131915758	NM_177047:1102477	Auts2	INSIDE	1.496	4.855	1835.06	8909.31	7.265	1385.90	10069.19
A_68_P26018982	chr8:86773469-86773513	NM_001007571:170	D8Ertd738e	INSIDE	1.496	4.477	3650.41	16344.52	6.698	2731.43	18295.77
A_68_P28291796	chr12:25516059-25516103	NM_001083341:-383	Mboat2	PROMOTER	1.496	2.432	781.87	1901.35	3.639	595.30	2166.22
A_68_P28457433	chr12:57634159-57634203	NM_001146198:1913	Nkx2-1	INSIDE	1.496	4.586	2023.54	9279.60	6.859	1756.49	12048.05
A_68_P30368658	chr15:79634975-79635019	NM_030689:143	Nptxr	INSIDE	1.496	1.954	1162.70	2271.90	2.922	1261.40	3686.23
A_68_P32415817	chrX:58147657-58147701	NM_009237:-1073	Sox3	PROMOTER	1.496	4.941	926.43	4577.92	7.391	691.04	5107.77
A_68_P20737712	chr1:157264214-157264258	NM_011273:338	Xpr1	INSIDE	1.496	1.619	2493.29	4035.43	2.421	1928.05	4667.12
A_68_P31620951	chr18:36090196-36090240			Unknown	1.496	3.298	274.83	906.53	4.936	237.68	1173.16
A_68_P28175452	chr11:118902740-118902784	NM_013926:-535	Cbx8	PROMOTER	1.495	1.563	1619.67	2532.11	2.337	1329.59	3107.83
A_68_P28051744	chr11:97490870-97490916	NM_175332:138	E130012A19Rik	INSIDE	1.495	1.730	541.17	936.05	2.586	478.99	1238.69
A_68_P24613524	chr6:86992684-86992728	NM_013528:-133	Gfpt1	PROMOTER	1.495	2.284	888.58	2029.77	3.416	884.07	3020.06

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P30639626	chr16:30064558-30064602	NM_008235:-862	Hes1	PROMOTER	1.495	4.123	2347.01	9677.81	6.166	1933.93	11924.39
A_68_P28192109	chr11:121564851-121564895	NM_144797:1132	Metrnl	INSIDE	1.495	1.942	2716.65	5276.61	2.904	1976.74	5740.69
A_68_P21495965	chr2:105516343-105516387	NM_013627:-237	Pax6	DIVERGENT_PROMOTER	1.495	1.911	694.64	1327.46	2.857	606.61	1732.91
A_68_P20022046	chr1:9289451-9289495	NM_027671:339	Sntg1	INSIDE	1.495	1.833	443.34	812.55	2.740	419.04	1148.14
A_68_P24002091	chr5:114581110-114581154	NM_011677:-32	Ung	PROMOTER	1.495	2.127	2054.94	4371.54	3.181	1704.40	5421.67
A_68_P24596101	chr6:83864271-83864315	NM_001166371:-54	Zfml	PROMOTER	1.495	3.231	532.77	1721.39	4.831	496.47	2398.62
A_68_P30849195	chr16:70314120-70314164	NM_028803:-189	Gbe1	PROMOTER	1.494	2.616	1831.98	4791.95	3.907	1550.72	6058.97
A_68_P23322029	chr4:133843071-133843115	NM_001163794:76	Pdik1l	INSIDE	1.494	2.372	10225.48	24258.79	3.545	8594.51	30466.36
A_68_P30423622	chr15:88998029-88998073	NM_001159521:6230	Plxnb2	INSIDE	1.494	1.877	524.77	984.97	2.804	429.82	1205.04
A_68_P25410469	chr7:117008961-117009005	NM_020052:211	Scube2	INSIDE	1.494	5.181	868.74	4501.01	7.739	825.26	6386.80
A_68_P28744649	chr12:112776399-112776444	NR_033168:-2735	Snora28	PROMOTER	1.494	3.047	9826.32	29943.34	4.552	7671.96	34924.14
A_68_P27985536	chr11:85645744-85645788	NM_009324:-350	Tbx2	PROMOTER	1.494	1.835	2705.43	4964.16	2.741	2125.14	5824.30
A_68_P27466136	chr10:114238907-114238951	NM_146241:-502	Trhde	PROMOTER	1.494	1.663	869.87	1446.85	2.485	737.16	1832.11
A_68_P20421181	chr1:89904795-89904839	NM_001033291:310	Usp40	INSIDE	1.494	1.493	776.15	1158.90	2.231	660.26	1473.15
A_68_P30351229	A_68_P30351229			Unknown	1.494	4.281	1145.52	4904.46	6.397	1071.97	6857.53
A_68_P22262798	chr3:79091123-79091167	AK032506:-169		PROMOTER	1.494	2.337	1452.04	3392.81	3.492	1172.92	4095.33
A_68_P31161581	chr17:36034296-36034340	NM_001033630:5	2310061I04Rik	INSIDE	1.493	3.516	1094.62	3848.68	5.249	932.82	4895.98
A_68_P21754951	chr2:153269795-153269839	NM_001001986:399	8430427H17Rik	INSIDE	1.493	1.796	1084.60	1948.13	2.682	930.08	2494.60
A_68_P26890107	chr9:122478468-122478512	NR_015610:-3128	9530059O14Rik	PROMOTER	1.493	1.625	802.64	1303.97	2.425	628.18	1523.47
A_68_P28098880	chr11:105847454-105847498	NM_009598:10955	Ace	INSIDE	1.493	1.549	581.37	900.55	2.313	444.02	1026.80
A_68_P25093839	chr7:52825720-52825764	NM_009737:10	Bcat2	INSIDE	1.493	2.461	1979.07	4869.89	3.675	1656.09	6086.18
A_68_P30433470	chr15:90880052-90880096	NM_001109040:305	Kif21a	INSIDE	1.493	1.872	1133.72	2122.14	2.794	984.50	2750.42
A_68_P32266422	chrX:13063296-13063340	NM_173415:18521	Nyx	INSIDE	1.493	2.556	715.31	1828.01	3.816	512.63	1955.93
A_68_P26349531	chr9:21722321-21722365	NM_031874:223	Rab3d	INSIDE	1.493	2.793	847.44	2367.19	4.170	739.45	3083.42
A_68_P21851412	chr2:169956064-169956108	NM_001033299:634	Zfp217	INSIDE	1.493	2.203	383.89	845.52	3.289	346.43	1139.56
A_68_P27830382	chr11:58136668-58136712	NM_178761:158	Zfp672	INSIDE	1.493	1.613	493.52	796.12	2.408	499.73	1203.21
A_68_P24336409	chr6:31166646-31166691	ENSMUST00000115107:1765		INSIDE	1.493	2.097	1806.75	3789.15	3.132	1653.24	5178.09
A_68_P23425243	chr4:152857051-152857095	NM_001099299:-133	Ajap1	PROMOTER	1.492	4.288	1661.98	7127.39	6.399	1493.27	9555.03
A_68_P22941965	chr4:56878080-56878124	NM_018761:-19	Ctnnal1	PROMOTER	1.492	2.293	10764.22	24683.44	3.420	7836.12	26802.11
A_68_P25010200	chr7:26180775-26180819	NM_010719:210	Lipe	INSIDE	1.492	2.450	1203.56	2948.31	3.655	957.61	3500.53
A_68_P21742434	chr2:150864733-150864777	NM_026086:361	Nanp	INSIDE	1.492	3.383	725.58	2454.59	5.047	652.76	3294.63
A_68_P27551122	chr11:3190063-3190107	NM_019574:-375	Patz1	PROMOTER	1.492	3.884	2049.99	7961.96	5.796	1553.45	9004.29
A_68_P21351543	chr2:76486449-76486493	NM_011871:-419	Prkra	DIVERGENT_PROMOTER	1.492	1.899	4446.39	8444.13	2.833	3396.36	9622.74
A_68_P25571665	chr7:145589754-145589798	NM_183289:-363	Tcerg1l	PROMOTER	1.492	3.210	1121.24	3599.02	4.789	938.78	4496.17
A_68_P32196169	chr19:55816232-55816276	NM_001142918:-45	Tcf7l2	PROMOTER	1.492	3.108	5003.32	15550.53	4.637	3907.26	18118.76
A_68_P23183551	chr4:105989077-105989121	NM_183225:281	Usp24	INSIDE	1.492	30.482	1090.71	33247.34	45.472	799.65	36361.55
A_68_P27663517	chr11:26493581-26493625	NM_027260:318	Vrk2	INSIDE	1.492	1.570	1306.37	2050.94	2.343	1375.56	3222.57
A_68_P28739968	chr12:111976134-111976178	NM_027149:-2	Wdr20a	PROMOTER	1.492	1.771	1358.99	2406.85	2.642	1134.91	2998.01
A_68_P21713971	chr2:145500669-145500713	ENSMUST00000144661:-412		PROMOTER	1.492	3.041	8805.83	26779.05	4.538	6759.79	30676.79
A_68_P32186055	chr19:54120591-54120635	NM_007417:941	Adra2a	INSIDE	1.491	3.574	745.23	2663.79	5.331	602.49	3211.68
A_68_P20429509	chr1:91351220-91351264	NM_001037136:-143	Agap1	PROMOTER	1.491	2.172	1218.02	2645.15	3.237	1092.67	3536.90
A_68_P20258853	chr1:58480687-58480731	NM_001042634:224	Clk1	INSIDE	1.491	2.517	965.55	2430.58	3.754	821.43	3083.74
A_68_P30213289	chr15:51697145-51697189	NM_080635:-159	Eif3h	PROMOTER	1.491	4.118	811.57	3341.85	6.140	689.75	4235.10
A_68_P26248326	chr8:127421066-127421110	NM_198103:517	Exoc8	INSIDE	1.491	2.689	1459.41	3923.64	4.010	1160.08	4651.42
A_68_P27556420	chr11:4118164-4118208	NM_028022:-67	Gatsl3	PROMOTER	1.491	3.351	3994.43	13386.75	4.999	3124.31	15616.92
A_68_P20417068	chr1:89223852-89223896	NM_001110212:271	Gigyf2	INSIDE	1.491	5.680	1362.29	7738.35	8.472	1230.82	10427.60
A_68_P23627551	chr5:40035622-40035667	NM_010474:226	Hs3st1	INSIDE	1.491	2.146	4082.80	8763.09	3.201	3300.09	10564.46
A_68_P24325224	chr6:29162351-29162395	NM_011829:-101	Impdh1	PROMOTER	1.491	3.611	2888.66	10432.29	5.386	2362.75	12725.29
A_68_P22530123	chr3:130809073-130809117	NM_010703:-4294	Lef1	PROMOTER	1.491	13.626	995.20	13560.91	20.319	868.75	17651.82
A_68_P32565868	chrX:99044658-99044702	NM_001163610:-43	Nhsl2	PROMOTER	1.491	3.614	1420.71	5134.02	5.386	897.42	4833.88
A_68_P31067738	chr17:15963543-15963587	NM_178615:-14	Rgmb	PROMOTER	1.491	2.517	8925.03	22468.51	3.753	6475.95	24302.21

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P24127573	chr5:138228997-138229041	NM_001005426:-11	Zcwpw1	DIVERGENT_PROMOTER	1.491	1.562	697.44	1089.17	2.329	617.84	1438.97
A_68_P25959077	chr8:74446861-74446905	NM_133358:159	Zfp617	INSIDE	1.491	5.588	2263.07	12647.16	8.330	1860.47	15498.50
A_68_P31256671	chr17:56651263-56651307	NM_011483:622	Znrf4	INSIDE	1.491	3.365	1288.91	4337.82	5.019	1098.38	5513.26
A_68_P29527055	A_68_P29527055			Unknown	1.491	3.497	196.73	687.87	5.214	153.74	801.59
A_68_P28743060	chr12:112512501-112512545	NM_033603:3201	Amn	INSIDE	1.490	1.423	7033.05	10010.01	2.121	5389.09	11430.75
A_68_P22860481	chr4:41045310-41045354	NM_016689:-116	Aqp3	PROMOTER	1.490	4.660	1305.12	6081.64	6.945	1101.64	7650.92
A_68_P27849285	chr11:61393132-61393176	NM_010148:-1	Epn2	PROMOTER	1.490	2.945	2245.53	6613.71	4.388	1779.36	7807.81
A_68_P25616728	chr8:4238821-4238865	NM_001042557:103	Map2k7	INSIDE	1.490	1.822	1137.79	2072.92	2.715	1027.75	2790.18
A_68_P24536650	chr6:71444353-71444397	NM_009543:487	Rnf103	INSIDE	1.490	1.806	1872.30	3381.13	2.691	1641.75	4418.32
A_68_P22342531	chr3:94964250-94964300	NM_011351:-4021	Sema6c	PROMOTER	1.490	4.451	357.82	1592.58	6.634	354.91	2354.44
A_68_P26596714	chr9:66891475-66891519	NM_001164252:182	Tpm1	INSIDE	1.490	2.510	900.44	2260.05	3.741	720.21	2694.31
A_68_P30826541	chr16:65815730-65815774	NM_028572:-125	Vgll3	PROMOTER	1.490	3.059	712.43	2179.14	4.557	617.08	2811.93
A_68_P24850992	chr6:131383975-131384019			Unknown	1.490	2.161	1306.32	2823.15	3.221	1119.61	3605.74
A_68_P22630569	chr3:148652119-148652163	ENSMUST00000098518:140		INSIDE	1.490	1.650	1457.29	2405.23	2.459	1295.15	3185.08
A_68_P25027724	chr7:30303544-30303588	ENSMUST00000141713:-657		PROMOTER	1.490	1.774	1239.78	2198.95	2.644	1094.62	2893.71
A_68_P30558454	chr16:13672209-13672253	NM_025653:118	3110001I22Rik	INSIDE	1.489	2.198	1853.67	4074.40	3.272	1443.14	4721.77
A_68_P25525515	chr7:138080197-138080241	NM_019564:502	Htra1	INSIDE	1.489	1.895	1370.52	2597.52	2.823	1195.46	3374.46
A_68_P30585934	chr16:20097708-20097752	NM_029436:104	Klhl24	INSIDE	1.489	2.283	662.18	1512.05	3.399	645.27	2193.26
A_68_P25018407	chr7:28442995-28443039	NM_001081292:16601	Map3k10	INSIDE	1.489	5.153	1305.66	6727.86	7.673	1031.07	7911.18
A_68_P23331869	chr4:135609312-135609356	NM_025919:-48	Rpl11	PROMOTER	1.489	3.002	1260.15	3783.48	4.469	1027.83	4593.88
A_68_P24158560	chr5:144670456-144670500	NM_001172146:230	Aimp2	INSIDE	1.488	5.856	2490.98	14587.44	8.716	2174.48	18953.42
A_68_P23818500	chr5:77286506-77286550	NM_001163793:16905	C530008M17Rik	INSIDE	1.488	6.205	7896.04	48992.45	9.233	4990.86	46079.35
A_68_P22524273	chr3:129883661-129883705	NM_029838:-113	Col25a1	PROMOTER	1.488	6.654	699.40	4653.89	9.898	635.72	6292.63
A_68_P21428537	chr2:92273951-92273995	NM_009963:254	Cry2	INSIDE	1.488	1.459	782.43	1141.89	2.172	670.94	1457.25
A_68_P32383357	chrX:49965510-49965554	NM_016697:1619	Gpc3	INSIDE	1.488	2.556	704.94	1801.58	3.802	445.28	1693.02
A_68_P27271929	chr10:77531813-77531858	NM_015790:-277	Icosl	PROMOTER	1.488	2.482	1296.29	3217.58	3.694	1047.40	3868.77
A_68_P20639346	chr1:137327066-137327110	NM_153774:-20	Ipo9	PROMOTER	1.488	1.519	815.68	1238.76	2.259	767.03	1732.96
A_68_P26531872	chr9:55390256-55390300	NM_027397:1323	Isl2	INSIDE	1.488	4.671	1085.66	5070.71	6.951	978.25	6799.90
A_68_P25948235	chr8:72356375-72356419	NM_001024954:-206	Pbx4	PROMOTER	1.488	1.638	680.46	1114.66	2.438	581.17	1416.90
A_68_P26011770	chr8:85388368-85388412	NM_177378:1136	Rnf150	INSIDE	1.488	3.080	1079.30	3324.26	4.583	970.72	4448.36
A_68_P24769162	chr6:115085438-115085482	NM_013681:541	Syn2	INSIDE	1.488	4.224	615.78	2600.91	6.283	470.27	2954.76
A_68_P24760941	chr6:113647011-113647055	NM_001033463:-460	Tatdn2	PROMOTER	1.488	2.222	1072.54	2383.67	3.307	953.60	3153.27
A_68_P27886201	chr11:67735651-67735695	NM_173754:-17	Usp43	PROMOTER	1.488	2.241	486.73	1090.62	3.334	360.25	1201.16
A_68_P20737716	chr1:157264675-157264719	NM_011273:-122	Xpr1	PROMOTER	1.488	2.422	1335.19	3233.80	3.603	1135.65	4091.66
A_68_P25614202	chr8:3492951-3492995	NM_080461:-165	Zfp358	PROMOTER	1.488	1.596	6033.02	9628.47	2.375	4331.43	10288.39
A_68_P26349677	chr9:21748879-21748923	NM_144935:6183	BC018242	INSIDE	1.487	3.028	3130.24	9478.02	4.502	2573.97	11588.81
A_68_P25601080	chr7:150646296-150646340	NM_001161624:637	Cdkn1c	INSIDE	1.487	4.382	1274.18	5583.61	6.515	1004.83	6546.13
A_68_P27849286	chr11:61393305-61393349	NM_010148:-173	Epn2	PROMOTER	1.487	4.727	4819.02	22780.15	7.029	3257.06	22894.05
A_68_P23356930	chr4:139802256-139802300	NM_198610:448	Igsf21	INSIDE	1.487	2.045	786.67	1608.36	3.041	607.76	1848.19
A_68_P21389130	chr2:83564617-83564661	NM_008402:85	Itgav	INSIDE	1.487	2.157	1205.50	2600.52	3.207	1076.10	3451.24
A_68_P31120666	chr17:28279127-28279172	NM_001004366:-321	Scube3	PROMOTER	1.487	1.332	5679.82	7564.81	1.981	3576.07	7084.14
A_68_P22383782	chr3:102799932-102799976	NM_025679:292	Sike1	INSIDE	1.487	2.904	3165.15	9192.18	4.317	2396.96	10348.20
A_68_P31301690	chr17:65963450-65963494	NM_013933:-577	Vapa	PROMOTER	1.487	8.798	1010.79	8893.14	13.087	685.67	8973.47
A_68_P23296941	chr4:129177909-129177953	NM_001085491:9497	1700125D06Rik	DOWNSTREAM	1.486	2.494	959.72	2393.20	3.705	822.00	3045.18
A_68_P23956783	chr5:106128691-106128735	NM_001122768:-275	Lrrc8d	PROMOTER	1.486	1.842	1832.21	3375.58	2.737	1481.10	4053.61
A_68_P20640400	chr1:137481754-137481798	NM_173437:156	Nav1	INSIDE	1.486	1.516	848.35	1286.26	2.253	795.55	1792.57
A_68_P31112710	chr17:26976655-26976699	NM_008700:1834	Nkx2-5	INSIDE	1.486	2.074	1893.57	3926.91	3.082	1586.57	4890.57
A_68_P26135469	chr8:108225412-108225456	NM_001047435:-114	Pard6a	PROMOTER	1.486	3.119	449.62	1402.26	4.634	385.94	1788.30
A_68_P24338524	chr6:31513799-31513843	NM_013723:117	Podxl	INSIDE	1.486	1.746	769.41	1343.69	2.595	715.71	1856.99
A_68_P31102167	chr17:25325180-25325224	NM_001197024:-142	Unkl	PROMOTER	1.486	2.798	921.18	2577.58	4.159	811.41	3374.68
A_68_P28746261	chr12:113052815-113052859	NM_026752:456	Zfyve21	INSIDE	1.486	3.714	1302.12	4836.52	5.520	1086.85	5999.50

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28168166	chr11:117811203-117811247			Unknown	1.486	1.853	1410.42	2613.60	2.754	1231.53	3391.73
A_68_P27633195	chr11:20640941-20640985	NM_181411:525	Aftph	INSIDE	1.485	6.232	1309.64	8162.06	9.254	1017.41	9415.47
A_68_P25188282	chr7:73572179-73572223	NM_053080:163	Aldh1a3	INSIDE	1.485	1.775	482.69	856.84	2.636	411.20	1083.82
A_68_P32244416	chrX:8469520-8469564	NM_175327:64	B630019K06Rik	INSIDE	1.485	3.190	515.88	1645.62	4.736	267.16	1265.36
A_68_P31756138	chr18:61336272-61336316	NM_178277:409	Hmgxb3	INSIDE	1.485	1.870	2277.30	4258.67	2.777	1653.25	4591.76
A_68_P28041916	chr11:95867049-95867093	NM_009951:188	Igf2bp1	INSIDE	1.485	2.030	1304.20	2646.88	3.014	1157.60	3488.96
A_68_P22509730	chr3:127336734-127336778	NM_009718:694	Neurog2	INSIDE	1.485	5.671	1068.27	6058.09	8.419	859.81	7239.13
A_68_P23361259	chr4:140517609-140517653	NM_023374:445	Sdhb	INSIDE	1.485	5.325	986.50	5253.58	7.911	849.33	6718.97
A_68_P26932996	chr10:9621066-9621110	NM_001081344:-250	Stxbp5	PROMOTER	1.485	2.612	314.38	821.25	3.879	442.32	1715.69
A_68_P28078912	chr11:102180945-102180990	NM_011551:-557	Ubtf	PROMOTER	1.485	1.841	1467.58	2701.44	2.733	1097.83	3000.03
A_68_P31839441	chr18:75980377-75980421	NM_145356:567	Zbtb7c	INSIDE	1.485	1.935	940.22	1819.10	2.874	811.86	2333.14
A_68_P30331748	chr15:73475653-73475697	ENSMUST00000150409:101		INSIDE	1.485	5.345	5095.75	27234.62	7.939	3654.55	29013.70
A_68_P22789806	chr4:25208898-25208942	NM_026194:48	1810074P20Rik	INSIDE	1.484	1.911	1480.86	2829.19	2.836	1269.09	3598.53
A_68_P23607908	chr5:36827600-36827644	NM_025725:386	Ccdc96	INSIDE	1.484	5.235	2489.82	13033.21	7.770	1941.17	15083.03
A_68_P26168095	chr8:113917768-113917812	NM_178086:-69	Fa2h	PROMOTER	1.484	6.080	1257.89	7648.54	9.026	1008.97	9106.88
A_68_P27497681	chr10:119914095-119914139	NM_010441:-125	Hmga2	PROMOTER	1.484	2.135	2093.43	4468.85	3.168	1657.10	5250.27
A_68_P30267513	chr15:61816737-61816781	NM_001177352:-137	Myc	PROMOTER	1.484	3.242	3790.60	12290.28	4.810	2991.79	14391.14
A_68_P26024229	chr8:87823886-87823930	NM_001163791:378	Orc6	INSIDE	1.484	5.626	1217.96	6852.12	8.349	978.99	8173.95
A_68_P30139531	chr15:36539130-36539174	NM_008774:-424	Pabpc1	PROMOTER	1.484	2.124	1105.00	2347.11	3.151	925.10	2915.31
A_68_P22129906	chr3:51287666-51287710	NM_016858:-199	Rab33b	PROMOTER	1.484	3.575	3179.94	11369.76	5.304	2674.89	14188.17
A_68_P28051170	chr11:97396005-97396049	NM_018873:40414	Srcin1	INSIDE	1.484	2.729	1143.80	3121.76	4.052	991.18	4015.84
A_68_P22411406	chr3:108029457-108029501	NM_008596:39	Sypl2	INSIDE	1.484	2.930	2603.75	7628.82	4.348	1948.88	8474.21
A_68_P30497401	chr15:102180872-102180916	NM_153416:296	Aaas	INSIDE	1.483	1.718	4393.93	7547.58	2.548	3456.38	8806.91
A_68_P27255925	chr10:74779618-74779662	NM_009630:-47	Adora2a	PROMOTER	1.483	2.081	3518.28	7321.57	3.086	2975.00	9180.44
A_68_P28533193	chr12:73765645-73765689	NM_025522:149	Dhrs7	INSIDE	1.483	1.684	1131.18	1904.55	2.498	939.62	2346.87
A_68_P28669125	chr12:99497683-99497727	NM_008079:-157	Galc	DIVERGENT_PROMOTER	1.483	2.241	1222.21	2738.64	3.322	1049.95	3488.01
A_68_P23756018	chr5:65771113-65771157	NM_031180:31485	Klb	INSIDE	1.483	4.473	1280.38	5727.59	6.635	1092.86	7251.53
A_68_P31731698	chr18:56867506-56867550	NM_010721:62	Lmnb1	INSIDE	1.483	1.891	1001.30	1893.37	2.804	868.82	2436.10
A_68_P26991379	chr10:20879243-20879287	NM_001198914:1526	Myb	INSIDE	1.483	4.136	1333.68	5516.51	6.135	1248.56	7659.30
A_68_P22325410	chr3:90270013-90270057	NM_008727:-246	Npr1	PROMOTER	1.483	2.568	1376.39	3535.17	3.809	1090.25	4152.71
A_68_P20876659	chr1:182498959-182499003	NM_007415:-125	Parp1	PROMOTER	1.483	5.070	2443.18	12386.49	7.518	1978.81	14877.19
A_68_P27838986	chr11:59600830-59600874	NM_183139:307	Pld6	INSIDE	1.483	2.031	820.37	1665.86	3.011	692.96	2086.64
A_68_P29419901	chr14:14953551-14953595	NM_025550:-154	Psmd6	PROMOTER	1.483	5.375	1361.25	7316.32	7.971	1043.09	8314.32
A_68_P27554683	chr11:3813912-3813956	NM_153142:733	Slc35e4	INSIDE	1.483	3.181	5584.46	17766.24	4.718	4111.19	19396.84
A_68_P28183961	chr11:120209795-120209839	NM_009609:-18	Actg1	DIVERGENT_PROMOTER	1.482	4.193	1639.68	6875.37	6.213	1414.71	8790.24
A_68_P30284258	chr15:64753242-64753286	NM_009623:594	Adcy8	INSIDE	1.482	2.953	6285.38	18562.99	4.376	4889.33	21396.26
A_68_P24950090	chr7:4658912-4658956	NM_001003920:16405	Brsk1	INSIDE	1.482	2.699	4374.20	11806.01	4.000	3848.05	15392.56
A_68_P27227733	chr10:69559705-69559749	NM_001111121:-142	Ccdc6	PROMOTER	1.482	5.110	3870.06	19777.68	7.576	2600.34	19699.88
A_68_P23980414	chr5:110973587-110973631	NM_198306:245	Galnt9	INSIDE	1.482	4.093	1922.29	7867.08	6.063	1572.34	9533.56
A_68_P22301527	chr3:86028160-86028204	NM_001077687:-429	Lrba	PROMOTER	1.482	1.595	746.77	1190.92	2.363	658.90	1556.83
A_68_P25995588	chr8:82163767-82163811	NM_001081164:214	Otud4	INSIDE	1.482	3.426	421.02	1442.45	5.079	366.04	1859.13
A_68_P28238663	chr12:11462730-11462774	NM_001111118:-132	Rad51ap2	PROMOTER	1.482	2.658	3232.76	8594.13	3.940	2793.60	11007.71
A_68_P20233544	chr1:53842063-53842107	NM_133810:-25	Stk17b	PROMOTER	1.482	1.878	2289.72	4300.75	2.784	1885.34	5248.64
A_68_P24951873	chr7:5014151-5014195	NM_001205231:428	U2af2	INSIDE	1.482	3.304	2306.57	7620.07	4.897	1919.29	9399.65
A_68_P26529570	chr9:54996803-54996847	NM_180600:-351	Ube2q2	PROMOTER	1.482	2.667	1031.63	2750.92	3.953	925.31	3657.95
A_68_P27475464	chr10:115855274-115855318	NR_028107:120	1700058G18Rik	INSIDE	1.481	4.934	292.58	1443.64	7.307	244.85	1789.09
A_68_P27958482	chr11:80967088-80967132	NM_007384:-705	Accn1	PROMOTER	1.481	4.388	962.52	4223.79	6.500	813.40	5287.31
A_68_P20753949	chr1:160293080-160293124	NM_001205204:668	Astn1	INSIDE	1.481	1.918	5761.52	11049.78	2.840	4203.78	11939.94
A_68_P25272112	chr7:88599818-88599862	NM_007755:-278	Cpeb1	PROMOTER	1.481	2.359	1025.11	2418.14	3.493	831.90	2905.84
A_68_P32219567	chr19:59533292-59533336	NM_010132:135	Emx2	INSIDE	1.481	1.925	451.55	869.14	2.851	413.29	1178.37
A_68_P32383368	chrX:49966913-49966957	NM_016697:217	Gpc3	INSIDE	1.481	2.480	1551.13	3847.02	3.674	1061.86	3901.58

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P23361559	chr4:140566637-140566681	NM_008546:107	Mfap2	INSIDE	1.481	1.545	1918.29	2964.27	2.289	1684.65	3855.41
A_68_P24132976	chr5:139471493-139471537	NM_008808:-607	Pdgfa	PROMOTER	1.481	4.271	882.01	3766.82	6.325	815.04	5155.40
A_68_P29578866	chr14:47501811-47501855	NM_001037221:-807	Samd4	PROMOTER	1.481	3.095	2088.77	6465.44	4.585	1551.32	7112.98
A_68_P22413523	chr3:108394473-108394517	NM_181400:299	Wdr47	INSIDE	1.481	1.823	830.50	1513.68	2.700	719.16	1941.53
A_68_P30387966	chr15:83197892-83197936	NR_027980:-187	1700001L05Rik	PROMOTER	1.480	3.809	1597.10	6083.53	5.638	1346.38	7590.37
A_68_P27945542	chr11:78639981-78640025	NM_001076681:-94	1810012P15Rik	PROMOTER	1.480	1.923	2346.71	4511.92	2.846	2058.79	5859.47
A_68_P25952417	chr8:73047003-73047047	NM_029366:55	2810422J05Rik	INSIDE	1.480	1.630	1050.66	1712.07	2.411	849.65	2048.77
A_68_P31776707	chr18:64820614-64820658	NM_001001488:18	Atp8b1	INSIDE	1.480	2.527	709.08	1791.99	3.740	629.48	2354.57
A_68_P29005199	chr13:46059825-46059869	NM_009124:499	Atxn1	INSIDE	1.480	4.210	1091.25	4593.78	6.230	913.47	5690.97
A_68_P24476446	chr6:56664815-56664859	NM_030235:-62	Avl9	PROMOTER	1.480	3.367	2391.78	8053.22	4.982	1936.96	9649.44
A_68_P26119098	chr8:105308180-105308224	NM_009866:809	Cdh11	INSIDE	1.480	2.061	8473.02	17463.92	3.049	6293.29	19191.28
A_68_P26898893	chr10:3134939-3134983	NM_172546:657	Cnksr3	INSIDE	1.480	2.790	3564.58	9944.12	4.129	2849.51	11766.46
A_68_P21769580	chr2:155937622-155937666	NM_170588:57	Cpne1	INSIDE	1.480	2.533	6122.06	15507.23	3.748	4655.04	17448.24
A_68_P22318791	chr3:89154152-89154197	NM_029974:14987	Dcst1	INSIDE	1.480	2.249	710.24	1597.59	3.330	619.90	2064.17
A_68_P20140950	chr1:34899440-34899484	NM_001160235:433	Fam168b	INSIDE	1.480	2.391	1108.36	2650.23	3.539	877.79	3106.40
A_68_P24784008	chr6:117867198-117867242	NM_001166427:-91	Hnrnpf	PROMOTER	1.480	2.749	2925.73	8044.26	4.068	2294.90	9336.79
A_68_P29616398	chr14:55732626-55732670	NM_177049:3124	Jph4	INSIDE	1.480	1.870	926.03	1731.65	2.767	721.71	1996.85
A_68_P31552995	chr18:23197987-23198031	NM_001161483:-844	Nol4	PROMOTER	1.480	2.708	3982.48	10782.62	4.006	3148.81	12614.76
A_68_P28151868	chr11:115048748-115048792	NM_001033393:-30	Tmem104	DIVERGENT_PROMOTER	1.480	3.488	3588.34	12515.17	5.162	3236.22	16706.76
A_68_P30366258	chr15:79233359-79233403	NM_172608:353	Tmem184b	INSIDE	1.480	2.133	1972.86	4207.76	3.156	1659.57	5236.82
A_68_P20405965	chr1:84835584-84835628	NM_133975:273	Trip12	INSIDE	1.480	2.436	1733.53	4222.22	3.606	1450.76	5230.82
A_68_P25355272	chr7:105509671-105509715	NM_001024619:106	Tsku	INSIDE	1.480	1.578	789.68	1245.92	2.335	720.02	1681.44
A_68_P27910155	chr11:72021079-72021123	NM_026559:45	Txndc17	INSIDE	1.480	1.464	1165.15	1705.59	2.167	977.40	2117.86
A_68_P27554559	chr11:3794810-3794858	NM_026150:295	4921536K21Rik	INSIDE	1.479	1.995	823.65	1642.99	2.950	659.99	1946.71
A_68_P25645835	chr8:9977887-9977931	NM_001081119:192	Abhd13	INSIDE	1.479	8.814	857.51	7558.11	13.035	763.22	9948.28
A_68_P31759814	chr18:61946393-61946437	NM_178928:-98	Afap1l1	PROMOTER	1.479	2.041	3425.45	6990.74	3.018	3032.52	9153.63
A_68_P26818180	chr9:108984801-108984845	NM_183250:73	Ccdc72	INSIDE	1.479	1.486	6981.24	10376.87	2.199	5026.10	11050.19
A_68_P28914111	chr13:29947064-29947108	NM_144536:371	Cdkal1	INSIDE	1.479	3.371	944.34	3183.75	4.986	929.45	4633.90
A_68_P31715218	chr18:53904131-53904175	NM_178686:49	Cep120	INSIDE	1.479	1.731	2423.12	4193.44	2.560	1996.83	5112.27
A_68_P31101001	chr17:25151361-25151405	NM_020608:793	Cramp1l	INSIDE	1.479	2.667	3775.30	10067.56	3.943	3133.13	12353.35
A_68_P24620316	chr6:88143988-88144032	NM_008090:-4647	Gata2	PROMOTER	1.479	3.030	1870.87	5668.13	4.480	1565.73	7013.72
A_68_P24862663	chr6:134582475-134582519	NM_026345:10	Mansc1	INSIDE	1.479	3.308	1719.31	5688.01	4.892	1484.89	7264.64
A_68_P24894482	chr6:140372882-140372926	NM_144920:285	Plekha5	INSIDE	1.479	1.478	786.61	1162.51	2.186	680.70	1488.20
A_68_P22321898	chr3:89634943-89634987	NM_172530:-327	She	PROMOTER	1.479	2.768	1127.27	3120.33	4.094	1072.50	4390.86
A_68_P28118794	chr11:109334955-109334999	NM_001029842:-66	Slc16a6	PROMOTER	1.479	1.583	2491.68	3944.60	2.342	1947.22	4560.78
A_68_P20734232	chr1:156646813-156646857	AK046991:-6961		PROMOTER	1.479	3.585	816.76	2928.19	5.304	648.34	3438.64
A_68_P31292460	chr17:64213972-64214016	ENSMUST00000112829:631		INSIDE	1.479	1.881	1392.48	2618.96	2.781	1147.32	3191.23
A_68_P31398060	chr17:83675697-83675741	ENSMUST00000157785:6408		DOWNSTREAM	1.479	2.246	610.82	1371.64	3.321	602.51	2000.92
A_68_P24115156	chr5:135663662-135663706	NM_011714:492	Baz1b	INSIDE	1.478	1.392	1457.67	2028.70	2.057	1309.96	2694.99
A_68_P32982437	chr5:135114511-135114555	NM_033561:666	Eif4h	INSIDE	1.478	1.455	1737.39	2528.45	2.151	1363.07	2931.61
A_68_P32092668	chr19:36993413-36993457	NM_028263:655	Fgfbp3	INSIDE	1.478	3.750	1172.92	4398.74	5.545	945.62	5243.20
A_68_P23201329	chr4:109148711-109148755	NM_013876:378	Rnf11	INSIDE	1.478	2.590	15012.97	38881.78	3.829	12506.99	47883.74
A_68_P29233990	chr13:95055582-95055626	NM_029153:-368	Scamp1	PROMOTER	1.478	2.340	3444.93	8061.13	3.458	2510.77	8681.86
A_68_P24951790	chr7:5004491-5004536	NM_026900:1380	Zfp580	INSIDE	1.478	1.663	883.25	1468.74	2.457	733.71	1802.93
A_68_P29145780	chr13:74487726-74487770	NM_001168659:-16	Ccdc127	DIVERGENT_PROMOTER	1.477	1.989	1765.25	3510.96	2.938	1523.36	4475.30
A_68_P29631499	chr14:58694324-58694368	NM_013518:2824	Fgf9	INSIDE	1.477	2.331	3091.01	7204.39	3.443	2442.41	8408.05
A_68_P28043342	chr11:96133436-96133480	NM_008270:815	Hoxb9	INSIDE	1.477	3.738	3533.47	13209.48	5.520	2622.75	14478.89
A_68_P25089581	chr7:52094932-52094976	NM_010215:3297	Il4i1	INSIDE	1.477	3.776	2505.62	9461.75	5.578	1728.23	9639.62
A_68_P30290903	chr15:66118372-66118416	NM_152923:-608	Kcnq3	PROMOTER	1.477	2.368	814.02	1927.72	3.499	706.35	2471.19
A_68_P32299549	chrX:22942071-22942115	NM_026167:87	Klhl13	INSIDE	1.477	1.778	456.55	811.58	2.625	245.96	645.62
A_68_P23657073	chr5:45911523-45911567	NM_025895:77	Med28	INSIDE	1.477	2.740	677.29	1855.49	4.047	663.80	2686.45

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28202815	chr12:4881183-4881227	NM_001033488:-39	Mfsd2b	PROMOTER	1.477	3.023	1201.75	3632.72	4.464	1000.10	4464.73
A_68_P31621449	chr18:36178281-36178325	NM_001167891:178512	Nrg2	INSIDE	1.477	1.702	3373.35	5741.23	2.514	2787.93	7007.95
A_68_P31844540	chr18:77098052-77098096	NM_001109743:2931	Skor2	INSIDE	1.477	3.276	1955.84	6407.97	4.840	1593.65	7712.69
A_68_P21303493	chr2:68309091-68309135	NM_016866:926	Stk39	INSIDE	1.477	1.631	1186.56	1935.83	2.409	940.06	2264.78
A_68_P21763712	chr2:154876566-154876610	NM_015770:37283	a	INSIDE	1.476	2.976	2522.97	7508.93	4.393	2039.92	8962.22
A_68_P21068908	chr2:24790503-24790547	NM_001162485:277	Arrdc1	INSIDE	1.476	2.759	3219.05	8881.57	4.072	2742.21	11166.22
A_68_P28175493	chr11:118908126-118908170	NM_013926:-5921	Cbx8	PROMOTER	1.476	3.311	1112.60	3683.47	4.887	1022.16	4995.76
A_68_P29961483	chr14:122805935-122805979	NR_033326:44412	Gm5089	INSIDE	1.476	2.444	1001.95	2448.52	3.607	904.65	3263.19
A_68_P24687704	chr6:99643282-99643326	NM_008158:632	Gpr27	INSIDE	1.476	2.762	1794.15	4955.86	4.077	1534.99	6257.79
A_68_P30490486	chr15:101062223-101062267	NM_019518:7607	Grasp	INSIDE	1.476	3.723	1411.87	5256.42	5.494	1174.75	6454.27
A_68_P28540459	chr12:75009270-75009315	NM_010431:439	Hif1a	INSIDE	1.476	1.586	647.19	1026.57	2.341	554.41	1297.97
A_68_P25842937	chr8:48759109-48759153	NM_023503:1383	Ing2	INSIDE	1.476	4.309	13402.38	57746.43	6.362	10088.99	64183.56
A_68_P25095113	chr7:53050658-53050702	NM_001005511:11364	Lmtk3	INSIDE	1.476	3.613	2223.54	8034.61	5.333	1761.72	9394.45
A_68_P31937501	chr19:7131176-7131220	NM_134147:-59	Macrod1	PROMOTER	1.476	1.539	564.55	868.61	2.271	522.48	1186.46
A_68_P31108447	chr17:26260564-26260608	NM_024227:139	Mrpl28	INSIDE	1.476	2.097	887.71	1861.50	3.096	711.74	2203.30
A_68_P27647504	chr11:23671033-23671077	NM_009044:-84	Rel	PROMOTER	1.476	3.631	2050.13	7443.76	5.360	1691.62	9067.89
A_68_P30424512	chr15:89145509-89145553	NM_001081030:212	Sbf1	INSIDE	1.476	2.299	1415.78	3255.00	3.394	1200.13	4072.88
A_68_P31927885	chr19:5295364-5295408	NM_030109:69	Sf3b2	INSIDE	1.476	1.915	760.31	1456.16	2.828	580.86	1642.40
A_68_P25516577	chr7:136735544-136735588	NM_172255:190	Wdr11	INSIDE	1.476	2.364	1435.09	3393.22	3.491	1131.32	3949.42
A_68_P28729932	chr12:110032712-110032756	NM_009537:1214	Yy1	INSIDE	1.476	2.304	672.44	1549.27	3.400	504.55	1715.50
A_68_P24934667	chr6:147424670-147424714	NM_025911:300	Ccdc91	INSIDE	1.475	1.446	1335.79	1931.52	2.133	1180.74	2518.27
A_68_P31208746	chr17:46889025-46889069	NM_028065:115	Cnpy3	INSIDE	1.475	2.679	2370.77	6352.00	3.953	2092.09	8270.42
A_68_P22564417	chr3:137286650-137286694	NM_030143:37	Ddit4l	INSIDE	1.475	1.539	1359.15	2091.21	2.269	1223.36	2775.50
A_68_P25005644	chr7:25370658-25370702	NM_023154:-1881	Ethe1	PROMOTER	1.475	3.742	7705.46	28832.32	5.518	5065.39	27952.41
A_68_P31213683	chr17:47831917-47831961	NM_144939:-217	Frs3	DIVERGENT_PROMOTER	1.475	3.687	4050.49	14933.40	5.437	3058.19	16628.36
A_68_P28558333	chr12:78339907-78339951	NM_016893:-79	Fut8	PROMOTER	1.475	4.612	1535.76	7083.22	6.801	1349.59	9179.20
A_68_P31256045	chr17:56567492-56567536	NM_011218:48389	Ptprs	INSIDE	1.475	3.272	739.29	2419.22	4.827	634.65	3063.46
A_68_P30980682	chr16:94535261-94535305	ENSMUST00000163193:-112		PROMOTER	1.475	1.966	1953.55	3840.35	2.899	1530.36	4436.57
A_68_P22410430	chr3:107889618-107889662	NM_028779:-95	Ampd2	DIVERGENT_PROMOTER	1.474	2.476	2023.84	5010.93	3.650	1662.24	6066.48
A_68_P21105464	chr2:30683897-30683941	NM_133346:-98	Asb6	PROMOTER	1.474	2.095	2429.69	5091.41	3.090	1863.61	5758.05
A_68_P28731499	chr12:110271722-110271766	NM_001163175:34683	Begain	INSIDE	1.474	1.755	1061.50	1862.57	2.587	1268.33	3280.56
A_68_P22342938	chr3:95032702-95032746	NM_001038708:-149	Cdc42se1	PROMOTER	1.474	1.703	954.06	1624.94	2.511	824.34	2070.21
A_68_P24290981	chr6:22306235-22306279	NM_138587:-175	Fam3c	PROMOTER	1.474	2.029	914.58	1855.65	2.991	785.68	2350.17
A_68_P26676070	chr9:81757205-81757249	NM_175213:-124	Mei4	PROMOTER	1.474	5.220	1402.00	7318.95	7.693	1110.60	8544.04
A_68_P25090468	chr7:52241783-52241827	NM_019830:-102	Prmt1	PROMOTER	1.474	1.607	2363.69	3798.86	2.369	1816.10	4303.19
A_68_P24001336	chr5:114443642-114443686	NM_198109:102	Ssh1	INSIDE	1.474	4.300	884.83	3805.16	6.338	760.01	4816.69
A_68_P24425029	chr6:47893194-47893238	NR_027963:43	Zfp783	INSIDE	1.474	2.346	1905.66	4470.50	3.459	1740.08	6018.63
A_68_P32913428	A_68_P32913428			Unknown	1.474	2.135	546.97	1168.06	3.147	484.41	1524.41
A_68_P31936888	chr19:7026555-7026600	NM_007522:10233	Bad	DOWNSTREAM	1.473	1.814	420.70	763.12	2.671	360.42	962.84
A_68_P23327642	chr4:134829090-134829134	NM_013885:-437	Clic4	PROMOTER	1.473	2.877	1202.13	3458.33	4.238	1110.86	4707.56
A_68_P25307422	chr7:96553151-96553195	NM_008055:297	Fzd4	INSIDE	1.473	4.265	1247.89	5321.97	6.281	967.76	6078.42
A_68_P24991771	chr7:19742770-19742814	NM_001080815:8684	Gipr	INSIDE	1.473	1.415	964.19	1364.02	2.084	816.47	1701.45
A_68_P27279734	chr10:79383882-79383926	NM_053244:4189	Kiss1r	INSIDE	1.473	2.818	2528.95	7125.36	4.150	2110.00	8756.97
A_68_P22882678	chr4:45412906-45412950	NM_001009949:8710	Mcart1	INSIDE	1.473	3.680	1682.66	6191.40	5.420	1213.04	6574.76
A_68_P31947893	chr19:10092733-10092777	NM_144538:37	Rab3il1	INSIDE	1.473	2.026	2171.86	4400.28	2.985	1800.08	5373.28
A_68_P25434388	chr7:121260597-121260641	NM_025846:677	Rras2	INSIDE	1.473	2.462	1960.46	4826.78	3.626	1799.97	6525.85
A_68_P27942519	chr11:78115075-78115119	NM_017407:4	Spag5	INSIDE	1.473	1.878	1066.65	2003.56	2.767	949.08	2625.70
A_68_P28940415	chr13:34838970-34839014	NM_138746:7482	Fam50b	INSIDE	1.472	4.375	983.48	4303.21	6.443	877.56	5653.70
A_68_P24658385	chr6:94649976-94650020	NM_008377:141	Lrig1	INSIDE	1.472	2.625	1485.04	3898.55	3.863	1194.57	4614.70
A_68_P25957682	chr8:74116758-74116804	NM_025396:698	Pgls	INSIDE	1.472	3.782	238.51	902.11	5.567	196.15	1092.01
A_68_P32144302	chr19:46576160-46576204	NM_053100:45	Trim8	INSIDE	1.472	7.776	169.31	1316.65	11.445	147.21	1684.80

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28606269	chr12:87165967-87166011	NM_001081423:89	Ttll5	INSIDE	1.472	2.014	2091.25	4211.80	2.964	1633.16	4840.56
A_68_P27179603	chr10:60736419-60736463	NM_001081127:-254	Adamts14	PROMOTER	1.471	2.066	1282.18	2648.46	3.039	949.89	2886.88
A_68_P30221123	chr15:53177744-53177788	NM_010162:-28	Ext1	PROMOTER	1.471	2.194	858.05	1882.41	3.228	768.85	2481.85
A_68_P30278744	chr15:63829220-63829264	NM_144846:62768	Fam49b	INSIDE	1.471	2.677	3820.71	10227.82	3.938	3260.43	12839.04
A_68_P28470857	chr12:60320041-60320085	NM_001033156:408	Fbxo33	INSIDE	1.471	2.157	1060.35	2287.30	3.173	764.70	2426.15
A_68_P29631503	chr14:58694761-58694806	NM_013518:3261	Fgf9	INSIDE	1.471	2.692	4216.43	11351.25	3.960	2938.61	11637.08
A_68_P27946741	chr11:78858490-78858534	NM_013571:101344	Ksr1	INSIDE	1.471	5.982	3427.78	20503.67	8.798	2564.13	22559.04
A_68_P27284853	chr10:80153805-80153849	NM_172457:10739	Mobkl2a	INSIDE	1.471	1.689	400.71	676.92	2.485	310.65	771.97
A_68_P23364089	chr4:141001208-141001252	NM_009541:643	Zbtb17	INSIDE	1.471	1.663	1350.23	2246.10	2.446	1220.67	2986.11
A_68_P20148961	chr1:36604157-36604208	NM_026241:-136	Ankrd39	PROMOTER	1.470	2.684	1725.21	4631.27	3.947	1246.17	4918.90
A_68_P31458869	chr18:3507247-3507294	NM_026505:-684	Bambi	PROMOTER	1.470	5.395	495.23	2671.77	7.929	382.40	3032.14
A_68_P20561486	chr1:122238913-122238957	NM_207233:1776	C1ql2	INSIDE	1.470	1.678	855.66	1436.04	2.466	656.37	1618.88
A_68_P25610236	chr7:152129258-152129302	NM_007631:-3450	Ccnd1	PROMOTER	1.470	1.564	751.82	1175.58	2.299	574.03	1319.74
A_68_P31864637	chr18:80666392-80666436	NM_026295:-8	Ctdp1	PROMOTER	1.470	3.845	1779.09	6839.92	5.651	1596.78	9024.09
A_68_P31933635	chr19:6276972-6277016	NM_010119:99	Ehd1	INSIDE	1.470	1.513	1146.59	1734.21	2.224	911.20	2026.38
A_68_P26220864	chr8:123062616-123062660	NM_001145896:1330	Gse1	INSIDE	1.470	2.649	773.57	2049.13	3.893	694.67	2704.14
A_68_P24619086	chr6:87931330-87931374	NM_198622:124	H1fx	INSIDE	1.470	4.319	530.03	2289.23	6.347	452.06	2869.37
A_68_P30823193	chr16:65105676-65105720	NM_008310:-88	Htr1f	PROMOTER	1.470	3.713	536.70	1992.53	5.458	444.92	2428.27
A_68_P24759667	chr6:113419865-113419909	NM_001034029:10998	Il17re	INSIDE	1.470	4.822	1404.21	6771.30	7.088	1016.82	7207.65
A_68_P31029172	chr17:8994701-8994745	NM_011866:113	Pde10a	INSIDE	1.470	2.005	3853.22	7725.23	2.948	3130.87	9228.68
A_68_P32183825	chr19:53751761-53751805	NM_001170847:-13	Rbm20	PROMOTER	1.470	2.473	1485.31	3673.77	3.636	1185.94	4311.76
A_68_P23466247	chr5:8056554-8056598	NM_001080974:35	Sri	INSIDE	1.470	4.638	4087.16	18956.12	6.819	3246.30	22137.09
A_68_P25614882	chr8:3631030-3631074	NM_011503:-107	Stxbp2	DIVERGENT_PROMOTER	1.470	2.653	1940.51	5147.96	3.901	1699.86	6630.50
A_68_P31922247	chr19:4283414-4283458	NM_026720:-299	Ankrd13d	PROMOTER	1.469	3.237	851.81	2757.27	4.755	713.16	3391.01
A_68_P20347398	chr1:74283332-74283376	NM_029711:231	Arpc2	INSIDE	1.469	2.067	4621.98	9555.06	3.037	3605.94	10952.21
A_68_P26624019	chr9:71619304-71619348	NM_026599:83	Cgnl1	INSIDE	1.469	2.364	1632.58	3859.07	3.474	1414.90	4914.66
A_68_P24613526	chr6:86992962-86993006	NM_013528:145	Gfpt1	INSIDE	1.469	1.416	2116.35	2995.80	2.079	1656.41	3444.36
A_68_P27127237	chr10:49508470-49508514	NM_001111268:68	Grik2	INSIDE	1.469	2.389	940.44	2246.97	3.510	827.91	2906.39
A_68_P26954164	chr10:13687012-13687056	NM_010437:850	Hivep2	INSIDE	1.469	4.341	882.92	3832.82	6.377	692.35	4415.08
A_68_P29130726	chr13:72101391-72101435	NM_010573:-241	Irx1	PROMOTER	1.469	2.409	1015.37	2445.87	3.539	1123.70	3976.49
A_68_P27989203	chr11:86298068-86298112	NM_029788:-68	Rnft1	PROMOTER	1.469	3.318	3448.05	11440.91	4.873	2688.37	13099.53
A_68_P24590571	chr6:82889627-82889671	NM_011350:96	Sema4f	INSIDE	1.469	4.504	1390.53	6262.53	6.617	1245.93	8244.76
A_68_P21440134	chr2:94113837-94113881	ENSMUST00000167726:-8943		PROMOTER	1.469	2.315	5022.32	11624.23	3.399	4033.70	13711.46
A_68_P32704868	chrX:138159961-138160005	NM_010572:-222	Irs4	PROMOTER	1.468	1.836	1144.09	2100.11	2.695	660.25	1779.33
A_68_P25098813	chr7:53652081-53652125	NM_001112739:236	Kcnc1	INSIDE	1.468	4.084	1056.70	4316.07	5.996	1000.33	5997.67
A_68_P23331510	chr4:135528254-135528298	NM_011942:233	Lypla2	INSIDE	1.468	1.701	1471.16	2502.09	2.496	1180.83	2947.92
A_68_P28154417	chr11:115474024-115474068	NM_027162:-229	Mif4gd	PROMOTER	1.468	1.814	4942.93	8967.52	2.663	3768.32	10035.51
A_68_P31095629	chr17:24278798-24278842	NM_011062:-259	Pdpk1	PROMOTER	1.468	2.422	1361.05	3296.96	3.557	993.71	3534.40
A_68_P30348897	chr15:76353005-76353049	NM_130893:-467	Scrt1	PROMOTER	1.468	1.878	942.14	1769.61	2.757	740.71	2042.07
A_68_P22873079	chr4:43682099-43682143	NM_001085508:278	Tmem8b	INSIDE	1.468	3.001	2359.24	7081.21	4.405	1952.29	8600.32
A_68_P28166391	chr11:117517129-117517173	NM_198022:1548	Tnrc6c	INSIDE	1.468	2.606	2960.80	7715.59	3.825	2299.18	8794.43
A_68_P23576671	chr5:31441022-31441066	NM_021290:224	Ucn	INSIDE	1.468	3.501	2317.10	8112.83	5.142	1802.53	9267.79
A_68_P23272342	chr4:124805193-124805237	NM_153159:-89	Zc3h12a	PROMOTER	1.468	3.508	1523.15	5342.63	5.148	1237.05	6368.43
A_68_P23441289	chr4:155266283-155266327	NM_207223:321	Acap3	INSIDE	1.467	3.063	1838.00	5630.53	4.495	1604.68	7213.71
A_68_P32769554	chrX:154481205-154481249	NM_177751:-184	Cnksr2	PROMOTER	1.467	1.785	1035.89	1848.56	2.618	662.20	1733.68
A_68_P24009176	chr5:115798923-115798967	NM_007748:20	Cox6a1	INSIDE	1.467	3.389	3166.66	10730.30	4.969	2503.40	12440.52
A_68_P31347827	chr17:74059382-74059426	NM_027864:387	Galnt14	INSIDE	1.467	3.466	987.63	3423.01	5.085	958.75	4875.38
A_68_P31493066	chr18:11054906-11054950	NM_010258:2421	Gata6	INSIDE	1.467	4.748	2399.43	11393.63	6.966	2124.96	14802.92
A_68_P29581905	chr14:47993552-47993596	NM_001145953:40	Lgals3	INSIDE	1.467	2.547	2541.06	6470.88	3.736	2078.11	7763.12
A_68_P20806523	chr1:169619018-169619062	NM_033652:-648	Lmx1a	PROMOTER	1.467	3.092	1588.97	4913.37	4.536	1242.36	5635.68
A_68_P25934950	chr8:69384793-69384837	NM_001163564:699	Naf1	INSIDE	1.467	1.903	1890.51	3598.40	2.793	1778.06	4966.22

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31093355	chr17:23876913-23876957	NM_023824:363	Paqr4	INSIDE	1.467	1.879	1257.55	2362.82	2.756	997.12	2748.02
A_68_P31940079	chr19:7557572-7557616	NM_053076:177	Rtn3	INSIDE	1.467	1.906	2243.05	4274.38	2.795	1833.22	5124.16
A_68_P26892104	chr9:122832365-122832409	NM_009544:191	Zfp105	INSIDE	1.467	3.399	1751.18	5952.06	4.986	1650.02	8227.28
A_68_P25600927	chr7:150623918-150623962			Unknown	1.467	2.640	1461.25	3857.25	3.872	1226.22	4748.16
A_68_P32565204	chrX:98893057-98893101	ENSMUST00000073812:-5889		PROMOTER	1.467	6.825	7499.20	51181.65	10.011	3237.87	32412.92
A_68_P21105459	chr2:30683485-30683529	NM_133346:314	Asb6	INSIDE	1.466	1.854	831.64	1541.56	2.718	687.12	1867.83
A_68_P26235085	chr8:125202360-125202404	NM_001109873:-307	Cbfa2t3	PROMOTER	1.466	5.797	1592.00	9228.23	8.499	1563.32	13286.47
A_68_P25082512	chr7:50721931-50721975	NM_001164518:23441	Iglon5	DOWNSTREAM	1.466	6.673	1298.78	8666.90	9.782	1293.35	12651.86
A_68_P23560503	chr5:28397698-28397742	NM_153526:-231	Insig1	PROMOTER	1.466	2.699	830.23	2240.95	3.956	742.87	2938.95
A_68_P24838924	chr6:128374739-128374783	NM_133927:168	Itfg2	INSIDE	1.466	2.138	879.52	1880.20	3.135	701.85	2200.15
A_68_P21305453	chr2:68700233-68700278	NM_172856:642	Lass6	INSIDE	1.466	3.774	2495.47	9417.92	5.533	2252.29	12461.69
A_68_P32137226	chr19:45309781-45309825	NM_010691:-76	Lbx1	PROMOTER	1.466	11.283	1551.16	17502.06	16.539	1307.13	21618.77
A_68_P23260196	chr4:122673426-122673470	NM_008506:107	Mycl1	INSIDE	1.466	3.773	3472.25	13102.03	5.531	2920.99	16155.65
A_68_P23298638	chr4:129497304-129497348	NM_008974:-396	Ptp4a2	PROMOTER	1.466	2.069	1542.71	3191.27	3.033	1412.18	4283.62
A_68_P27949795	chr11:79404844-79404888	NM_175543:153	Rab11fip4	INSIDE	1.466	1.779	517.95	921.50	2.609	505.92	1319.93
A_68_P26569961	chr9:62190386-62190430	NM_009672:1259	Anp32a	INSIDE	1.465	2.912	3661.25	10661.31	4.265	2424.99	10342.80
A_68_P26135515	chr8:108231965-108232009	NM_198299:82	E130303B06Rik	INSIDE	1.465	2.072	5535.37	11468.49	3.036	4238.37	12868.85
A_68_P21940379	chr3:10012439-10012483	NM_010634:-145	Fabp5	PROMOTER	1.465	3.164	4173.05	13202.55	4.634	3534.74	16381.28
A_68_P21338643	chr2:74506367-74506411	NM_008275:22	Hoxd13	INSIDE	1.465	1.856	2823.18	5239.55	2.719	2470.82	6719.12
A_68_P25016216	chr7:28013358-28013402	NM_181593:236	Itpkc	INSIDE	1.465	1.916	810.49	1553.14	2.808	728.28	2045.11
A_68_P28290827	chr12:25336485-25336529	NM_178357:271	Klf11	INSIDE	1.465	1.528	4868.62	7437.65	2.239	3523.30	7887.89
A_68_P25617732	chr8:4493215-4493259	NM_026058:-168	Lass4	PROMOTER	1.465	2.568	11509.06	29554.92	3.763	7642.87	28758.22
A_68_P24159372	chr5:144861058-144861106	NM_001081109:-222	Lmtk2	PROMOTER	1.465	2.419	1587.58	3840.24	3.544	1278.35	4530.73
A_68_P31296466	chr17:64951197-64951241	NM_008549:230	Man2a1	INSIDE	1.465	1.975	798.17	1576.45	2.894	699.34	2024.02
A_68_P32384750	chrX:50265645-50265689	NM_027642:224	Phf6	INSIDE	1.465	2.584	518.16	1338.87	3.786	317.74	1202.89
A_68_P28103448	chr11:106640841-106640885	NM_015810:-11	Polg2	PROMOTER	1.465	2.977	1175.26	3498.35	4.361	987.01	4303.98
A_68_P31303252	chr17:66234323-66234367	NM_001198949:-81	Ralbp1	PROMOTER	1.465	2.500	1059.86	2650.05	3.662	858.46	3143.61
A_68_P25050063	chr7:36370599-36370643	NM_145840:-19	Rgs9bp	DIVERGENT_PROMOTER	1.465	2.928	2932.41	8585.37	4.289	2328.77	9987.40
A_68_P22049391	chr3:34549338-34549382	NM_011443:434	Sox2	INSIDE	1.465	2.631	565.14	1486.72	3.854	461.29	1777.59
A_68_P31210123	chr17:47147224-47147268	NM_001177374:235	Ubr2	INSIDE	1.465	2.951	1438.47	4244.75	4.324	1223.15	5288.34
A_68_P20737709	chr1:157263929-157263973	NM_011273:624	Xpr1	INSIDE	1.465	1.630	3904.60	6363.37	2.387	3173.16	7575.19
A_68_P29478601	chr14:26427680-26427724	NM_183208:149032	Zmiz1	INSIDE	1.465	3.821	2002.18	7651.11	5.600	1832.49	10261.89
A_68_P24044663	chr5:121902036-121902080	NM_026129:425	Erp29	INSIDE	1.464	2.054	1586.70	3258.30	3.006	1213.06	3646.79
A_68_P24397652	chr6:42273788-42273832	NM_001113327:829	Fam131b	INSIDE	1.464	1.928	4011.99	7734.52	2.823	2915.36	8228.84
A_68_P27087305	chr10:40792189-40792233	NM_199058:-820	Gpr6	PROMOTER	1.464	2.788	1679.17	4680.85	4.082	1357.03	5538.88
A_68_P24249109	chr6:13788674-13788718	NM_145066:1152	Gpr85	INSIDE	1.464	2.339	811.08	1896.88	3.423	698.33	2390.38
A_68_P29186150	chr13:83662891-83662935	NM_001170537:19880	Mef2c	INSIDE	1.464	2.933	282.49	828.67	4.294	332.88	1429.43
A_68_P26977748	chr10:18564800-18564844	NM_022032:-54	Perp	PROMOTER	1.464	4.788	899.74	4307.54	7.009	868.93	6090.44
A_68_P25262772	chr7:86866415-86866459	NM_001113471:11226	Plin1	INSIDE	1.464	1.697	461.93	784.11	2.484	394.86	981.02
A_68_P29033142	chr13:51662332-51662377	NM_009167:99	Shc3	INSIDE	1.464	2.474	2443.96	6045.47	3.622	2096.84	7594.48
A_68_P27915805	chr11:73013090-73013134	NM_029031:129	Shpk	INSIDE	1.464	4.681	893.22	4181.24	6.852	813.06	5571.09
A_68_P32341125	chrX:39502207-39502251	NM_001077712:-360	Stag2	PROMOTER	1.464	3.496	726.62	2540.10	5.118	473.46	2423.23
A_68_P20186939	chr1:43149198-43149242	NM_001013025:6247	Tgfbrap1	INSIDE	1.464	1.582	1869.01	2956.34	2.316	1806.50	4183.12
A_68_P26349635	chr9:21741759-21741803	NM_144935:-937	BC018242	PROMOTER	1.463	2.870	814.01	2336.54	4.200	613.10	2574.99
A_68_P23895412	chr5:93104159-93104203	NM_177230:-27	Ccdc158	DIVERGENT_PROMOTER	1.463	2.184	2971.54	6488.40	3.195	2388.53	7632.27
A_68_P28727032	chr12:109512870-109512914	NM_001159910:735	Ccdc85c	INSIDE	1.463	3.637	1292.84	4702.43	5.322	989.31	5264.62
A_68_P27495835	chr10:119638550-119638594	NM_028679:21	Irak3	INSIDE	1.463	1.455	1018.19	1481.09	2.128	954.18	2030.95
A_68_P24623141	chr6:88577383-88577427	NM_001142724:35	Kbtbd12	INSIDE	1.463	1.486	1134.15	1685.45	2.174	954.46	2075.22
A_68_P30363285	chr15:78765693-78765737	NM_133800:352	Nol12	INSIDE	1.463	2.228	927.44	2066.66	3.260	731.54	2384.58
A_68_P30167378	chr15:41620567-41620611	NM_001130163:-472	Oxr1	PROMOTER	1.463	5.835	1351.56	7886.92	8.537	1228.20	10485.06
A_68_P20015305	chr1:7078905-7078949	NM_183028:-74	Pcmtd1	PROMOTER	1.463	1.868	1307.36	2442.13	2.733	1061.13	2900.19

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25435751	chr7:121559514-121559558	NM_011055:769	Pde3b	INSIDE	1.463	5.170	900.72	4656.88	7.565	729.69	5520.09
A_68_P25504895	chr7:134417127-134417171	NM_009266:425	Sephs2	INSIDE	1.463	2.790	990.62	2763.79	4.081	1003.94	4097.31
A_68_P25482572	chr7:130267793-130267837	NM_144925:416	Tnrc6a	INSIDE	1.463	2.144	694.03	1488.05	3.136	563.02	1765.67
A_68_P33008823	chr4_random:109636-109680	NM_001033326:-143	Dhrsx	PROMOTER	1.462	5.931	7787.85	46191.47	8.670	5024.52	43561.95
A_68_P24218878	chr6:6831381-6831425	NM_010056:666	Dlx5	INSIDE	1.462	1.541	1552.47	2392.93	2.253	1183.51	2666.48
A_68_P32263511	chrX:12338951-12338995	NM_001048208:127	Med14	INSIDE	1.462	2.879	1207.83	3477.80	4.208	984.15	4141.68
A_68_P23618575	chr5:38668403-38668447	NM_172709:-218	Otop1	PROMOTER	1.462	1.997	3392.73	6775.24	2.920	2565.88	7491.60
A_68_P21417957	chr2:90420274-90420318	NM_008982:508	Ptprj	INSIDE	1.462	3.067	1620.25	4968.54	4.483	1335.27	5985.98
A_68_P29605618	chr14:52877257-52877301	NM_172601:21792	Rab2b	DOWNSTREAM	1.462	2.734	2916.60	7973.69	3.998	2339.42	9352.89
A_68_P31302582	chr17:66121758-66121802	NM_133685:312	Rab31	INSIDE	1.462	2.303	5249.27	12088.18	3.368	4134.74	13924.93
A_68_P31924143	chr19:4625643-4625687	NM_023131:-47	Rce1	PROMOTER	1.462	1.354	1807.90	2447.64	1.980	1502.27	2973.96
A_68_P21568741	chr2:119096977-119097021	NM_145530:-36	Rhov	PROMOTER	1.462	2.931	2635.94	7726.37	4.286	2156.95	9244.83
A_68_P21911578	chr2:181333602-181333646	NM_172676:228	Samd10	INSIDE	1.462	1.779	1637.73	2913.00	2.601	1257.33	3269.68
A_68_P31929910	chr19:5654473-5654517	NM_001164480:9213	Sipa1	INSIDE	1.462	1.743	4619.05	8051.53	2.549	3528.01	8992.71
A_68_P22611968	chr3:145651227-145651271	NM_001166064:415	Syde2	INSIDE	1.462	2.559	707.01	1809.58	3.743	622.20	2329.01
A_68_P25581340	chr7:147130450-147130494	NM_009482:718	Utf1	INSIDE	1.462	1.579	3203.71	5057.77	2.308	2204.81	5089.26
A_68_P29455108	chr14:22650786-22650830	NM_011695:26	Vdac2	INSIDE	1.462	8.363	669.25	5597.08	12.226	576.83	7052.33
A_68_P21775097	chr2:156904527-156904571	NM_001164663:453	9830001H06Rik	INSIDE	1.461	6.751	1401.95	9464.94	9.864	1289.26	12716.90
A_68_P27339932	chr10:90545143-90545187	NM_001042558:324	Apaf1	INSIDE	1.461	1.626	581.25	944.94	2.375	514.37	1221.49
A_68_P28525541	chr12:72419505-72419549	NM_001190466:8656	Dact1	INSIDE	1.461	3.271	948.47	3102.20	4.779	740.23	3537.29
A_68_P27540020	chr10:127631671-127631715	NM_001033264:2	Gls2	INSIDE	1.461	2.403	1119.85	2691.21	3.510	1006.38	3532.25
A_68_P22028772	chr3:30407701-30407745	NM_021442:687	Mecom	INSIDE	1.461	2.306	973.83	2245.24	3.368	814.47	2742.77
A_68_P32148151	chr19:47253878-47253922	NM_021360:591	Neurl1a	INSIDE	1.461	3.015	2347.76	7079.64	4.406	2046.66	9017.99
A_68_P20641449	chr1:137662705-137662749	NM_013750:65	Phlda3	INSIDE	1.461	3.491	4817.35	16815.45	5.101	4035.59	20586.57
A_68_P27163773	chr10:57909758-57909803	NM_011240:181	Ranbp2	INSIDE	1.461	2.070	1044.40	2161.81	3.024	955.85	2890.17
A_68_P21494381	chr2:105239586-105239630	NM_009037:-132	Rcn1	PROMOTER	1.461	2.834	960.25	2720.91	4.141	859.45	3559.00
A_68_P28031422	chr11:94072689-94072733	NM_009427:-57	Tob1	PROMOTER	1.461	2.069	3383.56	6999.79	3.022	2629.56	7945.46
A_68_P20451933	chr1:94803719-94803763	NM_175118:175	Dusp28	INSIDE	1.460	1.836	1000.17	1836.32	2.680	851.65	2282.69
A_68_P31424359	chr17:88039798-88039842	NM_008532:4502	Epcam	INSIDE	1.460	2.523	659.90	1665.23	3.684	541.12	1993.23
A_68_P25018411	chr7:28443445-28443489	NM_001081292:16151	Map3k10	INSIDE	1.460	2.763	3810.58	10527.58	4.033	2767.38	11161.07
A_68_P26539664	chr9:56843551-56843595	NM_019651:798	Ptpn9	INSIDE	1.460	2.050	548.75	1125.07	2.993	444.66	1330.79
A_68_P32099689	chr19:38199320-38199364	NM_011255:-41	Rbp4	PROMOTER	1.460	2.293	652.67	1496.39	3.348	581.81	1947.91
A_68_P20833904	chr1:174493216-174493260	NR_027644:3202	Vsig8	INSIDE	1.460	1.492	1794.63	2677.71	2.178	1418.87	3090.24
A_68_P31468065	chr18:5334203-5334247	NM_178722:213	Zfp438	INSIDE	1.460	3.748	1186.50	4446.93	5.472	1077.59	5896.12
A_68_P24438776	chr6:50516749-50516793	NR_015581:129	5430402O13Rik	INSIDE	1.459	1.688	1333.34	2251.10	2.464	1109.36	2733.16
A_68_P28553305	chr12:77425730-77425774	NM_001101471:-125	Akap5	PROMOTER	1.459	5.759	2747.26	15821.81	8.404	2184.46	18357.78
A_68_P27080339	chr10:39451377-39451421	NR_038037:415	E130307A14Rik	INSIDE	1.459	2.576	3212.43	8274.16	3.759	2879.49	10823.71
A_68_P21107216	chr2:30997021-30997065	NM_001038700:486	Fnbp1	INSIDE	1.459	1.721	1615.84	2780.84	2.510	1425.03	3576.91
A_68_P23510646	chr5:17866146-17866190	NM_010305:63	Gnai1	INSIDE	1.459	2.612	1092.96	2855.21	3.812	932.74	3555.40
A_68_P31381047	chr17:80461465-80461509	NM_144802:188	Hnrpll	INSIDE	1.459	5.020	1241.74	6233.03	7.323	1099.87	8054.72
A_68_P31826505	chr18:73732011-73732055	NM_001039214:-326	Mex3c	PROMOTER	1.459	1.754	2862.22	5019.82	2.558	2182.65	5583.74
A_68_P21839356	chr2:167906923-167906967	NM_021409:441	Pard6b	INSIDE	1.459	1.612	1921.41	3097.64	2.352	1712.76	4027.98
A_68_P22874082	chr4:43888324-43888368	NM_016678:-55	Reck	PROMOTER	1.459	4.573	1315.45	6015.70	6.671	1076.68	7182.01
A_68_P23325608	chr4:134487062-134487106	NM_026780:190	Syf2	INSIDE	1.459	1.768	617.65	1092.25	2.580	512.56	1322.59
A_68_P30476484	chr15:98623292-98623336	NM_021279:3027	Wnt1	INSIDE	1.459	5.005	944.81	4728.35	7.304	680.07	4966.93
A_68_P23244790	chr4:118967092-118967136	NM_011732:4	Ybx1	INSIDE	1.459	1.877	4211.74	7907.02	2.739	2896.16	7932.24
A_68_P27873632	chr11:65621027-65621071	NM_026107:303	Zkscan6	INSIDE	1.459	3.212	942.34	3027.10	4.688	847.63	3973.56
A_68_P21101977	chr2:30093187-30093231	NR_028299:-57	1700084E18Rik	DIVERGENT_PROMOTER	1.458	2.115	2810.65	5945.31	3.085	2342.34	7225.85
A_68_P25933298	chr8:69010075-69010123	NM_025465:308	1810029B16Rik	INSIDE	1.458	2.297	420.54	965.79	3.349	366.75	1228.11
A_68_P26273049	chr9:3199691-3199735	NR_027988:101	4930433N12Rik	INSIDE	1.458	9.650	3965.00	38263.77	14.072	2614.39	36790.53
A_68_P28002759	chr11:88725539-88725583	NM_001042541:340	Akap1	INSIDE	1.458	1.390	1362.89	1894.77	2.028	1133.86	2298.98

						Sham group			TiO$_2$-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P21023862	chr2:14976924-14976968	NM_029466:-42	Arl5b	DIVERGENT_PROMOTER	1.458	1.951	1371.22	2675.65	2.845	1248.84	3552.80
A_68_P27954537	chr11:80290536-80290580	NM_009871:11	Cdk5r1	INSIDE	1.458	3.634	10555.96	38360.57	5.299	9525.91	50479.30
A_68_P28202614	chr12:4848201-4848245	NM_016863:179	Fkbp1b	INSIDE	1.458	3.457	890.42	3078.30	5.040	753.94	3799.81
A_68_P29542521	chr14:37781798-37781842	NM_027045:130	Gcap14	INSIDE	1.458	1.822	1608.46	2930.62	2.657	1283.32	3409.15
A_68_P25092916	chr7:52661724-52661768	NM_010596:417	Kcna7	INSIDE	1.458	3.884	1484.75	5766.07	5.663	1337.18	7572.44
A_68_P22393168	chr3:104591684-104591728	NM_007484:-245	Rhoc	PROMOTER	1.458	3.384	2910.92	9851.91	4.934	2172.18	10716.60
A_68_P24939589	chr6:148303183-148303227	NR_003634:27	Rps4y2	INSIDE	1.458	2.311	403.52	932.55	3.369	366.69	1235.46
A_68_P22324942	chr3:90193856-90193900	NM_011988:-29	Slc27a3	PROMOTER	1.458	2.853	781.53	2229.86	4.159	719.70	2993.24
A_68_P21328883	chr2:72818359-72818403	NM_001098425:-1042	Sp3	PROMOTER	1.458	3.094	36100.64	111680.40	4.510	29854.51	134653.00
A_68_P26875611	chr9:119920380-119920424	NM_011724:12314	Xirp1	DOWNSTREAM	1.458	2.503	1178.16	2949.18	3.649	919.22	3354.32
A_68_P21575995	chr2:120389596-120389640	NM_011743:-51	Zfp106	DIVERGENT_PROMOTER	1.458	2.231	4259.53	9503.35	3.253	3837.58	12482.20
A_68_P21863763	chr2:172171241-172171285	NM_025912:186	2010011I20Rik	INSIDE	1.457	2.311	1062.68	2455.68	3.367	931.57	3136.61
A_68_P27843669	chr11:60351870-60351914	NM_172943:708	Alkbh5	INSIDE	1.457	3.672	929.96	3414.82	5.351	763.55	4085.77
A_68_P25957072	chr8:74009934-74009979	NM_001164679:10	Ano8	INSIDE	1.457	1.346	2736.69	3683.83	1.961	2053.58	4026.41
A_68_P28195048	chr12:3427213-3427257	NM_172421:351	Asxl2	INSIDE	1.457	3.449	1549.18	5343.48	5.026	1221.20	6137.28
A_68_P28731660	chr12:110290621-110290665	NM_001163175:15785	Begain	INSIDE	1.457	3.320	520.84	1728.97	4.836	521.48	2521.94
A_68_P28082431	chr11:102807578-102807622	NM_011795:175	C1ql1	INSIDE	1.457	6.794	514.32	3494.08	9.896	465.73	4609.07
A_68_P31022586	chr17:6987747-6987791	NM_009510:-639	Ezr	PROMOTER	1.457	1.571	752.56	1182.48	2.289	639.94	1464.77
A_68_P22483671	chr3:122323019-122323074	NM_001114665:-461	Fnbp1l	PROMOTER	1.457	3.387	944.45	3198.37	4.933	826.14	4075.32
A_68_P21052792	chr2:20891136-20891180	NR_033225:658	Gm13375	INSIDE	1.457	4.676	1729.00	8084.67	6.813	1409.02	9600.07
A_68_P25842949	chr8:48760597-48760641	NM_023503:-105	Ing2	PROMOTER	1.457	2.518	1788.88	4503.57	3.668	1504.15	5517.81
A_68_P20166596	chr1:39634041-39634085	NM_001033135:130	Rnf149	INSIDE	1.457	2.325	1362.29	3166.74	3.386	1243.87	4211.82
A_68_P20638511	chr1:137180229-137180273	NM_001159624:411	Rnpep	INSIDE	1.457	2.202	1517.55	3341.03	3.207	1262.64	4049.56
A_68_P30970962	chr16:92698887-92698931	NM_001111023:-1335	Runx1	PROMOTER	1.457	1.835	641.32	1176.91	2.675	530.30	1418.40
A_68_P24803059	chr6:121195955-121195999	NM_011909:53	Usp18	INSIDE	1.457	2.204	926.39	2041.83	3.212	1000.99	3215.04
A_68_P26815586	chr9:108481063-108481107	NM_031392:-83	Wdr6	PROMOTER	1.457	2.069	1765.90	3654.08	3.015	1426.63	4301.72
A_68_P23575215	chr5:31191120-31191164	NM_174849:-82	Agbl5	PROMOTER	1.456	2.933	607.02	1780.58	4.272	413.55	1766.63
A_68_P33005169	chr7:3366442-3366487	NM_133189:29780	Cacng7	INSIDE	1.456	1.529	1339.66	2048.53	2.227	991.30	2207.71
A_68_P23792211	chr5:72895109-72895153	NM_016869:317	Corin	INSIDE	1.456	1.865	1598.60	2981.29	2.716	1215.77	3302.39
A_68_P23416728	chr4:151505797-151505841	NM_019585:-2784	Espn	PROMOTER	1.456	1.612	1539.60	2481.95	2.346	1367.83	3209.46
A_68_P30630418	chr16:28446840-28446884	NM_183064:-1549	Fgf12	PROMOTER	1.456	2.036	569.25	1158.74	2.964	537.05	1591.64
A_68_P29388379	chr14:9046505-9046549	NM_027782:-135	Kctd6	PROMOTER	1.456	6.924	4007.28	27747.18	10.079	3170.03	31951.83
A_68_P24325043	chr6:29129618-29129662	NM_001101443:-56	Prrt4	PROMOTER	1.456	7.255	8481.06	61526.61	10.564	6185.29	65343.71
A_68_P31102749	chr17:25410196-25410240	NM_001177610:158	Ube2i	INSIDE	1.456	2.075	1046.40	2171.19	3.020	923.66	2789.66
A_68_P27997644	chr11:87881461-87881505	NM_016686:-360	Vezf1	PROMOTER	1.456	1.830	2438.54	4462.54	2.665	2358.99	6286.77
A_68_P23957857	chr5:106305585-106305629	NM_018759:20	Zfp326	INSIDE	1.456	2.246	415.39	932.83	3.269	423.88	1385.76
A_68_P31134871	chr17:30713349-30713393	NM_027060:-138	Btbd9	PROMOTER	1.455	2.181	1117.76	2438.28	3.173	1010.81	3207.63
A_68_P24993219	chr7:20006500-20006544	NM_007710:10080	Ckm	INSIDE	1.455	2.148	1288.84	2768.37	3.125	1070.58	3345.70
A_68_P23345560	chr4:137951782-137951826	NM_001081672:569	Fam43b	INSIDE	1.455	3.959	706.97	2799.21	5.763	601.77	3467.91
A_68_P23582152	chr5:32437568-32437612	NM_008037:-1254	Fosl2	PROMOTER	1.455	4.137	641.42	2653.38	6.018	616.21	3708.17
A_68_P31515586	chr18:15222359-15222403	NM_001142731:-289	Kctd1	PROMOTER	1.455	1.733	1386.30	2403.07	2.523	1097.60	2769.12
A_68_P27785188	chr11:49660391-49660435	NM_001163671:160	Mapk9	INSIDE	1.455	1.566	1886.97	2955.07	2.278	1586.85	3614.59
A_68_P25981540	chr8:79709769-79709813	NM_001083906:283384	Nr3c2	INSIDE	1.455	3.288	943.76	3102.85	4.785	725.24	3470.35
A_68_P20163208	chr1:39044668-39044712	NM_026850:32	Pdcl3	INSIDE	1.455	3.480	2919.10	10159.42	5.065	2028.94	10275.96
A_68_P27430008	chr10:107599648-107599692	NM_027892:215	Ppp1r12a	INSIDE	1.455	2.288	1378.25	3153.33	3.330	1209.49	4027.44
A_68_P24691288	chr6:100237003-100237047	NM_019743:328	Rybp	INSIDE	1.455	3.187	1046.04	3333.77	4.638	817.40	3791.10
A_68_P22286842	chr3:83569940-83569984	NM_009144:-280	Sfrp2	PROMOTER	1.455	1.712	2189.69	3748.71	2.492	1691.78	4215.27
A_68_P29052701	chr13:55097633-55097677	NM_153131:46862	Unc5a	INSIDE	1.455	2.295	1681.83	3859.82	3.339	1344.53	4489.11
A_68_P24979386	chr7:16647485-16647529	NM_001099277:-9784	Zfp541	PROMOTER	1.455	3.901	6432.66	25096.37	5.677	4589.99	26058.32
A_68_P30379093	chr15:81524108-81524152	NM_001164320:3587	Chadl	INSIDE	1.454	3.450	292.29	1008.53	5.017	330.10	1656.11
A_68_P24818548	chr6:125031803-125031847	NM_001163268:10530	Lpar5	INSIDE	1.454	1.700	1581.55	2689.12	2.473	1399.54	3460.97

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P23227558	chr4:115748182-115748226	NM_153521:135	Lrrc41	INSIDE	1.454	3.338	1274.86	4255.23	4.853	1149.75	5579.65
A_68_P21780569	chr2:157854821-157854865	NM_027434:313	Rprd1b	INSIDE	1.454	1.517	1485.79	2254.60	2.206	1097.49	2420.89
A_68_P31331151	chr17:71202362-71202406	NM_001164075:-1310	Tgif1	PROMOTER	1.454	2.468	1761.00	4345.77	3.589	1299.47	4663.50
A_68_P25850571	chr8:49928417-49928461	AK013771:58		INSIDE	1.454	2.771	1314.67	3642.66	4.028	1193.16	4806.45
A_68_P32217229	chr19:59150385-59150429	NM_001114312:153	4930506M07Rik	INSIDE	1.453	1.820	399.24	726.66	2.645	346.26	915.90
A_68_P31053606	chr17:12934729-12934773	NR_002853:574	Airn	INSIDE	1.453	3.100	634.08	1965.72	4.503	625.99	2819.07
A_68_P28925107	chr13:31900007-31900051	NM_008592:1514	Foxc1	INSIDE	1.453	2.368	1067.03	2527.10	3.441	888.61	3058.02
A_68_P29660091	chr14:63865134-63865179	NM_008092:-1059	Gata4	PROMOTER	1.453	7.098	511.45	3630.21	10.310	404.51	4170.34
A_68_P22898182	chr4:48060289-48060333	NM_015743:-3809	Nr4a3	PROMOTER	1.453	2.764	766.56	2118.88	4.017	589.66	2368.92
A_68_P26574084	chr9:62990320-62990364	NM_172446:4445	Skor1	INSIDE	1.453	2.763	1499.36	4143.06	4.015	1218.84	4894.05
A_68_P28938195	chr13:34436488-34436532	NM_001033167:541	Slc22a23	INSIDE	1.453	2.762	403.59	1114.57	4.014	358.05	1437.23
A_68_P24118171	chr5:136328011-136328055	NM_021403:34057	Srrm3	INSIDE	1.453	3.840	1032.86	3965.69	5.579	906.14	5055.25
A_68_P21751498	chr2:152673870-152673914	NM_001141975:193	Tpx2	INSIDE	1.453	2.514	2648.33	6656.99	3.651	2122.21	7748.70
A_68_P24979385	chr7:16647414-16647458	NM_001099277:-9854	Zfp541	PROMOTER	1.453	4.543	2956.79	13432.03	6.600	2184.19	14415.65
A_68_P25174399	chr7:71082777-71082821	NM_021366:1003	Klf13	INSIDE	1.452	4.175	3133.31	13082.74	6.062	2360.67	14310.05
A_68_P22887154	chr4:46151513-46151557	NM_001033201:152	Ncbp1	INSIDE	1.452	1.423	840.75	1196.44	2.066	754.96	1559.62
A_68_P27230706	chr10:70062237-70062281	NM_178621:-219	Phyhipl	PROMOTER	1.452	2.073	7987.04	16559.84	3.011	6789.13	20438.82
A_68_P32785482	chrX:158155524-158155568	NM_198409:62	Rai2	INSIDE	1.452	4.180	1229.62	5140.23	6.068	905.40	5493.85
A_68_P20157823	chr1:38186758-38186802	NM_019570:-273	Rev1	PROMOTER	1.452	2.296	1303.21	2992.19	3.335	1132.40	3776.31
A_68_P22753435	chr4:16090304-16090348	NM_138952:319	Ripk2	INSIDE	1.452	2.680	1070.14	2867.87	3.891	950.19	3697.39
A_68_P20885441	chr1:184054789-184054833	NM_012058:-57	Srp9	PROMOTER	1.452	2.437	1536.69	3744.66	3.539	1275.05	4512.09
A_68_P24954139	chr7:6084115-6084159	NM_001013012:23437	Zfp787	INSIDE	1.452	2.746	1342.01	3685.47	3.988	1257.91	5016.35
A_68_P30284251	chr15:64752515-64752559	NM_009623:1322	Adcy8	INSIDE	1.451	3.100	1343.62	4165.22	4.499	1107.10	4981.16
A_68_P20886156	chr1:184271169-184271213	NM_175127:547	Fbxo28	INSIDE	1.451	2.477	645.07	1597.68	3.593	543.63	1953.12
A_68_P21840388	chr2:168088389-168088433	NM_001081134:6421	Kcng1	INSIDE	1.451	1.671	942.82	1575.61	2.425	706.71	1713.57
A_68_P25176078	chr7:71432596-71432640	NM_172742:63	Mtmr10	INSIDE	1.451	1.816	781.96	1419.94	2.635	718.56	1893.58
A_68_P23239263	chr4:117933446-117933490	NM_011213:30534	Ptprf	INSIDE	1.451	6.603	3880.11	25620.73	9.581	3001.41	28755.82
A_68_P21476820	chr2:102240650-102240694	NM_020267:385	Trim44	INSIDE	1.451	2.474	373.14	923.15	3.591	352.20	1264.71
A_68_P30570063	chr16:16599690-16599734	ENSMUST00000162671:359		INSIDE	1.451	4.347	10461.80	45473.02	6.307	7454.08	47015.58
A_68_P24816769	chr6:124695789-124695833	NM_007881:10695	Atn1	INSIDE	1.450	6.660	552.01	3676.21	9.657	451.90	4364.14
A_68_P26600872	chr9:67607645-67607689	NM_001081314:423	C2cd4b	INSIDE	1.450	3.347	1542.11	5161.61	4.852	1305.26	6332.76
A_68_P25954643	chr8:73397351-73397395	NM_026964:17	Ccdc124	INSIDE	1.450	1.547	1591.20	2461.74	2.243	1363.71	3058.24
A_68_P24334443	chr6:30846924-30846968	NM_017478:-186	Copg2	PROMOTER	1.450	6.673	2212.72	14766.05	9.679	1733.39	16776.79
A_68_P32092666	chr19:36993233-36993277	NM_028263:835	Fgfbp3	INSIDE	1.450	6.685	1885.91	12606.49	9.692	1657.17	16061.23
A_68_P24610513	chr6:86475289-86475333	NM_011865:849	Pcbp1	INSIDE	1.450	3.509	1375.79	4827.22	5.088	1197.78	6094.21
A_68_P25092562	chr7:52601979-52602025	NM_029741:20387	Ppfia3	INSIDE	1.450	7.101	288.86	2051.21	10.300	297.84	3067.79
A_68_P24090826	chr5:130293163-130293207	NM_133900:-55	Psph	DIVERGENT_PROMOTER	1.450	3.228	1767.44	5705.91	4.680	1507.77	7055.94
A_68_P27325556	chr10:87922749-87922793	NM_011517:439	Sycp3	INSIDE	1.450	9.760	7040.68	68715.96	14.156	4470.72	63288.14
A_68_P25011335	chr7:26473118-26473162	NM_011577:1120	Tgfb1	INSIDE	1.450	4.692	406.37	1906.80	6.804	351.15	2389.26
A_68_P20302822	chr1:66514910-66514954	NM_175510:-88	Unc80	PROMOTER	1.450	1.796	1118.10	2008.23	2.605	909.12	2368.43
A_68_P26084570	chr8:98201548-98201592	ENSMUST00000041318:-414		PROMOTER	1.450	1.955	3405.68	6657.29	2.835	2737.00	7759.89
A_68_P23328301	chr4:134954162-134954206	NM_001168500:-42	A330049M08Rik	PROMOTER	1.449	2.446	11938.32	29200.64	3.544	9050.21	32075.46
A_68_P23264562	chr4:123427164-123427208	NM_023423:356	Akirin1	INSIDE	1.449	3.460	686.55	2375.57	5.014	603.99	3028.44
A_68_P24120341	chr5:136751221-136751265	NM_198602:292033	Cux1	INSIDE	1.449	2.086	434.49	906.44	3.023	389.30	1176.94
A_68_P28072079	chr11:100980744-100980788	NM_026501:372	Fam134c	INSIDE	1.449	2.544	5815.49	14794.36	3.687	3975.99	14659.23
A_68_P27787811	chr11:50105373-50105417	NM_175334:444	Maml1	INSIDE	1.449	1.874	448.97	841.25	2.716	406.52	1103.98
A_68_P31296462	chr17:64950677-64950721	NM_008549:-290	Man2a1	PROMOTER	1.449	3.363	771.63	2595.34	4.873	652.61	3180.49
A_68_P23318794	chr4:133228762-133228806	NM_001145955:-222	Pigv	PROMOTER	1.449	2.193	1112.08	2438.55	3.177	1046.86	3326.16
A_68_P28956736	chr13:37918899-37918943	NM_001039188:-341	Rreb1	PROMOTER	1.449	7.469	673.49	5030.59	10.824	647.42	7007.82
A_68_P21101100	chr2:29918302-29918346	NM_001204875:-3669	Set	PROMOTER	1.449	3.154	2323.74	7328.64	4.570	1936.20	8849.05
A_68_P25618724	chr8:4779472-4779516	NM_011369:40	Shcbp1	INSIDE	1.449	2.534	676.91	1715.14	3.672	595.88	2188.15

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31259834	chr17:57199854-57199898	NM_025877:-590	Slc25a23	DIVERGENT_PROMOTER	1.449	2.701	1618.44	4371.00	3.912	1334.36	5220.64
A_68_P26828805	chr9:111214091-111214135	NM_001164659:-130	Trank1	PROMOTER	1.449	1.976	1514.65	2993.04	2.863	1318.17	3774.06
A_68_P23195055	chr4:107890802-107890861	NM_001167936:-304	Zyg11a	PROMOTER	1.449	1.839	675.01	1241.37	2.664	614.10	1636.04
A_68_P26016847	chr8:86399178-86399222			Unknown	1.449	2.692	1231.64	3315.53	3.901	1043.50	4070.90
A_68_P21040878	chr2:18610287-18610336	NM_007552:11667	Bmi1	DOWNSTREAM	1.448	3.632	294.61	1069.87	5.260	290.08	1525.82
A_68_P28068816	chr11:100436337-100436381	NM_001146318:-846	Cnp	PROMOTER	1.448	2.750	627.90	1726.48	3.980	661.69	2633.81
A_68_P27480860	chr10:116813708-116813752	NM_001013391:299	Cpsf6	INSIDE	1.448	1.714	752.02	1289.24	2.483	783.49	1945.15
A_68_P25470625	chr7:127986822-127986866	NM_007908:448	Eef2k	INSIDE	1.448	2.070	1084.98	2245.87	2.996	836.11	2505.35
A_68_P23250309	chr4:119940503-119940547	NM_194060:19342	Foxo6	INSIDE	1.448	2.395	1510.25	3616.72	3.469	1410.17	4891.28
A_68_P27284036	chr10:80031664-80031708	NM_078477:8355	Klf16	INSIDE	1.448	4.069	2311.53	9405.84	5.892	1831.43	10791.15
A_68_P21375628	chr2:80421369-80421413	NM_016965:-268	Nckap1	PROMOTER	1.448	2.306	83389.97	192305.90	3.338	68067.69	227227.30
A_68_P31208523	chr17:46849258-46849302	NM_145488:869	Pex6	INSIDE	1.448	1.798	581.56	1045.46	2.602	550.63	1432.93
A_68_P21585947	chr2:122174316-122174360	NM_001013829:20316	Shf	DOWNSTREAM	1.448	2.057	1047.19	2154.30	2.979	855.43	2548.27
A_68_P20372367	chr1:78654608-78654652	NM_001136226:-384	Utp14b	PROMOTER	1.448	3.668	1579.09	5791.38	5.311	1255.14	6665.96
A_68_P25507825	chr7:135020108-135020152	NM_146259:207	Zfp668	INSIDE	1.448	3.589	1357.92	4874.13	5.198	1099.79	5716.33
A_68_P25533783	chr7:139508008-139508052	NR_028578:684	Gm10584	INSIDE	1.447	2.447	855.09	2092.47	3.541	701.10	2482.34
A_68_P23339947	chr4:137024556-137024600	NM_008305:-139	Hspg2	PROMOTER	1.447	2.626	2329.40	6116.84	3.800	1884.70	7162.11
A_68_P25111228	chr7:56501603-56501647	NM_175272:66	Nav2	INSIDE	1.447	2.135	576.28	1230.09	3.089	435.18	1344.10
A_68_P25949903	chr8:72635987-72636031	NM_007789:8735	Ncan	INSIDE	1.447	3.122	2376.67	7419.26	4.517	1958.07	8844.04
A_68_P27835020	chr11:58948880-58948924	NM_001171512:975	Obscn	INSIDE	1.447	1.743	2129.04	3710.06	2.522	1679.01	4233.84
A_68_P30250724	chr15:58721209-58721253	NM_175226:447	Rnf139	INSIDE	1.447	2.050	2787.49	5714.56	2.967	2205.36	6543.37
A_68_P31841968	chr18:76400994-76401038	NM_010754:-562	Smad2	PROMOTER	1.447	2.698	713.64	1925.68	3.906	649.33	2536.17
A_68_P31349753	chr17:74397223-74397267	NM_053188:12	Srd5a2	INSIDE	1.447	1.986	2811.36	5582.34	2.873	2314.99	6652.02
A_68_P27833865	chr11:58791958-58792002	NM_053168:363	Trim11	INSIDE	1.447	2.868	2392.15	6859.83	4.148	2095.30	8691.42
A_68_P23429340	chr4:153516608-153516652	NM_021499:150	Wdr8	INSIDE	1.447	1.822	1735.19	3162.07	2.637	1489.55	3928.05
A_68_P22289849	chr3:84063343-84063387	ENSMUST00000147901:-73		PROMOTER	1.447	1.594	959.99	1529.97	2.306	753.69	1737.68
A_68_P22659832	chr3:153607334-153607378	NM_007382:40	Acadm	INSIDE	1.446	1.899	4802.21	9120.06	2.746	3718.40	10209.88
A_68_P31151211	chr17:34088231-34088275	NM_019420:181	B3galt4	INSIDE	1.446	2.006	3132.92	6285.11	2.900	2383.16	6911.87
A_68_P24982502	chr7:17200404-17200448	NM_172739:-84	Grlf1	PROMOTER	1.446	1.896	1027.80	1948.83	2.742	911.75	2500.28
A_68_P25678159	chr8:15011427-15011471	NM_029116:424	Kbtbd11	INSIDE	1.446	2.572	2572.51	6616.93	3.719	2184.53	8123.62
A_68_P28246310	chr12:12948750-12948795	NM_008709:-130	Mycn	PROMOTER	1.446	4.960	400.32	1985.49	7.170	370.26	2654.57
A_68_P21839353	chr2:167906491-167906535	NM_021409:9	Pard6b	INSIDE	1.446	4.552	2533.08	11530.95	6.580	2153.19	14168.50
A_68_P23271971	chr4:124743753-124743797	NM_175246:-162	Snip1	DIVERGENT_PROMOTER	1.446	3.096	1982.96	6139.75	4.479	1676.90	7509.98
A_68_P25362157	chr7:106632148-106632192	NR_002172:-728	Snord15a	PROMOTER	1.446	7.682	550.34	4227.67	11.109	510.90	5675.68
A_68_P20799884	chr1:168309567-168309611	NM_030245:291	Tada1	INSIDE	1.446	1.471	1502.42	2210.58	2.127	1239.05	2635.54
A_68_P27556189	chr11:4087040-4087084	NM_134023:227	Tbc1d10a	INSIDE	1.446	1.590	1408.80	2239.65	2.298	1044.86	2401.22
A_68_P24117669	chr5:136219992-136220036	NM_172541:28	Tmem120a	INSIDE	1.446	2.355	751.09	1768.70	3.406	556.39	1894.83
A_68_P31501880	chr18:12802925-12802969	NM_028341:905	Ttc39c	INSIDE	1.446	2.736	2149.54	5880.10	3.955	1685.22	6664.96
A_68_P31801896	chr18:69358080-69358124	AK080553:328		INSIDE	1.446	1.594	5420.38	8640.82	2.306	3539.97	8162.16
A_68_P26631263	chr9:72951130-72951174	NM_025890:948	2410004A20Rik	INSIDE	1.445	2.753	1723.42	4744.36	3.977	1485.00	5905.53
A_68_P28183249	chr11:120098316-120098360	NM_198423:4078	Bahcc1	INSIDE	1.445	3.233	1865.23	6030.16	4.672	1598.00	7465.76
A_68_P26613990	chr9:69837096-69837140	NM_016787:-189	Bnip2	PROMOTER	1.445	2.128	1610.94	3428.29	3.075	1296.90	3988.08
A_68_P21084948	chr2:27330582-27330626	NM_023336:314	Brd3	INSIDE	1.445	1.974	1939.64	3827.94	2.851	1524.89	4347.46
A_68_P28109101	chr11:107655547-107655591	NM_019431:210	Cacng4	INSIDE	1.445	2.543	2098.32	5336.33	3.675	1621.04	5956.95
A_68_P31097739	chr17:24643626-24643670	NM_027937:17921	Caskin1	INSIDE	1.445	2.261	3569.09	8069.63	3.267	2568.06	8389.01
A_68_P31253493	chr17:56179827-56179871	NM_013733:10	Chaf1a	INSIDE	1.445	1.436	1683.65	2417.12	2.075	1388.40	2880.67
A_68_P28099218	chr11:105898189-105898233	NM_027946:25	Dcaf7	INSIDE	1.445	1.560	1245.12	1942.89	2.255	1031.77	2327.05
A_68_P21978659	chr3:20054868-20054912	NM_013755:105	Gyg	INSIDE	1.445	3.474	1014.97	3526.07	5.021	916.63	4602.41
A_68_P25574932	chr7:146132973-146133017	NM_028708:562	Jakmip3	INSIDE	1.445	2.076	1303.86	2707.15	3.000	1108.06	3324.63
A_68_P30575876	chr16:17815718-17815762	NM_153790:18366	Scarf2	DOWNSTREAM	1.445	1.579	675.06	1065.85	2.282	643.83	1468.97
A_68_P22086571	chr3:41546266-41546310	NM_001081411:148	Sclt1	INSIDE	1.445	2.216	402.28	891.35	3.201	350.35	1121.43

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P21070644	chr2:25079420-25079464	NM_146116:780	Tubb2c	INSIDE	1.445	3.611	2212.18	7987.44	5.218	1676.25	8746.17
A_68_P24974292	chr7:13623438-13623482	NM_145578:-133	Ube2m	PROMOTER	1.445	2.605	1051.12	2738.68	3.765	888.60	3345.28
A_68_P28221330	chr12:8309173-8309217	NM_013527:-434	Gdf7	PROMOTER	1.444	1.733	2430.71	4211.45	2.501	1763.10	4409.85
A_68_P32454253	chrX:68809673-68809717	NM_008253:527	Hmgb3	INSIDE	1.444	1.957	1150.23	2251.28	2.827	601.95	1701.70
A_68_P20619890	chr1:134086976-134087020	NM_001033250:-1014	Lemd1	PROMOTER	1.444	3.065	1704.52	5224.81	4.427	1248.97	5528.78
A_68_P22373271	chr3:100914318-100914362	NM_011197:-251	Ptgfrn	PROMOTER	1.444	1.657	1507.39	2498.00	2.393	1256.15	3006.40
A_68_P24119330	chr5:136559824-136559868	NM_133914:61	Rasa4	INSIDE	1.444	4.408	4686.10	20657.71	6.364	3329.09	21186.54
A_68_P25186098	chr7:73205391-73205435	NM_021336:191	Snrpa1	INSIDE	1.444	2.115	2902.41	6138.04	3.054	2257.62	6894.17
A_68_P24040430	chr5:121161722-121161766	NM_008052:-66	Dtx1	PROMOTER	1.443	2.128	2505.95	5332.54	3.070	1996.93	6129.86
A_68_P31473580	chr18:6490337-6490381	NM_027497:496	Epc1	INSIDE	1.443	1.556	1551.72	2413.95	2.245	1453.93	3264.77
A_68_P28576808	chr12:81744517-81744561	NM_007951:310	Erh	INSIDE	1.443	4.662	1605.88	7487.33	6.729	1315.59	8852.28
A_68_P26065141	chr8:94882239-94882283	NM_018826:566	Irx5	INSIDE	1.443	1.717	2239.54	3846.36	2.478	1825.56	4524.24
A_68_P32508788	chrX:83437640-83437684	NM_007430:549	Nr0b1	INSIDE	1.443	1.851	606.34	1122.20	2.671	315.94	843.85
A_68_P29753344	chr14:80169969-80170013	NM_001042726:1129	Pcdh8	INSIDE	1.443	1.983	980.90	1944.81	2.861	881.14	2520.64
A_68_P21836026	chr2:167363834-167363878	NM_011427:130	Snai1	INSIDE	1.443	2.092	3308.02	6921.51	3.019	2522.35	7614.93
A_68_P31251408	chr17:55621977-55622021	NM_172829:36984	St6gal2	INSIDE	1.443	2.069	709.30	1467.20	2.985	670.32	2001.04
A_68_P31753941	chr18:61008559-61008603	NM_001198984:38	Tcof1	INSIDE	1.443	1.590	814.67	1295.56	2.294	735.15	1686.43
A_68_P23316767	chr4:132833610-132833654	NM_025667:73	Tmem222	INSIDE	1.443	3.044	915.15	2786.12	4.394	784.52	3447.25
A_68_P29613713	chr14:55305483-55305527	NM_001085473:264	Acin1	INSIDE	1.442	1.827	1544.88	2822.00	2.633	1173.53	3090.32
A_68_P23364702	chr4:141102564-141102608	NR_030695:510	B330016D10Rik	INSIDE	1.442	4.796	2115.56	10146.69	6.917	1843.49	12751.85
A_68_P29055347	chr13:55589235-55589279	NM_001177371:181	Dbn1	INSIDE	1.442	2.776	1106.39	3070.84	4.004	931.15	3727.99
A_68_P30373737	chr15:80502053-80502097	NM_145986:-202	Fam83f	PROMOTER	1.442	1.675	1637.22	2741.83	2.416	1702.71	4112.99
A_68_P24449105	chr6:52161725-52161769	NM_010454:-3123	Hoxa6	PROMOTER	1.442	2.003	491.99	985.61	2.889	402.05	1161.53
A_68_P30267538	chr15:61819548-61819592	NM_001177352:2675	Myc	INSIDE	1.442	1.750	2848.24	4984.12	2.523	2256.37	5693.87
A_68_P21069553	chr2:24909996-24910040	NM_001039386:120	Nelf	INSIDE	1.442	7.550	1426.68	10771.43	10.888	1505.80	16395.05
A_68_P27447374	chr10:110602373-110602417	NM_001003717:537	Osbpl8	INSIDE	1.442	4.572	430.88	1970.03	6.594	395.39	2607.36
A_68_P31958010	chr19:11893171-11893215	NM_011502:191	Stx3	INSIDE	1.442	1.540	927.43	1427.99	2.220	880.02	1953.82
A_68_P27468583	chr10:114688211-114688255	NM_025706:317	Tbc1d15	INSIDE	1.442	2.122	1279.35	2714.54	3.061	1029.32	3150.38
A_68_P25836146	chr8:47556498-47556542	NM_007981:125	Acsl1	INSIDE	1.441	1.816	808.68	1468.43	2.617	740.08	1936.95
A_68_P28616635	chr12:88784339-88784383	NM_001102565:429	Alkbh1	INSIDE	1.441	1.623	2599.48	4219.74	2.339	2111.19	4937.21
A_68_P31624567	chr18:36720291-36720335	NM_175375:56	Ankhd1	INSIDE	1.441	1.737	2296.88	3989.94	2.503	1915.71	4794.36
A_68_P30387839	chr15:83180363-83180407	NM_025445:293	Arfgap3	INSIDE	1.441	4.649	671.96	3123.86	6.698	666.26	4462.37
A_68_P25313630	chr7:97592416-97592460	NM_145151:1148	Crebzf	INSIDE	1.441	2.192	1619.69	3550.02	3.158	1301.54	4110.89
A_68_P23236049	chr4:117354422-117354470	NM_023178:384	Dmap1	INSIDE	1.441	2.227	726.54	1618.20	3.210	514.11	1650.34
A_68_P27284764	chr10:80139113-80139157	NM_021462:-4413	Mknk2	PROMOTER	1.441	1.745	511.83	893.20	2.515	494.33	1243.01
A_68_P31621836	chr18:36228394-36228438	NM_001167891:128398	Nrg2	INSIDE	1.441	2.269	1281.16	2907.25	3.271	1086.22	3552.79
A_68_P29228005	chr13:93962476-93962520	NM_133905:-260	Papd4	PROMOTER	1.441	2.111	1789.75	3778.83	3.042	1418.22	4314.68
A_68_P26949006	chr10:12810713-12810757	NM_009538:141	Plagl1	INSIDE	1.441	2.528	588.30	1486.95	3.642	627.94	2286.66
A_68_P26803290	chr9:106331991-106332035	NM_009082:143	Rpl29	INSIDE	1.441	1.653	6921.88	11443.61	2.382	5791.60	13793.26
A_68_P26574137	chr9:62997201-62997245	NM_001163758:-454	Skor1	PROMOTER	1.441	4.119	751.18	3093.92	5.935	672.30	3989.81
A_68_P28781890	chr12:120087139-120087183	NM_177082:2359	Sp8	INSIDE	1.441	1.650	936.66	1545.46	2.377	825.74	1962.99
A_68_P31943259	chr19:8810305-8810349	NM_134139:-2	Wdr74	PROMOTER	1.441	0.437	1483.47	648.57	0.630	1294.98	815.99
A_68_P23319341	chr4:133308432-133308476	NM_001080819:1072	Arid1a	INSIDE	1.440	2.202	1146.43	2524.79	3.172	1025.72	3253.28
A_68_P29941247	chr14:119254329-119254375	NM_001160099:181	Cldn10	INSIDE	1.440	1.864	525.64	980.02	2.684	425.00	1140.85
A_68_P30115251	chr15:31532021-31532065	NM_026546:172	Fam173b	INSIDE	1.440	2.103	1173.93	2468.83	3.028	1082.18	3276.64
A_68_P25729953	chr8:27086780-27086824	NM_029884:414	Hgsnat	INSIDE	1.440	2.990	1651.60	4938.89	4.306	1338.21	5762.28
A_68_P21395111	chr2:84712344-84712388	NM_199223:14483	Rtn4rl2	INSIDE	1.440	1.981	897.15	1777.13	2.853	846.01	2413.72
A_68_P23457021	chr5:5694320-5694364	NM_001103156:-265	Steap2	PROMOTER	1.440	4.252	2226.24	9466.77	6.124	1932.28	11832.98
A_68_P27644759	chr11:23155418-23155462	NM_001035226:-600	Xpo1	PROMOTER	1.440	1.675	1183.87	1982.94	2.412	966.57	2331.03
A_68_P22833088	chr4:34830058-34830102	NM_013889:117	Zfp292	INSIDE	1.440	2.508	1761.58	4417.80	3.611	1647.46	5948.42
A_68_P27243858	chr10:72562474-72562518	ENSMUST00000053544:295		INSIDE	1.440	1.614	867.98	1400.85	2.324	758.66	1763.30

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25724840	chr8:26127185-26127229	NM_007404:188	Adam9	INSIDE	1.439	2.381	3131.51	7455.70	3.426	2457.23	8418.00
A_68_P22767955	chr4:19969272-19969316	NM_010281:96	Ggh	INSIDE	1.439	2.289	616.67	1411.79	3.294	582.19	1917.86
A_68_P25285302	chr7:91032885-91032929	NM_030705:-55	Mesdc1	DIVERGENT_PROMOTER	1.439	1.504	835.43	1256.80	2.165	719.20	1556.90
A_68_P22422571	chr3:109945742-109945786	NM_001163348:626	Ntng1	INSIDE	1.439	1.492	3545.15	5287.91	2.146	2603.80	5588.93
A_68_P24265237	chr6:17015070-17015114	NM_207176:-56	Tes	PROMOTER	1.439	2.753	677.63	1865.41	3.961	687.12	2721.79
A_68_P27579285	chr11:8564248-8564292	NM_001083587:268	Tns3	INSIDE	1.439	1.503	2113.83	3176.44	2.163	1622.08	3508.07
A_68_P26696139	chr9:85736432-85736476	NM_001164792:-4	Tpbg	PROMOTER	1.439	2.250	684.18	1539.46	3.239	607.52	1967.46
A_68_P25657380	chr8:11758231-11758275	NM_001113518:-77	Arhgef7	PROMOTER	1.438	1.934	2355.29	4554.16	2.780	1938.44	5388.59
A_68_P28731670	chr12:110291859-110291903	NM_001163175:14547	Begain	INSIDE	1.438	3.009	881.12	2650.91	4.326	738.81	3195.76
A_68_P27996044	chr11:87577886-87577930	NM_172449:3866	Bzrap1	INSIDE	1.438	10.339	1173.75	12135.82	14.864	930.53	13830.94
A_68_P30362471	chr15:78633225-78633269	NM_130859:226	Card10	INSIDE	1.438	2.720	1537.93	4183.67	3.911	1301.14	5088.44
A_68_P21768600	chr2:155782266-155782310	NM_001129999:-5	Cep250	PROMOTER	1.438	4.307	2156.21	9286.15	6.193	1805.15	11179.84
A_68_P22875167	chr4:44085230-44085274	NM_001190414:293	Gne	INSIDE	1.438	2.876	1746.94	5024.47	4.137	1460.08	6040.57
A_68_P31244142	chr17:53707297-53707341	NM_020005:1023	Kat2b	INSIDE	1.438	3.857	906.06	3494.38	5.547	732.76	4064.54
A_68_P30397620	chr15:84754050-84754094	NM_016714:215	Nup50	INSIDE	1.438	4.257	1234.08	5253.86	6.121	1122.13	6868.99
A_68_P22729893	chr4:11413533-11413577	NM_001081183:450	1110037F02Rik	INSIDE	1.437	2.024	921.23	1864.51	2.909	803.47	2337.16
A_68_P21635706	chr2:131388108-131388153	NM_013460:-109	Adra1d	PROMOTER	1.437	1.690	2413.40	4079.07	2.429	1981.92	4814.53
A_68_P26229921	chr8:124474582-124474626	NM_001110100:172	Banp	INSIDE	1.437	5.586	4178.75	23342.39	8.029	3019.79	24245.52
A_68_P33007794	chr4_random:128835-128879	NM_001033326:19055	Dhrsx	INSIDE	1.437	6.540	5179.04	33869.01	9.395	3481.04	32704.98
A_68_P24156001	chr5:144076400-144076444	NM_172726:617	E130309D02Rik	INSIDE	1.437	2.264	1046.72	2369.42	3.253	938.73	3053.43
A_68_P26234163	chr8:125075221-125075265	NM_001037298:-13	Fam38a	PROMOTER	1.437	1.552	1816.29	2818.83	2.230	1572.86	3507.22
A_68_P26348586	chr9:21528050-21528094	NM_010700:35	Ldlr	INSIDE	1.437	2.629	1020.50	2682.53	3.778	774.37	2925.79
A_68_P26640623	chr9:74710266-74710310	NM_008262:561	Onecut1	INSIDE	1.437	4.179	2079.83	8692.42	6.006	1664.86	9999.74
A_68_P32139052	chr19:45619644-45619688	NM_020032:15367	Poll	DOWNSTREAM	1.437	1.557	1450.24	2258.63	2.238	1110.43	2484.79
A_68_P22373269	chr3:100913808-100913852	NM_011197:259	Ptgfrn	INSIDE	1.437	4.539	568.12	2578.63	6.521	543.62	3544.99
A_68_P23395558	chr4:148000660-148000704	NM_001003898:423	Tardbp	INSIDE	1.437	1.704	942.11	1605.42	2.448	850.93	2083.30
A_68_P28747159	chr12:113205331-113205376	NM_027360:-165	2010107E04Rik	DIVERGENT_PROMOTER	1.436	4.443	430.49	1912.54	6.380	361.95	2309.12
A_68_P21040812	chr2:18602535-18602579	NM_007552:3912	Bmi1	INSIDE	1.436	2.230	864.18	1926.75	3.203	773.72	2477.95
A_68_P25782096	chr8:36889804-36889848	NM_027998:-213	Cldn23	PROMOTER	1.436	2.860	7034.43	20115.50	4.106	5042.34	20703.83
A_68_P28291022	chr12:25365866-25365910	NM_001004455:772	Cys1	INSIDE	1.436	6.877	15387.49	105817.20	9.873	10241.94	101120.00
A_68_P28739206	chr12:111839872-111839916	NM_030238:290	Dync1h1	INSIDE	1.436	3.659	1091.47	3993.69	5.255	949.14	4987.40
A_68_P29410660	chr14:13177298-13177342	NM_080433:1059	Fezf2	INSIDE	1.436	1.419	1519.40	2156.27	2.038	1195.93	2437.42
A_68_P31159077	chr17:35516814-35516858	NM_001143689:275	H2-Gs10	INSIDE	1.436	2.060	3376.15	6954.00	2.958	2713.51	8025.89
A_68_P26445380	chr9:40609023-40609067	NM_031165:-311	Hspa8	PROMOTER	1.436	3.428	2047.53	7018.47	4.923	1722.88	8481.76
A_68_P29232482	chr13:94827759-94827803	NM_172589:30	Lhfpl2	INSIDE	1.436	1.601	634.81	1016.46	2.300	807.44	1856.79
A_68_P31066197	chr17:15673753-15673797	NM_008799:-9509	Pdcd2	PROMOTER	1.436	1.850	3237.13	5989.84	2.657	2716.52	7216.98
A_68_P31938929	chr19:7343308-7343352	NM_054048:-923	Rcor2	PROMOTER	1.436	1.360	1602.52	2179.14	1.953	1371.04	2678.03
A_68_P20502873	chr1:107252976-107253020	NM_001160368:289	Rnf152	INSIDE	1.436	2.959	1833.21	5423.92	4.248	1574.50	6688.09
A_68_P23281727	chr4:126412759-126412803	NM_198960:733	Tcfap2e	INSIDE	1.436	2.178	5659.61	12327.52	3.128	4685.75	14657.59
A_68_P31092981	chr17:23813793-23813837	NM_001161746:602	Tnfrsf12a	INSIDE	1.436	1.736	3254.07	5648.40	2.492	2768.70	6900.88
A_68_P22889131	chr4:46520297-46520341	NM_029077:28698	Trim14	INSIDE	1.436	2.670	1020.35	2724.65	3.834	923.57	3541.36
A_68_P20936234	chr1:192921983-192922027	NM_030060:-288	Batf3	PROMOTER	1.435	29.784	1166.38	34739.93	42.739	825.04	35261.56
A_68_P26014851	chr8:85913804-85913848	NM_009904:37	Clgn	INSIDE	1.435	1.940	638.89	1239.70	2.785	561.10	1562.71
A_68_P31259849	chr17:57202154-57202198	NM_177638:477	Crb3	INSIDE	1.435	1.695	586.85	994.42	2.432	501.30	1219.36
A_68_P25416987	chr7:118226039-118226083	NM_001040131:484	Eif4g2	INSIDE	1.435	2.014	1141.51	2299.16	2.890	885.24	2558.19
A_68_P31493065	chr18:11054816-11054860	NM_010258:2331	Gata6	INSIDE	1.435	1.635	861.87	1409.53	2.346	825.43	1936.60
A_68_P31708188	chr18:52688501-52688545	NM_010728:840	Lox	INSIDE	1.435	1.560	899.11	1402.22	2.239	709.78	1588.99
A_68_P24658383	chr6:94649752-94649796	NM_008377:365	Lrig1	INSIDE	1.435	2.307	331.57	764.80	3.311	373.13	1235.34
A_68_P24929770	chr6:146591301-146591345	NM_025315:222	Med21	INSIDE	1.435	5.106	823.78	4206.26	7.325	733.79	5374.87
A_68_P23231034	chr4:116480288-116480332	NM_001159581:-28	Mutyh	DIVERGENT_PROMOTER	1.435	2.306	3347.25	7719.85	3.310	2488.78	8238.76
A_68_P29654920	chr14:62950855-62950899	NM_026001:-65	Rnaseh2b	PROMOTER	1.435	1.636	1693.75	2770.46	2.348	1418.53	3330.13

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27936386	chr11:77029527-77029571	NM_177710:-378	Ssh2	PROMOTER	1.435	4.453	1711.54	7622.33	6.391	1424.23	9102.77
A_68_P30427170	chr15:89672308-89672352	NM_018803:-39	Syt10	PROMOTER	1.435	1.861	449.45	836.50	2.671	474.25	1266.89
A_68_P26845372	chr9:114472029-114472073	NM_001042503:1437	Trim71	INSIDE	1.435	3.231	613.56	1982.19	4.636	571.03	2647.35
A_68_P23349884	chr4:138686603-138686647	NR_033745:328	2310028O11Rik	INSIDE	1.434	3.733	4615.82	17229.37	5.353	3667.75	19633.56
A_68_P28098903	chr11:105850138-105850182	NM_009598:13639	Ace	INSIDE	1.434	7.534	2074.55	15629.93	10.802	1527.36	16498.62
A_68_P30579184	chr16:18348951-18348995	NM_033474:606	Arvcf	INSIDE	1.434	1.813	2856.70	5178.21	2.600	2245.36	5838.14
A_68_P28836396	chr13:14046811-14046855	NM_178640:-108	B3galnt2	PROMOTER	1.434	1.910	1688.04	3223.64	2.739	1365.70	3741.01
A_68_P27172919	chr10:59649414-59649458	NM_016803:32572	Chst3	INSIDE	1.434	2.741	1198.84	3286.30	3.932	959.44	3772.08
A_68_P25542609	chr7:140968445-140968489	NM_133941:20	Dhx32	INSIDE	1.434	2.159	1087.44	2347.25	3.095	979.77	3032.14
A_68_P22722448	chr4:9771474-9771518	NM_013526:-22	Gdf6	PROMOTER	1.434	1.944	2644.16	5140.52	2.789	2155.11	6009.59
A_68_P22129907	chr3:51287845-51287889	NM_016858:-21	Rab33b	PROMOTER	1.434	2.009	1571.71	3158.03	2.881	1413.96	4073.24
A_68_P28774232	chr12:118772473-118772517	NM_175930:17543	Rapgef5	INSIDE	1.434	2.482	682.68	1694.31	3.559	590.93	2102.97
A_68_P27288599	chr10:80748500-80748544	NM_013769:5490	Tjp3	INSIDE	1.434	2.239	797.76	1786.15	3.210	758.90	2436.44
A_68_P30639250	chr16:30008917-30008961	NR_033631:186	4632428C04Rik	INSIDE	1.433	1.966	1133.92	2229.41	2.818	1021.92	2879.83
A_68_P29560848	chr14:41827140-41827184	NM_027464:-98	5730469M10Rik	PROMOTER	1.433	2.133	3828.39	8165.54	3.056	2835.11	8664.27
A_68_P31108899	chr17:26338048-26338092	NM_008113:225	Arhgdig	INSIDE	1.433	3.283	1886.82	6195.22	4.706	1667.91	7848.59
A_68_P24925470	chr6:145811720-145811764	NM_024469:2118	Bhlhe41	INSIDE	1.433	6.170	1965.15	12124.53	8.843	1757.58	15541.76
A_68_P31098015	chr17:24687028-24687072	NM_013630:156	Pkd1	INSIDE	1.433	1.657	615.84	1020.71	2.376	534.61	1269.97
A_68_P29570101	chr14:45949780-45949824	NM_025959:304	Psmc6	INSIDE	1.433	1.411	1408.37	1987.78	2.022	1043.34	2109.70
A_68_P24061314	chr5:124895322-124895366	NM_030241:5406	Setd8	INSIDE	1.433	2.904	696.58	2023.18	4.163	582.53	2425.26
A_68_P27985577	chr11:85650442-85650486	NM_009324:4348	Tbx2	INSIDE	1.433	1.927	2748.21	5296.65	2.763	2035.37	5622.82
A_68_P23339475	chr4:136913438-136913482	NM_009861:192	Cdc42	INSIDE	1.432	6.373	963.58	6140.62	9.125	784.19	7155.96
A_68_P30459322	chr15:95484732-95484776	NM_207533:448	Dbx2	INSIDE	1.432	1.907	1004.97	1916.43	2.731	945.93	2583.68
A_68_P23236052	chr4:117354732-117354776	NM_023178:76	Dmap1	INSIDE	1.432	1.837	2606.68	4788.42	2.630	2143.06	5635.52
A_68_P22881527	chr4:45197858-45197902	NM_001081172:103	Frmpd1	INSIDE	1.432	1.645	593.32	976.03	2.356	603.73	1422.44
A_68_P32022553	chr19:24355018-24355062	NM_008044:36	Fxn	INSIDE	1.432	3.163	980.13	3099.87	4.530	902.11	4086.42
A_68_P31985486	chr19:17431193-17431237	NM_173442:-57	Gcnt1	PROMOTER	1.432	2.980	4805.40	14321.45	4.267	3835.65	16366.47
A_68_P32454254	chrX:68810106-68810150	NM_008253:961	Hmgb3	INSIDE	1.432	2.964	561.61	1664.78	4.246	395.17	1677.91
A_68_P25730818	chr8:27229559-27229603	NM_207659:116	Hook3	INSIDE	1.432	1.751	589.68	1032.40	2.508	525.81	1318.73
A_68_P29469016	chr14:24824250-24824294	NM_010610:-845	Kcnma1	PROMOTER	1.432	2.251	1908.32	4294.72	3.223	1621.56	5226.01
A_68_P27282833	chr10:79844657-79844701	NM_198615:5718	Mex3d	INSIDE	1.432	1.680	460.08	772.90	2.405	345.08	830.04
A_68_P32118288	chr19:42055682-42055726	NM_028152:-78	Mms19	DIVERGENT_PROMOTER	1.432	1.902	1328.02	2526.36	2.724	1108.91	3020.85
A_68_P26015449	chr8:86090778-86090822	NM_025843:144	Ndufb7	INSIDE	1.432	1.721	978.95	1684.31	2.463	824.08	2030.04
A_68_P24360134	chr6:35127844-35127888	NM_027513:251	Nup205	INSIDE	1.432	2.248	1180.52	2653.29	3.218	985.48	3171.57
A_68_P23320011	chr4:133443491-133443535	NM_009097:202	Rps6ka1	INSIDE	1.432	2.188	964.88	2111.38	3.133	907.19	2842.10
A_68_P31254020	chr17:56263726-56263770	NM_013662:9527	Sema6b	INSIDE	1.432	4.319	3412.90	14741.84	6.187	2822.02	17459.94
A_68_P26743637	chr9:95650689-95650733	NM_011643:67	Trpc1	INSIDE	1.432	4.306	1965.66	8463.87	6.165	1585.33	9772.83
A_68_P29958337	chr14:122277966-122278010	NM_026861:161	Ubac2	INSIDE	1.432	2.751	1292.75	3555.77	3.939	1094.81	4312.57
A_68_P27268624	chr10:76978491-76978535	NM_133998:46	1810008A18Rik	INSIDE	1.431	0.469	1440.40	675.72	0.671	1259.75	845.41
A_68_P30482000	chr15:99556370-99556414	NM_183256:344	2310016M24Rik	INSIDE	1.431	1.868	2886.15	5391.15	2.673	2223.93	5944.40
A_68_P25608860	chr7:151924429-151924473	NM_178642:-67	Ano1	PROMOTER	1.431	2.740	1442.97	3953.40	3.920	1301.36	5100.80
A_68_P28082435	chr11:102808047-102808091	NM_011795:-293	C1ql1	PROMOTER	1.431	2.491	1229.97	3064.36	3.565	979.07	3490.33
A_68_P32454734	chrX:68917679-68917723	NM_010340:759	Gpr50	INSIDE	1.431	3.037	1714.79	5208.11	4.346	951.26	4133.82
A_68_P31110190	chr17:26568998-26569042	NM_001081656:17111	Neurl1b	INSIDE	1.431	2.158	1000.89	2160.10	3.089	786.14	2428.58
A_68_P24815137	chr6:124364678-124364722	NM_008995:385	Pex5	INSIDE	1.431	2.394	3352.00	8025.03	3.426	2428.36	8319.20
A_68_P23524108	chr5:20561799-20561843	NM_011203:-205	Ptpn12	PROMOTER	1.431	2.471	4084.29	10094.31	3.535	3490.85	12341.85
A_68_P29855888	chr14:102007522-102007566	NM_001081278:864	Tbc1d4	INSIDE	1.431	1.773	894.75	1586.73	2.537	710.50	1802.46
A_68_P30558456	chr16:13672419-13672463	NM_025653:328	3110001I22Rik	INSIDE	1.430	1.971	580.42	1144.12	2.818	492.14	1386.89
A_68_P24631552	chr6:90259348-90259392	NM_027928:15809	Chst13	INSIDE	1.430	2.267	383.03	868.53	3.243	324.29	1051.80
A_68_P29671620	chr14:65716836-65716880	NM_018788:85	Extl3	INSIDE	1.430	2.093	867.26	1815.24	2.993	790.34	2365.67
A_68_P26905361	chr10:4540405-4540449	NM_025995:-649	Fbxo5	PROMOTER	1.430	1.765	2432.62	4293.20	2.523	1969.64	4970.35

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P29631505	chr14:58694946-58694991	NM_013518:3446	Fgf9	INSIDE	1.430	1.519	1530.88	2325.70	2.173	1248.57	2712.79
A_68_P26406147	chr9:32348923-32348967	NM_008026:9	Fli1	INSIDE	1.430	10.643	1659.07	17657.64	15.216	1332.51	20275.29
A_68_P31215016	chr17:48061356-48061400	NM_001110824:203	Foxp4	INSIDE	1.430	2.065	544.46	1124.39	2.952	431.86	1274.98
A_68_P28307233	chr12:28023729-28023773	NM_009234:3833	Sox11	INSIDE	1.430	1.917	1761.58	3377.42	2.741	1572.18	4309.91
A_68_P20878653	chr1:182872689-182872733	NM_144794:62	Tmem63a	INSIDE	1.430	3.461	1110.82	3844.24	4.949	1171.34	5796.88
A_68_P23296885	chr4:129168578-129168622	NM_001085491:167	1700125D06Rik	INSIDE	1.429	3.440	2205.27	7585.94	4.916	1839.76	9044.09
A_68_P28599343	chr12:85958262-85958306	NM_008992:132	Abcd4	INSIDE	1.429	2.059	496.59	1022.34	2.942	438.31	1289.71
A_68_P29080189	chr13:59658365-59658409	NM_023328:294	Agtpbp1	INSIDE	1.429	2.420	614.39	1486.84	3.458	529.07	1829.46
A_68_P32260333	chrX:11664076-11664120	NM_029510:-6419	Bcor	PROMOTER	1.429	1.463	2105.42	3079.95	2.091	1135.40	2373.82
A_68_P31369865	chr17:78599190-78599234	NM_015800:-375	Crim1	PROMOTER	1.429	3.631	2214.04	8039.99	5.188	1981.30	10278.47
A_68_P27212423	chr10:66998199-66998243	NM_010118:-2396	Egr2	PROMOTER	1.429	1.970	2569.89	5061.85	2.814	2176.70	6125.52
A_68_P27561404	chr11:4998804-4998848	NM_007968:254	Ewsr1	INSIDE	1.429	2.514	1332.85	3351.21	3.594	1126.92	4050.26
A_68_P24038706	chr5:120886174-120886218	NM_008499:4302	Lhx5	INSIDE	1.429	3.656	1390.51	5084.34	5.225	1145.84	5987.14
A_68_P30370814	chr15:80042595-80042639	NM_010795:38466	Mgat3	INSIDE	1.429	3.499	1181.13	4133.12	5.000	930.76	4653.43
A_68_P31207194	chr17:46624614-46624658	NM_001162864:-12	Ttbk1	DIVERGENT_PROMOTER	1.429	4.060	5421.37	22008.46	5.802	4083.42	23694.01
A_68_P26168806	chr8:114060945-114060989	NM_001168623:-1276	Znrf1	PROMOTER	1.429	1.938	1653.27	3204.55	2.771	1338.26	3707.84
A_68_P20370563	chr1:78214303-78214348			Unknown	1.429	1.638	1002.23	1641.76	2.341	768.30	1798.39
A_68_P25465270	chr7:126887848-126887892	ENSMUST00000004569:4431		DOWNSTREAM	1.429	2.309	971.07	2241.91	3.300	817.53	2697.78
A_68_P21977359	chr3:19795207-19795251	NR_027985:358	4632415L05Rik	INSIDE	1.428	1.482	1056.60	1565.64	2.115	866.83	1833.64
A_68_P21745336	chr2:151527951-151527995	NM_001160363:229	5430405G05Rik	INSIDE	1.428	9.637	702.25	6767.77	13.762	645.46	8882.48
A_68_P23542075	chr5:23980487-23980531	NM_139153:22514	Agap3	INSIDE	1.428	4.539	342.01	1552.25	6.483	350.72	2273.86
A_68_P24615404	chr6:87285370-87285414	NM_054041:377	Antxr1	INSIDE	1.428	3.198	3444.45	11013.90	4.568	2856.12	13045.70
A_68_P26022317	chr8:87381112-87381157	NM_025648:250	Farsa	INSIDE	1.428	1.769	496.37	878.07	2.527	424.29	1072.13
A_68_P23582164	chr5:32439192-32439236	NM_008037:370	Fosl2	INSIDE	1.428	2.722	2139.46	5824.04	3.888	2060.63	8011.77
A_68_P24817421	chr6:124811227-124811271	NM_013533:2687	Gpr162	INSIDE	1.428	3.167	1147.31	3633.33	4.524	916.44	4145.62
A_68_P26992095	chr10:21016178-21016222	NM_001145209:416	Hbs1l	INSIDE	1.428	1.591	2034.89	3237.98	2.272	1469.59	3339.49
A_68_P29154201	chr13:76521736-76521780	NM_030174:-650	Mctp1	PROMOTER	1.428	1.812	399.29	723.68	2.588	329.09	851.68
A_68_P30376706	chr15:81020912-81020956	NM_001082536:253	Mkl1	INSIDE	1.428	1.494	2829.65	4228.59	2.135	2432.01	5191.43
A_68_P26319360	chr9:14589324-14589368	NM_018736:196	Mre11a	INSIDE	1.428	4.375	4559.98	19951.51	6.246	3897.17	24342.17
A_68_P32565875	chrX:99045611-99045655	NM_001163610:909	Nhsl2	INSIDE	1.428	2.674	1582.43	4230.92	3.819	1220.26	4660.05
A_68_P21904290	chr2:180234531-180234575	NM_018766:-128	Ntsr1	PROMOTER	1.428	3.278	1431.59	4693.16	4.682	1179.37	5522.04
A_68_P22282897	chr3:82859249-82859293	NM_016784:-189	Plrg1	DIVERGENT_PROMOTER	1.428	1.983	3661.91	7262.64	2.832	2941.09	8329.96
A_68_P21152642	chr2:39046414-39046458	NM_178778:-186	Scai	PROMOTER	1.428	3.775	2173.82	8206.59	5.390	1657.02	8931.67
A_68_P25957635	chr8:74108819-74108863	NM_011977:16015	Slc27a1	INSIDE	1.428	1.924	591.76	1138.79	2.748	566.17	1555.89
A_68_P20218124	chr1:50983912-50983956	NM_019790:-432	Tmeff2	PROMOTER	1.428	1.552	2887.89	4483.16	2.217	2124.27	4710.17
A_68_P32217690	chr19:59244706-59244750	NM_009501:-209	Vax1	PROMOTER	1.428	2.418	3335.67	8065.71	3.453	2981.87	10297.34
A_68_P24594973	chr6:83652821-83652865	NR_002873:8084	Vax2os1	INSIDE	1.428	2.156	1206.72	2602.19	3.079	1009.76	3108.97
A_68_P30214226	chr15:51871837-51871881	NM_175503:206	Aard	INSIDE	1.427	1.916	304.81	584.06	2.733	277.47	758.45
A_68_P28743039	chr12:112510049-112510093	NM_033603:749	Amn	INSIDE	1.427	1.669	1149.82	1918.80	2.381	1011.30	2408.18
A_68_P32576282	chrX:101395577-101395621	NM_001077354:858	C77370	INSIDE	1.427	3.457	1964.90	6793.41	4.933	1171.01	5776.06
A_68_P25806164	chr8:41596758-41596802	NM_011135:-122	Cnot7	DIVERGENT_PROMOTER	1.427	2.515	7808.35	19635.50	3.588	5707.77	20481.14
A_68_P32539668	chrX:91881915-91881959	NM_008179:529	Gspt2	INSIDE	1.427	3.643	222.73	811.43	5.200	158.32	823.29
A_68_P30345339	chr15:75824110-75824154	NM_177922:-66	Mapk15	PROMOTER	1.427	1.919	786.89	1509.80	2.738	701.70	1921.46
A_68_P24981707	chr7:17061268-17061312	NM_008718:839	Npas1	INSIDE	1.427	3.402	567.40	1930.32	4.854	516.92	2509.31
A_68_P26521207	chr9:53345172-53345216	NM_001081152:43	Npat	INSIDE	1.427	2.439	1302.14	3175.88	3.481	978.04	3404.83
A_68_P32745696	chrX:147955251-147955299	NM_177201:60	Phf8	INSIDE	1.427	2.556	706.50	1805.96	3.647	342.37	1248.75
A_68_P31140484	chr17:31702098-31702142	NM_016670:403	Pknox1	INSIDE	1.427	2.201	875.94	1927.71	3.141	748.66	2351.44
A_68_P21132198	chr2:35056008-35056052	NM_026697:610	Rab14	INSIDE	1.427	3.344	1140.50	3814.24	4.773	998.62	4766.42
A_68_P32237966	chrX:6895899-6895943	ENSMUST00000132126:376		INSIDE	1.427	2.569	326.36	838.34	3.665	265.67	973.79
A_68_P29092064	chr13:63341467-63341511	NM_028079:225195	2010111I01Rik	INSIDE	1.426	2.239	3623.94	8114.95	3.193	2653.34	8472.99
A_68_P22862943	chr4:41516655-41516699	NM_001159583:-116	2310028H24Rik	DIVERGENT_PROMOTER	1.426	1.638	902.59	1478.41	2.335	741.87	1732.59

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27835441	chr11:59015919-59015963	NR_037964:-7	2610507I01Rik	DIVERGENT_PROMOTER	1.426	1.494	5723.64	8553.26	2.131	4391.28	9355.86
A_68_P31154762	chr17:34742611-34742655	NM_001163379:-173	Agpat1	DIVERGENT_PROMOTER	1.426	1.883	1330.03	2504.28	2.685	1020.33	2739.42
A_68_P27902137	chr11:70501182-70501226	NM_001190376:403	Camta2	INSIDE	1.426	1.816	1627.44	2955.45	2.590	1387.32	3593.52
A_68_P30483526	chr15:99869552-99869596	NM_001159361:480	Dip2b	INSIDE	1.426	2.682	882.59	2367.54	3.824	733.53	2805.01
A_68_P23203783	chr4:109656467-109656511	NM_172296:5859	Dmrta2	DOWNSTREAM	1.426	5.320	1612.88	8579.90	7.583	1244.48	9437.45
A_68_P28915538	chr13:30228234-30228278	NM_153546:-102	Mboat1	PROMOTER	1.426	1.618	656.21	1061.57	2.306	544.40	1255.51
A_68_P31257221	chr17:56743113-56743157	NM_001163300:18730	Safb	INSIDE	1.426	1.822	1742.72	3175.71	2.599	1293.65	3362.09
A_68_P26544601	chr9:57788261-57788305	NM_011352:341	Sema7a	INSIDE	1.426	2.228	1064.64	2371.54	3.176	854.68	2714.05
A_68_P28908962	chr13:29043905-29043949	NM_009238:1625	Sox4	INSIDE	1.426	2.876	1566.80	4505.62	4.102	1228.16	5037.66
A_68_P24912677	chr6:143781866-143781912	NM_001113559:376190	Sox5	INSIDE	1.426	1.675	487.02	815.64	2.388	383.16	915.04
A_68_P31253704	chr17:56213984-56214028	NM_024432:406	Ubxn6	INSIDE	1.426	2.904	13803.75	40089.43	4.142	9650.79	39974.27
A_68_P29247842	chr13:97518179-97518223			Unknown	1.426	3.100	3663.27	11355.10	4.420	3179.69	14054.99
A_68_P33005882	A_68_P33005882			Unknown	1.426	3.817	528.30	2016.67	5.443	431.27	2347.38
A_68_P23288223	chr4:127665242-127665286	ENSMUST00000144298:-23		PROMOTER	1.426	2.757	870.54	2400.34	3.933	774.97	3048.08
A_68_P31053612	chr17:12935271-12935317	NR_002853:1118	Airn	INSIDE	1.425	1.664	1280.94	2130.98	2.371	1005.54	2384.52
A_68_P27855080	chr11:62461500-62461544	NM_198861:503	BC046404	INSIDE	1.425	1.607	2660.83	4276.27	2.290	2054.16	4703.79
A_68_P28865538	chr13:20182700-20182744	NM_080288:347	Elmo1	INSIDE	1.425	3.480	2282.78	7943.04	4.958	1633.16	8097.72
A_68_P28814402	chr13:9093309-9093353	NM_172585:180	Larp4b	INSIDE	1.425	4.285	719.83	3084.31	6.105	641.17	3914.29
A_68_P31934662	chr19:6428439-6428483	NM_001205234:9723	Nrxn2	INSIDE	1.425	3.398	357.26	1213.98	4.843	285.18	1381.15
A_68_P25610029	chr7:152101203-152101247	NM_028184:126	Oraov1	INSIDE	1.425	1.363	1473.54	2008.57	1.943	1225.30	2380.48
A_68_P31929908	chr19:5654240-5654284	NM_001164480:9445	Sipa1	INSIDE	1.425	2.172	973.46	2114.71	3.096	854.47	2645.64
A_68_P30544728	chr16:10835113-10835157	NM_001162932:-17	A630055G03Rik	PROMOTER	1.424	4.746	1288.36	6115.03	6.759	1085.06	7334.04
A_68_P21576975	chr2:120556771-120556815	NM_026891:461	Cdan1	INSIDE	1.424	1.974	465.11	918.33	2.811	412.87	1160.65
A_68_P29361890	chr13:118009924-118009968	NM_010330:567	Emb	INSIDE	1.424	1.512	1520.73	2299.62	2.153	1205.35	2595.48
A_68_P32383370	chrX:49967260-49967304	NM_016697:-131	Gpc3	PROMOTER	1.424	3.095	9985.31	30905.65	4.408	4300.38	18956.13
A_68_P26220850	chr8:123061186-123061230	NM_001145896:-100	Gse1	PROMOTER	1.424	2.484	842.06	2092.04	3.537	662.22	2342.54
A_68_P25264894	chr7:87260253-87260297	NM_173011:-38	Idh2	PROMOTER	1.424	3.376	660.39	2229.50	4.806	570.14	2740.19
A_68_P31863637	chr18:80519734-80519778	NM_001190373:41237	Kcng2	INSIDE	1.424	4.185	4794.85	20068.50	5.960	3894.16	23210.21
A_68_P23837519	chr5:81449181-81449225	NM_198702:-1415	Lphn3	PROMOTER	1.424	3.380	834.56	2820.42	4.813	670.50	3227.44
A_68_P20937430	chr1:193141794-193141838	NM_025424:181	Nenf	INSIDE	1.424	3.519	756.69	2663.14	5.011	634.83	3181.09
A_68_P23637083	chr5:42099031-42099075	NM_027295:342	Rab28	INSIDE	1.424	2.210	737.77	1630.38	3.146	643.81	2025.58
A_68_P31836528	chr18:75526822-75526866	NM_001042660:-174	Smad7	PROMOTER	1.424	2.291	514.95	1179.88	3.263	471.35	1538.00
A_68_P27709784	chr11:35793975-35794019	NM_170779:-405	Wwc1	PROMOTER	1.424	2.341	284.11	665.18	3.334	258.24	861.07
A_68_P21290382	chr2:65962425-65962469	NM_015736:404	Galnt3	INSIDE	1.423	2.078	874.59	1817.17	2.956	765.48	2262.47
A_68_P26587426	chr9:65239326-65239370	NM_028974:111	Kbtbd13	INSIDE	1.423	1.711	395.84	677.41	2.435	347.04	845.19
A_68_P21089694	chr2:28061599-28061643	NM_001038612:412	Olfm1	INSIDE	1.423	2.364	1458.26	3447.64	3.365	1185.01	3987.49
A_68_P20053923	chr1:16095671-16095715	NM_133832:-270	Rdh10	DIVERGENT_PROMOTER	1.423	2.090	560.23	1170.67	2.974	551.98	1641.71
A_68_P30140493	chr15:36722578-36722622	NM_011740:1693	Ywhaz	INSIDE	1.423	1.348	2080.18	2803.46	1.918	1581.01	3032.76
A_68_P30245918	chr15:57907631-57907675	NM_001042438:392	Zhx1	INSIDE	1.423	2.738	938.73	2570.11	3.897	833.40	3247.82
A_68_P26074975	chr8:96535903-96535947	NM_011787:616	Amfr	INSIDE	1.422	1.492	1949.22	2908.74	2.123	1624.85	3449.13
A_68_P24046040	chr5:122161910-122161954	NM_009125:315	Atxn2	INSIDE	1.422	2.027	1749.81	3547.00	2.882	1488.38	4290.02
A_68_P32260262	chrX:11655805-11655849	NM_029510:1853	Bcor	INSIDE	1.422	1.371	1911.85	2621.27	1.949	979.23	1908.57
A_68_P25095390	chr7:53088658-53088702	NM_008172:33371	Grin2d	INSIDE	1.422	3.563	1262.40	4498.44	5.067	1114.50	5646.78
A_68_P29613087	chr14:55194747-55194791	NM_010590:1730	Jub	INSIDE	1.422	2.416	2460.45	5944.98	3.436	1982.73	6812.18
A_68_P28095285	chr11:105153865-105153909	NM_008626:-73	Mrc2	PROMOTER	1.422	4.225	3447.09	14562.36	6.007	2430.85	14601.31
A_68_P25092625	chr7:52613255-52613299	NM_029741:9113	Ppfia3	INSIDE	1.422	3.194	663.98	2120.53	4.542	530.13	2407.97
A_68_P25500162	chr7:133520602-133520646	NM_023712:824	Spns1	INSIDE	1.422	2.871	572.14	1642.66	4.083	501.94	2049.58
A_68_P31187133	chr17:43153476-43153520	NM_178589:-5	Tnfrsf21	PROMOTER	1.422	1.782	735.33	1310.66	2.534	663.27	1680.81
A_68_P27365515	chr10:94978265-94978309	NM_080560:491	Ube2n	INSIDE	1.422	3.809	830.13	3161.90	5.418	722.87	3916.47
A_68_P27186307	chr10:61949576-61949620	NM_133672:-45	Vps26a	PROMOTER	1.422	3.902	1404.97	5482.65	5.548	1070.91	5941.57
A_68_P30345267	chr15:75812246-75812290	NM_001163518:447	2410075B13Rik	INSIDE	1.421	1.377	1690.90	2327.70	1.956	1348.63	2637.73

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26989977	chr10:20672484-20672528	NM_026203:154	Ahi1	INSIDE	1.421	3.099	796.25	2467.77	4.405	848.36	3737.14
A_68_P26841767	chr9:113650601-113650645	NM_001114347:32	Clasp2	INSIDE	1.421	2.491	1132.02	2820.18	3.541	996.51	3528.69
A_68_P23222201	chr4:114574854-114574898	NM_008593:6627	Foxd2	DOWNSTREAM	1.421	3.263	625.49	2040.92	4.638	580.94	2694.51
A_68_P23812523	chr5:76373731-76373775	NM_010612:701	Kdr	INSIDE	1.421	1.552	911.79	1415.15	2.206	757.69	1671.14
A_68_P30378912	chr15:81494223-81494269	NM_145993:-119	L3mbtl2	PROMOTER	1.421	1.964	1468.91	2884.74	2.790	1163.64	3247.14
A_68_P24816267	chr6:124612992-124613036	NM_145130:-107	Lpcat3	PROMOTER	1.421	2.819	6204.39	17491.88	4.007	5172.70	20725.45
A_68_P30382866	chr15:82169438-82169482	NM_008669:-204	Naga	DIVERGENT_PROMOTER	1.421	2.621	903.69	2368.91	3.726	716.73	2670.73
A_68_P27551120	chr11:3189836-3189880	NM_019574:-601	Patz1	PROMOTER	1.421	2.600	566.69	1473.37	3.694	434.89	1606.33
A_68_P30651715	chr16:32277893-32277937	NM_027355:368	Rnf168	INSIDE	1.421	1.480	1228.71	1819.02	2.104	1036.11	2180.33
A_68_P22392367	chr3:104442522-104442566	NM_009196:-46	Slc16a1	PROMOTER	1.421	1.538	3067.84	4719.16	2.186	2499.13	5462.55
A_68_P23607900	chr5:36826413-36826457	NM_001170454:500	Tada2b	INSIDE	1.421	2.162	4646.76	10045.98	3.073	3440.19	10570.87
A_68_P26542618	chr9:57437330-57437374	NM_027895:94	Ulk3	INSIDE	1.421	2.757	987.59	2722.90	3.917	924.14	3620.05
A_68_P22953712	chr4:58956665-58956709	NM_001099323:187	Zkscan16	INSIDE	1.421	2.680	1467.68	3933.53	3.809	1115.69	4249.89
A_68_P29388382	A_68_P29388382			Unknown	1.421	5.787	645.09	3733.38	8.222	598.38	4919.56
A_68_P26872167	chr9:119311485-119311529	NM_007397:-112	Acvr2b	PROMOTER	1.420	1.894	306.96	581.52	2.690	293.65	789.98
A_68_P23990789	chr5:112656382-112656426	NR_003718:1564	Miat	INSIDE	1.420	3.657	3521.20	12877.97	5.195	2718.77	14122.74
A_68_P26144000	chr8:109818386-109818430	NM_018823:1039	Nfat5	INSIDE	1.420	1.406	989.41	1390.67	1.995	906.75	1809.35
A_68_P32071922	chr19:32831644-32831688	NM_008960:-400	Pten	PROMOTER	1.420	3.731	1652.64	6166.00	5.299	1164.64	6171.60
A_68_P26038364	chr8:90484174-90484218	NM_033327:-702	Zfp423	PROMOTER	1.420	2.690	1218.54	3278.46	3.821	1085.88	4149.67
A_68_P22888266	chr4:46358077-46358121	NM_183298:1033	Foxe1	INSIDE	1.419	2.861	1769.83	5064.28	4.061	1543.70	6269.47
A_68_P22885282	chr4:45839676-45839720	NM_018741:1	Igfbpl1	INSIDE	1.419	1.847	961.74	1776.69	2.622	899.33	2357.68
A_68_P25842953	chr8:48761063-48761107	NM_023503:-571	Ing2	PROMOTER	1.419	1.707	607.79	1037.38	2.422	540.57	1309.40
A_68_P26770182	chr9:100446024-100446068	NM_010878:426	Nck1	INSIDE	1.419	1.911	1209.36	2311.66	2.713	970.35	2632.31
A_68_P20282814	chr1:62750008-62750052	NM_001077406:140	Nrp2	INSIDE	1.419	1.496	2768.18	4140.50	2.123	2068.88	4392.13
A_68_P31962487	chr19:12869271-12869315	NR_024093:1321	U05342	INSIDE	1.419	3.008	2234.52	6720.66	4.267	1880.57	8024.34
A_68_P22833091	chr4:34830379-34830423	NM_013889:-203	Zfp292	PROMOTER	1.419	2.359	1941.85	4580.08	3.346	1615.31	5405.37
A_68_P24602878	chr6:85019144-85019188	NM_177077:341	Exoc6b	INSIDE	1.418	2.092	1503.87	3146.46	2.967	1052.23	3121.95
A_68_P24591430	chr6:83052100-83052144	NM_026744:-6979	Mrpl53	PROMOTER	1.418	2.520	513.50	1294.26	3.575	510.65	1825.60
A_68_P26949004	chr10:12810446-12810490	NM_009538:-125	Plagl1	PROMOTER	1.418	2.735	620.49	1697.16	3.880	532.72	2066.77
A_68_P28567253	chr12:80130122-80130166	NM_181073:-5	Plekhh1	PROMOTER	1.418	3.469	750.42	2603.38	4.918	614.61	3022.44
A_68_P23441284	chr4:155265872-155265916	NM_001033490:-23	Pusl1	DIVERGENT_PROMOTER	1.418	2.215	1826.83	4047.07	3.142	1459.89	4586.74
A_68_P30348873	chr15:76350063-76350107	NM_130893:2475	Scrt1	INSIDE	1.418	2.237	2107.41	4714.76	3.172	1649.29	5230.77
A_68_P27807186	chr11:53705037-53705081	NM_011396:147	Slc22a5	INSIDE	1.418	1.943	3064.09	5952.44	2.755	2449.95	6749.51
A_68_P26142730	chr8:109555781-109555825	NM_126165:577	Vps4a	INSIDE	1.418	3.159	742.40	2345.28	4.479	589.76	2641.60
A_68_P22715817	chr4:8619031-8619075	NM_001081417:985	Chd7	INSIDE	1.417	1.514	9548.50	14453.91	2.144	6606.79	14167.87
A_68_P27924600	chr11:74983847-74983891	NM_010430:-111	Hic1	DIVERGENT_PROMOTER	1.417	2.286	1116.06	2550.97	3.238	884.80	2865.09
A_68_P20614486	chr1:133141955-133141999	NM_018750:-221	Rassf5	PROMOTER	1.417	2.281	1232.45	2811.73	3.234	1041.72	3368.61
A_68_P27842503	chr11:60166349-60166393	NM_001039092:37	Tom1l2	INSIDE	1.417	2.063	4182.55	8628.75	2.923	3261.48	9534.34
A_68_P24162463	chr5:145529030-145529074	NM_001081362:-608	Trrap	DIVERGENT_PROMOTER	1.417	3.214	3512.09	11288.62	4.556	2712.99	12359.52
A_68_P25663081	chr8:12672535-12672579	NM_198031:-456	Tubgcp3	PROMOTER	1.417	3.452	2330.06	8043.53	4.891	1945.10	9514.34
A_68_P32751543	chrX:149442021-149442065	NM_001137547:1031	Usp51	INSIDE	1.417	3.561	1928.35	6866.94	5.047	1138.77	5746.86
A_68_P24536898	chr6:71494106-71494150	NM_025783:281	Vps24	INSIDE	1.417	2.320	708.74	1644.28	3.287	567.62	1865.79
A_68_P26074978	chr8:96536308-96536352	NM_011787:210	Amfr	INSIDE	1.416	3.311	1388.52	4596.77	4.687	1274.11	5971.61
A_68_P24062297	chr5:125079741-125079785	NM_011596:115	Atp6v0a2	INSIDE	1.416	1.559	562.67	877.39	2.208	554.78	1224.70
A_68_P29287628	chr13:104711178-104711222	NM_001005868:-606	Erbb2ip	PROMOTER	1.416	1.835	1257.68	2308.12	2.599	1169.33	3039.51
A_68_P25730817	chr8:27229449-27229493	NM_207659:226	Hook3	INSIDE	1.416	2.553	3049.89	7785.12	3.616	2441.25	8826.48
A_68_P32016043	chr19:23210311-23210355	NM_010638:-5383	Klf9	PROMOTER	1.416	4.067	888.34	3613.11	5.759	697.02	4013.92
A_68_P26540423	chr9:56978779-56978823	NM_028636:217	Man2c1	INSIDE	1.416	2.713	653.92	1774.18	3.843	629.24	2417.98
A_68_P25953728	chr8:73267438-73267482	NM_201607:19498	Pde4c	INSIDE	1.416	2.036	858.33	1747.23	2.882	833.15	2401.31
A_68_P32575424	chrX:101176475-101176519	NM_011276:127	Rlim	INSIDE	1.416	2.853	8693.10	24805.08	4.042	6236.87	25207.16
A_68_P21704898	chr2:143837238-143837282	NM_024281:-261	Rrbp1	PROMOTER	1.416	2.615	1426.50	3730.43	3.704	1309.78	4851.46

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27541473	chr10:127896021-127896065	NM_001114096:-249	Smarcc2	PROMOTER	1.416	1.550	1630.99	2528.10	2.195	1385.29	3040.92
A_68_P27977899	chr11:84327083-84327127	NM_019816:-101	Aatf	PROMOTER	1.415	1.558	523.54	815.46	2.204	444.21	978.92
A_68_P28610312	chr12:87811484-87811528	NM_011934:48913	Esrrb	INSIDE	1.415	3.514	1014.32	3564.09	4.972	806.86	4011.80
A_68_P29075362	chr13:58909694-58909740	NM_001025074:523	Ntrk2	INSIDE	1.415	3.545	1141.26	4045.28	5.014	821.72	4120.05
A_68_P22101761	chr3:45183553-45183597	NM_011043:1255	Pcdh10	INSIDE	1.415	1.576	2007.04	3163.72	2.230	1703.03	3798.26
A_68_P30728925	chr16:45844534-45844578	NM_153412:-65	Phldb2	PROMOTER	1.415	3.345	1302.97	4359.06	4.735	1194.07	5653.92
A_68_P27540451	chr10:127707541-127707585	NM_019963:-69	Stat2	PROMOTER	1.415	1.729	2245.50	3882.21	2.446	1746.72	4272.53
A_68_P28402112	chr12:46175110-46175154	NM_144552:338	Stxbp6	INSIDE	1.415	1.850	3113.93	5759.59	2.617	2470.93	6466.73
A_68_P21920096	chr3:5219661-5219705	NM_030708:1129	Zfhx4	INSIDE	1.415	3.152	1282.92	4043.32	4.461	1384.14	6174.88
A_68_P20319169	chr1:69423807-69423851			Unknown	1.415	2.964	555.40	1646.05	4.193	466.30	1955.39
A_68_P23537869	chr5:23181744-23181788	ENSMUST00000157734:-1567		PROMOTER	1.415	2.503	1679.74	4204.56	3.542	1537.53	5446.32
A_68_P28530097	chr12:73186365-73186409	NM_026038:-86	2810055F11Rik	DIVERGENT_PROMOTER	1.414	1.866	3408.96	6362.14	2.640	2516.52	6642.89
A_68_P22407403	chr3:107398682-107398726	NM_007441:756	Alx3	INSIDE	1.414	2.074	1436.96	2980.63	2.933	1240.18	3637.72
A_68_P30751463	chr16:50432288-50432332	NM_027444:192	Bbx	INSIDE	1.414	1.904	328.99	626.29	2.692	303.84	817.80
A_68_P22151284	chr3:54859150-54859194	NM_007628:-195	Ccna1	PROMOTER	1.414	1.485	1402.96	2083.08	2.099	1405.54	2950.93
A_68_P32287122	chrX:19637760-19637804	NM_021715:1087	Chst7	INSIDE	1.414	2.815	968.09	2725.52	3.980	588.99	2344.32
A_68_P21820018	chr2:164658706-164658751	NM_001038492:356	Ctsa	INSIDE	1.414	2.708	566.82	1534.69	3.830	530.30	2030.87
A_68_P28925097	chr13:31898615-31898660	NM_008592:123	Foxc1	INSIDE	1.414	1.421	1066.47	1515.41	2.009	1209.38	2429.45
A_68_P22954220	chr4:59048156-59048200	NM_025277:151	Gng10	INSIDE	1.414	5.807	989.26	5744.38	8.209	856.33	7029.87
A_68_P30684003	chr16:38088656-38088700	NM_019827:-408	Gsk3b	PROMOTER	1.414	1.435	1193.56	1712.45	2.029	1142.32	2318.16
A_68_P27995150	chr11:87430698-87430742	NM_001045527:55	Hsf5	INSIDE	1.414	3.298	1976.62	6519.18	4.663	1723.73	8036.94
A_68_P25652455	chr8:11009184-11009228	NM_001081212:-776	Irs2	PROMOTER	1.414	2.138	1613.53	3449.83	3.024	1491.62	4510.74
A_68_P23819023	chr5:77380662-77380706	NM_172146:-81	Ppat	PROMOTER	1.414	3.590	3968.51	14247.09	5.075	3214.29	16312.63
A_68_P27921385	chr11:74403747-74403791	NM_001015046:-108	Rap1gap2	PROMOTER	1.414	1.794	920.25	1650.72	2.537	807.88	2049.41
A_68_P20451965	chr1:94807505-94807549	NM_181405:125	Rnpepl1	INSIDE	1.414	3.410	1465.86	4998.88	4.822	1215.11	5859.83
A_68_P26365992	chr9:25060005-25060049	NM_001205367:-13	Septin7	PROMOTER	1.414	2.049	1041.49	2133.69	2.897	923.47	2674.98
A_68_P31850942	chr18:78244032-78244076	NM_001101038:9953	Siglec15	INSIDE	1.414	3.049	393.30	1199.14	4.310	413.77	1783.29
A_68_P23973160	chr5:109058811-109058855	NM_001163531:4	Tmem175	INSIDE	1.414	3.467	380.53	1319.33	4.901	384.66	1885.27
A_68_P25614227	chr8:3496122-3496166	NM_080461:3007	Zfp358	INSIDE	1.414	2.617	496.37	1298.83	3.699	392.65	1452.42
A_68_P20026600	chr1:10222313-10222357	NM_001102430:417	Arfgef1	INSIDE	1.413	1.931	1534.02	2961.89	2.728	1158.33	3160.39
A_68_P29977214	chr15:3976915-3976959	NR_028266:470	BC037032	INSIDE	1.413	2.675	1415.05	3784.72	3.780	1172.61	4432.52
A_68_P25420899	chr7:118923736-118923780	NM_173739:-267	Galntl4	PROMOTER	1.413	3.673	2958.55	10865.71	5.190	2430.84	12615.98
A_68_P26135759	chr8:108282466-108282510	NM_027469:19	Gfod2	INSIDE	1.413	1.523	1541.04	2347.57	2.152	1181.67	2543.51
A_68_P21874393	chr2:174110277-174110321	NM_019690:478	Gnas	INSIDE	1.413	2.154	2046.31	4406.79	3.042	1642.18	4995.92
A_68_P25023656	chr7:29594118-29594162	NM_177301:-1768	Hnrnpl	PROMOTER	1.413	2.687	1331.04	3576.01	3.795	1074.61	4078.44
A_68_P26809623	chr9:107471781-107471825	NM_010489:309	Hyal2	INSIDE	1.413	4.236	5054.64	21410.10	5.986	3419.86	20470.32
A_68_P30478822	chr15:99055021-99055065	NM_010601:-364	Kcnh3	PROMOTER	1.413	3.462	317.84	1100.28	4.891	338.85	1657.16
A_68_P21809534	chr2:162769378-162769422	NM_001081338:200	L3mbtl1	INSIDE	1.413	3.093	968.62	2996.17	4.372	841.69	3679.62
A_68_P24610520	chr6:86475945-86475989	NM_011865:193	Pcbp1	INSIDE	1.413	2.626	1858.75	4881.48	3.710	1609.11	5969.99
A_68_P20442663	chr1:93355837-93355883	NM_011066:45	Per2	INSIDE	1.413	3.657	6446.43	23575.61	5.166	5308.25	27421.77
A_68_P25092684	chr7:52622218-52622262	NM_029741:149	Ppfia3	INSIDE	1.413	1.409	1337.34	1884.40	1.991	1117.01	2223.57
A_68_P23327089	chr4:134731774-134731818	NM_019732:55237	Runx3	INSIDE	1.413	2.139	298.22	637.88	3.022	218.63	660.62
A_68_P23395562	chr4:148001229-148001274	NM_001003898:-146	Tardbp	PROMOTER	1.413	1.494	1928.57	2881.24	2.110	1656.26	3495.28
A_68_P26023340	chr8:87562055-87562099	NM_001122843:1010	Tnpo2	INSIDE	1.413	2.301	2992.19	6884.41	3.251	2164.18	7036.24
A_68_P31118855	chr17:27993453-27993497	NM_001080769:23	Uhrf1bp1	INSIDE	1.413	3.683	777.08	2862.23	5.206	680.20	3541.08
A_68_P24951458	chr7:4945401-4945445	NM_026741:2281	Zfp579	INSIDE	1.413	2.367	3124.98	7396.80	3.345	2462.47	8236.76
A_68_P29021091	chr13:48828074-48828118	BC167198:235103		INSIDE	1.413	2.604	1695.84	4416.64	3.681	1315.86	4843.55
A_68_P25890689	chr8:59819744-59819788	ENSMUST00000132988:8852		DOWNSTREAM	1.413	2.087	997.48	2081.66	2.948	802.38	2365.63
A_68_P32957256	chr17:8476298-8476342	NM_018819:-357	Brp44l	PROMOTER	1.412	2.317	559.09	1295.31	3.271	543.39	1777.50
A_68_P26019658	chr8:86939377-86939421	NM_007578:136	Cacna1a	INSIDE	1.412	3.848	1672.03	6434.41	5.433	1364.80	7414.42
A_68_P30371906	chr15:80203104-80203152	NM_001044308:85461	Cacna1i	INSIDE	1.412	4.922	136.27	670.65	6.947	83.75	581.84

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P22728452	chr4:11117767-11117811	NM_001037134:-712	Ccne2	PROMOTER	1.412	2.320	339.08	786.68	3.277	284.19	931.30
A_68_P28313702	chr12:29236975-29237019	NM_001177964:-3794	Dcdc2c	PROMOTER	1.412	2.750	1290.20	3548.29	3.884	1046.53	4065.16
A_68_P30569150	chr16:16359116-16359160	NM_001025947:-15	Dnm1l	PROMOTER	1.412	10.245	353.34	3619.79	14.461	335.43	4850.62
A_68_P27284176	chr10:80049548-80049592	NM_145421:3516	Fam108a	INSIDE	1.412	2.481	1696.54	4208.31	3.504	1437.16	5035.41
A_68_P23787602	chr5:72048882-72048926	NM_010251:643	Gabra4	INSIDE	1.412	1.663	2656.01	4416.65	2.349	1936.04	4547.33
A_68_P24119633	chr5:136611987-136612031	NM_027891:-64	Lrwd1	DIVERGENT_PROMOTER	1.412	1.868	4287.48	8007.90	2.637	2922.79	7708.54
A_68_P27882408	chr11:67111986-67112033	NM_177369:21384	Myh8	INSIDE	1.412	2.711	235.50	638.38	3.829	202.89	776.82
A_68_P21723786	chr2:147191194-147191239	NM_008780:487	Pax1	INSIDE	1.412	11.427	1168.71	13355.35	16.130	889.81	14352.68
A_68_P20874691	chr1:182186344-182186388	NM_001128605:65	Psen2	INSIDE	1.412	2.020	634.12	1280.71	2.852	529.21	1509.22
A_68_P27902925	chr11:70658259-70658303	NM_019400:16	Rabep1	INSIDE	1.412	1.763	1828.38	3224.09	2.489	1509.22	3757.14
A_68_P28707014	chr12:106270570-106270614	NR_003145:-103	Snhg10	DIVERGENT_PROMOTER	1.412	2.559	751.25	1922.41	3.614	723.34	2614.10
A_68_P32958522	chr17:8627015-8627059	NM_009309:-251	T	PROMOTER	1.412	1.744	1177.05	2052.94	2.463	1001.67	2466.93
A_68_P25952182	chr8:73013396-73013440	NM_182991:-2161	Tmem59l	DIVERGENT_PROMOTER	1.412	2.404	1488.13	3577.32	3.394	1368.06	4642.54
A_68_P22861756	chr4:41296379-41296423	NM_023305:372	Ubap1	INSIDE	1.412	1.899	2409.65	4575.33	2.680	1781.80	4775.54
A_68_P22410425	chr3:107889046-107889090	NM_028779:477	Ampd2	INSIDE	1.411	1.872	3075.40	5756.63	2.641	2414.79	6378.00
A_68_P29695817	chr14:69955362-69955406	NM_026174:177	Entpd4	INSIDE	1.411	1.639	1867.34	3060.75	2.313	1690.78	3910.85
A_68_P30356791	chr15:77786971-77787015	NM_001017983:160	Foxred2	INSIDE	1.411	2.358	2890.26	6815.42	3.328	2449.53	8152.29
A_68_P23757987	chr5:66155002-66155046	NM_001024917:265	N4bp2	INSIDE	1.411	2.078	490.71	1019.55	2.932	461.90	1354.40
A_68_P23057168	chr4:82150339-82150383	NM_001113209:852	Nfib	INSIDE	1.411	2.024	1268.08	2566.46	2.856	1209.56	3454.91
A_68_P25021286	chr7:29124000-29124044	NM_013676:-284	Supt5h	PROMOTER	1.411	2.093	1024.49	2144.66	2.953	951.93	2811.44
A_68_P21101048	chr2:29904402-29904446	NM_001008498:-25	Wdr34	PROMOTER	1.411	2.596	1068.05	2772.33	3.662	950.24	3480.16
A_68_P31152233	chr17:34258866-34258910	NM_010238:-196	Brd2	PROMOTER	1.410	1.630	877.15	1430.03	2.299	840.32	1931.76
A_68_P25083584	chr7:50932175-50932219	NM_145582:4796	Ctu1	INSIDE	1.410	2.203	489.91	1079.14	3.106	410.59	1275.12
A_68_P27281161	chr10:79594591-79594635	NM_001195268:5520	Dos	INSIDE	1.410	2.666	1813.03	4832.69	3.759	1417.47	5328.88
A_68_P30468154	chr15:97077540-97077584	NM_172293:25	Fam113b	INSIDE	1.410	5.074	999.43	5071.38	7.154	834.90	5972.61
A_68_P24817835	chr6:124881155-124881199	NM_001170341:-229	Mlf2	PROMOTER	1.410	2.519	3481.95	8770.99	3.552	3025.57	10748.07
A_68_P25261270	chr7:86610733-86610777	NM_017462:405	Polg	INSIDE	1.410	1.887	2237.30	4221.82	2.661	1842.14	4901.97
A_68_P30576627	chr16:17928257-17928301	NM_153150:34	Slc25a1	INSIDE	1.410	1.496	833.86	1247.16	2.109	719.36	1517.25
A_68_P25235399	chr7:81699616-81699660	NM_001038643:28	Slco3a1	INSIDE	1.410	5.257	915.21	4811.55	7.415	790.12	5858.61
A_68_P30562963	chr16:14705930-14705974	NM_011415:1	Snai2	INSIDE	1.410	1.377	1658.17	2283.48	1.942	1325.17	2573.25
A_68_P30787362	chr16:57606693-57606737	NM_025599:266	2610528E23Rik	INSIDE	1.409	1.377	1366.06	1880.56	1.939	1110.63	2153.52
A_68_P30655032	chr16:32877777-32877821	NM_001159349:-71	Fyttd1	DIVERGENT_PROMOTER	1.409	3.794	690.93	2621.64	5.344	673.85	3601.39
A_68_P32401470	chrX:54756780-54756824	NM_001033360:132	Gpr101	INSIDE	1.409	2.418	865.27	2092.26	3.408	449.92	1533.16
A_68_P27182284	chr10:61246043-61246087	NM_207000:548	H2afy2	INSIDE	1.409	3.237	4096.24	13260.25	4.561	3206.81	14626.86
A_68_P25846169	chr8:49314467-49314511	NM_001145937:445556	Odz3	INSIDE	1.409	3.159	728.27	2300.32	4.451	652.82	2906.04
A_68_P20768946	chr1:162837198-162837242	NM_001024952:679	Rc3h1	INSIDE	1.409	2.773	621.82	1724.47	3.908	536.69	2097.56
A_68_P23294679	chr4:128735519-128735563	NM_029219:26	Rnf19b	INSIDE	1.409	2.908	1340.86	3899.06	4.098	1187.25	4865.85
A_68_P22392370	chr3:104442843-104442887	NM_009196:274	Slc16a1	INSIDE	1.409	3.586	1227.30	4400.60	5.052	1130.60	5711.85
A_68_P27365030	chr10:94878524-94878568	NM_001168656:-428	Socs2	PROMOTER	1.409	2.684	970.86	2605.41	3.781	842.34	3184.83
A_68_P26685862	chr9:83728264-83728308	NM_001110265:-9	Ttk	PROMOTER	1.409	1.703	3577.40	6092.03	2.400	2394.02	5745.88
A_68_P20679676	chr1:145549881-145549925	NM_145991:-88	Cdc73	PROMOTER	1.408	1.476	5325.64	7862.49	2.079	4869.18	10121.53
A_68_P20453266	chr1:94997065-94997109	NM_001110315:1356	Kif1a	INSIDE	1.408	1.643	3795.87	6235.33	2.313	2801.91	6480.75
A_68_P24479790	chr6:57652980-57653024	NM_133737:554	Lancl2	INSIDE	1.408	2.430	794.70	1931.28	3.421	691.36	2364.89
A_68_P22661976	chr3:153991190-153991234	NM_010713:2312	Lhx8	INSIDE	1.408	1.540	3483.43	5364.29	2.168	2801.56	6074.45
A_68_P22793481	chr4:26274038-26274083	NM_172865:-261	Manea	PROMOTER	1.408	2.675	2801.31	7494.27	3.766	2411.79	9082.95
A_68_P27980118	chr11:84694015-84694059	NM_001077636:-249	Pigw	PROMOTER	1.408	1.569	699.70	1097.73	2.209	622.33	1374.67
A_68_P32141866	chr19:46131585-46131629	NM_001081214:578	Pprc1	INSIDE	1.408	1.563	2301.83	3598.49	2.201	1881.74	4142.35
A_68_P32806534	chrX:162917700-162917744	NM_019773:77	Rab9	INSIDE	1.408	2.038	766.79	1562.78	2.870	390.07	1119.42
A_68_P30250720	chr15:58720614-58720658	NM_175226:-147	Rnf139	PROMOTER	1.408	3.567	2289.85	8166.88	5.021	1927.49	9678.51
A_68_P31244849	chr17:53828675-53828719	NM_028232:-56	Sgol1	PROMOTER	1.408	2.141	1821.99	3901.06	3.014	1701.11	5126.64
A_68_P29240371	chr13:96145165-96145209	NM_025630:103	Aggf1	INSIDE	1.407	2.350	738.00	1733.96	3.305	740.57	2447.36

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25089705	chr7:52109937-52109981	NM_026270:5362	Akt1s1	INSIDE	1.407	2.093	1940.17	4060.15	2.944	1664.79	4901.91
A_68_P32536862	chrX:91225843-91225889	NR_028320:11872	AU015836	DOWNSTREAM	1.407	2.633	433.55	1141.38	3.705	250.43	927.87
A_68_P24055184	chr5:123794688-123794734	NM_029850:254	Bcl7a	INSIDE	1.407	0.431	1429.58	615.62	0.606	1174.64	711.76
A_68_P21569151	chr2:119163754-119163798	NM_019454:12257	Dll4	DOWNSTREAM	1.407	2.068	1210.07	2502.81	2.909	1026.27	2985.64
A_68_P25405199	chr7:116094716-116094760	NM_025344:16810	Eif3f	DOWNSTREAM	1.407	1.942	363.10	704.98	2.731	271.25	740.85
A_68_P20227608	chr1:52557632-52557676	NM_008667:-362	Nab1	PROMOTER	1.407	1.821	1276.26	2324.40	2.562	1135.61	2909.38
A_68_P21842488	chr2:168427130-168427174	NM_001037178:3	Nfatc2	INSIDE	1.407	3.598	4227.71	15210.75	5.063	3218.50	16294.33
A_68_P23894271	chr5:92863563-92863607	NM_183392:641	Nup54	INSIDE	1.407	2.401	2087.01	5011.84	3.380	1927.99	6516.10
A_68_P31156112	chr17:34987286-34987330	NM_001045863:-27	Rdbp	DIVERGENT_PROMOTER	1.407	1.602	936.61	1500.90	2.255	907.16	2045.32
A_68_P31156004	chr17:34973557-34973601	NM_019442:270	Stk19	INSIDE	1.407	2.874	3122.89	8976.41	4.043	2434.15	9842.26
A_68_P26035029	chr8:89996288-89996332	NM_019626:181	Cbln1	INSIDE	1.406	3.564	8407.66	29968.20	5.012	6059.68	30368.11
A_68_P24011284	chr5:116181838-116181882	NM_001080808:-292	Ccdc64	PROMOTER	1.406	1.875	2306.58	4325.59	2.638	1864.46	4917.56
A_68_P31254440	chr17:56323216-56323260	NM_080837:105	D17Wsu104e	INSIDE	1.406	2.193	1001.83	2197.02	3.083	887.19	2735.36
A_68_P27055772	chr10:33927102-33927146	NM_172508:233	Dse	INSIDE	1.406	2.291	1326.27	3038.19	3.220	1109.05	3571.66
A_68_P20637452	chr1:137001893-137001941	NM_001033409:-63	Lgr6	PROMOTER	1.406	6.787	7856.61	53326.08	9.545	5134.92	49011.52
A_68_P31123145	chr17:28712577-28712621	NM_026571:-65	Lhfpl5	PROMOTER	1.406	1.795	762.16	1367.86	2.524	659.41	1664.28
A_68_P27635062	chr11:20991838-20991882	NM_023324:534	Peli1	INSIDE	1.406	2.699	1651.07	4455.42	3.794	1394.60	5290.94
A_68_P29054323	chr13:55423060-55423104	NM_009000:259	Rab24	INSIDE	1.406	2.908	1715.27	4988.57	4.090	1431.38	5853.72
A_68_P23254536	chr4:120689836-120689880	NM_133716:-6	Smap2	PROMOTER	1.406	2.137	1799.58	3844.83	3.003	1896.83	5696.91
A_68_P29964718	chr14:123382401-123382445	NM_028651:61	Tmtc4	INSIDE	1.406	0.451	1631.66	736.13	0.634	1548.36	981.86
A_68_P30592417	chr16:21423184-21423228	NM_001081366:16	Vps8	INSIDE	1.406	1.700	651.68	1107.59	2.390	586.24	1401.27
A_68_P24793727	chr6:119494261-119494305	NM_009525:83	Wnt5b	INSIDE	1.406	1.856	635.81	1180.32	2.610	534.46	1394.95
A_68_P30931895	chr16:85900243-85900287	NM_011782:1106	Adamts5	INSIDE	1.405	1.414	864.81	1223.15	1.988	842.52	1674.73
A_68_P25500905	chr7:133646409-133646453	NM_183020:386	Atxn2l	INSIDE	1.405	3.122	1715.00	5353.63	4.386	1486.82	6521.92
A_68_P31020949	chr17:6079867-6079911	NM_181392:61	Gtf2h5	INSIDE	1.405	1.509	1025.28	1547.57	2.120	822.53	1744.03
A_68_P28431899	chr12:52930265-52930309	NM_144788:237	Hectd1	INSIDE	1.405	3.721	395.03	1469.73	5.229	349.96	1829.86
A_68_P29117879	chr13:69948975-69949019	NM_138596:237	Med10	INSIDE	1.405	2.470	509.97	1259.71	3.470	452.22	1569.13
A_68_P23269531	chr4:124337466-124337523	NM_011141:2606	Pou3f1	INSIDE	1.405	6.180	201.62	1246.01	8.680	203.38	1765.43
A_68_P23238885	chr4:117884835-117884879	NM_011213:79146	Ptprf	INSIDE	1.405	5.342	1806.98	9653.34	7.506	1584.46	11893.57
A_68_P32750676	chrX:149203868-149203912	NM_172441:114	Shroom2	INSIDE	1.405	2.139	894.45	1913.59	3.007	560.54	1685.34
A_68_P24544425	chr6:72908782-72908826	NM_001190327:-62	Tmsb10	PROMOTER	1.405	2.237	1467.27	3282.32	3.144	1175.79	3696.58
A_68_P21620795	chr2:128512977-128513021	NM_008569:133	Anapc1	INSIDE	1.404	1.694	1441.96	2443.33	2.379	1286.45	3060.30
A_68_P32745112	chrX:147779006-147779050	NM_198105:263	Fam120c	INSIDE	1.404	2.058	2046.86	4213.02	2.891	1083.97	3133.24
A_68_P21609427	chr2:126500825-126500869	NM_010249:376	Gabpb1	INSIDE	1.404	5.171	1070.08	5533.26	7.258	919.71	6675.09
A_68_P28577474	chr12:81859527-81859571	NM_001008423:2154	Gm1568	INSIDE	1.404	3.088	946.54	2923.19	4.336	841.54	3648.63
A_68_P23644447	chr5:43625680-43625724	NR_028417:891	Gm7854	INSIDE	1.404	2.190	1122.39	2457.65	3.074	936.76	2879.42
A_68_P32536211	chrX:91077428-91077472	NM_145630:-16	Pdk3	PROMOTER	1.404	1.589	1225.88	1947.97	2.231	635.73	1418.11
A_68_P30575813	chr16:17807076-17807120	NM_153790:9724	Scarf2	INSIDE	1.404	2.276	4243.24	9657.92	3.195	3306.28	10564.39
A_68_P32259784	chrX:11584144-11584188			Unknown	1.404	1.722	6852.99	11799.17	2.417	3456.14	8353.28
A_68_P26885056	chr9:121619308-121619352	NM_026794:-176	Deb1	DIVERGENT_PROMOTER	1.403	1.680	998.84	1677.58	2.356	783.40	1845.53
A_68_P33007792	chr4_random:128621-128665	NM_001033326:18841	Dhrsx	INSIDE	1.403	2.689	4244.61	11413.45	3.771	3341.64	12602.76
A_68_P31936679	chr19:6996326-6996370	NM_007953:-50	Esrra	PROMOTER	1.403	2.076	1004.40	2085.48	2.914	812.87	2368.73
A_68_P31601519	chr18:32322742-32322786	NM_011946:22	Map3k2	INSIDE	1.403	1.491	710.88	1060.03	2.092	704.25	1472.97
A_68_P24757359	chr6:113027455-113027499	NM_028385:-156	Setd5	DIVERGENT_PROMOTER	1.403	3.215	2571.75	8268.07	4.512	2248.85	10147.12
A_68_P31142311	chr17:31992646-31992690	NM_010831:69	Sik1	INSIDE	1.403	1.467	2539.21	3723.82	2.057	2085.33	4290.14
A_68_P29421307	chr14:15536004-15536048	NM_001033270:488	Slc4a7	INSIDE	1.403	3.711	691.17	2564.99	5.208	592.83	3087.32
A_68_P25926490	chr8:67471009-67471053	NM_001163747:-53	Tmem192	PROMOTER	1.403	1.627	811.49	1320.02	2.282	731.54	1669.41
A_68_P24136156	chr5:140020220-140020264	NM_013702:391	Uncx	INSIDE	1.403	2.655	1505.01	3996.43	3.726	1276.00	4753.82
A_68_P24639205	chr6:91423217-91423261	NM_133928:179	Chchd4	INSIDE	1.402	1.712	1123.21	1923.19	2.401	875.72	2102.71
A_68_P26166334	chr8:113581188-113581232	NM_028274:972	Exosc6	INSIDE	1.402	2.006	1168.33	2343.79	2.813	996.51	2802.98
A_68_P31948450	chr19:10176095-10176139	NM_019699:-123	Fads2	PROMOTER	1.402	1.380	1397.41	1929.06	1.936	1083.93	2098.42

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27591951	chr11:11585898-11585942	NM_001025597:-295	Ikzf1	PROMOTER	1.402	2.070	730.08	1511.22	2.901	599.41	1739.11
A_68_P22139473	chr3:52845232-52845276	NM_175386:-214	Lhfp	PROMOTER	1.402	3.719	2004.22	7453.29	5.213	1562.39	8145.14
A_68_P23316583	chr4:132806890-132806934	NM_016693:10180	Map3k6	INSIDE	1.402	1.507	895.06	1348.55	2.112	732.59	1547.47
A_68_P25478239	chr7:129432560-129432604	NM_008855:-56	Prkcb	PROMOTER	1.402	2.667	505.17	1347.19	3.738	432.90	1618.16
A_68_P20354815	chr1:75543006-75543050	NM_009208:188	Slc4a3	INSIDE	1.402	1.770	518.97	918.77	2.482	430.74	1069.06
A_68_P31469354	chr18:5592137-5592181	NM_011546:270	Zeb1	INSIDE	1.402	2.753	1966.58	5414.65	3.861	1502.43	5801.01
A_68_P28185535	chr11:120459852-120459896	NM_001038230:29	Anapc11	INSIDE	1.401	1.827	749.13	1368.39	2.559	589.68	1509.19
A_68_P25947954	chr8:72315394-72315438	NM_133224:355	Atp13a1	INSIDE	1.401	5.952	863.09	5137.52	8.341	743.89	6204.59
A_68_P31567774	chr18:25911745-25911789	NM_001146292:718	Celf4	INSIDE	1.401	1.931	353.29	682.11	2.706	290.12	784.96
A_68_P30181643	chr15:44451360-44451404	NM_019480:196	Ebag9	INSIDE	1.401	1.552	2230.43	3461.83	2.175	1838.06	3996.93
A_68_P26166328	chr8:113580417-113580461	NM_028274:200	Exosc6	INSIDE	1.401	6.399	499.21	3194.31	8.964	463.31	4152.94
A_68_P32139831	chr19:45734262-45734306	NM_013907:399	Fbxw4	INSIDE	1.401	1.512	587.99	889.29	2.119	532.35	1127.87
A_68_P23577610	chr5:31597885-31597929	NM_022424:344	Fndc4	INSIDE	1.401	2.391	2561.88	6124.91	3.349	2078.32	6959.31
A_68_P25101651	chr7:54101747-54101791	NM_001136069:-683	Ldha	PROMOTER	1.401	2.910	447.71	1302.65	4.075	390.23	1590.14
A_68_P21706641	chr2:144156468-144156512	NM_152947:608	Ovol2	INSIDE	1.401	6.539	4320.91	28254.59	9.164	3330.70	30522.49
A_68_P30140494	chr15:36722668-36722712	NM_011740:1603	Ywhaz	INSIDE	1.401	1.704	2603.52	4437.13	2.388	1951.87	4661.74
A_68_P20349427	chr1:74634546-74634590	NM_029888:34	Zfp142	INSIDE	1.401	1.664	2069.36	3443.62	2.332	1793.48	4182.06
A_68_P31929033	chr19:5490488-5490532	NM_007687:56	Cfl1	INSIDE	1.400	1.869	798.40	1491.89	2.616	769.74	2013.88
A_68_P27533642	chr10:126478457-126478501	NM_001205036:-28	LOC100504608	DIVERGENT_PROMOTER	1.400	3.818	2175.23	8304.52	5.343	2058.67	11000.07
A_68_P27788131	chr11:50172882-50172926	NR_030529:-1523	Mir804	PROMOTER	1.400	2.253	2303.11	5189.26	3.155	1863.17	5879.04
A_68_P27215086	chr10:67442552-67442596	NM_001081346:229	Rtkn2	INSIDE	1.400	2.426	1259.75	3055.84	3.396	1153.03	3916.15
A_68_P22659975	chr3:153636613-153636657	NM_001081263:235	Slc44a5	INSIDE	1.400	1.638	1233.09	2019.54	2.293	1001.03	2295.80
A_68_P24833353	chr6:127511414-127511458			Unknown	1.400	1.740	1231.76	2142.93	2.436	1108.95	2701.05
A_68_P27756941	chr11:44431946-44431990	NM_007897:333	Ebf1	INSIDE	1.399	1.745	394.68	688.61	2.441	362.89	885.87
A_68_P20226307	chr1:52289184-52289228	NM_001081081:870	Gls	INSIDE	1.399	2.484	1200.72	2982.60	3.475	1081.89	3759.12
A_68_P30681056	chr16:37539468-37539512	NM_028812:365	Gtf2e1	INSIDE	1.399	2.322	1872.10	4347.39	3.250	1573.84	5114.56
A_68_P23611441	chr5:37482522-37482566	NM_178394:40449	Jakmip1	INSIDE	1.399	2.144	743.36	1593.77	2.998	643.30	1928.90
A_68_P25263205	chr7:86937995-86938039	NM_008588:460	Mesp1	INSIDE	1.399	3.289	629.69	2070.96	4.600	556.40	2559.24
A_68_P24591487	chr6:83059326-83059370	NM_026744:247	Mrpl53	INSIDE	1.399	1.585	820.52	1300.18	2.217	677.96	1503.31
A_68_P30480281	chr15:99287653-99287697	NM_001001884:505	Nckap5l	INSIDE	1.399	1.686	2209.21	3724.04	2.358	1458.67	3438.90
A_68_P27279098	chr10:79281731-79281775	NM_001161747:25436	Palm	INSIDE	1.399	3.382	602.57	2037.78	4.733	558.73	2644.35
A_68_P31208520	chr17:46848930-46848974	NM_145488:541	Pex6	INSIDE	1.399	2.065	1808.51	3735.42	2.890	1669.19	4823.98
A_68_P27942686	chr11:78142057-78142101	NM_201406:155	Pigs	INSIDE	1.399	2.322	3187.24	7400.05	3.248	2820.21	9160.18
A_68_P20011682	chr1:6204945-6204989	NM_009826:224	Rb1cc1	INSIDE	1.399	6.011	107.23	644.54	8.411	99.08	833.42
A_68_P27926518	chr11:75324220-75324264	NM_001029938:647	Rilp	INSIDE	1.399	4.585	3632.75	16656.98	6.417	2896.51	18586.14
A_68_P23542975	chr5:24107899-24107943	NM_025891:-100	Smarcd3	PROMOTER	1.399	1.953	382.91	747.98	2.732	354.36	968.08
A_68_P20409779	chr1:87915105-87915149	NM_027029:-3390	Spata3	PROMOTER	1.399	2.606	369.43	962.76	3.645	329.67	1201.68
A_68_P29428732	chr14:17198090-17198134	NM_009409:393	Top2b	INSIDE	1.399	3.732	693.33	2587.49	5.223	598.73	3127.03
A_68_P27789375	chr11:50415810-50415854	NM_175643:246	Adamts2	INSIDE	1.398	2.253	2651.57	5973.66	3.151	2404.30	7575.02
A_68_P25065437	chr7:38892310-38892354	NM_007633:177	Ccne1	INSIDE	1.398	1.867	578.86	1080.99	2.611	461.28	1204.19
A_68_P27282061	chr10:79727895-79727939	NM_001122604:181	Dazap1	INSIDE	1.398	3.911	1487.01	5815.28	5.468	1279.79	6997.54
A_68_P23235083	chr4:117223023-117223067	NM_080469:-54	Eri3	PROMOTER	1.398	5.781	754.89	4364.04	8.084	638.76	5163.45
A_68_P29953204	chr14:121435005-121435049	NM_134082:231	Farp1	INSIDE	1.398	2.932	995.92	2920.48	4.099	921.82	3778.72
A_68_P29529251	chr14:35124024-35124068	NM_008133:134	Glud1	INSIDE	1.398	2.579	2250.19	5802.24	3.605	1990.22	7175.04
A_68_P24757357	chr6:113027235-113027279	NR_027010:-18	Gt(ROSA)26Sor	DIVERGENT_PROMOTER	1.398	2.086	588.75	1228.17	2.915	544.79	1588.32
A_68_P24325223	chr6:29162126-29162170	NM_011829:123	Impdh1	INSIDE	1.398	1.871	5279.77	9878.35	2.615	3665.18	9584.02
A_68_P32148149	chr19:47253623-47253667	NM_021360:335	Neurl1a	INSIDE	1.398	2.625	1198.87	3147.37	3.669	959.99	3522.42
A_68_P32565873	chrX:99045311-99045356	NM_001163610:610	Nhsl2	INSIDE	1.398	1.771	1001.28	1772.96	2.475	607.83	1504.35
A_68_P29009460	chr13:46822473-46822517	NM_175749:724	Nup153	INSIDE	1.398	1.677	3751.32	6291.94	2.344	2854.35	6691.14
A_68_P31375202	chr17:79452069-79452113	NM_027455:845	Qpct	INSIDE	1.398	2.331	1879.36	4380.77	3.259	1644.52	5359.97
A_68_P23820630	chr5:77694944-77694988	NM_011263:448	Rest	INSIDE	1.398	1.947	5298.87	10319.06	2.723	4359.51	11869.89

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P21365118	chr2:78709482-78709526	NM_009454:301	Ube2e3	INSIDE	1.398	4.528	1600.81	7247.78	6.330	1381.60	8745.66
A_68_P29448497	chr14:21526842-21526886	NM_027996:91	2310021P13Rik	INSIDE	1.397	1.393	2174.38	3028.32	1.946	1834.85	3570.00
A_68_P20769692	chr1:162965131-162965175	NR_002840:-144	Gas5	DIVERGENT_PROMOTER	1.397	3.524	2582.17	9100.43	4.923	1793.34	8827.97
A_68_P30482737	chr15:99705642-99705686	NM_001113545:223	Lima1	INSIDE	1.397	4.162	1490.10	6202.30	5.814	1170.51	6805.88
A_68_P31236180	chr17:51952405-51952449	NM_001163630:-1047	Satb1	PROMOTER	1.397	2.008	618.50	1242.07	2.805	632.48	1774.17
A_68_P24725198	chr6:106719039-106719083	NM_027296:-105	Trnt1	PROMOTER	1.397	5.081	1506.70	7656.14	7.099	1137.75	8077.29
A_68_P32257886	chrX:11241995-11242039			Unknown	1.397	3.581	665.18	2381.66	5.004	371.14	1857.01
A_68_P28183960	chr11:120209674-120209718	NM_009609:102	Actg1	INSIDE	1.396	1.642	541.23	888.58	2.291	499.59	1144.79
A_68_P21492619	chr2:104966561-104966605	NR_015462:85	AI314831	INSIDE	1.396	2.308	940.63	2170.96	3.222	704.81	2271.21
A_68_P31053607	chr17:12934828-12934873	NR_002853:674	Airn	INSIDE	1.396	2.003	564.26	1130.13	2.796	529.19	1479.46
A_68_P24864229	chr6:134869881-134869925	NM_009875:-516	Cdkn1b	PROMOTER	1.396	1.394	1252.13	1745.42	1.946	1149.29	2237.07
A_68_P22893294	chr4:47221270-47221314	NM_009928:409	Col15a1	INSIDE	1.396	1.957	7873.75	15410.43	2.733	6249.31	17078.71
A_68_P25422971	chr7:119301817-119301861	NM_015814:733	Dkk3	INSIDE	1.396	6.658	4315.43	28730.11	9.294	2768.78	25732.05
A_68_P29863770	chr14:103498866-103498910	NM_015822:-162	Fbxl3	PROMOTER	1.396	2.589	973.82	2521.37	3.613	902.17	3259.82
A_68_P28480021	chr12:62624233-62624277	NM_178714:-1364	Lrfn5	PROMOTER	1.396	1.666	443.87	739.42	2.325	369.37	858.89
A_68_P25091650	chr7:52437190-52437234	NM_053256:848	Pth2	DOWNSTREAM	1.396	1.506	1846.75	2781.72	2.102	1450.07	3048.37
A_68_P27646885	chr11:23565657-23565701	NM_001033654:5	Pus10	INSIDE	1.396	1.369	1802.33	2467.43	1.911	1579.50	3019.08
A_68_P21077274	chr2:26092670-26092714	NM_153559:248	Qsox2	INSIDE	1.396	1.944	2133.27	4147.70	2.715	1864.67	5062.62
A_68_P25092432	chr7:52582657-52582701	NM_175130:6472	Trpm4	INSIDE	1.396	2.555	1622.52	4144.76	3.566	1367.67	4876.75
A_68_P24819389	chr6:125165905-125165949	NM_001080557:328	Vamp1	INSIDE	1.396	1.869	954.47	1783.85	2.609	844.70	2204.17
A_68_P27033518	chr10:28868262-28868306	NM_026138:4483	6330407J23Rik	INSIDE	1.395	1.534	2436.88	3737.10	2.139	1828.86	3912.70
A_68_P23192159	chr4:107356053-107356097	NM_019872:693	Dmrtb1	INSIDE	1.395	1.903	441.89	840.91	2.655	421.38	1118.83
A_68_P27067359	chr10:36693905-36693949	NM_008229:-423	Hdac2	PROMOTER	1.395	2.956	2512.26	7426.68	4.123	1989.08	8200.42
A_68_P31731697	chr18:56867382-56867426	NM_010721:-62	Lmnb1	PROMOTER	1.395	2.458	549.59	1350.75	3.428	488.07	1673.23
A_68_P22038555	chr3:32428477-32428521	NM_024200:95	Mfn1	INSIDE	1.395	3.778	1062.72	4015.10	5.272	1025.16	5404.92
A_68_P32183819	chr19:53750945-53750989	NM_001170847:-829	Rbm20	PROMOTER	1.395	1.383	1942.31	2685.80	1.929	1608.32	3102.19
A_68_P31738737	chr18:58039024-58039069	NM_009194:715	Slc12a2	INSIDE	1.395	1.668	1207.21	2013.50	2.326	1010.92	2351.78
A_68_P32008153	chr19:21852916-21852960	NM_001033759:107	Tmem2	INSIDE	1.395	3.709	1218.89	4520.81	5.173	1023.30	5294.04
A_68_P23874561	A_68_P23874561			Unknown	1.395	7.260	319.56	2320.13	10.131	308.34	3123.78
A_68_P26749715	chr9:96789502-96789546	NM_153420:317	Acpl2	INSIDE	1.394	1.692	12101.53	20476.82	2.358	7410.41	17477.14
A_68_P23315382	chr4:132595283-132595327	NM_146155:27884	Ahdc1	INSIDE	1.394	3.767	896.38	3377.11	5.252	793.29	4166.12
A_68_P21569149	chr2:119163546-119163590	NM_019454:12049	Dll4	DOWNSTREAM	1.394	4.287	1272.36	5454.83	5.977	1115.32	6666.14
A_68_P22081217	chr3:40549685-40549729	NM_011020:172	Hspa4l	INSIDE	1.394	1.992	1461.33	2911.48	2.777	1265.58	3514.48
A_68_P24759766	chr6:113432543-113432587	NM_134159:11116	Il17rc	INSIDE	1.394	4.030	2414.78	9732.27	5.617	1971.48	11073.56
A_68_P31791016	chr18:67448771-67448815	NM_053261:-84	Impa2	PROMOTER	1.394	5.242	21630.25	113388.70	7.309	13337.96	97486.45
A_68_P25954564	chr8:73386897-73386941	NM_032397:-6011	Kcnn1	PROMOTER	1.394	6.923	863.31	5976.70	9.648	731.30	7055.72
A_68_P20080973	chr1:21951507-21951551	NM_001160139:495	Kcnq5	INSIDE	1.394	1.983	1766.27	3502.03	2.764	1556.32	4301.49
A_68_P21203206	chr2:49475493-49475538	NM_008449:682	Kif5c	INSIDE	1.394	2.658	1117.53	2970.46	3.706	947.98	3513.10
A_68_P25954066	chr8:73311865-73311909	NM_199308:4446	Mast3	INSIDE	1.394	1.885	3213.06	6055.79	2.627	2384.39	6264.26
A_68_P24192244	chr5:151476355-151476399	NM_175310:-25	Pds5b	DIVERGENT_PROMOTER	1.394	1.880	2011.69	3782.47	2.620	1713.43	4490.00
A_68_P25114628	chr7:57034222-57034266	NM_133740:517	Prmt3	INSIDE	1.394	2.031	1557.36	3163.39	2.832	1345.01	3809.64
A_68_P26165837	chr8:113494378-113494429	NM_009179:50639	St3gal2	INSIDE	1.394	4.067	281.97	1146.83	5.670	250.48	1420.12
A_68_P25806165	chr8:41596899-41596943	NM_033560:-216	Vps37a	DIVERGENT_PROMOTER	1.394	2.268	3052.89	6923.55	3.162	2440.41	7716.95
A_68_P32414051	chrX:57657552-57657596	NM_001001798:-418	Atp11c	PROMOTER	1.393	3.236	1169.61	3785.34	4.509	898.54	4051.94
A_68_P25091981	chr7:52489690-52489734	NM_007645:4497	Cd37	INSIDE	1.393	3.706	1418.20	5256.43	5.164	1190.30	6146.77
A_68_P25187993	chr7:73532543-73532587	NM_146191:663	Lrrk1	INSIDE	1.393	1.898	3028.57	5747.25	2.644	2787.26	7368.42
A_68_P25016747	chr7:28118579-28118623	NM_001113549:67	Ltbp4	INSIDE	1.393	3.093	2893.09	8948.48	4.309	2424.53	10446.94
A_68_P31866300	chr18:80904546-80904590	NM_001164111:344	Nfatc1	INSIDE	1.393	3.042	622.87	1894.76	4.238	571.47	2421.71
A_68_P29294054	chr13:105844417-105844461	NM_029879:572	Rgs7bp	INSIDE	1.393	4.855	1066.43	5177.25	6.761	999.80	6759.52
A_68_P23012913	chr4:71860924-71860968	NM_011599:1007	Tle1	INSIDE	1.393	1.763	2197.50	3873.44	2.456	1831.01	4496.95
A_68_P20804421	chr1:169238701-169238745	NM_001039483:-78	Tmco1	PROMOTER	1.393	1.455	3612.53	5257.39	2.028	2927.21	5935.77

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25508612	chr7:135153559-135153603	NM_001079932:5689	Trim72	INSIDE	1.393	3.632	6264.66	22752.62	5.060	4584.63	23199.60
A_68_P30446388	chr15:93166877-93166921	NM_024189:468	Yaf2	INSIDE	1.393	1.789	459.90	822.73	2.492	410.73	1023.67
A_68_P27473557	chr10:115550809-115550853	NM_001161855:143	4933416C03Rik	INSIDE	1.392	1.775	841.21	1492.90	2.471	700.50	1730.61
A_68_P23952640	chr5:104937435-104937479	NM_001166581:86	BC005561	INSIDE	1.392	3.221	917.87	2956.25	4.484	900.73	4038.50
A_68_P31602500	chr18:32537426-32537470	NM_001083334:578	Bin1	INSIDE	1.392	2.016	1367.56	2757.24	2.807	1075.46	3018.73
A_68_P32121152	chr19:42507077-42507121	NM_145123:-825	Crtac1	PROMOTER	1.392	1.346	2500.39	3365.95	1.874	2134.04	3999.26
A_68_P32224194	chr19:60302569-60302613	NM_029648:10	D19Ertd737e	INSIDE	1.392	2.462	712.38	1753.56	3.427	651.94	2234.20
A_68_P21708094	chr2:144425869-144425913	NM_025314:202	Dtd1	INSIDE	1.392	2.707	1902.22	5149.00	3.769	1721.20	6486.54
A_68_P30287849	chr15:65618481-65618525	NM_133766:-100	Efr3a	PROMOTER	1.392	2.069	456.57	944.77	2.880	376.12	1083.26
A_68_P32087899	chr19:36132232-36132276	NM_008315:-404	Htr7	PROMOTER	1.392	3.060	1869.92	5721.76	4.258	1584.05	6744.81
A_68_P26258349	chr8:129107965-129108009	NM_001164598:9350	Irf2bp2	DOWNSTREAM	1.392	4.946	787.26	3893.53	6.883	617.74	4252.15
A_68_P22530174	chr3:130815152-130815196	NM_010703:1786	Lef1	INSIDE	1.392	1.934	1766.84	3416.36	2.691	1447.40	3894.72
A_68_P22289187	chr3:83959390-83959434	NM_029797:296	Mnd1	INSIDE	1.392	3.022	590.88	1785.42	4.205	507.76	2135.18
A_68_P26770183	chr9:100446090-100446134	NM_010878:360	Nck1	INSIDE	1.392	1.694	1160.50	1966.16	2.359	1027.67	2424.48
A_68_P21630523	chr2:130402275-130402319	NM_011025:388	Oxt	INSIDE	1.392	2.016	2820.56	5687.33	2.807	2397.92	6731.12
A_68_P29011801	chr13:47218477-47218521	NM_146042:410	Rnf144b	INSIDE	1.392	1.546	1748.77	2703.86	2.152	1491.46	3209.47
A_68_P23328080	chr4:134908744-134908788	NM_001130477:363	Srrm1	INSIDE	1.392	2.562	1269.99	3254.29	3.567	1131.87	4036.84
A_68_P30784286	chr16:57122130-57122174	NM_138599:326	Tomm70a	INSIDE	1.392	5.873	2134.34	12535.32	8.177	1613.28	13192.50
A_68_P31509672	chr18:14129799-14129843	NM_145492:1422	Zfp521	INSIDE	1.392	1.346	2572.26	3462.43	1.874	2083.95	3905.19
A_68_P28729767	chr12:109996277-109996321			Unknown	1.392	2.215	2800.23	6201.96	3.083	2176.21	6709.01
A_68_P23767822	chr5:67818022-67818066	NM_001164806:994	Bend4	INSIDE	1.391	1.964	2706.33	5314.51	2.732	2302.94	6292.60
A_68_P29787829	chr14:87541024-87541070	NM_019670:-125	Diap3	PROMOTER	1.391	1.480	4821.44	7138.04	2.060	3649.49	7516.66
A_68_P31201910	chr17:45710240-45710284	NM_008302:-52	Hsp90ab1	PROMOTER	1.391	1.931	2513.45	4852.98	2.685	2103.94	5649.86
A_68_P24431605	chr6:49164853-49164897	NM_023670:79	Igf2bp3	INSIDE	1.391	1.783	1060.06	1890.47	2.481	892.70	2215.10
A_68_P20832387	chr1:174255748-174255792	NM_008429:3624	Kcnj9	INSIDE	1.391	3.128	3509.47	10978.33	4.352	2542.31	11064.65
A_68_P31257382	chr17:56766395-56766439	NM_028782:-90	Lonp1	DIVERGENT_PROMOTER	1.391	2.748	5430.44	14925.43	3.824	3946.84	15092.92
A_68_P22190750	chr3:63100022-63100066	NM_008604:251	Mme	INSIDE	1.391	3.594	1374.41	4939.93	4.998	1143.34	5714.37
A_68_P31187137	chr17:43153945-43153989	NM_178589:463	Tnfrsf21	INSIDE	1.391	2.094	2666.64	5583.34	2.912	2260.14	6581.90
A_68_P28818477	chr13:9763394-9763438	NM_001199141:1144	Zmynd11	INSIDE	1.391	2.739	1885.24	5162.99	3.810	1673.44	6376.01
A_68_P32565209	chrX:98893628-98893674	ENSMUST00000073812:-6461		PROMOTER	1.391	3.079	936.61	2883.76	4.284	327.68	1403.82
A_68_P30931273	chr16:85802461-85802505	NM_009621:878	Adamts1	INSIDE	1.390	3.403	1563.18	5318.88	4.729	1329.86	6288.30
A_68_P24593651	chr6:83407070-83407114	NR_028382:15344	B230319C09Rik	DOWNSTREAM	1.390	1.651	1604.03	2648.16	2.295	1366.64	3136.95
A_68_P28191921	chr11:121534336-121534380	NM_178664:107	B3gntl1	INSIDE	1.390	2.023	813.65	1646.24	2.813	683.65	1922.94
A_68_P31166953	chr17:37183108-37183152	NM_019439:220	Gabbr1	INSIDE	1.390	2.246	545.54	1225.43	3.122	433.24	1352.77
A_68_P20293513	chr1:64663621-64663665	NM_025964:100	Mettl21a	INSIDE	1.390	7.059	1748.89	12345.54	9.810	1306.19	12813.78
A_68_P21934677	chr3:8923780-8923824	NM_025434:55	Mrps28	INSIDE	1.390	2.404	1130.38	2717.52	3.342	1012.75	3384.86
A_68_P32082675	chr19:34953035-34953079	NM_023792:-649	Pank1	PROMOTER	1.390	1.862	609.80	1135.72	2.588	620.50	1605.87
A_68_P26760867	chr9:98743140-98743184	NM_001134660:157	Prr23a	INSIDE	1.390	3.725	2610.95	9724.83	5.178	2298.06	11898.87
A_68_P23794550	chr5:73305332-73305376	NM_001113423:-201	Slain2	PROMOTER	1.390	1.421	1679.49	2387.30	1.976	1309.27	2587.76
A_68_P30487544	chr15:100592074-100592119	NM_021530:-81	Slc4a8	PROMOTER	1.390	1.893	878.86	1663.74	2.632	686.91	1807.95
A_68_P25089709	chr7:52110332-52110376	NM_026270:5758	Akt1s1	INSIDE	1.389	1.646	1948.90	3207.99	2.287	1590.76	3637.56
A_68_P30337621	chr15:74350207-74350251	NM_174991:3603	Bai1	INSIDE	1.389	1.830	1937.76	3547.01	2.542	1660.99	4222.91
A_68_P23299543	chr4:129665364-129665408	NM_001199696:3065	Bai2	INSIDE	1.389	4.824	1005.48	4850.09	6.698	818.53	5482.78
A_68_P27289988	chr10:80945144-80945188	NM_176954:288	Celf5	INSIDE	1.389	3.138	7031.28	22066.79	4.360	5090.20	22193.73
A_68_P20997455	chr2:9799133-9799177	NM_008091:1073	Gata3	INSIDE	1.389	2.203	1407.39	3101.06	3.060	1213.21	3711.88
A_68_P27286724	chr10:80448504-80448548	NM_001038655:15584	Gng7	INSIDE	1.389	2.779	5471.48	15203.85	3.859	4309.14	16628.08
A_68_P26346113	chr9:21043510-21043554	NM_001110305:244	Keap1	INSIDE	1.389	2.738	1066.07	2919.34	3.804	977.31	3717.21
A_68_P31462886	chr18:4375807-4375851	NM_026157:239	Mtpap	INSIDE	1.389	1.781	1407.85	2507.38	2.473	1354.18	3349.23
A_68_P23637417	chr5:42154620-42154664	NM_007524:817	Nkx3-2	INSIDE	1.389	1.588	3754.70	5962.47	2.206	2920.74	6441.82
A_68_P31757535	chr18:61559223-61559268	NM_133249:840	Ppargc1b	INSIDE	1.389	2.054	4873.75	10011.88	2.854	3783.56	10798.66
A_68_P21769250	chr2:155890860-155890904	NM_139151:-66	Spag4	PROMOTER	1.389	2.324	596.43	1386.03	3.229	546.75	1765.42

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27644767	chr11:23156427-23156471	NM_001035226:408	Xpo1	INSIDE	1.389	1.998	524.57	1048.31	2.776	417.92	1160.20
A_68_P28048035	chr11:96858653-96858697			Unknown	1.389	2.884	1597.67	4607.66	4.006	1231.51	4933.87
A_68_P22262794	chr3:79090694-79090738	AK032506:-597		PROMOTER	1.389	1.987	809.05	1607.50	2.761	754.96	2084.19
A_68_P32589659	chrX:105011372-105011416	NM_025921:279	2610002M06Rik	INSIDE	1.388	3.761	4965.52	18676.02	5.219	2295.18	11979.46
A_68_P24134879	chr5:139801058-139801102	NM_172723:338	Adap1	INSIDE	1.388	0.416	3250.82	1352.27	0.577	2894.34	1671.39
A_68_P31516123	chr18:15309505-15309549	NM_134112:429	Kctd1	INSIDE	1.388	1.414	3242.69	4584.00	1.962	2543.33	4989.28
A_68_P28738216	chr12:111684724-111684768	NM_001135001:-642	Ppp2r5c	PROMOTER	1.388	2.129	4451.31	9478.89	2.956	3140.30	9281.26
A_68_P20770876	chr1:163181287-163181331	NM_007453:-11	Prdx6	PROMOTER	1.388	1.612	7474.68	12051.29	2.238	5273.32	11802.44
A_68_P22572447	chr3:138737478-138737522	NM_001040690:663	Rap1gds1	INSIDE	1.388	2.478	2028.06	5026.53	3.440	1758.57	6049.20
A_68_P21557413	chr2:117168443-117168487	NM_011246:149	Rasgrp1	INSIDE	1.388	2.134	448.72	957.44	2.961	404.89	1198.97
A_68_P29715888	chr14:73543452-73543496	NR_033185:883	Rcbtb2	INSIDE	1.388	2.304	1611.48	3712.43	3.198	1358.60	4344.63
A_68_P26823109	chr9:110235990-110236034	NM_001001144:216	Scap	INSIDE	1.388	1.776	1006.73	1787.90	2.465	936.32	2308.19
A_68_P30425916	chr15:89388272-89388316	NM_021423:58007	Shank3	INSIDE	1.388	2.300	963.68	2216.92	3.194	959.09	3063.19
A_68_P30364761	chr15:78993943-78993987	NM_011437:956	Sox10	INSIDE	1.388	1.372	1741.41	2389.96	1.905	1480.70	2820.63
A_68_P23321805	chr4:133805694-133805738	NM_024215:-4210	Zfp593	PROMOTER	1.388	2.078	568.36	1181.10	2.885	373.34	1077.17
A_68_P26350214	chr9:21855080-21855124	NM_010487:1365	Elavl3	INSIDE	1.387	1.879	1127.71	2118.45	2.605	987.56	2572.23
A_68_P31215014	chr17:48061036-48061080	NM_001110824:523	Foxp4	INSIDE	1.387	3.489	1284.81	4483.10	4.841	1017.48	4925.13
A_68_P21874746	chr2:174153286-174153330	NR_003258:-106	Gnas	PROMOTER	1.387	1.563	557.01	870.38	2.168	460.07	997.43
A_68_P27996400	chr11:87630599-87630643	NM_080420:8996	Lpo	INSIDE	1.387	2.331	3454.61	8052.90	3.233	2408.00	7783.99
A_68_P31930919	chr19:5803763-5803807	NR_002847:-1113	Malat1	PROMOTER	1.387	3.632	3709.80	13474.98	5.039	2884.96	14537.26
A_68_P25285292	chr7:91031812-91031856	NM_030705:1017	Mesdc1	INSIDE	1.387	1.854	1987.57	3685.71	2.573	1610.70	4144.00
A_68_P23439968	chr4:155043128-155043172	NM_145124:186	Mib2	INSIDE	1.387	0.439	1003.59	440.94	0.609	1058.62	645.06
A_68_P31542302	chr18:21120354-21120398	NM_026301:17251	Rnf125	INSIDE	1.387	3.232	1806.35	5838.05	4.482	1432.12	6418.86
A_68_P32136240	chr19:45139857-45139901	NM_001178012:17813	Sfxn3	DOWNSTREAM	1.387	2.930	1865.52	5465.30	4.062	1583.58	6432.72
A_68_P27288939	chr10:80795142-80795186	NM_009325:3689	Tbxa2r	INSIDE	1.387	2.434	820.12	1996.51	3.377	677.70	2288.73
A_68_P23255470	chr4:120887662-120887706	ENSMUST00000056635:5		INSIDE	1.387	1.989	1497.95	2979.89	2.760	1185.81	3272.51
A_68_P26617806	chr9:70527432-70527476	NM_007399:647	Adam10	INSIDE	1.386	4.446	897.40	3989.47	6.163	771.76	4756.74
A_68_P27176090	chr10:60149152-60149197	NM_023370:10064	Cdh23	INSIDE	1.386	10.499	320.92	3369.37	14.546	282.00	4102.07
A_68_P25512010	chr7:135831942-135831986	NM_178641:77086	Inpp5f	INSIDE	1.386	3.071	1024.72	3146.72	4.256	926.84	3944.48
A_68_P22934417	chr4:55543327-55543371	NM_010637:1999	Klf4	INSIDE	1.386	2.954	2248.19	6640.92	4.094	1724.91	7061.55
A_68_P31130477	chr17:30026875-30026919	NM_001081160:-2069	Mdga1	PROMOTER	1.386	2.242	770.76	1728.12	3.107	603.50	1875.07
A_68_P27922752	chr11:74651542-74651586	NM_010813:7139	Mnt	INSIDE	1.386	1.680	496.56	834.26	2.329	347.28	808.66
A_68_P29001573	chr13:45484920-45484964	NM_153789:-168	Mylip	PROMOTER	1.386	2.542	1859.71	4727.59	3.523	1466.18	5165.83
A_68_P31112706	chr17:26976161-26976205	NM_008700:2328	Nkx2-5	INSIDE	1.386	1.920	555.70	1067.23	2.663	529.20	1409.09
A_68_P20506812	chr1:108069726-108069770	NM_133821:1303	Phlpp1	INSIDE	1.386	0.442	1093.08	482.98	0.612	988.03	605.05
A_68_P29578876	chr14:47503079-47503123	NM_001037221:461	Samd4	INSIDE	1.386	2.731	1230.87	3361.27	3.786	1130.55	4279.76
A_68_P23081886	chr4:86520283-86520327	NM_139306:-13	Acer2	PROMOTER	1.385	1.376	1471.41	2024.91	1.906	1311.14	2499.13
A_68_P28081265	chr11:102622917-102622961	NM_001110778:186	Adam11	INSIDE	1.385	1.343	4557.53	6122.12	1.860	3493.31	6498.27
A_68_P25954612	chr8:73392998-73393042	NM_026964:4369	Ccdc124	INSIDE	1.385	5.066	149.73	758.54	7.018	132.41	929.27
A_68_P21612764	chr2:127162058-127162102	NM_010090:186	Dusp2	INSIDE	1.385	3.209	1458.87	4681.39	4.445	1289.22	5730.87
A_68_P30480288	chr15:99288482-99288527	NM_001001884:-325	Nckap5l	PROMOTER	1.385	2.314	337.82	781.56	3.205	286.71	918.82
A_68_P26772514	chr9:100935310-100935354	NM_025835:-38	Pccb	PROMOTER	1.385	2.186	736.85	1610.80	3.028	620.75	1879.44
A_68_P28549418	chr12:76696906-76696950	NM_012024:259	Ppp2r5e	INSIDE	1.385	1.423	1358.66	1932.97	1.971	1145.58	2257.54
A_68_P30447921	chr15:93426390-93426434	NM_001033217:-90	Prickle1	PROMOTER	1.385	1.576	625.87	986.42	2.182	603.39	1316.77
A_68_P24092506	chr5:130647910-130647954	NM_001199059:244	Rabgef1	INSIDE	1.385	1.536	704.41	1081.84	2.128	612.31	1302.86
A_68_P26782297	chr9:102737533-102737577	NM_001042607:305	Ryk	INSIDE	1.385	1.916	530.94	1017.41	2.654	555.68	1474.61
A_68_P31386733	chr17:81464391-81464435	NM_028138:13	Thumpd2	INSIDE	1.385	2.672	501.61	1340.18	3.699	445.20	1646.93
A_68_P22594408	chr3:142763801-142763845			Unknown	1.385	2.405	1253.99	3015.34	3.331	1139.39	3794.97
A_68_P27938081	chr11:77329399-77329443	NM_026185:802	Abhd15	INSIDE	1.384	1.651	1075.96	1776.09	2.285	893.15	2041.00
A_68_P31097619	chr17:24625915-24625959	NM_027937:209	Caskin1	INSIDE	1.384	6.079	2677.94	16279.90	8.413	2045.41	17207.47
A_68_P23203782	chr4:109656380-109656424	NM_172296:5773	Dmrta2	DOWNSTREAM	1.384	3.514	1461.45	5135.93	4.864	1229.56	5980.70

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P29626310	chr14:57752221-57752265	NM_008128:-8184	Gjb6	PROMOTER	1.384	2.282	684.04	1561.29	3.159	668.13	2110.85
A_68_P25023673	chr7:29596377-29596421	NM_177301:490	Hnrnpl	INSIDE	1.384	2.347	1864.68	4377.06	3.249	1656.71	5383.10
A_68_P28530098	chr12:73186548-73186592	NM_001205067:-255	Jkamp	DIVERGENT_PROMOTER	1.384	2.022	1860.70	3762.19	2.798	1158.76	3241.72
A_68_P25176079	chr7:71432668-71432712	NM_172742:135	Mtmr10	INSIDE	1.384	2.188	1366.94	2991.38	3.028	1213.24	3673.97
A_68_P25016937	chr7:28149369-28149413	NM_001199235:30135	Spnb4	INSIDE	1.384	4.256	450.84	1918.83	5.890	388.56	2288.49
A_68_P24929724	chr6:146582793-146582837	NM_026281:300	Tm7sf3	INSIDE	1.384	2.488	1029.62	2561.28	3.444	814.79	2806.13
A_68_P20444766	chr1:93698474-93698518	NM_007855:443	Twist2	INSIDE	1.384	2.254	2341.47	5277.33	3.120	1896.89	5918.08
A_68_P31292365	chr17:64199012-64199056			Unknown	1.384	1.783	1971.01	3513.41	2.468	1488.53	3673.51
A_68_P30221125	chr15:53177961-53178005	NM_010162:-244	Ext1	PROMOTER	1.383	1.695	850.39	1441.42	2.345	757.81	1776.96
A_68_P24932468	chr6:147040234-147040278	NM_001081237:660	Klhdc5	INSIDE	1.383	4.799	492.26	2362.45	6.635	486.13	3225.65
A_68_P28246270	chr12:12944193-12944237	NM_008709:4428	Mycn	INSIDE	1.383	1.799	1343.75	2416.97	2.488	1094.02	2721.69
A_68_P31848618	chr18:77803995-77804039	NM_001164504:-141	Rnf165	PROMOTER	1.383	1.500	1536.57	2304.59	2.074	1326.48	2750.58
A_68_P31120665	chr17:28278842-28278886	NM_001004366:-606	Scube3	PROMOTER	1.383	3.106	1273.71	3956.08	4.294	1103.17	4737.50
A_68_P31682245	chr18:47528367-47528411	NM_018744:134	Sema6a	INSIDE	1.383	2.207	659.59	1455.48	3.051	574.22	1751.82
A_68_P25716368	chr8:24522869-24522913	NM_013834:917	Sfrp1	INSIDE	1.383	1.613	2227.30	3593.62	2.231	1935.21	4317.32
A_68_P24039145	chr5:120961107-120961151	NM_001177594:-72	Slc24a6	DIVERGENT_PROMOTER	1.383	1.486	4781.84	7103.62	2.054	3617.40	7431.95
A_68_P23364649	chr4:141094339-141094383	NM_019763:152	Spen	INSIDE	1.383	1.992	2347.37	4676.34	2.756	1958.71	5398.44
A_68_P23238477	chr4:117807306-117807350	NM_009176:167	St3gal3	INSIDE	1.383	2.005	540.61	1083.76	2.773	510.76	1416.34
A_68_P29072110	chr13:58316632-58316676	NM_026842:360	Ubqln1	INSIDE	1.383	2.096	560.88	1175.53	2.898	535.81	1552.68
A_68_P30382917	chr15:82176766-82176812	NM_026914:313	1500032L24Rik	INSIDE	1.382	3.347	912.41	3053.90	4.627	745.99	3451.56
A_68_P26920734	chr10:7500514-7500558	NM_145418:179	BC013529	INSIDE	1.382	1.710	990.54	1693.60	2.363	880.38	2080.26
A_68_P21111660	chr2:31701435-31701479	NM_178887:69	Fibcd1	INSIDE	1.382	2.715	1341.96	3643.49	3.753	1101.84	4135.43
A_68_P22081213	chr3:40549234-40549278	NM_011020:-278	Hspa4l	PROMOTER	1.382	2.443	1011.96	2472.12	3.375	784.50	2647.61
A_68_P28055738	chr11:98195652-98195696	NM_010895:-4715	Neurod2	PROMOTER	1.382	1.669	2668.79	4452.94	2.306	2176.79	5019.22
A_68_P31921055	chr19:4101179-4101223	NM_008851:579	Pitpnm1	INSIDE	1.382	1.719	420.25	722.25	2.375	310.95	738.64
A_68_P26079858	chr8:97381751-97381795	NM_009090:423	Polr2c	INSIDE	1.382	2.436	1507.50	3672.30	3.366	1204.30	4054.04
A_68_P23668870	chr5:48377571-48377615	NM_178804:3199	Slit2	INSIDE	1.382	2.559	2256.35	5774.06	3.537	1713.19	6060.08
A_68_P26504312	chr9:50369341-50369385	NM_025687:11	Tex12	INSIDE	1.382	3.272	1507.58	4933.34	4.523	1344.59	6081.12
A_68_P24115622	chr5:135752511-135752555			Unknown	1.382	2.149	2790.05	5996.38	2.970	2278.78	6767.93
A_68_P31933962	chr19:6320206-6320250	NM_001033342:13772	Cdc42bpg	INSIDE	1.381	3.899	1882.50	7340.23	5.385	1508.45	8123.72
A_68_P32820569	chrX:165758461-165758505	NM_008222:-207	Hccs	PROMOTER	1.381	3.000	691.81	2075.27	4.142	442.18	1831.64
A_68_P25005400	chr7:25318962-25319006	NM_153134:3318	Irgq	INSIDE	1.381	2.764	1793.18	4955.65	3.818	1547.70	5908.62
A_68_P28998903	chr13:44998308-44998352	NM_001205043:171691	Jarid2	INSIDE	1.381	3.750	2610.28	9788.20	5.180	2206.54	11430.73
A_68_P32122315	chr19:42687286-42687330	NM_001164311:-12	Loxl4	PROMOTER	1.381	5.696	2747.26	15647.16	7.863	2171.28	17072.43
A_68_P23985655	chr5:111846403-111846447	NM_001081235:-761	Mn1	PROMOTER	1.381	3.121	952.83	2973.79	4.311	746.99	3220.03
A_68_P23292285	chr4:128332448-128332492	NM_001195130:525	Phc2	INSIDE	1.381	2.352	1220.71	2871.13	3.248	867.57	2817.74
A_68_P21432198	chr2:92885847-92885891	NM_001177536:433	Prdm11	INSIDE	1.381	2.016	2664.89	5372.70	2.784	2130.21	5930.78
A_68_P22883652	chr4:45543353-45543397	NM_001033306:326	Shb	INSIDE	1.381	1.440	1244.64	1792.30	1.989	1018.36	2025.13
A_68_P29936814	chr14:118531918-118531962	NM_029578:47	Tgds	INSIDE	1.381	2.107	848.15	1787.14	2.909	718.51	2090.03
A_68_P20046436	chr1:14496639-14496683			Unknown	1.381	1.790	1532.18	2743.32	2.473	1331.58	3292.41
A_68_P22832218	chr4:34663760-34663804	NM_027041:13673	1700003M02Rik	INSIDE	1.380	2.400	327.86	786.83	3.313	316.86	1049.66
A_68_P23225501	chr4:115410210-115410254	NM_172698:-445	4732418C07Rik	PROMOTER	1.380	1.596	2393.59	3820.41	2.202	1950.35	4295.52
A_68_P23966390	chr5:107760143-107760187	NM_001079873:-48	Brdt	PROMOTER	1.380	1.925	1143.18	2200.75	2.657	1031.75	2741.32
A_68_P30589166	chr16:20716372-20716416	NM_009900:315	Clcn2	INSIDE	1.380	1.526	1428.09	2178.81	2.105	1153.03	2427.48
A_68_P23222742	chr4:114659539-114659583	NM_025647:273	Cmpk1	INSIDE	1.380	5.083	1829.05	9297.78	7.013	1581.23	11088.78
A_68_P31694513	chr18:49915007-49915051	NM_001170960:227	Dtwd2	INSIDE	1.380	4.950	2036.11	10079.53	6.830	1655.93	11309.80
A_68_P22009690	chr3:27052485-27052529	NM_001177625:270	Ect2	INSIDE	1.380	1.652	4969.44	8207.66	2.280	3935.17	8970.84
A_68_P27284175	chr10:80049466-80049510	NM_145421:3598	Fam108a	INSIDE	1.380	4.596	1189.87	5468.94	6.343	1018.45	6459.94
A_68_P22702204	chr4:5571466-5571510	NM_173426:163	Fam110b	INSIDE	1.380	1.694	809.27	1370.98	2.338	736.49	1722.06
A_68_P24429121	chr6:48693073-48693117	NM_008376:4049	Gimap1	INSIDE	1.380	2.233	1776.08	3965.19	3.080	1429.23	4401.83
A_68_P23333240	chr4:135866700-135866744	NM_028871:-168	Hnrnpr	PROMOTER	1.380	2.154	1180.61	2542.84	2.972	1064.75	3164.30

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28185589	chr11:120469914-120469958	NM_153288:146	Npb	INSIDE	1.380	1.724	626.95	1080.66	2.378	563.76	1340.59
A_68_P23696527	chr5:53133072-53133116	NM_025951:282	Pi4k2b	INSIDE	1.380	3.064	616.45	1889.00	4.230	538.73	2278.62
A_68_P23374912	chr4:142984306-142984350	NM_031377:-15	Pramel1	PROMOTER	1.380	6.083	4431.85	26959.06	8.397	3035.40	25488.68
A_68_P20779531	chr1:164670132-164670176	NM_001081290:533	Prrc2c	INSIDE	1.380	1.464	1019.61	1492.29	2.019	862.65	1741.74
A_68_P30990391	chr16:96212295-96212339	NM_019537:194	Psmg1	INSIDE	1.380	1.645	2589.44	4259.35	2.270	2009.46	4560.84
A_68_P27901831	chr11:70460715-70460759	NM_024211:-241	Slc25a11	DIVERGENT_PROMOTER	1.380	2.844	1614.27	4590.39	3.925	1332.11	5228.40
A_68_P20172918	chr1:40738845-40738889	NM_001033289:310	Slc9a2	INSIDE	1.380	1.589	1993.26	3167.76	2.193	1698.03	3723.11
A_68_P31846337	chr18:77424326-77424370	NM_013666:-237	St8sia5	PROMOTER	1.380	1.438	1106.77	1591.43	1.984	926.23	1837.71
A_68_P22889661	chr4:46627029-46627073	NM_198664:36021	Tbc1d2	INSIDE	1.380	2.524	978.10	2468.45	3.482	838.18	2918.50
A_68_P29506489	chr14:31362538-31362582	NM_009388:226	Tkt	INSIDE	1.380	4.247	1327.69	5639.28	5.860	1239.52	7264.01
A_68_P24155694	chr5:144016617-144016661	NM_017467:15063	Zfp316	INSIDE	1.380	4.227	2787.80	11782.74	5.832	3116.04	18172.71
A_68_P31755200	chr18:61195546-61195590	NM_009880:285	Cdx1	INSIDE	1.379	3.032	739.77	2242.91	4.181	703.01	2939.13
A_68_P25564249	chr7:144390277-144390323	NM_001113414:115828	Ebf3	INSIDE	1.379	8.357	3043.67	25435.00	11.525	2012.21	23191.66
A_68_P24477004	chr6:56782166-56782210	NM_012056:136	Fkbp9	INSIDE	1.379	3.039	1936.77	5886.78	4.190	1684.97	7060.59
A_68_P24129311	chr5:138635844-138635888	NM_177878:325	Mblac1	INSIDE	1.379	1.861	1250.14	2326.95	2.566	1257.67	3227.68
A_68_P30252139	chr15:58912975-58913019	NM_001146180:585	Mtss1	INSIDE	1.379	4.491	2342.42	10520.33	6.192	1909.09	11820.70
A_68_P23281395	chr4:126355065-126355109	NM_011970:200	Psmb2	INSIDE	1.379	1.555	610.53	949.65	2.145	491.93	1055.12
A_68_P30546791	chr16:11203150-11203194	NM_025546:213	Rsl1d1	INSIDE	1.379	2.630	4731.03	12440.96	3.626	4018.95	14572.39
A_68_P26506991	chr9:50816720-50816764	NM_178710:436	Sik2	INSIDE	1.379	1.394	3412.25	4755.79	1.922	2627.82	5049.66
A_68_P30436285	chr15:91403260-91403304	NM_001033633:410	Slc2a13	INSIDE	1.379	6.148	784.46	4822.57	8.478	676.56	5735.66
A_68_P20456741	chr1:95532187-95532231	NM_021537:96	Stk25	INSIDE	1.379	2.702	1331.87	3598.85	3.726	1122.47	4182.07
A_68_P32806692	chrX:162947996-162948040	NM_001007577:392	Tceanc	INSIDE	1.379	2.785	1571.63	4377.73	3.842	810.69	3114.39
A_68_P31385964	chr17:81344186-81344230	NM_026516:237	Tmem178	INSIDE	1.379	1.688	2239.28	3779.05	2.328	1997.79	4650.03
A_68_P31320413	chr17:69190632-69190676	NM_001206661:4179	Tmem200c	INSIDE	1.379	3.280	1315.62	4315.33	4.524	1228.76	5558.54
A_68_P32744218	chrX:147530920-147530964	NM_001164578:144	Tsr2	INSIDE	1.379	1.849	1593.64	2946.93	2.549	884.15	2253.95
A_68_P28029564	chr11:93746411-93746455	NM_001013375:648	Utp18	INSIDE	1.379	3.233	7724.07	24970.39	4.457	6462.51	28801.15
A_68_P29623591	chr14:57190486-57190530	NM_001014996:175	Cenpj	INSIDE	1.378	2.599	1315.91	3419.70	3.581	1026.85	3676.94
A_68_P31620307	chr18:35990504-35990548	NM_133687:1055	Cxxc5	INSIDE	1.378	2.707	1313.88	3556.03	3.729	1077.64	4018.54
A_68_P30678530	chr16:37012233-37012277	NM_001159369:383	Polq	INSIDE	1.378	1.598	710.95	1136.21	2.202	600.92	1323.31
A_68_P24994377	chr7:20204860-20204904	NM_009046:9905	Relb	INSIDE	1.378	2.654	2286.08	6067.75	3.657	1835.48	6713.10
A_68_P27786170	chr11:49838566-49838610	NM_021540:-244	Rnf130	PROMOTER	1.378	1.429	1226.49	1753.24	1.970	1132.76	2231.12
A_68_P31196997	chr17:44873430-44873474	NM_001145920:145	Runx2	INSIDE	1.378	2.438	917.75	2237.63	3.360	915.27	3074.90
A_68_P28332011	chr12:32244102-32244146	NM_011867:710	Slc26a4	INSIDE	1.378	5.869	464.29	2724.78	8.089	473.71	3831.95
A_68_P28087051	chr11:103634875-103634919	NM_009521:-592	Wnt3	PROMOTER	1.378	2.144	2186.97	4688.89	2.955	1748.70	5167.87
A_68_P28703312	chr12:105685478-105685522			Unknown	1.378	4.544	1247.37	5668.27	6.264	1078.33	6754.76
A_68_P31560300	chr18:24625872-24625916	NM_026529:-3477	2700062C07Rik	PROMOTER	1.377	2.091	1837.99	3843.87	2.880	1537.54	4428.68
A_68_P20872226	chr1:181733791-181733835	NM_026375:334	Ahctf1	INSIDE	1.377	1.483	1020.63	1513.38	2.042	953.61	1947.41
A_68_P26641128	chr9:74800966-74801010	NM_001113283:129	BC031353	INSIDE	1.377	1.421	935.86	1330.00	1.957	757.06	1481.86
A_68_P26229677	chr8:124431978-124432022	NM_001033485:268	BC048644	INSIDE	1.377	1.832	3606.16	6605.22	2.522	2702.89	6815.57
A_68_P24993659	chr7:20092410-20092454	NM_177692:1248	Bloc1s3	INSIDE	1.377	1.527	817.62	1248.89	2.103	736.93	1549.64
A_68_P23415125	chr4:151235092-151235136	NM_001081557:763	Camta1	INSIDE	1.377	1.933	1640.21	3170.34	2.661	1284.07	3416.84
A_68_P28175792	chr11:118951266-118951310	NM_007625:-3737	Cbx4	PROMOTER	1.377	1.724	1989.94	3429.86	2.373	1495.37	3548.44
A_68_P30347072	chr15:76077510-76077554	NM_023168:296	Grina	INSIDE	1.377	1.644	4149.13	6822.67	2.264	3082.56	6979.74
A_68_P25770373	chr8:34842329-34842373	NM_001167921:-35	Gtf2e2	PROMOTER	1.377	3.104	596.25	1850.67	4.273	555.40	2373.50
A_68_P23300610	chr4:129815848-129815892	NM_001163027:-75	Hcrtr1	PROMOTER	1.377	3.703	712.34	2637.77	5.099	651.74	3323.44
A_68_P21104807	chr2:30567268-30567312	NR_037272:-9439	Mir3089	PROMOTER	1.377	1.905	1670.97	3182.87	2.623	1314.14	3447.47
A_68_P31110244	chr17:26575843-26575887	NM_001081656:23955	Neurl1b	INSIDE	1.377	2.750	354.52	974.95	3.786	392.75	1486.86
A_68_P31992143	chr19:18706329-18706373	NM_017375:-47	Ostf1	DIVERGENT_PROMOTER	1.377	3.356	665.77	2234.11	4.620	579.61	2677.94
A_68_P27310783	chr10:85334508-85334552	NM_133993:-45	Pwp1	PROMOTER	1.377	4.295	2751.45	11818.80	5.915	2115.68	12513.39
A_68_P21370050	chr2:79475696-79475740	NM_080558:137	Ssfa2	INSIDE	1.377	3.999	1978.05	7909.62	5.507	1706.95	9399.62
A_68_P29647966	chr14:61656769-61656813	NM_001164155:34	Tnfrsf19	INSIDE	1.377	1.838	6260.09	11508.96	2.532	4828.77	12228.67

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P22314483	chr3:88357962-88358006	NM_033526:347	Ubqln4	INSIDE	1.377	1.901	4250.16	8080.01	2.618	3593.31	9407.82
A_68_P24302940	chr6:24615184-24615228	NM_028459:-211	Wasl	PROMOTER	1.377	3.177	5056.14	16063.79	4.373	3996.07	17476.81
A_68_P24164949	chr5:145992823-145992867	NM_028298:217	Zfp655	INSIDE	1.377	2.062	389.23	802.68	2.839	344.22	977.21
A_68_P23434211	chr4:154176443-154176487			Unknown	1.377	1.561	543.93	849.12	2.149	381.65	820.32
A_68_P28430596	chr12:52694381-52694425	NM_001198835:75	Coch	INSIDE	1.376	0.478	1309.17	626.02	0.658	1116.29	734.38
A_68_P29699005	chr14:70475525-70475569	NM_018781:-1705	Egr3	PROMOTER	1.376	1.394	1438.22	2004.90	1.918	1157.31	2219.84
A_68_P26319144	chr9:14556142-14556186	NM_010242:402	Fut4	INSIDE	1.376	3.074	1203.39	3699.80	4.231	1121.20	4744.15
A_68_P26084325	chr8:98157711-98157755	NM_030198:274	Gins3	INSIDE	1.376	1.883	985.87	1856.77	2.592	859.02	2226.91
A_68_P26228892	chr8:124308825-124308869	NM_020605:54388	Jph3	INSIDE	1.376	1.724	995.29	1715.95	2.372	838.23	1988.43
A_68_P25362045	chr7:106617271-106617315	NM_028145:2779	Klhl35	INSIDE	1.376	2.305	526.96	1214.56	3.171	454.24	1440.49
A_68_P23391245	chr4:147278506-147278550	NM_133201:400	Mfn2	INSIDE	1.376	3.309	1814.59	6004.03	4.552	1323.36	6024.14
A_68_P25261415	chr7:86644791-86644835	NR_029818:-5337	Mir9-3	PROMOTER	1.376	3.090	1236.50	3820.81	4.251	1120.30	4762.78
A_68_P23567786	chr5:29804560-29804604	NM_019944:428	Mnx1	INSIDE	1.376	2.546	1206.43	3072.06	3.503	1201.39	4208.33
A_68_P29009458	chr13:46822289-46822335	NM_175749:906	Nup153	INSIDE	1.376	1.969	2573.51	5068.11	2.710	1813.46	4914.81
A_68_P20774854	chr1:163899508-163899552	NM_001039045:212	Pigc	INSIDE	1.376	2.331	1042.59	2430.21	3.208	898.56	2882.98
A_68_P30346606	chr15:76010797-76010841	NM_201394:15322	Plec	INSIDE	1.376	2.047	535.71	1096.39	2.815	444.76	1252.19
A_68_P30566363	chr16:15638071-15638115	NM_011159:134	Prkdc	INSIDE	1.376	1.710	1088.29	1861.23	2.354	930.80	2190.88
A_68_P29256277	chr13:98976271-98976315	NM_012026:-172	Rgnef	PROMOTER	1.376	3.274	1412.57	4624.77	4.504	1243.93	5602.44
A_68_P23576986	chr5:31495832-31495876	NM_153680:178	Snx17	INSIDE	1.376	1.840	2165.65	3985.33	2.533	1787.83	4528.59
A_68_P27579022	chr11:8524378-8524422	NM_001083587:40138	Tns3	INSIDE	1.376	1.548	2177.26	3369.77	2.130	1779.43	3789.85
A_68_P28961200	chr13:38619778-38619822	NM_145367:529	Txndc5	INSIDE	1.376	3.821	5245.05	20040.92	5.259	3912.62	20576.59
A_68_P20833903	chr1:174493113-174493157	NR_027644:3098	Vsig8	INSIDE	1.376	1.793	2249.43	4033.83	2.468	1999.11	4933.52
A_68_P27646190	chr11:23397665-23397709	NM_172391:260	Ahsa2	INSIDE	1.375	1.715	1621.39	2781.47	2.359	1351.90	3189.46
A_68_P29514239	chr14:32644087-32644131	NM_001024604:-507	Ankrd28	PROMOTER	1.375	1.676	1130.69	1895.08	2.304	944.60	2176.30
A_68_P32414052	chrX:57657724-57657768	NM_001001798:-590	Atp11c	PROMOTER	1.375	1.643	538.41	884.38	2.259	296.57	669.91
A_68_P27933360	chr11:76479988-76480032	NM_177182:-5961	Bhlha9	PROMOTER	1.375	3.983	364.29	1450.84	5.478	383.99	2103.54
A_68_P21768605	chr2:155782745-155782804	NM_001129999:481	Cep250	INSIDE	1.375	5.441	118.40	644.25	7.479	128.96	964.52
A_68_P26880500	chr9:120842272-120842316	NM_007614:-223	Ctnnb1	PROMOTER	1.375	2.419	2400.00	5804.42	3.326	2000.36	6653.02
A_68_P22152359	chr3:55046645-55046689	NM_001111053:219	Dclk1	INSIDE	1.375	3.624	8361.76	30303.38	4.984	6503.71	32416.85
A_68_P20137271	chr1:34234808-34234852	NM_133833:166161	Dst	INSIDE	1.375	3.461	716.17	2478.51	4.760	596.28	2838.31
A_68_P28493839	chr12:66176820-66176864	NM_178912:250	Fancm	INSIDE	1.375	2.779	3973.93	11044.06	3.820	3275.45	12511.94
A_68_P25965606	chr8:75876811-75876855	NM_010687:-377	Large	PROMOTER	1.375	2.625	2341.04	6144.85	3.610	1995.36	7202.71
A_68_P30425292	chr15:89288332-89288376	NM_021921:4013	Mapk8ip2	INSIDE	1.375	3.266	229.60	749.97	4.492	227.71	1022.91
A_68_P28269969	chr12:17355438-17355482	NR_037226:-6737	Mir3066	PROMOTER	1.375	2.091	685.61	1433.87	2.876	587.58	1689.64
A_68_P26904675	chr10:4424482-4424526	NM_001161822:364	Rgs17	INSIDE	1.375	1.732	1542.84	2671.65	2.381	1583.48	3770.68
A_68_P31598790	chr18:31769072-31769116	NM_026165:462	Slc25a46	INSIDE	1.375	6.570	998.35	6559.36	9.031	852.54	7699.27
A_68_P32260673	chrX:11717563-11717607	NM_001168321:19897	Bcor	INSIDE	1.374	2.878	826.98	2380.40	3.955	499.68	1976.01
A_68_P23927393	chr5:100468878-100468922	NM_001163035:-112	Enoph1	DIVERGENT_PROMOTER	1.374	1.509	1248.13	1882.91	2.073	955.75	1981.28
A_68_P24143544	chr5:141306207-141306251	NM_010302:157	Gna12	INSIDE	1.374	3.560	907.44	3230.87	4.890	814.68	3984.00
A_68_P30350023	chr15:76528479-76528523	NM_182805:1307	Gpt	INSIDE	1.374	1.770	971.90	1720.43	2.432	862.92	2098.74
A_68_P21794482	chr2:160191240-160191284	NM_010658:1539	Mafb	INSIDE	1.374	1.503	3066.50	4609.26	2.065	2286.40	4721.48
A_68_P32579358	chrX:102316971-102317015	NM_053201:1258	Magee1	INSIDE	1.374	2.382	719.09	1712.51	3.272	498.39	1630.53
A_68_P23006652	chr4:70195652-70195696	NM_172694:288	Megf9	INSIDE	1.374	2.072	963.32	1996.32	2.847	830.41	2363.84
A_68_P21132204	chr2:35056598-35056642	NM_026697:20	Rab14	INSIDE	1.374	1.586	6464.98	10254.22	2.179	5245.70	11430.34
A_68_P25092756	chr7:52632188-52632232	NM_009224:18807	Snrnp70	INSIDE	1.374	3.300	2001.33	6604.55	4.534	1404.80	6368.80
A_68_P32565202	chrX:98892756-98892800	ENSMUST00000073812:-5589		PROMOTER	1.374	6.762	4957.84	33525.38	9.293	2152.12	19999.37
A_68_P22069325	chr3:38355009-38355053	NM_001167883:28708	Ankrd50	INSIDE	1.373	1.625	837.43	1360.69	2.231	684.92	1527.92
A_68_P28050583	chr11:97301455-97301499	NM_021493:-9997	Arhgap23	PROMOTER	1.373	2.380	1152.01	2741.29	3.267	924.38	3019.91
A_68_P22311221	chr3:87801100-87801144	NM_007529:3156	Bcan	INSIDE	1.373	2.311	651.53	1505.78	3.174	611.78	1941.94
A_68_P20350875	chr1:74901471-74901515	NM_009872:-110	Cdk5r2	PROMOTER	1.373	1.914	784.58	1501.78	2.628	687.29	1806.35
A_68_P26526112	chr9:54349310-54349354	NM_172771:101	Dmxl2	INSIDE	1.373	2.680	1768.03	4738.66	3.680	1451.46	5341.14

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31122729	chr17:28622707-28622751	NM_010220:329	Fkbp5	INSIDE	1.373	1.817	636.24	1155.99	2.495	613.11	1529.42
A_68_P30960667	chr16:91044987-91045031	NM_026110:-384	Gcfc1	PROMOTER	1.373	2.734	1560.00	4264.53	3.753	1215.01	4560.42
A_68_P32539367	chrX:91787344-91787392	NM_019791:45	Maged1	INSIDE	1.373	2.267	4377.50	9923.92	3.112	1911.15	5948.14
A_68_P31425842	chr17:88374222-88374266	NM_010830:-145	Msh6	PROMOTER	1.373	1.615	1220.04	1969.95	2.217	1081.66	2397.57
A_68_P30000047	chr15:8394313-8394357	NM_027707:129	Nipbl	INSIDE	1.373	2.319	673.55	1561.95	3.183	505.75	1609.85
A_68_P31622624	chr18:36356271-36356315	NM_001167891:522	Nrg2	INSIDE	1.373	3.532	1864.27	6583.97	4.848	1729.99	8387.74
A_68_P31934660	chr19:6428244-6428288	NM_001205234:9529	Nrxn2	INSIDE	1.373	4.464	641.73	2864.66	6.130	517.31	3171.36
A_68_P24043140	chr5:121641038-121641082	NM_001109992:346	Ptpn11	INSIDE	1.373	2.484	994.92	2471.65	3.410	895.24	3052.50
A_68_P30477114	chr15:98711909-98711953	NM_026967:-85	Rhebl1	PROMOTER	1.373	1.647	627.51	1033.80	2.262	510.71	1155.47
A_68_P23896973	chr5:93371964-93372008	NM_001077596:44963	Shroom3	INSIDE	1.373	3.531	278.13	982.12	4.847	237.92	1153.27
A_68_P30778635	chr16:55974040-55974084	NM_173026:146	Zbtb11	INSIDE	1.373	2.188	485.07	1061.14	3.003	449.64	1350.30
A_68_P20625950	chr1:135061005-135061049			Unknown	1.373	2.926	2328.63	6813.40	4.016	1832.13	7357.84
A_68_P23573892	chr5:30969470-30969514	NM_007681:218	Cenpa	INSIDE	1.372	2.370	2278.59	5401.33	3.253	1830.57	5955.37
A_68_P31992642	chr19:18787440-18787484	NM_177640:-263	D030056L22Rik	PROMOTER	1.372	2.103	1545.40	3249.62	2.885	1352.69	3903.16
A_68_P26659816	chr9:78329333-78329377	NM_010106:177	Eef1a1	INSIDE	1.372	1.469	695.01	1021.26	2.016	626.18	1262.24
A_68_P23280299	chr4:126146120-126146166	NM_153403:-477	Eif2c1	PROMOTER	1.372	1.714	1628.50	2791.35	2.352	1222.62	2875.57
A_68_P25016727	chr7:28116145-28116189	NM_001113549:2501	Ltbp4	INSIDE	1.372	4.066	1296.28	5270.71	5.579	991.80	5533.22
A_68_P21081858	chr2:26883547-26883591	NM_172659:-50	Slc2a6	PROMOTER	1.372	1.937	521.29	1009.54	2.658	391.90	1041.65
A_68_P20121785	chr1:30930713-30930757	ENSMUST00000046443:-195		PROMOTER	1.372	9.708	671.62	6520.36	13.321	660.88	8803.74
A_68_P27675038	chr11:29447584-29447633	NM_001163521:-341	1700034F02Rik	PROMOTER	1.371	1.827	1378.55	2518.92	2.505	1090.59	2731.52
A_68_P20743645	chr1:158488645-158488689	NM_001136104:-251	Abl2	PROMOTER	1.371	1.999	940.19	1879.19	2.739	830.12	2274.10
A_68_P27868560	chr11:64792596-64792640	NM_023479:82	Elac2	INSIDE	1.371	1.715	2034.10	3487.49	2.351	1612.28	3790.58
A_68_P22892661	chr4:47105201-47105245	NM_172693:398	Galnt12	INSIDE	1.371	2.988	5173.15	15456.04	4.097	3825.02	15672.85
A_68_P31253728	chr17:56219108-56219152	NM_008233:51	Hdgfrp2	INSIDE	1.371	1.367	2289.37	3129.31	1.873	1816.94	3404.02
A_68_P26658189	chr9:77960962-77961006	NM_019987:-60	Ick	PROMOTER	1.371	2.883	1000.73	2884.64	3.952	895.54	3539.20
A_68_P25088776	chr7:51926206-51926250	NM_028021:-5355	Myh14	PROMOTER	1.371	7.363	1447.93	10661.22	10.097	1179.84	11912.56
A_68_P25179906	chr7:72017792-72017836	NM_023239:112	Ndnl2	INSIDE	1.371	2.516	572.71	1440.90	3.449	502.13	1732.03
A_68_P27273029	chr10:77707518-77707562	NM_001081055:-153	Trappc10	PROMOTER	1.371	2.506	572.85	1435.32	3.434	519.86	1785.44
A_68_P27099070	chr10:42894837-42894881	NM_172419:349	9030612E09Rik	INSIDE	1.370	1.604	1165.63	1870.02	2.199	908.73	1997.96
A_68_P24040428	chr5:121161477-121161521	NM_008052:180	Dtx1	INSIDE	1.370	1.414	2522.17	3567.04	1.937	1907.99	3696.06
A_68_P25954902	chr8:73438710-73438754	NM_173013:8860	Mtap1s	INSIDE	1.370	2.956	1750.82	5175.23	4.049	1434.24	5806.80
A_68_P32289246	chrX:20195326-20195370	NM_001167776:464	Rbm10	INSIDE	1.370	2.689	312.43	840.02	3.684	216.81	798.64
A_68_P28599771	chr12:86039461-86039505	NM_001033334:275	Tmem90a	INSIDE	1.370	1.496	1077.57	1611.93	2.049	954.20	1955.36
A_68_P30133050	chr15:35301092-35301136	NM_177151:-186	Vps13b	PROMOTER	1.370	1.559	605.88	944.33	2.136	405.16	865.25
A_68_P24114683	chr5:135565547-135565591			Unknown	1.370	6.231	5435.73	33867.69	8.538	4289.37	36622.50
A_68_P22283292	chr3:82932341-82932385	ENSMUST00000047876:806		INSIDE	1.370	1.540	1362.03	2097.64	2.110	1337.53	2822.76
A_68_P23151254	chr4:100449214-100449258	NM_198037:-47	Cachd1	PROMOTER	1.369	1.924	484.95	932.84	2.632	426.95	1123.94
A_68_P33007797	chr4_random:129202-129246	NM_001033326:19423	Dhrsx	INSIDE	1.369	3.132	1160.60	3634.66	4.289	966.03	4143.07
A_68_P21704238	chr2:143741481-143741525	NM_019771:436	Dstn	INSIDE	1.369	2.307	1017.02	2346.25	3.158	850.15	2685.09
A_68_P27945140	chr11:78565152-78565196	NM_197989:57	Fam58b	INSIDE	1.369	2.862	900.85	2578.09	3.918	754.39	2955.42
A_68_P21562932	chr2:118082494-118082538	NM_027759:186	Fsip1	INSIDE	1.369	1.651	5276.17	8710.22	2.261	4159.80	9404.29
A_68_P28883194	chr13:23830758-23830802	NM_015786:105	Hist1h1c	INSIDE	1.369	2.192	380.66	834.42	3.002	334.35	1003.65
A_68_P28161571	chr11:116704550-116704594	NM_033398:191	Jmjd6	INSIDE	1.369	1.664	2018.24	3357.39	2.278	1617.83	3685.48
A_68_P21122750	chr2:33495287-33495331	NM_010725:723	Lmx1b	INSIDE	1.369	2.211	1750.94	3871.10	3.027	1471.58	4454.33
A_68_P25587306	chr7:148380913-148380957	NM_153777:-107	Lrrc56	PROMOTER	1.369	4.543	360.12	1636.08	6.221	318.47	1981.20
A_68_P32777673	chrX:156426105-156426149	NM_001163085:-238	Map3k15	PROMOTER	1.369	2.374	360.63	856.04	3.249	289.33	939.97
A_68_P20015303	chr1:7078680-7078724	NM_183028:-298	Pcmtd1	PROMOTER	1.369	3.266	2213.15	7228.65	4.471	1704.15	7618.55
A_68_P24344497	chr6:32538021-32538065	NM_175750:150	Plxna4	INSIDE	1.369	2.431	405.17	984.91	3.327	335.28	1115.48
A_68_P28738219	chr12:111685115-111685159	NM_001135001:-252	Ppp2r5c	PROMOTER	1.369	2.398	1728.54	4145.07	3.284	1481.02	4863.54
A_68_P27109370	chr10:44787342-44787386	NM_011156:345	Prep	INSIDE	1.369	2.529	859.35	2173.64	3.462	777.81	2692.76
A_68_P28301681	chr12:27100085-27100129	NM_001081977:15	Rnf144a	INSIDE	1.369	4.189	2490.92	10434.65	5.736	1991.84	11425.37

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P23434595	chr4:154229865-154229909	NM_172878:-422	Ttc34	PROMOTER	1.369	1.886	364.52	687.62	2.581	350.58	905.03
A_68_P21105116	chr2:30627229-30627273			Unknown	1.369	3.274	1242.96	4069.44	4.482	1097.87	4920.44
A_68_P31467175	chr18:5163131-5163175	ENSMUST00000150337:2577		INSIDE	1.369	1.758	2368.93	4165.65	2.408	1900.57	4576.71
A_68_P27971504	chr11:83254254-83254300	NM_025492:3081	1700020L24Rik	INSIDE	1.368	2.805	780.50	2189.34	3.839	560.42	2151.21
A_68_P22892545	chr4:47069865-47069909	NM_001024136:292	Anks6	INSIDE	1.368	1.768	448.56	792.95	2.419	413.33	999.74
A_68_P26169913	chr8:114256102-114256146	NM_001198839:-88	Bcar1	PROMOTER	1.368	1.606	1267.97	2036.39	2.196	1083.80	2380.48
A_68_P21338757	chr2:74520450-74520494	NM_008273:23	Hoxd11	INSIDE	1.368	1.926	1431.74	2757.97	2.636	1127.49	2972.01
A_68_P21137837	chr2:35960605-35960649	NM_001083126:-1046	Lhx6	PROMOTER	1.368	1.750	2410.01	4216.87	2.393	2224.30	5322.58
A_68_P26759567	chr9:98501957-98502001	NM_025485:120	Mrps22	INSIDE	1.368	3.823	1312.87	5019.01	5.230	1138.42	5953.87
A_68_P30670430	chr16:35490785-35490829	NM_028295:153	Pdia5	INSIDE	1.368	2.441	13750.31	33567.02	3.339	10387.86	34680.90
A_68_P30655993	chr16:33056579-33056624	NM_021338:2	Rpl35a	INSIDE	1.368	2.063	1663.09	3431.42	2.822	1331.72	3758.29
A_68_P32396717	chrX:53863261-53863305	NM_172780:271	Slc9a6	INSIDE	1.368	1.889	2597.25	4907.16	2.584	1089.97	2816.44
A_68_P26845378	chr9:114472828-114472872	NM_001042503:637	Trim71	INSIDE	1.368	1.578	472.26	745.14	2.158	428.19	924.04
A_68_P24835542	chr6:127837749-127837793	NM_026743:131	Tspan11	INSIDE	1.368	1.988	2799.60	5564.83	2.719	2337.58	6355.58
A_68_P25005689	chr7:25378891-25378935	NM_001033205:-6252	Zfp575	PROMOTER	1.368	6.844	2705.24	18515.49	9.360	2044.84	19140.21
A_68_P21865360	chr2:172553949-172553993			Unknown	1.368	1.612	1090.82	1757.87	2.204	925.20	2039.16
A_68_P32977628	A_68_P32977628			Unknown	1.368	2.466	2769.34	6828.19	3.373	1619.11	5461.68
A_68_P31292459	chr17:64213804-64213848	ENSMUST00000112829:463		INSIDE	1.368	1.558	2470.65	3849.48	2.132	2091.44	4458.68
A_68_P28706883	chr12:106247987-106248031	NM_172500:11	4831426I19Rik	INSIDE	1.367	1.677	950.15	1593.03	2.292	785.95	1801.11
A_68_P30542888	chr16:10545617-10545661	NM_001204229:207	Clec16a	INSIDE	1.367	1.675	1662.27	2784.25	2.290	1314.90	3011.56
A_68_P25532700	chr7:139346324-139346368	NM_018867:78	Cpxm2	INSIDE	1.367	4.021	2274.54	9147.03	5.496	1804.75	9918.85
A_68_P23349533	chr4:138631065-138631109	NM_021358:-382	Htr6	PROMOTER	1.367	3.012	3354.55	10105.39	4.117	2563.39	10554.44
A_68_P29009466	chr13:46823130-46823174	NM_175749:66	Nup153	INSIDE	1.367	1.694	1586.03	2687.08	2.316	1294.00	2996.38
A_68_P31629950	chr18:37927496-37927540	NM_033595:2285	Pcdhga12	INSIDE	1.367	2.105	393.75	828.98	2.879	371.08	1068.22
A_68_P32240903	chrX:7500233-7500277	NM_013892:3307	Pcsk1n	INSIDE	1.367	3.291	1079.03	3550.77	4.497	639.10	2874.21
A_68_P24117609	chr5:136209766-136209810	NM_008898:44705	Por	INSIDE	1.367	2.931	887.84	2602.55	4.006	739.59	2962.73
A_68_P32462208	chrX:70599329-70599373	NM_001160229:11391	Zfp275	INSIDE	1.367	3.264	322.68	1053.14	4.461	179.68	801.62
A_68_P32145408	chr19:46764549-46764593	NM_025563:175	2010012O05Rik	INSIDE	1.366	4.452	1229.58	5474.42	6.081	1084.00	6591.45
A_68_P27565303	chr11:5762324-5762369	NM_009636:478	Aebp1	INSIDE	1.366	2.865	2978.57	8532.66	3.913	2426.65	9494.28
A_68_P27899584	chr11:70042574-70042618	NM_007528:704	Bcl6b	INSIDE	1.366	2.798	708.68	1983.09	3.823	594.48	2272.99
A_68_P20645802	chr1:138311830-138311874	NM_026500:5	Ddx59	INSIDE	1.366	2.654	593.77	1575.57	3.624	505.83	1833.18
A_68_P27542236	chr10:128027435-128027479	NM_010153:-899	Erbb3	PROMOTER	1.366	2.487	615.00	1529.48	3.397	550.29	1869.55
A_68_P21374844	chr2:80287643-80287687	NM_011356:-111	Frzb	PROMOTER	1.366	2.653	278.41	738.54	3.624	232.57	842.79
A_68_P20122141	chr1:31006006-31006050	NR_002688:527	Gm13363	INSIDE	1.366	3.458	957.64	3311.41	4.722	802.74	3790.64
A_68_P21489524	chr2:104333565-104333609	NM_001145824:1060	Hipk3	INSIDE	1.366	2.527	4985.82	12597.99	3.450	4054.64	13990.46
A_68_P25652450	chr8:11008619-11008663	NM_001081212:-210	Irs2	PROMOTER	1.366	3.243	1037.10	3363.20	4.431	913.30	4046.50
A_68_P30491676	chr15:101242719-101242763	NM_033073:-93	Krt7	PROMOTER	1.366	2.265	2270.88	5144.58	3.096	1817.82	5627.44
A_68_P24656008	chr6:94234014-94234058	NM_001029850:-138	Magi1	PROMOTER	1.366	2.915	3017.70	8797.05	3.983	2358.96	9395.79
A_68_P21071913	chr2:25258906-25258950	NM_008721:326	Npdc1	INSIDE	1.366	4.097	2136.86	8754.80	5.597	1746.94	9778.14
A_68_P26542458	chr9:57408773-57408817	NM_022813:44	Scamp2	INSIDE	1.366	2.322	1662.49	3859.71	3.171	1201.75	3811.15
A_68_P27098031	chr10:42741435-42741479	NM_175407:152880	Sobp	INSIDE	1.366	2.616	436.98	1143.02	3.574	364.82	1303.85
A_68_P27937053	chr11:77161754-77161798	NM_177710:131850	Ssh2	INSIDE	1.366	1.996	388.31	774.94	2.726	401.06	1093.45
A_68_P28087325	chr11:103671166-103671210	NM_009521:35700	Wnt3	INSIDE	1.366	2.438	1160.65	2829.73	3.331	1066.06	3551.03
A_68_P31509674	chr18:14130093-14130137	NM_145492:1128	Zfp521	INSIDE	1.366	2.488	711.15	1769.61	3.399	569.89	1936.82
A_68_P26710067	A_68_P26710067			Unknown	1.366	2.734	9332.13	25516.35	3.736	6010.72	22454.09
A_68_P27892803	chr11:68873789-68873833	NM_028005:534	2310047M10Rik	INSIDE	1.365	1.753	1835.32	3217.20	2.392	1543.35	3691.98
A_68_P30686068	chr16:38452791-38452835	NM_007414:-43	Adprh	DIVERGENT_PROMOTER	1.365	1.811	429.23	777.53	2.473	423.67	1047.63
A_68_P23961351	chr5:106886587-106886631	NM_001005477:577	Barhl2	INSIDE	1.365	5.453	6035.95	32914.14	7.441	4374.52	32552.81
A_68_P29487113	chr14:28242620-28242665	NM_001114879:610	D14Abb1e	INSIDE	1.365	2.278	937.43	2135.62	3.111	760.25	2365.00
A_68_P29699027	chr14:70478576-70478620	NM_018781:1347	Egr3	INSIDE	1.365	2.225	2968.91	6606.06	3.036	1916.90	5820.15
A_68_P22882726	chr4:45421447-45421491	NM_001009949:170	Mcart1	INSIDE	1.365	1.978	1515.41	2998.06	2.701	1358.02	3667.33

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P30884142	chr16:76372860-76372904	NM_173440:412	Nrip1	INSIDE	1.365	1.630	829.32	1351.42	2.224	791.79	1761.14
A_68_P21495967	chr2:105516620-105516664	NM_013627:41	Pax6	INSIDE	1.365	1.404	1409.12	1978.78	1.917	1251.03	2398.75
A_68_P27940746	chr11:77796693-77796737	NM_174852:397	Phf12	INSIDE	1.365	1.576	896.82	1412.96	2.150	747.20	1606.34
A_68_P29482222	chr14:27353534-27353578	NM_032008:-330	Slmap	PROMOTER	1.365	3.503	1597.70	5596.47	4.781	1401.51	6700.50
A_68_P26696151	chr9:85737666-85737710	NM_001164792:1230	Tpbg	INSIDE	1.365	1.601	1639.80	2625.68	2.186	1476.94	3228.44
A_68_P31090924	chr17:23013653-23013697	NM_001110254:-9573	Zfp945	PROMOTER	1.365	3.268	2013.01	6578.76	4.460	1739.67	7759.32
A_68_P29308200	chr13:108680217-108680261	NM_145456:20	Zswim6	INSIDE	1.365	3.452	1029.65	3554.78	4.711	912.24	4297.77
A_68_P22217922	chr3:68674470-68674514	NM_001167996:985	1110032F04Rik	INSIDE	1.364	1.514	3760.24	5692.53	2.065	2765.18	5709.65
A_68_P30339175	chr15:74551980-74552024	NM_198607:339	4930572J05Rik	INSIDE	1.364	4.736	981.45	4647.90	6.460	773.94	5000.06
A_68_P27938078	chr11:77329061-77329105	NM_026185:464	Abhd15	INSIDE	1.364	1.489	948.03	1411.60	2.031	734.04	1491.14
A_68_P28175760	chr11:118947373-118947417	NM_007625:157	Cbx4	INSIDE	1.364	1.991	1552.36	3091.16	2.715	1329.48	3609.96
A_68_P24980083	chr7:16760918-16760963	NM_008627:212	Meis3	INSIDE	1.364	1.724	1918.07	3306.37	2.352	1537.74	3616.61
A_68_P20005799	chr1:4482580-4482624	NM_011441:3892	Sox17	INSIDE	1.364	2.873	1902.00	5463.89	3.918	1576.06	6174.50
A_68_P31201703	chr17:45682394-45682438	NM_001013749:4210	Tmem151b	INSIDE	1.364	2.039	2284.65	4657.56	2.781	1929.60	5367.08
A_68_P25477112	chr7:129211243-129211287	NM_138589:553	Ubfd1	INSIDE	1.364	5.681	694.56	3946.07	7.747	632.13	4896.98
A_68_P20778496	chr1:164501404-164501449	NM_016796:468	Vamp4	INSIDE	1.364	2.376	727.00	1727.60	3.241	610.91	1980.14
A_68_P26158504	chr8:112229332-112229376	NM_001167946:-94	Zfp821	PROMOTER	1.364	1.357	2785.29	3778.49	1.850	2238.75	4141.09
A_68_P27288852	chr10:80783503-80783547	NM_027381:-323	2510012J08Rik	PROMOTER	1.363	1.438	2241.07	3223.18	1.960	1897.65	3720.15
A_68_P32238972	chrX:7150718-7150762	NR_029473:15	4930524L23Rik	INSIDE	1.363	1.425	892.18	1270.99	1.941	467.23	906.99
A_68_P29940455	chr14:119105820-119105864	NM_001033336:-401	Abcc4	PROMOTER	1.363	2.192	444.95	975.45	2.989	386.60	1155.38
A_68_P27543828	chr10:128347300-128347344	NM_007653:401	Cd63	INSIDE	1.363	1.593	2565.47	4086.57	2.172	2080.95	4519.18
A_68_P29454311	chr14:22506206-22506253	NM_001013826:27569	Dupd1	INSIDE	1.363	2.232	524.85	1171.62	3.044	433.34	1318.94
A_68_P21903062	chr2:180068497-180068541	NM_008093:866	Gata5	INSIDE	1.363	3.218	783.22	2520.57	4.386	679.87	2981.68
A_68_P29613086	chr14:55194659-55194703	NM_010590:1818	Jub	INSIDE	1.363	2.489	1979.72	4926.86	3.391	1677.56	5688.85
A_68_P24383013	chr6:39369919-39369963	NM_018810:428	Mkrn1	INSIDE	1.363	2.549	1425.23	3632.38	3.473	1207.82	4195.23
A_68_P21652765	chr2:134612489-134612533	NM_001145830:611	Plcb1	INSIDE	1.363	1.493	4111.13	6137.50	2.034	3304.93	6723.05
A_68_P26818266	chr9:108998036-108998080	NM_172775:109	Plxnb1	INSIDE	1.363	2.414	582.67	1406.34	3.289	549.93	1808.78
A_68_P24537771	chr6:71657856-71657900	NM_178608:204	Reep1	INSIDE	1.363	3.930	1707.76	6711.48	5.355	1465.87	7849.29
A_68_P29871957	chr14:104921836-104921880	NM_026047:25	Rnf219	INSIDE	1.363	2.386	1614.12	3850.86	3.251	1506.69	4898.83
A_68_P23318415	chr4:133155946-133155990	NM_018754:2115	Sfn	DOWNSTREAM	1.363	2.560	2353.04	6023.00	3.488	1731.94	6041.65
A_68_P20412460	chr1:88400352-88400396			Unknown	1.363	1.843	1127.38	2077.21	2.511	924.65	2321.98
A_68_P28914784	chr13:30077124-30077168	NM_010093:786	E2f3	INSIDE	1.362	3.509	1126.80	3954.07	4.779	1102.66	5269.22
A_68_P27281572	chr10:79649620-79649664	NM_007909:7416	Efna2	INSIDE	1.362	2.532	1752.70	4437.39	3.448	1292.57	4456.30
A_68_P23404991	chr4:149610981-149611025	NM_023119:-303	Eno1	PROMOTER	1.362	1.847	622.32	1149.25	2.516	550.40	1384.84
A_68_P24908774	chr6:143115559-143115603	NM_029250:-169	Etnk1	PROMOTER	1.362	1.491	1244.29	1855.55	2.032	1106.83	2248.53
A_68_P23570788	chr5:30441008-30441052	NM_001167879:9295	Fam59b	INSIDE	1.362	1.603	1468.31	2353.99	2.184	1158.64	2530.82
A_68_P23438941	chr4:154865679-154865723	NM_001160016:231	Gnb1	INSIDE	1.362	3.548	2529.70	8975.40	4.831	2211.89	10686.38
A_68_P21717098	chr2:146047771-146047815	NM_016889:60	Insm1	INSIDE	1.362	3.054	1048.62	3202.55	4.161	911.19	3791.03
A_68_P28067976	chr11:100276206-100276250	NM_176830:-95	Leprel4	DIVERGENT_PROMOTER	1.362	2.990	1008.38	3015.14	4.073	901.21	3670.91
A_68_P31106322	chr17:25933806-25933850	NM_133719:162	Metrn	INSIDE	1.362	1.699	689.09	1170.50	2.313	626.86	1449.91
A_68_P20348302	chr1:74438798-74438842	NR_029743:-2063	Mir26b	PROMOTER	1.362	2.584	636.14	1643.58	3.519	801.80	2821.38
A_68_P27901890	chr11:70467341-70467385	NM_011072:790	Pfn1	INSIDE	1.362	3.593	1101.08	3956.38	4.895	1022.58	5005.37
A_68_P20941542	chr1:193916523-193916567	NM_011633:-99	Traf5	PROMOTER	1.362	2.493	3521.84	8780.89	3.395	2869.11	9740.55
A_68_P29117525	chr13:69878696-69878740	NM_001145162:57	Ube2ql1	INSIDE	1.362	2.858	1370.47	3916.86	3.894	1265.64	4928.35
A_68_P30571780	chr16:17070460-17070504	NM_023249:79	Ypel1	INSIDE	1.362	2.294	633.96	1453.98	3.125	532.71	1664.56
A_68_P32564025	chrX:98615354-98615398	NM_001177985:-123	Zmym3	PROMOTER	1.362	1.536	1503.86	2309.65	2.092	872.43	1825.25
A_68_P22291852	chr3:84386166-84386211	NM_001081093:359	Arfip1	INSIDE	1.361	1.874	1862.27	3490.66	2.551	1534.47	3914.95
A_68_P26815969	chr9:108551009-108551053	NM_011790:681	Arih2	INSIDE	1.361	1.913	910.96	1742.30	2.603	809.45	2107.36
A_68_P31845029	chr18:77182994-77183040	NM_001039201:-140	Hdhd2	PROMOTER	1.361	2.124	1149.86	2442.61	2.891	1039.55	3005.11
A_68_P26467130	chr9:44152085-44152129	NM_001110251:-1642	Hmbs	PROMOTER	1.361	2.192	1107.48	2428.13	2.983	1031.07	3075.71
A_68_P27862295	chr11:63735348-63735392	NM_018805:416	Hs3st3b1	INSIDE	1.361	1.969	1565.83	3083.71	2.680	1195.83	3204.44

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P23399811	chr4:148681546-148681590	NM_207682:239	Kif1b	INSIDE	1.361	2.065	441.00	910.65	2.811	399.56	1123.33
A_68_P23164367	chr4:102792385-102792429	NM_001039081:412	Mier1	INSIDE	1.361	1.931	1119.80	2162.68	2.629	899.38	2364.38
A_68_P31425848	chr17:88374947-88374991	NM_010830:579	Msh6	INSIDE	1.361	2.086	1162.99	2425.55	2.839	1098.30	3117.65
A_68_P26772688	chr9:100978469-100978513	NM_001100451:40	Msl2	INSIDE	1.361	1.465	1259.57	1845.10	1.993	1116.02	2224.57
A_68_P27687498	chr11:32121990-32122034	NM_010117:281	Rhbdf1	INSIDE	1.361	1.857	1146.02	2128.65	2.528	942.75	2382.92
A_68_P31003195	chr17:3114834-3114878	NM_134123:-115	Scaf8	PROMOTER	1.361	1.598	476.21	760.78	2.174	473.73	1029.91
A_68_P22411698	chr3:108087081-108087125	NM_019972:53	Sort1	INSIDE	1.361	1.897	3132.01	5941.00	2.581	2374.06	6127.71
A_68_P31958009	chr19:11893089-11893134	NM_011502:272	Stx3	INSIDE	1.361	1.890	2811.58	5314.04	2.573	2393.25	6157.28
A_68_P24946870	chr7:3646016-3646060	NM_024168:-71	Tsen34	PROMOTER	1.361	2.702	3686.60	9962.49	3.677	2903.22	10675.36
A_68_P26685864	chr9:83728415-83728459	NM_001110265:141	Ttk	INSIDE	1.361	1.839	3798.36	6984.55	2.503	3015.76	7548.85
A_68_P26465578	chr9:43893359-43893403	NM_198091:378	Usp2	INSIDE	1.361	1.883	1890.54	3560.74	2.564	1506.49	3862.12
A_68_P20046440	chr1:14497095-14497139			Unknown	1.361	5.292	2590.68	13710.41	7.203	1986.94	14312.50
A_68_P22875972	chr4:44247099-44247143	ENSMUST00000153116:-459		PROMOTER	1.361	1.884	809.90	1525.58	2.563	729.11	1868.62
A_68_P26749718	chr9:96789794-96789838	NM_153420:25	Acpl2	INSIDE	1.360	2.516	1208.35	3040.42	3.423	1060.90	3631.22
A_68_P24639207	chr6:91423387-91423431	NM_133928:9	Chchd4	INSIDE	1.360	1.479	1769.31	2617.20	2.011	1498.62	3014.42
A_68_P25592938	chr7:149280400-149280444	NM_008748:767	Dusp8	INSIDE	1.360	2.194	789.10	1731.38	2.985	574.57	1714.93
A_68_P27560006	chr11:4749005-4749049	NM_010898:504	Nf2	INSIDE	1.360	2.734	1101.42	3011.51	3.719	910.36	3385.51
A_68_P21939653	chr3:9833472-9833516	NM_001195031:185	Pag1	INSIDE	1.360	1.918	767.65	1472.10	2.609	635.03	1656.72
A_68_P24381543	chr6:39067895-39067939	NM_172893:432	Parp12	INSIDE	1.360	2.227	1642.62	3658.04	3.028	1483.86	4493.75
A_68_P28036286	chr11:94902671-94902715	NM_133667:-7	Pdk2	PROMOTER	1.360	2.254	1330.35	2999.21	3.067	1225.86	3759.60
A_68_P32694937	chrX:136145542-136145586	NM_023270:406	Rnf128	INSIDE	1.360	1.800	733.51	1319.95	2.447	365.61	894.79
A_68_P26129567	chr8:107154779-107154823	NM_019662:421	Rrad	INSIDE	1.360	1.446	1182.94	1710.77	1.967	1040.72	2047.28
A_68_P22871354	chr4:43394705-43394749	NM_001037709:-127	Rusc2	PROMOTER	1.360	2.432	951.83	2315.00	3.307	871.20	2881.09
A_68_P31058947	chr17:14416697-14416741	NM_022315:206	Smoc2	INSIDE	1.360	1.903	1483.75	2823.56	2.588	1295.92	3353.82
A_68_P21986766	chr3:21976041-21976085	NM_030732:489	Tbl1xr1	INSIDE	1.360	2.448	1397.89	3421.62	3.328	1312.91	4369.70
A_68_P27365516	chr10:94978402-94978446	NM_080560:629	Ube2n	INSIDE	1.360	2.455	1631.46	4005.41	3.340	1469.29	4906.85
A_68_P20803943	chr1:169156624-169156668	NM_030724:58612	Uck2	INSIDE	1.360	8.497	3753.86	31896.72	11.552	2329.16	26907.04
A_68_P20735710	chr1:156930629-156930673	ENSMUST00000128143:-254		PROMOTER	1.360	1.551	1935.62	3001.40	2.110	1615.07	3407.05
A_68_P31158463	chr17:35373372-35373416	NM_023179:-146	Atp6v1g2	DIVERGENT_PROMOTER	1.359	1.914	2497.39	4780.43	2.600	2011.96	5232.05
A_68_P27796700	chr11:51781220-51781264	NM_029976:110	Cdkn2aipnl	INSIDE	1.359	2.363	1411.32	3335.26	3.211	1298.73	4170.55
A_68_P22412527	chr3:108217228-108217273	NM_001004177:1162	Celsr2	INSIDE	1.359	2.437	327.37	797.66	3.312	271.86	900.52
A_68_P31620310	chr18:35990907-35990952	NM_133687:1458	Cxxc5	INSIDE	1.359	2.002	279.55	559.53	2.721	229.64	624.73
A_68_P24449527	chr6:52210204-52210248	NM_008264:648	Hoxa13	INSIDE	1.359	3.967	1308.24	5189.28	5.389	1142.69	6157.76
A_68_P21006641	chr2:11457093-11457137	NM_001177758:18442	Pfkfb3	INSIDE	1.359	2.507	1694.90	4249.41	3.407	1346.83	4588.87
A_68_P31655273	chr18:42555254-42555298	NM_138945:1026	Pou4f3	INSIDE	1.359	1.688	2210.55	3732.33	2.295	1843.32	4230.40
A_68_P23916643	chr5:98614905-98614949	NM_029947:5039	Prdm8	INSIDE	1.359	1.869	628.31	1174.47	2.540	506.16	1285.51
A_68_P29718153	chr14:73952777-73952821	NM_011506:206	Sucla2	INSIDE	1.359	2.144	427.53	916.50	2.913	397.88	1159.23
A_68_P28974184	chr13:40826354-40826399	NM_001122948:-564	Tcfap2a	PROMOTER	1.359	3.705	5820.36	21562.28	5.033	4575.69	23028.54
A_68_P33005816	A_68_P33005816			Unknown	1.359	2.659	388.66	1033.63	3.615	323.22	1168.46
A_68_P23692834	chr5:52507355-52507399	AK076709:-1175		PROMOTER	1.359	1.615	1889.57	3052.55	2.195	1493.69	3279.23
A_68_P25587958	chr7:148480452-148480496	NM_007878:2570	Drd4	INSIDE	1.358	1.707	1909.73	3259.96	2.318	1638.20	3796.62
A_68_P31769415	chr18:63546129-63546173	NM_001039485:687	Fam38b	INSIDE	1.358	2.290	1864.44	4269.70	3.110	1624.13	5051.65
A_68_P26467611	chr9:44248858-44248902	NM_001033469:71	Foxr1	INSIDE	1.358	2.455	1282.79	3149.56	3.335	957.04	3191.29
A_68_P20058119	chr1:17081907-17081951	NM_020604:6042	Jph1	INSIDE	1.358	2.532	479.42	1213.87	3.439	443.56	1525.24
A_68_P25098809	chr7:53651661-53651705	NM_008421:-155	Kcnc1	PROMOTER	1.358	3.971	520.29	2066.17	5.395	528.12	2848.95
A_68_P31123750	chr17:28826626-28826670	NM_001168508:-1638	Mapk14	PROMOTER	1.358	2.749	1067.98	2935.78	3.733	901.71	3366.23
A_68_P20088276	chr1:23389423-23389467	NM_001081079:570	Ogfrl1	INSIDE	1.358	3.591	630.15	2262.87	4.877	523.96	2555.37
A_68_P29509082	chr14:31814863-31814907	NM_026911:-32	Spcs1	PROMOTER	1.358	7.876	445.18	3506.37	10.697	415.82	4447.88
A_68_P21370052	chr2:79475902-79475946	NM_080558:343	Ssfa2	INSIDE	1.358	1.723	2895.47	4988.92	2.340	2403.07	5623.52
A_68_P24907675	chr6:142912528-142912572	NM_011374:422	St8sia1	INSIDE	1.358	1.772	1785.69	3164.63	2.407	1266.13	3047.71
A_68_P24951676	chr7:4982246-4982290	NM_001033383:10291	Zfp865	INSIDE	1.358	2.423	1233.64	2989.54	3.290	975.09	3207.93

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27288263	chr10:80702990-80703034	NM_001034895:7105	Zfr2	INSIDE	1.358	3.781	647.33	2447.83	5.134	514.02	2639.05
A_68_P27765615	chr11:45869497-45869541	NM_009616:30	Adam19	INSIDE	1.357	2.475	1814.11	4490.02	3.359	1298.58	4361.56
A_68_P30473398	chr15:97975961-97976005	NM_001170710:151	Asb8	INSIDE	1.357	2.239	2378.64	5324.89	3.038	1972.24	5992.46
A_68_P21897026	chr2:179176969-179177013	NM_009867:-192	Cdh4	PROMOTER	1.357	2.400	941.21	2259.13	3.256	808.82	2633.70
A_68_P25958451	chr8:74233667-74233711	NM_028715:15892	Fcho1	INSIDE	1.357	2.488	2287.70	5691.25	3.376	1781.15	6012.42
A_68_P29228410	chr13:94074181-94074225	NM_011982:-247	Homer1	PROMOTER	1.357	2.763	1506.26	4161.77	3.750	1305.27	4895.03
A_68_P21812073	chr2:163201933-163201977	NM_021566:21755	Jph2	INSIDE	1.357	2.387	517.55	1235.46	3.240	440.74	1427.76
A_68_P31424878	chr17:88145892-88145936	NM_199251:51420	Kcnk12	INSIDE	1.357	1.503	1312.07	1971.76	2.039	1064.52	2170.80
A_68_P22868863	chr4:42929796-42929840	NM_172690:-304	N28178	PROMOTER	1.357	3.146	467.50	1470.79	4.269	417.48	1782.29
A_68_P25050058	chr7:36370084-36370128	NM_145840:495	Rgs9bp	INSIDE	1.357	2.270	661.86	1502.42	3.080	603.50	1858.72
A_68_P30255504	chr15:59479090-59479134	NM_144549:-1096	Trib1	PROMOTER	1.357	1.527	949.03	1449.63	2.073	723.73	1499.94
A_68_P28741417	chr12:112215277-112215321	NM_175207:1933	Ankrd9	INSIDE	1.356	2.526	336.41	849.76	3.425	312.11	1069.03
A_68_P28669124	chr12:99497596-99497640	NM_008079:-71	Galc	DIVERGENT_PROMOTER	1.356	2.292	1424.45	3264.84	3.107	1240.70	3855.38
A_68_P28290299	chr12:25257426-25257470	NM_145890:-8135	Grhl1	PROMOTER	1.356	1.773	1594.35	2827.16	2.404	1278.35	3073.66
A_68_P31255286	chr17:56465347-56465391	NM_172132:-104	Kdm4b	PROMOTER	1.356	3.863	1908.78	7373.43	5.239	1735.55	9092.43
A_68_P22882724	chr4:45421232-45421276	NM_001009949:384	Mcart1	INSIDE	1.356	1.897	1805.70	3425.43	2.572	1310.37	3370.89
A_68_P27795021	chr11:51449266-51449310	NM_025346:110	Rmnd5b	INSIDE	1.356	4.161	516.21	2147.72	5.642	508.89	2871.36
A_68_P20024136	chr1:9788012-9788056	NM_133220:-176	Sgk3	PROMOTER	1.356	4.194	1044.55	4380.35	5.688	908.73	5168.57
A_68_P31381749	chr17:80606236-80606280	NM_001195485:387	Srsf7	INSIDE	1.356	1.494	7234.62	10806.48	2.026	5253.97	10642.61
A_68_P27971718	chr11:83286618-83286662	NM_027427:31	Taf15	INSIDE	1.356	8.044	1308.94	10529.64	10.909	1225.83	13372.08
A_68_P31209392	chr17:47027759-47027803	NM_178385:211	Tbcc	INSIDE	1.356	1.883	3135.97	5904.23	2.553	2378.32	6072.48
A_68_P30484944	chr15:100111219-100111263	NM_183109:-27	Tmprss12	PROMOTER	1.356	2.156	415.05	895.01	2.924	316.24	924.60
A_68_P30328150	chr15:72891418-72891462	NM_029640:-5198	Trappc9	PROMOTER	1.356	1.371	2665.84	3654.67	1.858	2154.79	4004.25
A_68_P32533199	chrX:90533865-90533909	NM_007492:1902	Arx	INSIDE	1.355	2.142	1899.44	4068.56	2.903	1239.21	3597.10
A_68_P31399352	chr17:83913503-83913547	NM_001159529:149	Cox7a2l	INSIDE	1.355	1.556	848.42	1320.11	2.109	742.39	1565.67
A_68_P24423150	chr6:47404743-47404787	NM_012042:442	Cul1	INSIDE	1.355	1.800	723.60	1302.32	2.439	653.62	1593.97
A_68_P23325561	chr4:134479965-134480009	NM_023665:447	D4Wsu53e	INSIDE	1.355	3.398	2142.02	7278.91	4.605	1818.26	8373.31
A_68_P30113005	chr15:31154387-31154431	NM_146057:269	Dap	INSIDE	1.355	1.369	1518.58	2079.26	1.856	1191.38	2211.13
A_68_P24138257	chr5:140384753-140384797	NM_175522:878	Elfn1	INSIDE	1.355	1.525	811.28	1237.10	2.065	768.93	1588.21
A_68_P21338547	chr2:74493903-74493947	NM_007967:3552	Evx2	INSIDE	1.355	3.343	349.06	1166.95	4.530	318.51	1442.81
A_68_P21428052	chr2:92211160-92211204	NM_001166633:11	Gyltl1b	INSIDE	1.355	2.320	1224.27	2840.76	3.144	959.15	3015.32
A_68_P22218631	chr3:68809558-68809602	NR_029529:-4113	Mir15b	PROMOTER	1.355	1.957	1913.91	3745.63	2.652	1423.59	3775.34
A_68_P22342633	chr3:94977194-94977238	NM_011351:8921	Sema6c	INSIDE	1.355	2.157	1867.57	4028.64	2.922	1490.67	4355.66
A_68_P31421397	chr17:87534362-87534421	NM_019654:27373	Socs5	INSIDE	1.355	2.229	258.24	575.61	3.021	242.91	733.71
A_68_P28051188	chr11:97398038-97398082	NM_018873:38380	Srcin1	INSIDE	1.355	2.770	1139.86	3157.30	3.754	924.48	3470.35
A_68_P23223183	chr4:114736145-114736189	NM_011527:4035	Tal1	INSIDE	1.355	3.038	538.70	1636.78	4.117	415.29	1709.74
A_68_P27985546	chr11:85647033-85647077	NM_009324:938	Tbx2	INSIDE	1.355	5.637	4673.73	26343.99	7.638	3623.94	27678.21
A_68_P23297751	chr4:129318057-129318101	NM_001005506:-29	Txlna	PROMOTER	1.355	1.833	5046.79	9250.43	2.483	3828.55	9505.34
A_68_P23358589	chr4:140071100-140071144	NM_001112723:133549	Arhgef10l	INSIDE	1.354	2.587	423.43	1095.63	3.504	399.52	1399.80
A_68_P25274217	chr7:88973759-88973803	NM_146193:537	Btbd1	INSIDE	1.354	2.131	829.29	1767.39	2.887	778.59	2247.43
A_68_P30508958	chr16:4214152-4214196	NM_001025432:-770	Crebbp	PROMOTER	1.354	3.169	968.07	3068.05	4.291	889.88	3818.04
A_68_P23320290	chr4:133524024-133524068	NM_016957:-140	Hmgn2	PROMOTER	1.354	2.333	2847.55	6643.49	3.158	2230.36	7044.42
A_68_P29010691	chr13:47024841-47024885	NM_010617:225	Kif13a	INSIDE	1.354	3.743	2168.68	8117.07	5.068	1869.97	9476.71
A_68_P28206077	chr12:5382789-5382833	NM_001164493:-322	Klhl29	DIVERGENT_PROMOTER	1.354	2.654	871.38	2312.70	3.593	700.41	2516.89
A_68_P24947984	chr7:4101189-4101233	NM_175529:264	Leng9	INSIDE	1.354	1.783	683.29	1218.35	2.414	631.11	1523.52
A_68_P20007250	chr1:4797717-4797761	NM_008866:-235	Lypla1	PROMOTER	1.354	3.212	454.86	1461.19	4.351	455.05	1979.79
A_68_P20849642	chr1:177622972-177623016	NM_010098:-273	Opn3	DIVERGENT_PROMOTER	1.354	3.511	3696.49	12979.44	4.755	2887.33	13729.03
A_68_P31421395	chr17:87534146-87534190	NM_019654:27150	Socs5	INSIDE	1.354	2.103	500.87	1053.44	2.848	331.39	943.73
A_68_P28402111	chr12:46175015-46175059	NM_144552:434	Stxbp6	INSIDE	1.354	2.043	8270.30	16896.14	2.767	6107.35	16899.76
A_68_P30349160	chr15:76406761-76406805	NM_172960:-6	Adck5	PROMOTER	1.353	1.912	1435.20	2744.49	2.587	1309.33	3387.57
A_68_P21901913	chr2:179906128-179906172	NM_019822:-142	Adrm1	PROMOTER	1.353	2.249	536.72	1207.15	3.043	546.14	1661.97

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P29413816	chr14:13655475-13655519	NM_001042617:97	Cadps	INSIDE	1.353	2.294	1232.12	2827.09	3.103	1014.73	3149.20
A_68_P24154206	chr5:143722119-143722163	NM_007984:107	Fscn1	INSIDE	1.353	2.117	1448.25	3066.19	2.864	1282.20	3672.75
A_68_P20799113	chr1:168168950-168168994	NM_175296:-97	Mael	PROMOTER	1.353	2.194	792.66	1738.88	2.967	621.81	1844.92
A_68_P22825640	chr4:33275997-33276041	NM_001034867:694	Pm20d2	INSIDE	1.353	1.769	751.45	1329.68	2.394	836.59	2003.17
A_68_P20636473	chr1:136852289-136852333	NM_001081307:207	Ppp1r12b	INSIDE	1.353	5.648	1800.34	10168.16	7.642	1490.00	11385.87
A_68_P27561411	chr11:4999553-4999597	NM_177370:134	Rhbdd3	INSIDE	1.353	2.588	756.61	1957.93	3.502	639.15	2238.47
A_68_P23317104	chr4:132894918-132894962	NM_199306:290	Wdtc1	INSIDE	1.353	2.205	791.17	1744.65	2.983	755.02	2252.60
A_68_P24951576	chr7:4967342-4967386	NM_025324:255	Zfp524	INSIDE	1.353	3.487	1823.33	6357.48	4.718	1604.79	7571.15
A_68_P21622683	chr2:128864800-128864844	ENSMUST00000145798:16689		INSIDE	1.353	2.007	928.98	1864.50	2.716	839.61	2280.31
A_68_P25357074	chr7:105804627-105804671	NM_172280:431	2210018M11Rik	INSIDE	1.352	3.522	2626.25	9249.25	4.763	2332.64	11110.79
A_68_P28449510	chr12:55963628-55963672	NM_007688:214	Cfl2	INSIDE	1.352	3.331	1397.96	4657.07	4.503	1155.87	5205.38
A_68_P28143432	chr11:113545919-113545963	NM_177777:215	D11Wsu47e	INSIDE	1.352	2.503	3355.22	8398.52	3.385	2468.17	8355.60
A_68_P24501227	chr6:63205942-63205990	NM_008167:-884	Grid2	PROMOTER	1.352	3.292	166.72	548.82	4.452	156.51	696.82
A_68_P31425165	chr17:88198232-88198276	NM_199251:-920	Kcnk12	PROMOTER	1.352	2.405	858.46	2064.29	3.251	787.51	2560.10
A_68_P28516078	chr12:70825634-70825678	NM_145443:205	L2hgdh	INSIDE	1.352	1.922	2372.19	4558.42	2.598	2034.28	5285.87
A_68_P21081081	chr2:26766063-26766107	NM_001033908:78	Med22	INSIDE	1.352	1.373	6011.65	8253.93	1.857	4490.83	8339.26
A_68_P28831284	chr13:12350487-12350531	NM_001081128:-241	Mtr	PROMOTER	1.352	1.899	1347.79	2559.38	2.567	1046.52	2686.24
A_68_P27857775	chr11:62945991-62946035	NM_008885:1001	Pmp22	INSIDE	1.352	3.144	1566.53	4925.80	4.251	1451.94	6172.10
A_68_P21820792	chr2:164793405-164793449	NM_020333:-61	Slc12a5	PROMOTER	1.352	1.914	754.00	1443.04	2.588	676.97	1751.94
A_68_P26238818	chr8:125778428-125778472	NM_020497:356	Zfp276	INSIDE	1.352	1.703	968.26	1649.17	2.302	713.76	1643.32
A_68_P25735806	chr8:28088778-28088822	NM_001101502:993	Zfp703	INSIDE	1.352	1.463	2200.89	3219.55	1.978	1519.14	3004.28
A_68_P22509004	chr3:127201898-127201942	ENSMUST00000104965:-1		PROMOTER	1.352	3.319	1159.32	3847.87	4.486	944.78	4238.11
A_68_P29656176	chr14:63174690-63174734	ENSMUST00000160745:101		INSIDE	1.352	12.068	731.90	8832.82	16.313	732.20	11944.22
A_68_P30568280	chr16:16146642-16146686	NM_146068:262	2310008H04Rik	INSIDE	1.351	3.121	1423.97	4444.92	4.217	1239.77	5228.61
A_68_P22942710	chr4:57003066-57003110	NM_001142965:175	6430704M03Rik	INSIDE	1.351	3.860	405.32	1564.37	5.213	526.59	2744.90
A_68_P29747537	chr14:79124881-79124925	NM_001081336:-6	Dgkh	PROMOTER	1.351	2.255	848.39	1913.52	3.048	683.30	2082.64
A_68_P32541781	chrX:92639710-92639754	NM_175179:447	Fam123b	INSIDE	1.351	2.399	2316.60	5557.38	3.240	1138.92	3690.06
A_68_P28997659	chr13:44826258-44826302	NM_001205043:-359	Jarid2	PROMOTER	1.351	1.460	893.50	1304.83	1.972	875.17	1726.24
A_68_P21421187	chr2:91023173-91023217	NM_001177720:-3716	Madd	PROMOTER	1.351	3.258	1096.95	3574.40	4.403	958.05	4218.22
A_68_P22949803	chr4:58218825-58218869	NM_022814:622	Svep1	INSIDE	1.351	2.522	578.72	1459.31	3.406	486.29	1656.44
A_68_P30566187	chr16:15594249-15594293	NM_001159351:341	Ube2v2	INSIDE	1.351	2.127	4254.61	9048.22	2.872	3286.73	9440.89
A_68_P24091119	chr5:130371741-130371785	NM_183088:170	2410018M08Rik	INSIDE	1.350	4.754	1452.40	6904.13	6.418	1168.93	7501.85
A_68_P21631948	chr2:130665681-130665725	NM_029432:144	4930402H24Rik	INSIDE	1.350	1.883	1526.30	2873.28	2.542	1369.48	3481.37
A_68_P27958472	chr11:80965947-80965991	NM_007384:437	Accn1	INSIDE	1.350	2.931	228.85	670.79	3.958	228.19	903.09
A_68_P23315180	chr4:132568310-132568354	NM_146155:912	Ahdc1	INSIDE	1.350	2.566	577.69	1482.17	3.464	557.57	1931.48
A_68_P24990327	chr7:19479355-19479399	NM_001033314:16377	Ccdc61	INSIDE	1.350	4.732	4065.99	19240.24	6.387	3400.00	21717.34
A_68_P26236516	chr8:125394674-125394718	NM_007662:22423	Cdh15	DOWNSTREAM	1.350	4.613	1240.67	5722.78	6.225	973.31	6058.68
A_68_P27894661	chr11:69182323-69182367	NM_146019:584	Chd3	INSIDE	1.350	1.733	598.91	1037.71	2.340	511.00	1195.65
A_68_P23155324	chr4:101169410-101169454	NM_198412:180	Dnajc6	INSIDE	1.350	1.697	1936.17	3284.88	2.290	1410.10	3228.90
A_68_P23309924	chr4:131604876-131604920	NM_001128606:95	Epb4.1	INSIDE	1.350	4.441	2377.59	10558.25	5.995	2028.13	12159.05
A_68_P26224362	chr8:123609059-123609103	NM_010426:707	Foxf1a	INSIDE	1.350	2.194	1213.76	2662.70	2.961	920.81	2726.96
A_68_P24620344	chr6:88147093-88147137	NM_008090:-1543	Gata2	PROMOTER	1.350	2.203	587.48	1294.48	2.974	532.80	1584.60
A_68_P29613096	chr14:55195734-55195778	NM_010590:742	Jub	INSIDE	1.350	7.990	2719.59	21729.66	10.785	2234.76	24101.80
A_68_P27528046	chr10:125403373-125403417	NM_177152:120	Lrig3	INSIDE	1.350	4.085	1673.97	6838.45	5.516	1338.69	7384.71
A_68_P22209747	chr3:67178066-67178110	NM_001039543:70	Mlf1	INSIDE	1.350	1.503	1142.03	1716.40	2.028	1022.81	2074.71
A_68_P21840226	chr2:168056561-168056605	NM_001160330:461	Mocs3	INSIDE	1.350	4.757	442.98	2107.05	6.422	371.87	2388.16
A_68_P26500015	chr9:49606210-49606254	NM_001081445:942	Ncam1	INSIDE	1.350	2.107	750.15	1580.35	2.844	631.11	1794.89
A_68_P26477175	chr9:45792523-45792567	NM_008775:410	Pafah1b2	INSIDE	1.350	1.712	1861.35	3187.50	2.312	1644.22	3802.17
A_68_P29116256	chr13:69673614-69673658	NM_001169131:-894	Papd7	PROMOTER	1.350	1.569	2724.26	4273.30	2.117	2356.71	4989.79
A_68_P27551126	chr11:3190443-3190488	NM_019574:6	Patz1	INSIDE	1.350	1.532	1497.99	2294.67	2.067	1338.58	2767.13
A_68_P27949793	chr11:79404552-79404596	NM_175543:-139	Rab11fip4	PROMOTER	1.350	2.519	1244.98	3136.67	3.401	1099.13	3737.89

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27907304	chr11:71565101-71565145	NM_177618:918	Wscd1	INSIDE	1.350	1.817	798.47	1450.58	2.452	704.74	1728.38
A_68_P32111692	chr19:40969658-40969702	NM_028319:486	Zfp518a	INSIDE	1.350	2.005	5300.44	10629.34	2.707	4430.67	11994.26
A_68_P22300151	chr3:85775250-85775294	ENSMUST00000158452:-8518		PROMOTER	1.350	2.485	692.09	1720.00	3.354	680.90	2283.78
A_68_P30382914	chr15:82176511-82176555	NM_026914:57	1500032L24Rik	INSIDE	1.349	4.575	1510.15	6909.63	6.171	1513.47	9339.25
A_68_P24098222	chr5:131916544-131916588	NM_177047:1101647	Auts2	INSIDE	1.349	4.268	378.96	1617.35	5.756	342.54	1971.59
A_68_P30478823	chr15:99055100-99055144	NM_010601:-284	Kcnh3	PROMOTER	1.349	1.660	545.35	905.02	2.239	508.01	1137.66
A_68_P30682957	chr16:37868699-37868743	NM_177093:235	Lrrc58	INSIDE	1.349	2.636	1457.85	3842.19	3.557	1184.30	4211.97
A_68_P24731710	chr6:108090490-108090549	NM_145937:45058	Sumf1	INSIDE	1.349	5.960	233.08	1389.11	8.038	185.59	1491.64
A_68_P29448169	chr14:21480603-21480647	NM_175132:6904	Synpo2l	INSIDE	1.349	1.484	656.87	974.96	2.002	569.66	1140.74
A_68_P23282960	chr4:126645057-126645101	NM_001114399:89	Zmym4	INSIDE	1.349	2.115	2067.77	4373.83	2.854	1783.97	5092.09
A_68_P26663734	chr9:79190352-79190396			Unknown	1.349	2.174	1089.87	2369.86	2.933	884.61	2594.65
A_68_P23593955	chr5:34713045-34713089	ENSMUST00000042234:5		INSIDE	1.349	4.173	510.56	2130.77	5.630	450.09	2534.10
A_68_P31154763	chr17:34742756-34742800	NM_001163379:-27	Agpat1	DIVERGENT_PROMOTER	1.348	1.589	1297.92	2062.07	2.141	1067.47	2285.71
A_68_P24540594	chr6:72185394-72185438	NM_153778:155	Atoh8	INSIDE	1.348	2.927	1388.35	4063.95	3.945	1073.45	4234.55
A_68_P26234162	chr8:125075132-125075176	NM_001037298:75	Fam38a	INSIDE	1.348	2.716	835.72	2269.80	3.661	879.62	3220.14
A_68_P20351021	chr1:74929129-74929173	NM_153111:2832	Fev	INSIDE	1.348	3.448	1564.46	5394.70	4.649	1378.08	6407.18
A_68_P30490428	chr15:101054889-101054933	NM_019518:273	Grasp	INSIDE	1.348	0.394	1524.89	600.94	0.531	1193.36	634.07
A_68_P31489152	chr18:10325147-10325191	NM_001083628:-8	Greb1l	PROMOTER	1.348	4.009	1463.51	5866.73	5.403	1090.28	5890.53
A_68_P26349535	chr9:21722823-21722867	NM_031874:-279	Rab3d	PROMOTER	1.348	1.640	4313.75	7073.43	2.211	2985.88	6600.80
A_68_P31930774	chr19:5771196-5771240	NM_023912:183	Scyl1	INSIDE	1.348	0.402	1293.41	519.44	0.541	1001.35	541.92
A_68_P21623516	chr2:129024287-129024331	NM_001159593:-200	Slc20a1	PROMOTER	1.348	2.524	1562.08	3942.32	3.402	1464.39	4981.84
A_68_P30580561	chr16:18582686-18582730	NM_011532:4354	Tbx1	INSIDE	1.348	1.717	761.91	1308.00	2.315	639.79	1480.99
A_68_P27590826	chr11:11362086-11362130	NM_001185153:314	Zpbp	INSIDE	1.348	6.592	539.80	3558.60	8.889	478.90	4257.03
A_68_P24591142	chr6:83004903-83004947	NM_007517:278	Aup1	INSIDE	1.347	1.420	1180.63	1676.14	1.913	980.14	1874.80
A_68_P27812114	chr11:54601209-54601253	NM_178626:-25	Cdc42se2	PROMOTER	1.347	3.405	812.15	2765.33	4.587	734.19	3367.84
A_68_P31166952	chr17:37183039-37183083	NM_019439:150	Gabbr1	INSIDE	1.347	1.632	1349.72	2202.16	2.198	1103.62	2425.58
A_68_P25301153	chr7:95278950-95278994	NM_001081414:546295	Grm5	INSIDE	1.347	2.153	795.64	1713.16	2.901	698.56	2026.33
A_68_P26348588	chr9:21528254-21528298	NM_010700:239	Ldlr	INSIDE	1.347	4.817	292.19	1407.62	6.490	322.47	2092.75
A_68_P21475550	chr2:102026219-102026263	NM_178886:294	Ldlrad3	INSIDE	1.347	1.932	3546.53	6851.72	2.602	2729.63	7102.60
A_68_P27969031	chr11:82721501-82721545	NM_145431:375	Nle1	INSIDE	1.347	1.508	1683.38	2538.58	2.031	1353.98	2749.68
A_68_P29904272	chr14:112075171-112075215	NM_198865:856	Slitrk5	INSIDE	1.347	2.108	911.50	1921.46	2.839	781.50	2218.40
A_68_P32264678	chrX:12649125-12649169	NM_009481:523	Usp9x	INSIDE	1.347	2.170	1564.01	3393.55	2.922	867.52	2534.63
A_68_P24992394	chr7:19856763-19856807	NM_009499:419	Vasp	INSIDE	1.347	1.565	1471.11	2302.67	2.108	1180.72	2489.50
A_68_P24954288	chr7:6106767-6106811	NM_001013012:785	Zfp787	INSIDE	1.347	1.487	1545.68	2297.86	2.002	1290.12	2582.61
A_68_P24983771	chr7:17470567-17470612	NM_001081655:9924	Dact3	INSIDE	1.346	2.158	696.75	1503.57	2.904	694.21	2016.01
A_68_P23232037	chr4:116692073-116692117	NM_175135:82	Eif2b3	INSIDE	1.346	2.096	1100.19	2306.35	2.822	977.06	2757.37
A_68_P28513502	chr12:70342816-70342860	NM_178253:20	Klhdc1	INSIDE	1.346	2.317	870.11	2016.35	3.120	700.60	2185.64
A_68_P23950022	chr5:104475737-104475781	NM_028794:-271	Nudt9	PROMOTER	1.346	1.393	1131.89	1577.11	1.875	993.45	1862.75
A_68_P28513108	chr12:70260224-70260268	NM_009093:-73	Rps29	DIVERGENT_PROMOTER	1.346	1.580	1551.10	2450.61	2.127	1334.72	2839.08
A_68_P29218721	chr13:91600629-91600673	NM_024186:-51	Ssbp2	PROMOTER	1.346	2.895	1245.08	3604.99	3.896	1126.61	4389.72
A_68_P26805310	chr9:106724832-106724876	NM_001015507:548	Vprbp	INSIDE	1.346	1.700	1624.83	2762.47	2.288	1326.87	3036.44
A_68_P26552554	chr9:59139473-59139517	NM_028121:116	Adpgk	INSIDE	1.345	3.966	546.33	2166.48	5.334	559.45	2984.12
A_68_P27843676	chr11:60352657-60352701	NM_172943:1494	Alkbh5	INSIDE	1.345	1.803	1111.47	2003.81	2.426	936.19	2270.89
A_68_P25587962	chr7:148480819-148480877	NM_007878:2944	Drd4	INSIDE	1.345	2.296	319.06	732.54	3.087	247.41	763.84
A_68_P25827838	chr8:46095952-46095996	NM_001081286:60413	Fat1	INSIDE	1.345	2.345	1020.73	2393.43	3.153	804.20	2535.83
A_68_P31949295	chr19:10315203-10315247	NM_001033481:14	Gm98	INSIDE	1.345	2.226	2762.80	6150.31	2.993	2332.90	6982.74
A_68_P25262701	chr7:86855086-86855130	NM_010626:3964	Kif7	INSIDE	1.345	4.186	342.03	1431.64	5.631	321.35	1809.63
A_68_P31731695	chr18:56867197-56867241	NM_010721:-248	Lmnb1	PROMOTER	1.345	3.064	1742.74	5339.03	4.122	1496.70	6169.25
A_68_P23164324	chr4:102787243-102787287	NM_001039081:-4730	Mier1	PROMOTER	1.345	2.885	1527.16	4405.40	3.881	1239.86	4811.59
A_68_P31100163	chr17:25032650-25032694	NM_023260:608	Mrps34	INSIDE	1.345	1.470	829.83	1219.61	1.977	727.19	1437.34
A_68_P27565429	chr11:5778293-5778337	NM_008894:-55	Pold2	PROMOTER	1.345	1.484	6769.19	10048.55	1.996	4910.58	9801.50

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P29619515	chr14:56341110-56341154	NM_019519:-119	Rabggta	PROMOTER	1.345	1.837	1069.75	1965.49	2.472	872.78	2157.61
A_68_P24428192	chr6:48544047-48544091	NM_001079901:187	Repin1	INSIDE	1.345	1.620	4432.65	7182.98	2.180	3673.76	8008.99
A_68_P30424513	chr15:89145595-89145639	NM_001081030:126	Sbf1	INSIDE	1.345	1.646	977.58	1608.85	2.214	832.48	1842.77
A_68_P29145779	chr13:74487622-74487666	NM_023281:44	Sdha	INSIDE	1.345	1.769	3823.23	6762.77	2.379	3142.66	7474.94
A_68_P32363781	chrX:45638888-45638932	NM_028276:28800	Utp14a	DOWNSTREAM	1.345	4.508	4499.91	20285.34	6.065	2344.00	14216.05
A_68_P28577654	chr12:81892119-81892163	NM_178682:595	4933426M11Rik	INSIDE	1.344	1.873	402.24	753.31	2.517	370.66	932.86
A_68_P30367720	chr15:79489229-79489273	NM_029407:136	4933432B09Rik	INSIDE	1.344	1.571	1644.90	2584.60	2.112	1249.73	2639.32
A_68_P31794495	chr18:68092683-68092727	NM_172631:-206	D18Ertd653e	PROMOTER	1.344	5.098	868.15	4425.93	6.852	728.89	4994.12
A_68_P30346594	chr15:76009406-76009450	NM_201394:16712	Plec	INSIDE	1.344	2.929	1053.43	3084.97	3.935	909.12	3577.10
A_68_P21351539	chr2:76486029-76486073	NM_011871:1	Prkra	INSIDE	1.344	3.292	1449.40	4771.65	4.424	1126.06	4981.41
A_68_P31096042	chr17:24342530-24342574	NM_001163847:-45	Tbc1d24	PROMOTER	1.344	2.127	1128.60	2400.42	2.859	930.85	2661.29
A_68_P32562267	chrX:98254914-98254958	NM_031384:42	Tex11	INSIDE	1.344	2.185	1466.51	3204.23	2.937	759.57	2230.79
A_68_P28614746	chr12:88540796-88540840	NM_001033475:361	Tmed8	INSIDE	1.344	1.730	3353.98	5801.61	2.324	2617.69	6083.77
A_68_P21070953	chr2:25118574-25118618	NM_175286:479	Tprn	INSIDE	1.344	1.619	2392.55	3873.83	2.176	1987.89	4324.89
A_68_P25948524	chr8:72411743-72411787	NM_026818:-473	Cilp2	PROMOTER	1.343	2.962	1181.69	3500.32	3.979	846.69	3368.65
A_68_P23797494	chr5:73797444-73797488	NM_181323:150	Cwh43	INSIDE	1.343	1.827	1940.94	3545.24	2.452	1713.72	4202.67
A_68_P28553890	chr12:77518775-77518819	NM_001163103:211	Gm70	INSIDE	1.343	1.890	847.73	1602.10	2.539	734.25	1864.00
A_68_P26585802	chr9:64949678-64949722	NM_020043:399	Igdcc4	INSIDE	1.343	2.113	2532.28	5349.72	2.838	1862.59	5286.39
A_68_P31220004	chr17:49070978-49071022	NM_027452:-906	Lrfn2	PROMOTER	1.343	2.745	3083.98	8465.89	3.687	2419.79	8921.06
A_68_P20897581	chr1:186635006-186635050	NM_001081361:164	Mosc1	INSIDE	1.343	1.441	1974.58	2846.13	1.936	1701.70	3293.85
A_68_P29591680	chr14:49685967-49686011	NM_144535:-181	Mudeng	PROMOTER	1.343	2.974	782.10	2325.97	3.994	718.01	2868.04
A_68_P22346838	chr3:95799917-95799961	NM_023320:-176	Plekho1	PROMOTER	1.343	3.746	995.77	3729.99	5.032	1010.56	5084.78
A_68_P29177384	chr13:81850152-81850196	NM_001081176:-162	Polr3g	DIVERGENT_PROMOTER	1.343	1.758	1624.81	2856.71	2.361	1401.46	3308.73
A_68_P26701864	chr9:86774762-86774806	NM_013669:423	Snap91	INSIDE	1.343	2.241	2263.56	5071.87	3.009	1966.54	5917.00
A_68_P26770650	chr9:100543637-100543681	NM_009282:-383	Stag1	PROMOTER	1.343	3.029	521.91	1580.85	4.067	522.70	2125.96
A_68_P23892499	chr5:92566763-92566807	NM_019490:-179	Uso1	PROMOTER	1.343	1.352	3090.94	4179.57	1.816	2605.61	4732.47
A_68_P30665799	chr16:34745459-34745503	ENSMUST00000155268:185		INSIDE	1.343	2.697	1401.94	3780.96	3.622	1146.42	4152.87
A_68_P22611613	chr3:145587280-145587324	NM_009740:-39	Bcl10	PROMOTER	1.342	1.846	1465.19	2704.33	2.476	1240.37	3071.52
A_68_P28149797	chr11:114653726-114653770	NM_028055:3458	Btbd17	INSIDE	1.342	1.735	878.36	1524.07	2.329	704.61	1641.20
A_68_P22151285	chr3:54859248-54859292	NM_007628:-293	Ccna1	PROMOTER	1.342	2.456	1542.30	3787.73	3.297	1328.02	4378.25
A_68_P24157327	chr5:144383303-144383347	NM_011182:9	Cyth3	INSIDE	1.342	2.206	732.54	1615.92	2.961	752.32	2227.69
A_68_P32140229	chr19:45817346-45817390	NM_001166361:6	Fgf8	INSIDE	1.342	2.813	896.25	2521.01	3.775	850.84	3212.33
A_68_P28431895	chr12:52929741-52929785	NM_144788:761	Hectd1	INSIDE	1.342	2.458	362.51	891.20	3.299	334.68	1104.11
A_68_P25528897	chr7:138685710-138685754	NM_008257:-744	Hmx3	PROMOTER	1.342	4.723	1970.61	9306.45	6.340	1736.99	11012.01
A_68_P25954891	chr8:73437387-73437431	NM_173013:7536	Mtap1s	INSIDE	1.342	4.074	1656.66	6750.02	5.469	1363.98	7459.09
A_68_P22165653	chr3:57651276-57651320	NM_019410:381	Pfn2	INSIDE	1.342	2.233	966.34	2157.50	2.996	881.45	2640.61
A_68_P32700062	chrX:137133645-137133689	NM_001077364:1395	Tsc22d3	INSIDE	1.342	3.679	648.42	2385.47	4.936	495.78	2447.01
A_68_P25957039	chr8:74005499-74005543	NM_001164679:4446	Ano8	INSIDE	1.341	4.935	612.86	3024.27	6.617	520.56	3444.58
A_68_P32130260	chr19:44144019-44144063	NM_145502:136	Erlin1	INSIDE	1.341	1.536	3085.79	4740.97	2.060	2339.82	4819.63
A_68_P21052788	chr2:20890736-20890780	NR_033225:258	Gm13375	INSIDE	1.341	1.874	3948.02	7398.32	2.513	3064.35	7701.04
A_68_P23344527	chr4:137772352-137772396	NM_001122896:-167	Hp1bp3	PROMOTER	1.341	2.571	1612.56	4146.00	3.449	1364.94	4707.40
A_68_P23333958	chr4:135999081-135999125	NM_008309:19664	Htr1d	INSIDE	1.341	3.546	2662.08	9439.13	4.754	2030.57	9653.41
A_68_P28041933	chr11:95868905-95868949	NM_009951:-1668	Igf2bp1	PROMOTER	1.341	2.490	2490.68	6202.21	3.338	1816.66	6064.22
A_68_P28748394	chr12:113413797-113413841	NM_001097621:29400	Kif26a	INSIDE	1.341	2.524	1151.21	2906.20	3.385	992.17	3358.66
A_68_P25308743	chr7:96781285-96781329	NM_181407:-21	Me3	PROMOTER	1.341	4.545	937.57	4261.60	6.093	730.00	4448.16
A_68_P32778405	chrX:156575888-156575932	NM_008810:358	Pdha1	INSIDE	1.341	1.893	1655.40	3133.51	2.538	761.33	1932.45
A_68_P20335741	chr1:72301294-72301338	NM_023523:29572	Pecr	DOWNSTREAM	1.341	2.547	2164.50	5512.47	3.416	1799.10	6145.68
A_68_P29194041	chr13:85429220-85429264	NM_145452:-151	Rasa1	PROMOTER	1.341	1.531	2338.75	3581.60	2.054	2082.23	4276.98
A_68_P28145843	chr11:113928475-113928519	NM_172800:-1231	Sdk2	PROMOTER	1.341	1.523	863.20	1314.51	2.042	722.08	1474.48
A_68_P31019379	chr17:5841808-5841852	NM_025664:451	Snx9	INSIDE	1.341	2.188	1208.94	2645.75	2.935	1063.24	3120.64
A_68_P28307257	chr12:28026632-28026676	NM_009234:929	Sox11	INSIDE	1.341	2.549	1939.58	4944.88	3.420	1530.73	5234.53

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P21303500	chr2:68309909-68309953	NM_016866:108	Stk39	INSIDE	1.341	0.485	1005.88	488.07	0.651	982.39	639.18
A_68_P24838523	chr6:128305849-128305893	NM_011657:-1	Tulp3	PROMOTER	1.341	1.922	8087.35	15543.80	2.577	5603.71	14438.80
A_68_P30133054	chr15:35301504-35301548	NM_177151:226	Vps13b	INSIDE	1.341	1.790	494.98	886.08	2.400	409.02	981.74
A_68_P31836390	chr18:75503087-75503131			Unknown	1.341	2.940	1694.58	4981.64	3.941	1214.78	4787.82
A_68_P30591270	chr16:21248808-21248852	ENSMUST00000152179:48115		INSIDE	1.341	1.983	537.39	1065.58	2.659	443.74	1179.77
A_68_P33012182	chr9_random:57481-57526	NR_027950:2811	4930526I15Rik	DOWNSTREAM	1.340	1.803	1443.26	2602.19	2.417	1106.91	2675.29
A_68_P25352111	chr7:104886841-104886885	NM_175105:-105	Aqp11	PROMOTER	1.340	1.566	2330.02	3648.13	2.098	1761.88	3695.74
A_68_P20645417	chr1:138242409-138242453	NM_001081360:251	Camsap1l1	INSIDE	1.340	1.793	488.83	876.41	2.402	429.57	1031.69
A_68_P20794602	chr1:167390651-167390695	NM_028759:-78	Dcaf6	DIVERGENT_PROMOTER	1.340	1.682	1369.42	2303.47	2.253	1193.27	2688.65
A_68_P24218728	chr6:6813006-6813052	NM_010057:-305	Dlx6	PROMOTER	1.340	3.124	463.90	1449.06	4.184	343.38	1436.81
A_68_P23590785	chr5:34065022-34065066	NM_001163216:90	Fgfr3	INSIDE	1.340	1.500	1441.38	2161.81	2.010	1196.27	2404.98
A_68_P29257132	chr13:99125852-99125896	NM_008242:1675	Foxd1	INSIDE	1.340	3.574	465.45	1663.66	4.791	406.12	1945.74
A_68_P26803574	chr9:106367984-106368028	NM_001159652:265	Gpr62	INSIDE	1.340	1.427	3088.38	4408.24	1.912	2350.54	4494.43
A_68_P20453280	chr1:94998488-94998532	NM_001110315:-68	Kif1a	PROMOTER	1.340	4.133	1535.83	6347.31	5.537	1108.13	6136.10
A_68_P31442546	chr17:91487752-91487796	NM_020252:4368	Nrxn1	INSIDE	1.340	4.217	690.47	2911.36	5.651	647.49	3658.63
A_68_P26824202	chr9:110434375-110434420	NM_001081340:-703	Setd2	PROMOTER	1.340	1.892	467.14	883.91	2.536	352.86	894.77
A_68_P27176492	chr10:60215582-60215626	NM_023596:-74	Slc29a3	PROMOTER	1.340	2.681	5444.55	14594.76	3.592	3669.82	13180.77
A_68_P27682717	chr11:31269557-31269601	NM_011491:483	Stc2	INSIDE	1.340	1.669	1237.89	2066.49	2.237	1094.87	2449.72
A_68_P32136800	chr19:45228638-45228682	NM_021901:3456	Tlx1	INSIDE	1.340	3.369	748.09	2520.00	4.512	686.92	3099.60
A_68_P32554230	chrX:96412300-96412344			Unknown	1.340	1.351	1922.99	2598.74	1.811	994.30	1800.28
A_68_P30959225	chr16:90831355-90831399	NM_001199210:273	4931408A02Rik	INSIDE	1.339	2.098	570.28	1196.22	2.809	771.21	2166.00
A_68_P23882644	chr5:90795790-90795834	NM_030886:-601	Ankrd17	PROMOTER	1.339	1.716	3282.73	5632.05	2.297	2759.58	6339.29
A_68_P26323900	chr9:15432364-15432408	NM_181816:-9	Ccdc67	PROMOTER	1.339	1.842	1156.73	2130.38	2.466	973.67	2401.32
A_68_P26475231	chr9:45480834-45480878	NM_001081270:242481	Dscaml1	INSIDE	1.339	1.652	1172.34	1936.21	2.211	914.02	2021.00
A_68_P31740998	chr18:58369127-58369171	NM_010181:432	Fbn2	INSIDE	1.339	1.482	3111.41	4611.22	1.985	2320.40	4605.24
A_68_P28082092	chr11:102754466-102754510	NM_010277:4026	Gfap	INSIDE	1.339	1.665	1707.38	2842.56	2.228	1362.45	3036.12
A_68_P24226577	chr6:8460033-8460077	NM_133236:459	Glcci1	INSIDE	1.339	2.909	1410.44	4102.79	3.895	1231.12	4795.38
A_68_P29330809	chr13:112599173-112599217	NM_011945:-3	Map3k1	PROMOTER	1.339	0.427	1060.33	452.65	0.571	1039.45	593.98
A_68_P21839352	chr2:167906373-167906417	NM_021409:-109	Pard6b	PROMOTER	1.339	4.844	374.56	1814.38	6.487	288.36	1870.76
A_68_P23398661	chr4:148473893-148473937	NM_019781:7	Pex14	INSIDE	1.339	1.577	2035.14	3209.18	2.112	1587.54	3353.13
A_68_P32464005	chrX:70905148-70905192	NM_001199351:23	Pnck	INSIDE	1.339	2.115	1153.88	2440.12	2.832	575.03	1628.51
A_68_P28736915	chr12:111426863-111426907	AK044800:1099		INSIDE	1.339	2.545	872.42	2220.13	3.408	737.57	2513.97
A_68_P27281467	chr10:79634488-79634532	NM_027207:-1178	1600002K03Rik	PROMOTER	1.338	3.721	3827.22	14240.89	4.977	3317.73	16513.05
A_68_P30350790	chr15:76648746-76648790	NM_001168288:-168	Arhgap39	PROMOTER	1.338	1.790	1276.86	2286.01	2.395	1173.22	2809.87
A_68_P20331600	chr1:71603721-71603765	NM_026195:13	Atic	INSIDE	1.338	2.362	3141.08	7419.09	3.160	2564.54	8104.76
A_68_P22551964	chr3:135086455-135086499	NM_025902:-79	Cisd2	PROMOTER	1.338	2.027	266.75	540.60	2.711	283.56	768.81
A_68_P28923671	chr13:31650063-31650107	NM_008239:46	Foxq1	INSIDE	1.338	1.997	1114.18	2225.43	2.673	983.38	2628.11
A_68_P24449299	chr6:52184163-52184207	NM_008263:754	Hoxa10	INSIDE	1.338	2.076	455.15	945.07	2.779	425.78	1183.31
A_68_P25092917	chr7:52661860-52661904	NM_010596:553	Kcna7	INSIDE	1.338	2.607	531.73	1386.00	3.487	497.20	1733.82
A_68_P24992159	chr7:19813899-19813943	NM_207525:183	Opa3	INSIDE	1.338	1.911	2633.79	5033.31	2.558	2126.72	5439.79
A_68_P30346607	chr15:76010905-76010949	NM_201394:15214	Plec	INSIDE	1.338	8.869	2737.52	24278.32	11.865	2149.78	25506.15
A_68_P28160474	chr11:116485631-116485675	NM_001167680:-86	Rhbdf2	PROMOTER	1.338	3.174	5177.67	16434.58	4.248	3799.05	16139.05
A_68_P30368252	chr15:79573047-79573091	NM_001205345:-102	Sun2	PROMOTER	1.338	2.064	1709.94	3529.13	2.762	1574.09	4347.12
A_68_P32672209	chrX:131010003-131010047	NM_028958:1005	Taf7l	INSIDE	1.338	1.414	2478.92	3505.23	1.892	1251.69	2368.81
A_68_P31335267	chr17:71948102-71948146	NR_015549:-23	Trmt61b	PROMOTER	1.338	2.084	1345.43	2803.78	2.789	1114.42	3107.82
A_68_P30125733	chr15:33617621-33617665	NM_001085421:-4	Tspyl5	PROMOTER	1.338	2.298	2155.98	4954.41	3.075	1620.37	4982.26
A_68_P28736904	chr12:111425727-111425771	AK044800:-37		DIVERGENT_PROMOTER	1.338	3.048	1148.32	3500.06	4.077	1097.52	4474.22
A_68_P31458282	chr18:3383392-3383436	NM_029402:192	Cul2	INSIDE	1.337	3.211	2117.97	6800.27	4.292	1751.61	7517.97
A_68_P22520451	chr3:129236724-129236768	NM_130450:1443	Elovl6	INSIDE	1.337	4.256	616.20	2622.36	5.692	541.72	3083.33
A_68_P21834174	chr2:167014089-167014133	NM_008420:189	Kcnb1	INSIDE	1.337	1.753	524.44	919.24	2.344	527.04	1235.51
A_68_P27453319	chr10:111708984-111709028	NM_001025581:828	Kcnc2	INSIDE	1.337	2.028	1498.18	3038.83	2.713	1243.51	3373.36

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P20127130	chr1:32229462-32229506	NM_133235:-166	Khdrbs2	PROMOTER	1.337	2.312	2254.58	5212.73	3.091	1987.15	6141.96
A_68_P26133049	chr8:107850154-107850198	NM_177449:0	Lrrc29	INSIDE	1.337	3.266	1227.99	4010.66	4.365	1021.93	4461.19
A_68_P30777937	chr16:55822273-55822317	NM_001159394:-43	Nfkbiz	PROMOTER	1.337	2.175	2129.70	4632.62	2.908	1709.94	4972.36
A_68_P25779457	chr8:36439788-36439832	NM_177741:1016	Ppp1r3b	INSIDE	1.337	2.316	504.42	1168.21	3.097	408.12	1264.11
A_68_P29267242	chr13:100878272-100878316	NM_011353:321	Serf1	INSIDE	1.337	1.446	1531.30	2214.12	1.934	1407.30	2721.17
A_68_P28875421	chr13:22037070-22037115	NM_183014:130	Zfp184	INSIDE	1.337	1.661	896.06	1488.71	2.221	746.96	1658.69
A_68_P21851419	chr2:169956951-169956995	NM_001033299:-252	Zfp217	PROMOTER	1.337	1.763	975.08	1719.13	2.357	860.78	2028.53
A_68_P23296944	chr4:129178242-129178286	NM_001085491:9831	1700125D06Rik	DOWNSTREAM	1.336	3.582	2075.79	7434.50	4.785	1806.94	8646.07
A_68_P28574822	chr12:81361237-81361281	NM_134156:100	Actn1	INSIDE	1.336	3.621	938.72	3399.35	4.840	864.72	4185.02
A_68_P25024597	chr7:29747515-29747559	NM_021895:-237	Actn4	PROMOTER	1.336	1.478	852.53	1259.82	1.975	795.54	1571.06
A_68_P20872222	chr1:181733328-181733372	NM_026375:796	Ahctf1	INSIDE	1.336	2.979	486.39	1448.99	3.980	359.47	1430.54
A_68_P30379106	chr15:81525333-81525377	NM_001164320:2363	Chadl	INSIDE	1.336	4.624	1302.11	6020.74	6.176	1129.61	6976.41
A_68_P31227865	chr17:50432360-50432404	NM_010021:542	Dazl	INSIDE	1.336	2.581	370.51	956.21	3.449	302.26	1042.39
A_68_P31161462	chr17:36016904-36016948	NM_026987:204	Dhx16	INSIDE	1.336	4.865	710.65	3457.34	6.500	533.57	3468.25
A_68_P27937920	chr11:77307416-77307460	NM_001004144:525	Git1	INSIDE	1.336	1.872	3343.68	6260.74	2.501	2574.44	6438.23
A_68_P29141936	chr13:73901069-73901113	NM_011390:-54	Slc12a7	PROMOTER	1.336	5.352	1349.31	7222.09	7.153	1152.16	8241.44
A_68_P27325554	chr10:87922543-87922587	NM_011517:233	Sycp3	INSIDE	1.336	3.252	1820.93	5920.98	4.345	1391.20	6045.37
A_68_P20680088	chr1:145624700-145624744	NM_001159866:315	Uchl5	INSIDE	1.336	1.508	818.20	1233.96	2.016	654.47	1319.14
A_68_P30356301	chr15:77688150-77688194			Unknown	1.336	1.916	1408.52	2698.29	2.560	1253.57	3209.38
A_68_P22747701	chr4:14858053-14858097	ENSMUST00000152024:252		INSIDE	1.336	1.862	1307.55	2434.08	2.487	1130.94	2812.33
A_68_P21092002	chr2:28438501-28438545	NM_148928:277	Gtf3c5	INSIDE	1.335	3.024	1189.90	3598.21	4.036	961.92	3882.22
A_68_P21338754	chr2:74520144-74520188	NM_008273:-283	Hoxd11	PROMOTER	1.335	4.895	964.44	4721.07	6.534	934.03	6103.35
A_68_P21666845	chr2:136941868-136941912	NM_013822:366	Jag1	INSIDE	1.335	1.437	1804.87	2592.90	1.918	1445.41	2772.97
A_68_P23120719	chr4:94719459-94719503	NM_010591:-567	Jun	PROMOTER	1.335	2.009	7357.97	14785.66	2.682	5167.60	13857.99
A_68_P24862701	chr6:134591261-134591305	NM_026371:325	Loh12cr1	INSIDE	1.335	2.315	1231.51	2851.23	3.091	1058.55	3271.87
A_68_P31100078	chr17:25023059-25023105	NM_011956:213	Nubp2	INSIDE	1.335	2.560	1166.37	2985.90	3.419	923.21	3156.12
A_68_P27808204	chr11:53914341-53914385	NM_001136076:-63	P4ha2	PROMOTER	1.335	2.153	739.34	1592.04	2.874	676.91	1945.71
A_68_P22309854	chr3:87572957-87573001	NM_001032413:-103	Pear1	PROMOTER	1.335	2.770	1235.72	3422.55	3.697	1098.60	4061.88
A_68_P25169315	chr7:69608941-69608985	NM_013788:434	Peg12	INSIDE	1.335	2.966	433.72	1286.34	3.961	376.26	1490.24
A_68_P25024908	chr7:29804801-29804845	NM_009109:105348	Ryr1	INSIDE	1.335	1.502	652.69	980.15	2.004	893.28	1790.28
A_68_P25735809	chr8:28089115-28089159	NM_001101502:1329	Zfp703	INSIDE	1.335	2.225	15940.06	35462.73	2.970	13259.88	39380.86
A_68_P20293905	chr1:64737459-64737503	NR_038009:-247	2810408I11Rik	DIVERGENT_PROMOTER	1.334	4.130	700.14	2891.44	5.509	590.88	3254.91
A_68_P21768923	chr2:155833524-155833568	NM_001145351:-3383	6430550D23Rik	PROMOTER	1.334	1.486	1918.07	2850.26	1.982	1568.36	3108.55
A_68_P23352771	chr4:139130470-139130514	NM_001205173:-142	Iffo2	PROMOTER	1.334	1.834	5321.49	9762.17	2.446	3868.28	9463.00
A_68_P25503042	chr7:134072295-134072339	NM_172747:-76	Kctd13	PROMOTER	1.334	2.072	2909.54	6027.35	2.763	2401.59	6636.46
A_68_P28052177	chr11:97560932-97560976	NM_001163307:-256	Pcgf2	PROMOTER	1.334	3.014	323.96	976.35	4.021	264.30	1062.62
A_68_P31257082	chr17:56724139-56724183	NM_001029979:-154	Safb2	DIVERGENT_PROMOTER	1.334	2.397	1326.14	3178.53	3.197	1326.10	4239.77
A_68_P26885415	chr9:121672022-121672066	NM_001166644:2894	Zfp651	INSIDE	1.334	3.001	367.72	1103.34	4.002	323.52	1294.84
A_68_P25264340	chr7:87172009-87172053	NM_175433:917	Zfp710	INSIDE	1.334	2.542	1323.19	3363.81	3.391	1157.96	3926.24
A_68_P32257885	chrX:11241764-11241808			Unknown	1.334	1.843	2993.62	5515.87	2.458	2032.34	4995.40
A_68_P28731504	chr12:110272212-110272256	NM_001163175:34193	Begain	INSIDE	1.333	2.767	351.11	971.62	3.690	331.43	1222.84
A_68_P26880510	chr9:120843613-120843657	NM_001165902:939	Ctnnb1	INSIDE	1.333	2.029	1273.94	2584.83	2.705	1019.34	2757.35
A_68_P26512426	chr9:51771455-51771499	NM_007996:162	Fdx1	INSIDE	1.333	2.638	1623.96	4284.49	3.517	1384.14	4868.40
A_68_P28923686	chr13:31651815-31651859	NM_008239:1798	Foxq1	INSIDE	1.333	2.485	1040.59	2586.20	3.312	840.99	2785.69
A_68_P26035037	chr8:89997425-89997469	NR_033430:736	Gm2694	INSIDE	1.333	3.330	422.27	1406.31	4.441	364.08	1616.82
A_68_P21902331	chr2:179960697-179960741	NM_001081171:-154	Lama5	PROMOTER	1.333	1.805	1144.46	2065.74	2.406	1145.28	2755.15
A_68_P25010203	chr7:26181112-26181156	NM_010719:-128	Lipe	PROMOTER	1.333	2.248	2863.62	6436.32	2.997	2214.24	6635.82
A_68_P20241002	chr1:55294197-55294241	NM_175439:198	Mars2	INSIDE	1.333	2.175	1906.21	4145.37	2.898	1719.83	4984.92
A_68_P31553001	chr18:23198592-23198636	NM_001161483:-1450	Nol4	PROMOTER	1.333	1.905	955.04	1819.39	2.539	751.14	1907.10
A_68_P21114136	chr2:32092306-32092350	NM_145145:126	Pomt1	INSIDE	1.333	1.860	1785.50	3321.77	2.480	1471.03	3648.84
A_68_P24117360	chr5:136164660-136164704	NM_008898:-401	Por	PROMOTER	1.333	1.400	2742.36	3840.04	1.867	2286.08	4267.59

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P30380957	chr15:81846273-81846317	NM_134095:276	Pppde2	INSIDE	1.333	2.057	2296.06	4724.11	2.743	1977.13	5423.42
A_68_P25228919	chr7:80554204-80554248	NM_177740:33821	Rgma	INSIDE	1.333	3.125	1593.04	4978.61	4.164	1257.76	5237.77
A_68_P30575781	chr16:17803149-17803193	NM_153790:5796	Scarf2	INSIDE	1.333	2.172	1337.19	2904.51	2.895	1270.17	3677.27
A_68_P29507582	chr14:31529438-31529482	NM_001166532:660	Sfmbt1	INSIDE	1.333	2.054	2040.89	4192.46	2.737	1920.06	5255.83
A_68_P24120070	chr5:136708234-136708278	NM_018825:12517	Sh2b2	INSIDE	1.333	2.738	276.24	756.47	3.650	197.08	719.35
A_68_P30425529	chr15:89329556-89329600	NM_021423:-709	Shank3	PROMOTER	1.333	3.568	1757.17	6269.47	4.757	1409.19	6703.29
A_68_P23187164	chr4:106585031-106585075	NM_023672:978	Ssbp3	INSIDE	1.333	2.840	979.04	2780.22	3.785	811.06	3069.92
A_68_P30385309	chr15:82729893-82729937	NR_027799:-1023	Tbrg3	PROMOTER	1.333	2.843	332.55	945.29	3.790	351.26	1331.45
A_68_P30572943	chr16:17277156-17277200	NM_177473:786	Tmem191c	INSIDE	1.333	1.574	2471.21	3889.63	2.098	2174.32	4562.63
A_68_P28696867	chr12:104563817-104563863	NM_023049:30371	Asb2	INSIDE	1.332	6.609	655.44	4332.12	8.807	474.02	4174.57
A_68_P26470343	chr9:44728440-44728484	NM_013795:363	Atp5l	INSIDE	1.332	0.502	1215.35	610.51	0.669	1031.13	690.09
A_68_P22523145	chr3:129672979-129673023	NM_025779:124	Ccdc109b	INSIDE	1.332	1.964	752.91	1479.05	2.616	688.48	1801.39
A_68_P31607790	chr18:33623473-33623517	NM_001109989:-93	D0H4S114	PROMOTER	1.332	1.825	540.07	985.73	2.430	490.14	1191.28
A_68_P20422165	chr1:90102210-90102254	NM_008299:91	Dnajb3	INSIDE	1.332	2.473	690.38	1707.28	3.295	585.58	1929.29
A_68_P26658159	chr9:77956440-77956484	NM_023605:1	Fbxo9	INSIDE	1.332	3.803	1019.33	3876.55	5.066	912.99	4625.60
A_68_P20264189	chr1:59539520-59539564	NM_008057:552	Fzd7	INSIDE	1.332	1.795	1363.25	2446.54	2.390	1114.11	2663.22
A_68_P27500269	chr10:120335461-120335505	NM_177092:545	Msrb3	INSIDE	1.332	1.914	1787.68	3421.72	2.550	1542.80	3934.06
A_68_P21722728	chr2:147009701-147009745	NR_030769:-96	Nkx2-2as	PROMOTER	1.332	1.500	810.16	1214.93	1.997	767.80	1533.39
A_68_P31682250	chr18:47528856-47528900	NM_018744:-356	Sema6a	PROMOTER	1.332	1.808	935.61	1691.99	2.409	814.14	1961.36
A_68_P24046794	chr5:122286634-122286678	NM_008507:154	Sh2b3	INSIDE	1.332	2.434	950.55	2313.86	3.242	834.37	2704.65
A_68_P23238480	chr4:117807649-117807693	NM_001161774:-151	St3gal3	PROMOTER	1.332	2.806	2923.17	8200.99	3.736	2211.63	8261.91
A_68_P25576308	chr7:146374357-146374401	NM_021302:15	Stk32c	INSIDE	1.332	2.699	993.13	2680.68	3.596	915.61	3292.55
A_68_P31098879	chr17:24806802-24806846	NM_183149:128	Zfp598	INSIDE	1.332	0.419	1813.18	759.99	0.558	1540.66	860.45
A_68_P26160580	chr8:112603835-112603879	NM_175480:223	Zfp612	INSIDE	1.332	1.437	2261.02	3248.90	1.914	1850.82	3542.32
A_68_P30821643	chr16:64770368-64770412	NM_026273:375	4930453N24Rik	INSIDE	1.331	1.725	1018.18	1756.51	2.296	832.14	1910.38
A_68_P23602808	chr5:36100579-36100623	NM_001177696:72	Ablim2	INSIDE	1.331	1.664	718.64	1195.51	2.214	653.94	1447.58
A_68_P31939551	chr19:7456653-7456699	NM_001033139:840	AI846148	INSIDE	1.331	2.226	646.62	1439.53	2.964	578.22	1713.62
A_68_P24593643	chr6:83406064-83406108	NR_028382:14338	B230319C09Rik	DOWNSTREAM	1.331	1.961	1529.67	2999.72	2.611	1309.39	3418.30
A_68_P32464345	chrX:70961700-70961744	NM_012060:-208	Bcap31	DIVERGENT_PROMOTER	1.331	1.867	2442.66	4561.11	2.485	1185.74	2946.87
A_68_P27360779	chr10:94151657-94151701	NM_029852:144	Ccdc41	INSIDE	1.331	1.374	1423.70	1955.77	1.828	1289.37	2357.44
A_68_P32096195	chr19:37625247-37625291	NM_175353:361	Exoc6	INSIDE	1.331	2.964	518.11	1535.82	3.946	585.86	2311.77
A_68_P26228654	chr8:124277231-124277275	NM_020605:22794	Jph3	INSIDE	1.331	2.378	754.46	1794.34	3.166	785.56	2486.72
A_68_P31515588	chr18:15222716-15222760	NM_001142731:-647	Kctd1	PROMOTER	1.331	3.505	1556.81	5457.17	4.667	1481.41	6913.96
A_68_P28457453	chr12:57636766-57636810	NM_001146198:-695	Nkx2-1	PROMOTER	1.331	2.333	6807.31	15879.70	3.105	5163.41	16032.11
A_68_P20870654	chr1:181447812-181447856	NM_027188:300	Smyd3	INSIDE	1.331	1.548	4397.46	6807.52	2.060	3135.10	6459.42
A_68_P21823565	chr2:165213622-165213666	NM_178411:115	Zfp334	INSIDE	1.331	1.801	1360.15	2449.20	2.397	1128.76	2705.35
A_68_P25504795	chr7:134398033-134398077	NM_177362:10015	Zfp771	INSIDE	1.331	2.801	722.05	2022.40	3.729	710.19	2648.52
A_68_P24183980	chr5:150040675-150040719	AK155259:18562		DOWNSTREAM	1.331	2.303	304.15	700.36	3.066	269.40	825.98
A_68_P27111542	chr10:45205927-45205971	ENSMUST00000099847:-365		PROMOTER	1.331	1.624	2466.59	4006.89	2.162	2163.36	4678.11
A_68_P25027733	chr7:30304368-30304412	ENSMUST00000141713:167		INSIDE	1.331	2.366	489.83	1159.16	3.149	411.67	1296.37
A_68_P21110673	chr2:31544152-31544196	NM_001112703:99	Abl1	INSIDE	1.330	2.593	1393.98	3614.26	3.447	1188.79	4097.93
A_68_P23541452	chr5:23893732-23893776	NM_001002897:4207	Atg9b	INSIDE	1.330	1.663	494.34	822.07	2.212	416.14	920.65
A_68_P27828609	chr11:57822259-57822303	NM_028451:-285	Larp1	PROMOTER	1.330	2.175	1919.17	4173.64	2.893	1632.70	4723.18
A_68_P31938322	chr19:7240010-7240054	NM_134147:108775	Macrod1	INSIDE	1.330	3.244	197.20	639.76	4.316	156.80	676.76
A_68_P29224476	chr13:93300612-93300656	NM_173392:131	Zfyve16	INSIDE	1.330	1.564	1215.33	1900.52	2.079	1033.25	2148.53
A_68_P27921684	chr11:74463331-74463375	NM_001081158:356	1300001I01Rik	INSIDE	1.329	2.131	649.07	1383.17	2.833	529.41	1499.69
A_68_P20861822	chr1:179726539-179726583	NM_007422:80	Adss	INSIDE	1.329	1.576	1110.22	1749.31	2.094	852.39	1785.30
A_68_P26236514	chr8:125394402-125394446	NM_007662:22151	Cdh15	DOWNSTREAM	1.329	2.720	1831.61	4982.14	3.614	1550.16	5602.88
A_68_P26695698	chr9:85642712-85642756	NM_001081282:207	Ibtk	INSIDE	1.329	4.457	487.82	2174.07	5.924	537.96	3186.74
A_68_P28290824	chr12:25336101-25336145	NM_178357:-113	Klf11	PROMOTER	1.329	2.060	906.85	1867.82	2.737	773.95	2118.22
A_68_P24591361	chr6:83037609-83037653	NM_010692:1272	Lbx2	INSIDE	1.329	2.250	737.02	1658.65	2.991	627.50	1877.06

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31784509	chr18:66162457-66162501	NM_027400:-189	Lman1	PROMOTER	1.329	1.864	2581.80	4812.40	2.477	1946.21	4820.43
A_68_P21747603	chr2:151918965-151919009	NM_001160410:11722	Scrt2	INSIDE	1.329	1.802	874.71	1576.53	2.394	735.01	1759.97
A_68_P26365997	chr9:25060616-25060660	NM_001205367:599	Septin7	INSIDE	1.329	2.708	1613.18	4368.05	3.598	1635.78	5885.79
A_68_P23991345	chr5:112736931-112736975	NM_009419:31226	Tpst2	INSIDE	1.329	2.709	958.79	2597.34	3.600	790.67	2846.33
A_68_P27889184	chr11:68213153-68213197	ENSMUST00000108674:1151		INSIDE	1.329	2.210	6659.31	14716.33	2.936	5271.16	15476.48
A_68_P30425032	chr15:89240650-89240694	NM_001162882:22	1700007E06Rik	INSIDE	1.328	3.837	641.17	2459.90	5.097	593.91	3026.98
A_68_P31304171	chr17:66426811-66426855	NM_001025572:-446	Ankrd12	PROMOTER	1.328	1.740	1184.72	2060.95	2.311	1028.02	2375.55
A_68_P32111327	chr19:40905758-40905802	NM_172839:12	Ccnj	INSIDE	1.328	1.806	337.55	609.64	2.399	338.98	813.34
A_68_P32054108	chr19:29722693-29722737	NM_001081213:196	Ermp1	INSIDE	1.328	1.378	2497.19	3442.12	1.830	2094.02	3833.04
A_68_P24518615	chr6:66846390-66846434	NM_001177558:-472	Gng12	PROMOTER	1.328	3.354	1881.29	6309.00	4.454	1803.62	8032.63
A_68_P20939666	chr1:193542578-193542622	NM_001134829:327	Lpgat1	INSIDE	1.328	2.532	1456.79	3689.26	3.363	1359.30	4571.15
A_68_P26017625	chr8:86535356-86535400	NR_035431:154	Mir1199	DOWNSTREAM	1.328	2.383	289.76	690.47	3.164	247.17	782.08
A_68_P27708863	chr11:35648179-35648223	NM_025936:-170	Rars	PROMOTER	1.328	2.661	1297.55	3453.16	3.534	1109.70	3922.11
A_68_P27277984	chr10:79100620-79100664	NM_001024539:21	Shc2	INSIDE	1.328	2.265	1849.31	4188.43	3.008	1539.84	4632.16
A_68_P27985585	chr11:85651342-85651386	NM_009324:5248	Tbx2	INSIDE	1.328	2.422	537.79	1302.68	3.218	535.62	1723.58
A_68_P23317102	chr4:132894698-132894742	NM_199306:510	Wdtc1	INSIDE	1.328	2.257	1980.31	4469.28	2.997	1700.34	5095.96
A_68_P31054979	chr17:13184902-13184946	NM_001113533:201	Wtap	INSIDE	1.328	1.592	480.14	764.31	2.113	490.52	1036.67
A_68_P31839436	chr18:75979559-75979603	NM_145356:-251	Zbtb7c	PROMOTER	1.328	3.054	1281.61	3913.84	4.056	1122.07	4551.36
A_68_P21863764	chr2:172171330-172171374	NM_025912:276	2010011I20Rik	INSIDE	1.327	2.582	980.11	2530.58	3.425	836.76	2866.20
A_68_P30478152	chr15:98918819-98918863	NM_001024702:-681	C1ql4	PROMOTER	1.327	1.812	1095.73	1985.63	2.406	926.74	2229.38
A_68_P21761656	chr2:154482914-154482958	NM_029362:175	Chmp4b	INSIDE	1.327	2.086	1477.06	3080.69	2.767	1247.02	3450.68
A_68_P21772343	chr2:156439879-156439923	NM_146128:460	Dlgap4	INSIDE	1.327	4.427	527.59	2335.58	5.875	478.94	2813.59
A_68_P23203768	chr4:109654665-109654709	NM_172296:4057	Dmrta2	INSIDE	1.327	2.445	731.29	1788.17	3.245	722.67	2345.00
A_68_P27561405	chr11:4998913-4998957	NM_007968:146	Ewsr1	INSIDE	1.327	1.582	3416.84	5404.07	2.099	2668.71	5601.04
A_68_P21826982	chr2:165818442-165818486	NM_008679:328	Ncoa3	INSIDE	1.327	2.219	749.00	1661.83	2.943	601.78	1771.19
A_68_P29509959	chr14:31952078-31952122	NM_027289:4062	Nt5dc2	INSIDE	1.327	6.149	5256.00	32320.87	8.159	3483.05	28419.71
A_68_P27994102	chr11:87218064-87218108	NM_053269:-89	Rad51c	DIVERGENT_PROMOTER	1.327	2.099	2291.40	4810.14	2.786	1906.29	5310.77
A_68_P28690583	chr12:103521466-103521510	NM_001161365:-362	Rin3	PROMOTER	1.327	3.033	1823.63	5531.38	4.025	1699.66	6841.70
A_68_P26626136	chr9:71959653-71959697	NM_011544:-48	Tcf12	PROMOTER	1.327	2.176	413.81	900.58	2.889	369.21	1066.56
A_68_P24973912	chr7:13556599-13556643	NM_178732:5408	Zfp324	INSIDE	1.327	2.365	596.32	1410.24	3.138	501.39	1573.22
A_68_P22415392	chr3:108743052-108743096	NM_001078646:-400	4921515J06Rik	PROMOTER	1.326	3.943	1193.06	4704.51	5.228	1075.53	5622.93
A_68_P23315375	chr4:132594527-132594571	NM_146155:27128	Ahdc1	INSIDE	1.326	1.780	1395.87	2485.03	2.360	1182.08	2789.86
A_68_P31992643	chr19:18787618-18787662	NM_177640:-85	D030056L22Rik	PROMOTER	1.326	1.684	745.29	1255.19	2.233	604.09	1348.65
A_68_P25371481	chr7:108257732-108257776	NM_001146010:466	Fchsd2	INSIDE	1.326	1.417	1431.97	2028.55	1.879	1190.75	2237.42
A_68_P21393860	chr2:84499188-84499232	NM_001145100:-25	Gm13718	DIVERGENT_PROMOTER	1.326	1.993	461.60	920.05	2.642	366.33	967.97
A_68_P26423570	chr9:35382219-35382263	NM_001167603:8	Gm6762	INSIDE	1.326	2.375	721.29	1713.06	3.149	599.39	1887.46
A_68_P20472800	chr1:99666322-99666367	NM_173760:325	Ppip5k2	INSIDE	1.326	1.502	1205.28	1810.01	1.991	1018.87	2028.53
A_68_P33012164	chr9_random:55526-55570	NM_011154:-516	Ppp2r3d	PROMOTER	1.326	1.883	1207.21	2273.69	2.498	1040.43	2598.63
A_68_P22383500	chr3:102739435-102739479	NM_011516:567	Sycp1	INSIDE	1.326	4.447	800.92	3561.39	5.896	729.86	4303.12
A_68_P20880198	chr1:183142413-183142457	NM_145514:-325	Wdr26	PROMOTER	1.326	3.450	811.74	2800.51	4.576	663.30	3035.36
A_68_P20734230	chr1:156646554-156646598	AK046991:-6703		PROMOTER	1.326	3.352	528.65	1771.80	4.445	611.00	2715.93
A_68_P32744435	chrX:147603926-147603970	ENSMUST00000151778:-294		PROMOTER	1.326	2.441	369.44	901.85	3.236	269.94	873.57
A_68_P26870880	chr9:119071809-119071853	NM_146230:-5619	Acaa1b	PROMOTER	1.325	2.532	209.50	530.41	3.355	199.15	668.13
A_68_P21429508	chr2:92440060-92440104	NM_023850:219	Chst1	INSIDE	1.325	3.221	1274.45	4104.95	4.267	1061.68	4530.38
A_68_P27596686	chr11:12364779-12364823	NM_172496:163	Cobl	INSIDE	1.325	1.630	1174.88	1914.68	2.160	879.30	1899.17
A_68_P23644441	chr5:43624695-43624739	NM_001177379:15	Cpeb2	INSIDE	1.325	1.720	758.50	1304.34	2.279	566.73	1291.42
A_68_P32467042	chrX:71491942-71491986	NM_010227:-91	Flna	DIVERGENT_PROMOTER	1.325	1.736	2304.77	4001.90	2.300	1207.98	2778.69
A_68_P26228891	chr8:124308748-124308792	NM_020605:54312	Jph3	INSIDE	1.325	2.148	1238.21	2660.24	2.846	994.77	2831.00
A_68_P27180702	chr10:60938602-60938646	NM_153542:44	Lrrc20	INSIDE	1.325	2.254	1350.93	3044.50	2.987	1157.71	3458.25
A_68_P24344494	chr6:32537701-32537745	NM_175750:470	Plxna4	INSIDE	1.325	4.779	906.23	4331.14	6.332	817.07	5173.42
A_68_P25261273	chr7:86611105-86611149	NM_017462:33	Polg	INSIDE	1.325	2.466	988.11	2437.11	3.269	783.30	2560.71

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P22373272	chr3:100914442-100914486	NM_011197:-375	Ptgfrn	PROMOTER	1.325	1.846	2116.48	3907.36	2.446	1668.49	4080.89
A_68_P31166410	chr17:37084116-37084160	NM_001099632:4143	Rnf39	INSIDE	1.325	5.307	804.66	4270.32	7.033	666.26	4685.86
A_68_P27502792	chr10:120747561-120747605	NM_029057:663	Tbc1d30	INSIDE	1.325	2.310	2694.13	6222.40	3.061	2143.82	6562.39
A_68_P27273028	chr10:77707431-77707475	NM_001081055:-65	Trappc10	PROMOTER	1.325	3.157	464.09	1465.08	4.183	452.55	1892.91
A_68_P30579667	chr16:18426465-18426509	NM_013711:-23	Txnrd2	PROMOTER	1.325	1.481	783.90	1161.05	1.963	638.69	1253.83
A_68_P20737711	chr1:157264084-157264128	NM_011273:468	Xpr1	INSIDE	1.325	2.450	1346.14	3298.40	3.246	1119.03	3632.03
A_68_P27939246	chr11:77576975-77577019	ENSMUST00000164315:-2108		PROMOTER	1.325	2.885	618.33	1783.74	3.822	584.18	2232.48
A_68_P32362521	chrX:45387855-45387899	NM_013912:153	Apln	INSIDE	1.324	2.085	784.66	1635.84	2.759	531.92	1467.67
A_68_P31013735	chr17:4994646-4994690	NM_001085355:-405	Arid1b	PROMOTER	1.324	4.513	834.47	3766.07	5.977	776.71	4642.31
A_68_P31497270	chr18:11998017-11998061	NM_001146287:256	Cables1	INSIDE	1.324	1.937	792.07	1534.37	2.566	698.72	1792.66
A_68_P31497275	chr18:11998719-11998763	NM_001146287:958	Cables1	INSIDE	1.324	3.779	866.26	3273.55	5.003	818.60	4095.46
A_68_P27856226	chr11:62693049-62693093	NM_026210:79	Fam18b	INSIDE	1.324	1.619	2108.69	3414.57	2.144	1632.20	3499.12
A_68_P28691639	chr12:103707284-103707328	NM_001199004:-37	Golga5	PROMOTER	1.324	6.824	728.83	4973.52	9.036	662.37	5985.37
A_68_P23595697	chr5:35003116-35003160	NM_001080743:111	Grk4	INSIDE	1.324	3.205	811.98	2602.50	4.245	698.69	2965.75
A_68_P26551398	chr9:58883897-58883941	NM_001042752:330	Neo1	INSIDE	1.324	2.352	598.47	1407.40	3.113	584.31	1818.90
A_68_P21099262	chr2:29602819-29602863	NM_001039086:127601	Rapgef1	DOWNSTREAM	1.324	1.773	2158.80	3827.34	2.347	1966.85	4616.65
A_68_P24061815	chr5:124991287-124991331	NM_019770:509	Tmed2	INSIDE	1.324	3.457	830.90	2872.79	4.579	726.16	3324.86
A_68_P27941693	chr11:77978890-77978934	NM_009423:140	Traf4	INSIDE	1.324	2.290	976.67	2236.09	3.031	1005.12	3046.52
A_68_P24974195	chr7:13610408-13610452	NM_011588:930	Trim28	INSIDE	1.324	1.826	4941.50	9023.02	2.417	3820.40	9233.04
A_68_P25805592	chr8:41509363-41509407	NM_178395:216	Zdhhc2	INSIDE	1.324	4.035	2183.74	8811.56	5.341	1808.12	9656.86
A_68_P27282404	chr10:79778048-79778092	NM_011789:13506	Apc2	INSIDE	1.323	2.930	1282.30	3757.48	3.878	1101.62	4272.28
A_68_P28731659	chr12:110290536-110290580	NM_001163175:15869	Begain	INSIDE	1.323	1.482	865.97	1283.25	1.960	693.49	1359.22
A_68_P24172982	chr5:148118030-148118074	NM_007673:773	Cdx2	INSIDE	1.323	1.526	745.96	1137.99	2.019	620.09	1251.70
A_68_P20884270	chr1:183853884-183853931	NM_001083120:96204	Enah	INSIDE	1.323	4.449	283.64	1261.81	5.883	245.23	1442.75
A_68_P30672048	chr16:35770485-35770529	NM_175111:35	Hspbap1	INSIDE	1.323	1.888	504.28	952.34	2.498	500.95	1251.18
A_68_P22301530	chr3:86028536-86028580	NM_001077687:-53	Lrba	PROMOTER	1.323	1.558	2396.45	3734.12	2.062	1823.34	3759.48
A_68_P30477059	chr15:98702362-98702406	NM_001033276:-770	Mll2	PROMOTER	1.323	0.489	1195.94	585.17	0.647	1062.71	687.82
A_68_P22129522	chr3:51220411-51220455	NM_053089:495	Naa15	INSIDE	1.323	3.886	2611.95	10149.18	5.142	2331.12	11986.67
A_68_P29962214	chr14:122933466-122933510	NM_144844:-61	Pcca	PROMOTER	1.323	2.679	806.16	2159.36	3.543	661.97	2345.13
A_68_P27926516	chr11:75323969-75324013	NM_001029938:395	Rilp	INSIDE	1.323	5.409	923.84	4997.02	7.158	875.77	6268.87
A_68_P20502876	chr1:107253429-107253473	NM_001160368:-163	Rnf152	PROMOTER	1.323	1.967	771.60	1518.09	2.603	700.33	1822.83
A_68_P32056100	chr19:30105268-30105312	NM_144873:288	Uhrf2	INSIDE	1.323	1.524	1487.05	2265.92	2.016	1267.08	2555.01
A_68_P27532843	chr10:126338419-126338463	NM_026858:-13	Xrcc6bp1	PROMOTER	1.323	3.405	5351.64	18221.11	4.504	3691.77	16628.77
A_68_P26744829	chr9:95855445-95855489	NM_011916:288	Xrn1	INSIDE	1.323	1.870	757.69	1417.19	2.474	690.29	1707.60
A_68_P25288546	chr7:91558357-91558401	NM_007488:91	Arnt2	INSIDE	1.322	2.099	764.77	1605.49	2.774	727.59	2018.56
A_68_P23909952	chr5:97426279-97426323	NM_080708:-407	Bmp2k	PROMOTER	1.322	2.863	2058.50	5893.04	3.785	1676.29	6345.46
A_68_P21134948	chr2:35516613-35516657	NM_001114124:39134	Dab2ip	INSIDE	1.322	2.312	2135.86	4937.48	3.057	1571.09	4802.63
A_68_P25728861	chr8:26864655-26864699	NM_028102:76	Ddhd2	INSIDE	1.322	3.597	1997.80	7186.27	4.756	1678.32	7982.86
A_68_P23981086	chr5:111082431-111082475	NM_027156:-17	Ddx51	DIVERGENT_PROMOTER	1.322	2.900	612.99	1777.46	3.835	595.78	2284.63
A_68_P23392750	chr4:147533918-147533962	NM_001161851:-236	Fbxo44	PROMOTER	1.322	2.102	1717.08	3610.11	2.779	1242.74	3453.90
A_68_P20306027	chr1:67085323-67085367	NM_001190984:64	Lancl1	INSIDE	1.322	2.292	2434.12	5579.96	3.030	2089.25	6330.04
A_68_P23188354	chr4:106739410-106739454	NM_025500:39	Mrpl37	INSIDE	1.322	2.233	1362.25	3042.43	2.952	1105.58	3263.30
A_68_P25806930	chr8:41720049-41720093	NM_001040699:76	Mtmr7	INSIDE	1.322	1.868	846.82	1581.48	2.469	711.06	1755.95
A_68_P25115908	chr7:57231147-57231191	NM_001037906:449	Nell1	INSIDE	1.322	1.503	757.62	1138.89	1.987	705.90	1402.58
A_68_P20625253	chr1:134942691-134942735	NM_001099276:124	Pik3c2b	INSIDE	1.322	1.948	999.52	1946.72	2.575	823.42	2120.49
A_68_P24774308	chr6:115944222-115944266	NM_026376:779	Plxnd1	INSIDE	1.322	1.750	1046.01	1830.01	2.313	852.82	1972.65
A_68_P23544155	chr5:24348677-24348721	NM_053075:-519	Rheb	PROMOTER	1.322	1.864	2804.58	5226.78	2.464	2232.16	5501.05
A_68_P26429692	chr9:37062811-37062855	NM_001145960:491	Slc37a2	INSIDE	1.322	1.616	5577.69	9012.00	2.136	3945.81	8426.96
A_68_P32287972	chrX:19869101-19869145	NM_177353:-232	Slc9a7	PROMOTER	1.322	2.514	1294.20	3253.30	3.324	852.12	2832.80
A_68_P22317588	chr3:88968981-88969026	NM_001163432:277	Clk2	INSIDE	1.321	1.518	1934.64	2936.72	2.005	1581.67	3170.46
A_68_P29246778	chr13:97313012-97313056	NM_001164222:345	Col4a3bp	INSIDE	1.321	1.625	1179.00	1916.11	2.148	1123.96	2413.79

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P24091776	chr5:130505164-130505208	NM_007761:11	Crcp	INSIDE	1.321	8.956	626.35	5609.50	11.831	547.25	6474.46
A_68_P24058535	chr5:124423625-124423669	NM_145070:10	Hip1r	INSIDE	1.321	2.395	2236.78	5356.70	3.163	1780.95	5632.28
A_68_P25956632	chr8:73905289-73905333	NM_010150:541	Nr2f6	INSIDE	1.321	1.811	433.75	785.73	2.393	366.94	878.09
A_68_P31709378	chr18:52927767-52927811	NM_001199154:-9	Sncaip	PROMOTER	1.321	1.496	4933.51	7378.29	1.976	3616.94	7147.28
A_68_P22363128	chr3:99057574-99057618	NM_009323:-86	Tbx15	PROMOTER	1.321	3.627	5475.86	19861.59	4.790	4531.13	21704.62
A_68_P24543633	chr6:72738096-72738140	NM_001079822:832	Tcf7l1	INSIDE	1.321	3.710	3090.85	11466.74	4.900	2656.84	13017.93
A_68_P26845370	chr9:114471876-114471920	NM_001042503:1589	Trim71	INSIDE	1.321	2.375	839.43	1993.48	3.137	804.38	2523.27
A_68_P27332826	chr10:89208214-89208258	NM_029166:501	Uhrf1bp1l	INSIDE	1.321	4.622	896.95	4146.03	6.104	667.30	4073.18
A_68_P32462207	chrX:70599165-70599209	NM_001160229:11227	Zfp275	INSIDE	1.321	2.975	477.54	1420.49	3.931	285.08	1120.50
A_68_P28011630	chr11:90279544-90279588	AK139414:-6564		PROMOTER	1.321	1.916	1131.88	2168.43	2.532	980.47	2482.21
A_68_P27330521	chr10:88807370-88807414	ENSMUST00000168681:115		INSIDE	1.321	2.051	223.51	458.37	2.710	240.47	651.64
A_68_P22726935	chr4:10801906-10801950	NM_026005:284	2610301B20Rik	INSIDE	1.320	1.516	1758.59	2666.84	2.001	1483.27	2968.67
A_68_P32202573	chr19:56796579-56796623	NM_007419:-261	Adrb1	PROMOTER	1.320	3.560	1510.97	5378.29	4.697	1303.70	6123.66
A_68_P22388171	chr3:103613470-103613514	NM_001163552:53	Ap4b1	INSIDE	1.320	2.902	670.75	1946.43	3.830	684.49	2621.58
A_68_P25657174	chr8:11728216-11728260	NM_001113517:134	Arhgef7	INSIDE	1.320	4.272	2013.22	8601.05	5.640	1690.72	9536.17
A_68_P24925489	chr6:145814071-145814115	NM_024469:-232	Bhlhe41	PROMOTER	1.320	2.428	2408.96	5849.72	3.204	1870.90	5995.06
A_68_P31746198	chr18:59334973-59335017	NM_001081328:1	Chsy3	INSIDE	1.320	0.393	1365.51	536.56	0.519	1369.65	710.52
A_68_P22318693	chr3:89141626-89141670	NM_007910:302	Efna4	INSIDE	1.320	2.758	517.65	1427.61	3.639	477.52	1737.92
A_68_P25637624	chr8:8661448-8661492	NM_010111:-697	Efnb2	PROMOTER	1.320	1.744	681.68	1188.93	2.302	668.01	1538.05
A_68_P22565464	chr3:137527246-137527290	NM_016750:-294	H2afz	PROMOTER	1.320	0.463	2174.78	1007.66	0.612	1794.34	1097.28
A_68_P21338759	chr2:74520621-74520665	NM_008273:193	Hoxd11	INSIDE	1.320	2.060	679.69	1400.29	2.719	543.50	1477.82
A_68_P30514376	chr16:5203769-5203813	NM_013796:315	Nagpa	INSIDE	1.320	2.344	1058.07	2479.86	3.094	1030.70	3189.24
A_68_P26345775	chr9:20970639-20970683	NM_183408:503	Pde4a	INSIDE	1.320	1.653	649.90	1074.00	2.181	628.84	1371.80
A_68_P26700011	chr9:86465251-86465295	NM_001163746:177	Pgm3	INSIDE	1.320	1.631	2316.46	3777.33	2.153	1896.78	4083.99
A_68_P31154947	chr17:34769261-34769305	NM_030890:2652	Prrt1	DOWNSTREAM	1.320	2.189	2412.13	5279.41	2.889	1946.67	5624.40
A_68_P28678694	chr12:101122653-101122697	NM_028354:-50	Tdp1	DIVERGENT_PROMOTER	1.320	3.553	464.84	1651.56	4.689	439.59	2061.40
A_68_P24951679	chr7:4982581-4982625	NM_001033383:10625	Zfp865	INSIDE	1.320	2.406	217.38	523.13	3.175	195.46	620.66
A_68_P20863554	chr1:180299211-180299255			Unknown	1.320	2.271	629.91	1430.31	2.996	579.01	1735.00
A_68_P31661525	chr18:43597987-43598031	ENSMUST00000121805:-68		PROMOTER	1.320	1.411	2721.78	3839.24	1.862	2099.50	3909.95
A_68_P30570068	chr16:16600185-16600230	ENSMUST00000162414:-75		PROMOTER	1.320	3.597	774.75	2786.93	4.748	678.05	3219.19
A_68_P26084574	chr8:98202070-98202114	ENSMUST00000166358:-52		PROMOTER	1.320	8.324	737.08	6135.13	10.985	646.80	7104.85
A_68_P21665423	chr2:136716895-136716939	NM_028201:-37	2210009G21Rik	PROMOTER	1.319	1.987	2290.35	4549.79	2.620	2013.89	5275.58
A_68_P24383687	chr6:39507859-39507903	NM_172477:-47	Dennd2a	PROMOTER	1.319	1.931	2240.18	4324.83	2.546	1784.98	4544.03
A_68_P25520723	chr7:137409825-137409869	NM_010207:476	Fgfr2	INSIDE	1.319	2.219	720.81	1599.73	2.926	714.70	2091.51
A_68_P31347829	chr17:74059599-74059643	NM_027864:171	Galnt14	INSIDE	1.319	5.333	1697.21	9051.21	7.032	1550.96	10906.59
A_68_P24632565	chr6:90412944-90412988	NM_023184:347	Klf15	INSIDE	1.319	2.825	1583.42	4472.47	3.724	1453.82	5414.34
A_68_P26159961	chr8:112485994-112486038	NM_212447:89	Marveld3	INSIDE	1.319	2.326	1310.01	3047.50	3.068	1049.69	3220.71
A_68_P26980661	chr10:19077130-19077174	NM_053008:808	Olig3	INSIDE	1.319	1.602	3972.90	6365.16	2.113	3129.88	6612.40
A_68_P30346610	chr15:76011282-76011326	NM_201394:14836	Plec	INSIDE	1.319	4.220	2274.76	9599.30	5.566	2082.10	11589.26
A_68_P25092682	chr7:52621989-52622033	NM_029741:379	Ppfia3	INSIDE	1.319	3.297	1302.15	4293.37	4.350	1083.03	4711.70
A_68_P20848445	chr1:177422484-177422528	NM_001199003:170	Rgs7	INSIDE	1.319	4.625	1420.26	6569.12	6.099	1880.03	11466.08
A_68_P31256956	chr17:56705945-56705989	NM_001029979:18040	Safb2	INSIDE	1.319	2.169	888.39	1926.95	2.861	748.12	2140.56
A_68_P32021818	chr19:24205720-24205764	NM_001198985:42888	Tjp2	INSIDE	1.319	3.260	1992.82	6497.09	4.300	1836.06	7895.64
A_68_P27886200	chr11:67735519-67735563	NM_173754:115	Usp43	INSIDE	1.319	2.168	1106.12	2397.93	2.859	1010.27	2887.95
A_68_P30499184	chr15:102523520-102523564			Unknown	1.319	2.082	1555.22	3237.48	2.746	1259.57	3458.69
A_68_P25782091	chr8:36889227-36889271	NM_027998:365	Cldn23	INSIDE	1.318	1.908	1666.44	3179.85	2.514	1326.53	3335.34
A_68_P22882282	chr4:45333130-45333174	NM_025513:323	Exosc3	INSIDE	1.318	1.446	2411.88	3486.72	1.906	1944.14	3705.42
A_68_P23577613	chr5:31598167-31598211	NM_022424:62	Fndc4	INSIDE	1.318	1.773	1145.28	2031.03	2.337	1017.31	2376.98
A_68_P23332312	chr4:135700753-135700797	NM_008321:1038	Id3	INSIDE	1.318	2.129	2120.22	4514.37	2.805	1786.75	5012.28
A_68_P24137557	chr5:140251443-140251487	NM_026748:168	Ints1	INSIDE	1.318	1.468	915.06	1342.90	1.934	798.05	1543.68
A_68_P24476402	chr6:56654577-56654621	NM_025520:95	Lsm5	INSIDE	1.318	2.109	1461.25	3081.26	2.780	1251.41	3478.55

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25210716	chr7:77496064-77496108	NM_009697:9393	Nr2f2	DOWNSTREAM	1.318	1.531	3364.96	5151.09	2.017	2659.38	5363.72
A_68_P24898883	chr6:141198105-141198149	NM_018779:337	Pde3a	INSIDE	1.318	1.967	1181.39	2323.47	2.593	1024.49	2656.20
A_68_P30403196	chr15:85652378-85652422	NM_011105:-237	Pkdrej	PROMOTER	1.318	2.450	1129.50	2767.12	3.228	959.14	3096.33
A_68_P21866928	chr2:172805309-172805353	NM_001083959:-12	Spo11	PROMOTER	1.318	2.220	487.00	1081.11	2.927	445.93	1305.23
A_68_P20147164	chr1:36300875-36300919	NM_198899:251	Uggt1	INSIDE	1.318	1.554	6959.13	10817.93	2.049	5371.50	11004.76
A_68_P26153110	chr8:111316387-111316431	NM_007496:77865	Zfhx3	INSIDE	1.318	1.759	1250.27	2199.65	2.319	1015.92	2356.18
A_68_P24155687	chr5:144015862-144015906	NM_017467:15817	Zfp316	INSIDE	1.318	2.428	1061.06	2576.73	3.200	953.54	3051.26
A_68_P25726105	chr8:26350956-26351000	AK190590:395		INSIDE	1.318	2.020	2706.47	5467.91	2.663	2103.71	5602.89
A_68_P26577166	chr9:63450424-63450468	NM_025857:-15	Aagab	DIVERGENT_PROMOTER	1.317	2.201	789.44	1737.57	2.898	785.77	2277.24
A_68_P32260263	chrX:11655948-11655992	NM_029510:1709	Bcor	INSIDE	1.317	1.450	1662.62	2410.33	1.910	944.99	1804.58
A_68_P26527664	chr9:54613648-54613692	NM_013496:1056	Crabp1	INSIDE	1.317	3.590	700.69	2515.53	4.726	547.75	2588.92
A_68_P26699340	chr9:86360809-86360853	NM_177208:70	Dopey1	INSIDE	1.317	3.081	452.97	1395.49	4.057	466.30	1891.79
A_68_P21517948	chr2:109757926-109757970	NM_172671:145	Lgr4	INSIDE	1.317	2.059	1364.16	2809.25	2.713	1274.38	3457.38
A_68_P32466328	chrX:71330831-71330875	NM_010788:80	Mecp2	INSIDE	1.317	1.608	3044.74	4895.49	2.117	1475.04	3123.20
A_68_P25285286	chr7:91031153-91031197	NM_030705:1677	Mesdc1	INSIDE	1.317	2.271	786.92	1786.81	2.990	595.14	1779.19
A_68_P25780633	chr8:36651446-36651490	NM_001081279:617	Mfhas1	INSIDE	1.317	3.439	1040.64	3578.81	4.530	892.16	4041.59
A_68_P25709495	chr8:23276840-23276884	NM_001162947:-3896	Nek3	PROMOTER	1.317	1.834	1288.04	2362.78	2.415	1231.44	2974.50
A_68_P29753348	chr14:80170386-80170430	NM_001042726:711	Pcdh8	INSIDE	1.317	1.591	863.36	1373.18	2.094	833.06	1744.50
A_68_P28035922	chr11:94852837-94852881	NM_172261:333	Ppp1r9b	INSIDE	1.317	1.664	1090.30	1814.24	2.191	892.40	1955.69
A_68_P24155330	chr5:143942270-143942314	NM_001045482:130	Rbak	INSIDE	1.317	2.620	712.56	1866.56	3.449	625.96	2159.09
A_68_P21817914	chr2:164268773-164268817	NM_011521:-106	Sdc4	PROMOTER	1.317	2.861	1038.43	2970.56	3.767	992.39	3738.59
A_68_P24950759	chr7:4788111-4788155	NM_172737:8166	Shisa7	INSIDE	1.317	2.924	1027.97	3006.28	3.850	868.11	3342.30
A_68_P26477006	chr9:45762946-45762990	NM_172257:364	Sidt2	INSIDE	1.317	1.784	898.87	1603.27	2.348	854.15	2005.80
A_68_P23575087	chr5:31172049-31172093	NM_144525:51	Tmem214	INSIDE	1.317	1.506	7935.28	11952.04	1.984	6042.37	11988.98
A_68_P28575795	chr12:81564283-81564327	NM_133798:223	Exd2	INSIDE	1.316	3.658	5153.17	18848.24	4.815	3636.13	17508.68
A_68_P29346590	chr13:115249262-115249306	NM_008046:-346	Fst	PROMOTER	1.316	1.653	2540.27	4200.22	2.175	2104.93	4578.71
A_68_P29469014	chr14:24824046-24824090	NM_010610:-641	Kcnma1	PROMOTER	1.316	1.484	878.85	1304.58	1.954	776.79	1517.81
A_68_P22934434	chr4:55545364-55545408	NM_010637:-39	Klf4	PROMOTER	1.316	2.394	1702.46	4075.57	3.151	1374.43	4330.43
A_68_P26983898	chr10:19654588-19654632	NM_008580:279	Map3k5	INSIDE	1.316	1.760	1671.56	2942.32	2.317	1513.87	3507.61
A_68_P32134821	chr19:44911447-44911492	NM_011037:79586	Pax2	INSIDE	1.316	1.500	3089.94	4634.51	1.974	2528.66	4991.94
A_68_P22878697	chr4:44723513-44723557	NM_008782:-222	Pax5	PROMOTER	1.316	3.224	1352.76	4361.46	4.242	1245.43	5283.32
A_68_P21834482	chr2:167065917-167065961	NM_008968:99	Ptgis	INSIDE	1.316	1.640	3977.78	6523.45	2.158	2785.35	6011.84
A_68_P27926562	chr11:75328897-75328941	NM_001004157:1876	Scarf1	INSIDE	1.316	2.051	1029.47	2111.34	2.700	897.94	2424.25
A_68_P24024080	chr5:118478322-118478366	NM_021344:512	Tesc	INSIDE	1.316	4.629	945.70	4377.53	6.091	838.74	5108.40
A_68_P31202525	chr17:45822791-45822835	NM_198167:355	Tmem63b	INSIDE	1.316	2.089	1211.65	2530.68	2.750	1011.81	2782.04
A_68_P27836014	chr11:59102302-59102346	NM_009522:1929	Wnt3a	INSIDE	1.316	2.997	382.20	1145.35	3.943	377.15	1487.10
A_68_P31412802	chr17:86199409-86199453	AK142122:208		INSIDE	1.316	1.854	5358.93	9934.05	2.439	3923.47	9570.58
A_68_P23947800	chr5:104084571-104084615	NM_028824:151	1700016H13Rik	INSIDE	1.315	2.463	1484.82	3656.51	3.237	1183.61	3831.77
A_68_P27934861	chr11:76759571-76759615	NM_178645:435	Blmh	INSIDE	1.315	1.589	1623.20	2580.04	2.090	1495.91	3126.22
A_68_P31186620	chr17:43013150-43013194	NM_009847:201	Cd2ap	INSIDE	1.315	1.968	1075.29	2115.69	2.588	976.54	2527.28
A_68_P23309921	chr4:131604501-131604545	NM_001128606:471	Epb4.1	INSIDE	1.315	5.420	2522.16	13670.18	7.125	2069.71	14747.50
A_68_P24046891	chr5:122302921-122302965	NM_175474:3906	Fam109a	INSIDE	1.315	2.427	1047.84	2542.75	3.190	849.76	2711.06
A_68_P29571200	chr14:46149352-46149396	NM_146054:366	Fermt2	INSIDE	1.315	1.812	1239.14	2245.38	2.383	1044.63	2488.84
A_68_P27594244	chr11:11925917-11925961	NM_001177629:2036	Grb10	INSIDE	1.315	4.773	1924.73	9187.03	6.276	1482.37	9303.42
A_68_P20556973	chr1:121318457-121318501	NM_008381:347	Inhbb	INSIDE	1.315	3.089	2105.89	6505.40	4.063	1555.58	6320.74
A_68_P21717097	chr2:146047662-146047707	NM_016889:-48	Insm1	PROMOTER	1.315	1.575	1716.91	2703.90	2.071	1521.54	3150.50
A_68_P26270748	chr8:131209625-131209669	NM_010578:93	Itgb1	INSIDE	1.315	1.669	1173.41	1958.52	2.195	1081.42	2373.62
A_68_P32051829	chr19:29326236-29326280	NM_001048177:-59	Jak2	PROMOTER	1.315	1.953	1573.61	3073.02	2.567	1283.59	3295.20
A_68_P25092919	chr7:52661992-52662036	NM_010596:685	Kcna7	INSIDE	1.315	2.433	798.30	1942.21	3.200	662.46	2119.90
A_68_P30359963	chr15:78267288-78267332	NM_001081367:8253	Kctd17	INSIDE	1.315	2.639	2635.29	6955.47	3.470	1700.55	5901.06
A_68_P20453265	chr1:94996931-94996975	NM_001110315:1490	Kif1a	INSIDE	1.315	3.015	2093.88	6313.38	3.964	1718.09	6810.50

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P30345385	chr15:75829377-75829421	NM_177922:5200	Mapk15	INSIDE	1.315	2.436	4535.10	11047.77	3.204	3380.91	10832.31
A_68_P23592026	chr5:34340043-34340087	NM_001001985:1432	Nat8l	INSIDE	1.315	2.110	377.84	797.40	2.774	325.05	901.76
A_68_P20231212	chr1:53353853-53353897	NM_153556:-34	Pms1	DIVERGENT_PROMOTER	1.315	6.054	2118.56	12825.81	7.960	1553.22	12363.36
A_68_P29094194	chr13:63669536-63669580	NM_008957:-2730	Ptch1	PROMOTER	1.315	1.537	1530.49	2351.68	2.020	1377.86	2783.49
A_68_P26540062	chr9:56920055-56920099	NM_001110350:-4106	Sin3a	PROMOTER	1.315	1.615	959.36	1549.82	2.125	816.42	1734.67
A_68_P22218905	chr3:68848719-68848763	NM_025863:-76	Trim59	PROMOTER	1.315	3.872	903.90	3499.83	5.091	841.47	4284.26
A_68_P30693866	chr16:39984614-39984658	AK082117:-71		PROMOTER	1.315	3.050	1025.21	3126.43	4.011	886.36	3554.84
A_68_P21127431	chr2:34262562-34262606	ENSMUST00000147337:-118		PROMOTER	1.315	2.202	2062.74	4541.97	2.895	1817.90	5263.15
A_68_P27901660	chr11:70429072-70429116	NM_001145537:-301	4930544D05Rik	PROMOTER	1.314	1.840	539.06	992.14	2.418	454.14	1098.33
A_68_P25598323	chr7:150238635-150238679	NM_133655:2	Cd81	INSIDE	1.314	2.764	445.68	1231.72	3.631	409.36	1486.40
A_68_P23339476	chr4:136913526-136913570	NM_009861:104	Cdc42	INSIDE	1.314	1.767	1242.91	2195.86	2.321	1185.61	2751.78
A_68_P21103095	chr2:30271038-30271082	NM_007760:208	Crat	INSIDE	1.314	3.125	1171.17	3660.15	4.106	992.30	4074.11
A_68_P25286994	chr7:91300218-91300262	NM_133722:163	Fam108c	INSIDE	1.314	2.967	933.15	2768.27	3.898	884.59	3447.80
A_68_P26021244	chr8:87225675-87225719	NM_008535:341	Lyl1	INSIDE	1.314	1.708	1373.03	2345.00	2.244	1062.52	2383.86
A_68_P24161575	chr5:145306253-145306297	NM_016789:-481	Nptx2	PROMOTER	1.314	1.650	717.78	1184.51	2.168	601.10	1303.28
A_68_P25377990	chr7:109416158-109416202	NM_009287:-157	Stim1	PROMOTER	1.314	1.883	965.18	1817.67	2.474	815.89	2018.84
A_68_P25182469	chr7:72516013-72516058	NM_001163574:95	Tjp1	INSIDE	1.314	1.683	1133.77	1908.56	2.212	1004.05	2221.14
A_68_P29733542	chr14:76814361-76814405	NM_207652:-1245	Tsc22d1	PROMOTER	1.314	3.076	405.83	1248.14	4.042	371.57	1501.92
A_68_P23610941	chr5:37379997-37380041	NM_011716:203	Wfs1	INSIDE	1.314	2.172	1264.79	2747.47	2.854	1084.02	3093.86
A_68_P31175249	chr17:39985581-39985625	ENSMUST00000062783:170		INSIDE	1.314	3.331	23670.85	78837.49	4.378	17964.65	78645.27
A_68_P31951639	chr19:10680032-10680076	NM_015735:-60	Ddb1	DIVERGENT_PROMOTER	1.313	1.880	1892.66	3557.63	2.468	1408.63	3477.00
A_68_P23202060	chr4:109349261-109349305	NM_007983:51	Faf1	INSIDE	1.313	2.204	899.95	1983.17	2.893	777.80	2249.83
A_68_P28928667	chr13:32430111-32430155	NM_146041:281	Gmds	INSIDE	1.313	4.076	1399.23	5703.60	5.352	1287.51	6890.28
A_68_P31866345	chr18:80909646-80909690	NM_001164111:-4756	Nfatc1	PROMOTER	1.313	5.078	3778.50	19186.36	6.668	3031.32	20211.49
A_68_P26253526	chr8:128258037-128258081	NM_025636:-44	Ntpcr	PROMOTER	1.313	2.307	1712.75	3950.85	3.028	1416.54	4289.92
A_68_P27921383	chr11:74403548-74403592	NM_001015046:90	Rap1gap2	INSIDE	1.313	1.487	2251.45	3348.42	1.953	1938.07	3785.75
A_68_P21099264	chr2:29603006-29603050	NM_001039086:127789	Rapgef1	DOWNSTREAM	1.313	1.473	1343.02	1978.17	1.934	1146.35	2217.20
A_68_P24428223	chr6:48547614-48547658	NM_001079901:3755	Repin1	INSIDE	1.313	3.260	927.15	3022.57	4.281	891.28	3815.31
A_68_P27554682	chr11:3813819-3813863	NM_153142:827	Slc35e4	INSIDE	1.313	2.454	3040.60	7460.32	3.222	2397.68	7725.96
A_68_P32766767	chrX:153929659-153929703	NM_009214:298	Sms	INSIDE	1.313	4.673	667.05	3117.10	6.135	514.12	3154.30
A_68_P23322941	chr4:134024349-134024393	NM_019641:136	Stmn1	INSIDE	1.313	2.772	2406.39	6671.71	3.639	1983.81	7219.85
A_68_P28974160	chr13:40823639-40823683	NM_001122948:2152	Tcfap2a	INSIDE	1.313	1.564	846.12	1323.49	2.054	725.71	1490.63
A_68_P26894032	chr9:123169639-123169683	NM_001002267:247	Tmem158	INSIDE	1.313	2.289	678.84	1554.04	3.007	672.75	2022.72
A_68_P27044453	chr10:31165715-31165759	NM_009413:-9	Tpd52l1	PROMOTER	1.313	1.513	1100.39	1664.77	1.987	926.62	1841.10
A_68_P27086292	chr10:40604319-40604365	NM_031877:1003	Wasf1	INSIDE	1.313	2.172	298.43	648.34	2.852	222.37	634.28
A_68_P30342957	chr15:75446831-75446875	NM_001044718:-262	Zfp41	PROMOTER	1.313	1.573	939.86	1478.67	2.066	768.12	1586.85
A_68_P28435276	chr12:53605530-53605574	AK041016:550		INSIDE	1.313	1.434	4253.89	6099.47	1.883	3479.01	6551.22
A_68_P30425161	chr15:89259781-89259825	NR_004843:556	BC090627	INSIDE	1.312	1.887	932.87	1760.34	2.477	882.45	2185.42
A_68_P30221122	chr15:53177633-53177677	NM_010162:84	Ext1	INSIDE	1.312	5.053	1784.62	9018.40	6.631	1423.70	9441.00
A_68_P30399218	chr15:85036672-85036716	NM_010180:257	Fbln1	INSIDE	1.312	3.036	2885.58	8760.74	3.985	2518.06	10033.89
A_68_P30630403	chr16:28445216-28445260	NM_183064:75	Fgf12	INSIDE	1.312	1.997	736.69	1471.52	2.622	666.78	1748.01
A_68_P29529256	chr14:35124536-35124580	NM_008133:646	Glud1	INSIDE	1.312	2.593	2761.15	7160.42	3.403	2344.05	7976.58
A_68_P27292918	chr10:82092906-82092950	NR_037190:342	Gm9855	INSIDE	1.312	1.873	1576.59	2953.07	2.457	1368.82	3362.63
A_68_P23332339	chr4:135704351-135704395	NM_008321:4636	Id3	DOWNSTREAM	1.312	2.086	3292.78	6869.03	2.737	2434.87	6665.09
A_68_P32451589	chrX:68303308-68303352	NM_001081354:-100	Mamld1	PROMOTER	1.312	2.609	2091.88	5457.59	3.423	1122.91	3843.46
A_68_P28291797	chr12:25516152-25516196	NM_001083341:-289	Mboat2	PROMOTER	1.312	2.255	720.01	1623.57	2.958	643.11	1902.49
A_68_P20625166	chr1:134921738-134921782	NM_008575:165	Mdm4	INSIDE	1.312	1.629	2572.84	4192.26	2.138	2107.13	4505.68
A_68_P25962048	chr8:75072006-75072050	NM_027485:181	Med26	INSIDE	1.312	1.914	984.30	1883.76	2.510	862.74	2165.75
A_68_P21902498	chr2:179992383-179992427	NM_025587:321	Rps21	INSIDE	1.312	0.355	1571.36	558.03	0.466	1223.89	570.12
A_68_P25499767	chr7:133435936-133435980	NM_145587:19826	Sbk1	INSIDE	1.312	2.745	479.90	1317.41	3.602	462.47	1665.81
A_68_P31054977	chr17:13185351-13185395	NM_001113533:-247	Wtap	PROMOTER	1.312	2.763	919.81	2540.98	3.626	814.74	2953.89

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27927818	chr11:75546834-75546878	NM_009536:468	Ywhae	INSIDE	1.312	1.568	2704.41	4239.29	2.057	2139.87	4401.64
A_68_P24397788	chr6:42300448-42300492	NM_011777:644	Zyx	INSIDE	1.312	1.390	6127.79	8516.22	1.823	4319.77	7876.43
A_68_P29020719	chr13:48764304-48764348	NM_007526:5922	Barx1	DOWNSTREAM	1.311	1.543	1293.74	1996.44	2.023	1056.36	2137.42
A_68_P28109100	chr11:107655405-107655449	NM_019431:352	Cacng4	INSIDE	1.311	1.578	1179.70	1861.41	2.069	816.49	1689.09
A_68_P27990839	chr11:86571533-86571577	NM_001003908:-560	Cltc	PROMOTER	1.311	2.236	964.60	2156.80	2.931	813.45	2384.61
A_68_P20472155	chr1:99558144-99558188	NM_133825:429	D1Ertd622e	INSIDE	1.311	2.736	2311.18	6324.15	3.587	1928.44	6917.33
A_68_P25780174	chr8:36558678-36558722	NM_026067:-113	Eri1	PROMOTER	1.311	4.426	2740.09	12126.52	5.800	2304.83	13367.43
A_68_P26467131	chr9:44152207-44152251	NM_001110251:-1764	Hmbs	PROMOTER	1.311	1.787	1258.18	2248.32	2.342	1130.11	2647.15
A_68_P24634433	chr6:90686814-90686858	NM_001134384:73281	Iqsec1	INSIDE	1.311	1.400	1584.56	2217.82	1.835	1407.07	2581.52
A_68_P24993122	chr7:19989220-19989264	NM_146182:-4037	Klc3	DIVERGENT_PROMOTER	1.311	4.396	754.28	3315.96	5.762	736.59	4244.40
A_68_P26920199	chr10:7401013-7401057	NM_010690:28	Lats1	INSIDE	1.311	3.150	1853.00	5836.10	4.128	1476.45	6094.39
A_68_P32252887	chrX:10294418-10294462	NM_001166635:-50	Mid1ip1	PROMOTER	1.311	3.114	1184.82	3689.99	4.084	805.83	3291.29
A_68_P28941009	chr13:34967839-34967883	NM_013830:498	Prpf4b	INSIDE	1.311	2.099	2031.31	4263.23	2.751	1584.41	4358.19
A_68_P20598625	chr1:129999853-129999897	NM_181750:-8	R3hdm1	DIVERGENT_PROMOTER	1.311	3.304	3560.20	11762.41	4.331	2728.21	11815.83
A_68_P31108132	chr17:26206355-26206399	NM_001162868:-254	Rab11fip3	PROMOTER	1.311	1.420	1282.51	1821.54	1.862	1102.44	2052.41
A_68_P23820629	chr5:77694724-77694768	NM_011263:228	Rest	INSIDE	1.311	1.414	2102.35	2973.67	1.855	1587.82	2945.14
A_68_P29454669	chr14:22569927-22569971	NM_026283:196	Samd8	INSIDE	1.311	2.418	983.65	2378.31	3.169	888.00	2813.80
A_68_P31738735	chr18:58038835-58038879	NM_009194:525	Slc12a2	INSIDE	1.311	3.333	750.33	2500.94	4.368	660.48	2885.31
A_68_P31202526	chr17:45822858-45822902	NM_198167:287	Tmem63b	INSIDE	1.311	1.841	1736.21	3195.60	2.414	1440.02	3475.98
A_68_P27836016	chr11:59102534-59102578	NM_009522:1697	Wnt3a	INSIDE	1.311	2.350	661.87	1555.58	3.081	560.35	1726.20
A_68_P22262797	chr3:79090995-79091039	AK032506:-297		PROMOTER	1.311	2.578	1072.39	2764.16	3.378	876.55	2961.01
A_68_P26813047	chr9:108008622-108008666	NM_007567:84070	Bsn	INSIDE	1.310	3.904	730.57	2852.43	5.115	618.33	3162.45
A_68_P26061569	chr8:94329516-94329560	NM_008393:-4265	Irx3	PROMOTER	1.310	1.559	3461.01	5396.80	2.043	2550.90	5212.10
A_68_P21419651	chr2:90758053-90758097	NM_025576:133	Ptpmt1	INSIDE	1.310	1.531	608.69	932.20	2.007	598.10	1200.20
A_68_P24061764	chr5:124981000-124981044	NM_021430:378	Rilpl1	INSIDE	1.310	2.979	866.48	2581.37	3.903	779.24	3041.07
A_68_P30467109	chr15:96884897-96884941	NM_027052:1469	Slc38a4	INSIDE	1.310	1.925	802.38	1544.79	2.521	700.47	1766.07
A_68_P24389053	chr6:40421556-40421600	NM_028358:165	Ssbp1	INSIDE	1.310	1.995	804.58	1605.29	2.614	633.49	1656.13
A_68_P28740916	chr12:112127614-112127658	NM_001081057:163	Tecpr2	INSIDE	1.310	1.754	2463.40	4320.80	2.297	1891.09	4343.88
A_68_P23575086	chr5:31171940-31171984	NM_144525:-57	Tmem214	PROMOTER	1.310	2.907	2082.81	6054.52	3.809	1773.46	6754.90
A_68_P30351140	chr15:76741911-76741955	NM_001168276:13946	Zfp647	INSIDE	1.310	2.952	809.49	2389.81	3.867	706.45	2731.85
A_68_P24060291	A_68_P24060291			Unknown	1.310	1.809	1709.86	3092.39	2.369	1447.76	3429.46
A_68_P30778641	chr16:55974831-55974875	NR_027965:-122	2310061J03Rik	PROMOTER	1.309	4.204	3177.75	13359.67	5.502	2637.44	14510.06
A_68_P28534551	chr12:74018450-74018494	NM_029444:280	4930447C04Rik	INSIDE	1.309	6.415	2114.90	13567.05	8.395	1681.74	14118.40
A_68_P28603261	chr12:86621337-86621381	NM_025421:27	Acyp1	INSIDE	1.309	1.898	979.89	1859.50	2.485	866.62	2153.45
A_68_P31155039	chr17:34784544-34784588	NM_017406:442	Atf6b	INSIDE	1.309	2.011	1755.10	3529.20	2.632	1452.66	3823.17
A_68_P29050817	chr13:54789017-54789062	NM_001146025:130	Rnf44	INSIDE	1.309	1.521	1711.26	2602.18	1.990	1451.17	2887.46
A_68_P29141935	chr13:73901004-73901048	NM_011390:-118	Slc12a7	PROMOTER	1.309	3.097	3078.56	9533.25	4.055	2465.41	9996.41
A_68_P21836564	chr2:167457070-167457114	NM_023230:413	Ube2v1	INSIDE	1.309	1.998	893.80	1785.54	2.615	710.32	1857.61
A_68_P30474027	chr15:98126645-98126689	NM_173769:-152	Zfp641	PROMOTER	1.309	1.647	1806.18	2975.30	2.157	1612.47	3477.93
A_68_P24603368	chr6:85105219-85105263	ENSMUST00000089584:242		INSIDE	1.309	2.108	542.87	1144.24	2.758	543.40	1498.92
A_68_P21537143	chr2:113688822-113688866	NM_181416:-26	Arhgap11a	PROMOTER	1.308	2.023	1745.08	3529.84	2.646	1416.55	3748.74
A_68_P25506862	chr7:134852430-134852474	NM_009746:-172	Bcl7c	DIVERGENT_PROMOTER	1.308	1.340	4589.62	6148.95	1.752	3607.14	6320.37
A_68_P26350530	chr9:21921461-21921505	NM_170777:-2869	Elof1	PROMOTER	1.308	1.675	1144.83	1917.14	2.191	1033.94	2265.10
A_68_P29241520	chr13:96373925-96373969	NM_010169:14442	F2r	INSIDE	1.308	2.828	360.86	1020.34	3.699	264.49	978.21
A_68_P28156895	chr11:115885168-115885212	NM_008211:628	H3f3b	INSIDE	1.308	2.496	1356.30	3385.90	3.265	1021.21	3334.10
A_68_P31051121	chr17:12511550-12511594	NM_011948:-46	Map3k4	PROMOTER	1.308	1.861	1220.76	2271.33	2.434	1135.96	2765.40
A_68_P27279588	chr10:79361859-79361903	NM_001163276:9803	Med16	INSIDE	1.308	3.352	3661.68	12273.38	4.384	2475.52	10853.27
A_68_P24383012	chr6:39369835-39369879	NM_018810:512	Mkrn1	INSIDE	1.308	2.097	1270.65	2664.88	2.744	1120.41	3074.60
A_68_P22006132	chr3:26230317-26230361	NM_138666:493	Nlgn1	INSIDE	1.308	1.457	1085.32	1581.60	1.906	913.41	1741.38
A_68_P29239503	chr13:95992534-95992578	NM_001170669:449	Pde8b	INSIDE	1.308	4.875	1256.92	6128.05	6.375	1102.46	7028.15
A_68_P21747515	chr2:151907678-151907722	NM_001160410:436	Scrt2	INSIDE	1.308	1.793	351.88	630.97	2.345	387.12	907.73

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P24973913	chr7:13556719-13556763	NM_178732:5528	Zfp324	INSIDE	1.308	1.928	475.96	917.86	2.522	400.57	1010.21
A_68_P24432031	chr6:49269387-49269431	NM_175098:57	Ccdc126	INSIDE	1.307	2.396	1144.52	2742.61	3.132	914.17	2863.03
A_68_P25948479	chr8:72406005-72406049	NM_026818:5265	Cilp2	INSIDE	1.307	2.258	521.32	1177.35	2.952	437.85	1292.49
A_68_P29747539	chr14:79125062-79125106	NM_001081336:-188	Dgkh	PROMOTER	1.307	3.032	1370.59	4155.45	3.964	1149.84	4557.84
A_68_P20566311	chr1:123224390-123224434	NM_133748:-73	Insig2	PROMOTER	1.307	1.804	475.82	858.56	2.358	419.44	989.19
A_68_P21421182	chr2:91022680-91022724	NM_001177720:-3224	Madd	PROMOTER	1.307	3.844	2550.05	9802.18	5.023	2460.76	12359.94
A_68_P27897811	chr11:69715610-69715654	NM_001013414:253	Neurl4	INSIDE	1.307	1.571	1025.78	1611.52	2.053	868.63	1783.29
A_68_P23194284	chr4:107704369-107704413	NM_172874:305	Podn	INSIDE	1.307	3.070	1491.45	4578.12	4.012	1262.85	5066.12
A_68_P20451967	chr1:94807773-94807817	NM_181405:393	Rnpepl1	INSIDE	1.307	1.690	1221.53	2064.62	2.210	1082.61	2392.29
A_68_P21635215	chr2:131318208-131318252	NM_001177833:633	Smox	INSIDE	1.307	1.829	1287.57	2354.76	2.390	1042.16	2490.54
A_68_P25017144	chr7:28189868-28189912	NM_001199236:-8318	Spnb4	PROMOTER	1.307	4.368	2637.82	11522.10	5.709	2009.34	11472.27
A_68_P21866929	chr2:172805440-172805484	NM_001083959:120	Spo11	INSIDE	1.307	2.174	268.48	583.75	2.841	239.13	679.40
A_68_P28161641	chr11:116713805-116713849	NM_011358:582	Srsf2	INSIDE	1.307	2.187	1722.99	3767.62	2.858	1494.57	4271.70
A_68_P31331149	chr17:71202044-71202088	NM_001164075:-992	Tgif1	PROMOTER	1.307	2.750	182.62	502.16	3.593	182.47	655.54
A_68_P24376582	chr6:38249064-38249108	NM_172467:173	Zc3hav1l	INSIDE	1.307	1.599	494.54	790.58	2.089	450.11	940.24
A_68_P29938688	chr14:118836379-118836423			Unknown	1.307	2.306	1426.31	3288.99	3.014	1434.90	4324.77
A_68_P29258006	chr13:99274352-99274396	AK135687:84239		INSIDE	1.307	3.076	834.43	2566.84	4.022	690.55	2777.20
A_68_P25230182	chr7:80763065-80763109	AK158912:183		INSIDE	1.307	1.774	1206.56	2140.97	2.319	1047.81	2429.74
A_68_P27279428	chr10:79337495-79337539	NM_001170935:-137	BC005764	DIVERGENT_PROMOTER	1.306	2.372	2183.07	5178.66	3.098	1624.04	5031.35
A_68_P23250424	chr4:119955496-119955540	NM_194060:4348	Foxo6	INSIDE	1.306	2.779	1829.84	5085.10	3.630	1633.22	5927.82
A_68_P28152362	chr11:115119477-115119521	NM_010350:9059	Grin2c	INSIDE	1.306	3.700	801.28	2964.80	4.834	682.32	3298.37
A_68_P24133865	chr5:139626414-139626458	NM_001081265:260	Heatr2	INSIDE	1.306	2.927	958.50	2805.89	3.824	758.37	2899.90
A_68_P25375722	chr7:108985190-108985234	NM_001122739:1126	Inppl1	INSIDE	1.306	2.147	1896.27	4071.65	2.804	1595.66	4474.06
A_68_P30482202	chr15:99602992-99603036	NM_028015:-68	Lass5	PROMOTER	1.306	1.807	6735.07	12172.06	2.360	5406.62	12758.44
A_68_P26548745	chr9:58430450-58430494	NM_009145:426	Nptn	INSIDE	1.306	1.555	1871.33	2909.89	2.030	1597.79	3244.12
A_68_P31934661	chr19:6428357-6428401	NM_001205234:9641	Nrxn2	INSIDE	1.306	3.818	704.80	2691.21	4.988	557.67	2781.49
A_68_P31943407	chr19:8831518-8831562	NM_016813:-52	Nxf1	PROMOTER	1.306	1.792	398.12	713.49	2.340	313.91	734.54
A_68_P27901903	chr11:70468945-70468989	NM_011072:-814	Pfn1	DIVERGENT_PROMOTER	1.306	2.751	525.83	1446.51	3.591	533.19	1914.91
A_68_P21888792	chr2:177877156-177877200	NM_028806:541	Phactr3	INSIDE	1.306	2.919	920.93	2687.97	3.813	776.29	2960.04
A_68_P21796699	chr2:160557598-160557642	NM_021280:575	Plcg1	INSIDE	1.306	2.503	539.07	1349.13	3.269	414.39	1354.74
A_68_P27080343	chr10:39452167-39452211	NM_011264:223	Rev3l	INSIDE	1.306	2.939	1588.48	4668.40	3.838	1333.46	5118.17
A_68_P20759140	chr1:161161812-161161856	NM_011931:-622	Rfwd2	PROMOTER	1.306	2.737	1207.32	3304.29	3.574	923.39	3300.49
A_68_P31412117	chr17:86087251-86087295	NM_011380:322	Six2	INSIDE	1.306	2.248	430.59	968.15	2.936	459.18	1347.94
A_68_P20940733	chr1:193730478-193730522	NM_009579:-159	Slc30a1	PROMOTER	1.306	1.484	1923.39	2855.27	1.939	1625.46	3152.48
A_68_P31351019	chr17:74738085-74738129	NM_001162870:-220	Spast	PROMOTER	1.306	1.403	2396.18	3361.47	1.832	2038.95	3735.31
A_68_P27513153	chr10:122633430-122633474	NM_027604:527	Usp15	INSIDE	1.306	1.918	1082.46	2076.40	2.505	1018.49	2551.28
A_68_P28931384	chr13:32894661-32894705	NM_030215:784	Wrnip1	INSIDE	1.306	4.902	1428.29	7001.87	6.403	1235.14	7908.42
A_68_P23998433	chr5:113920169-113920213	NM_177292:724	Wscd2	INSIDE	1.306	1.823	1093.18	1992.80	2.380	982.35	2338.42
A_68_P25947916	chr8:72298647-72298691	NM_177899:142	Zfp866	INSIDE	1.306	2.110	1943.12	4099.60	2.755	1700.55	4684.31
A_68_P32537534	chrX:91368825-91368869	NM_001044386:-100	Zfx	PROMOTER	1.306	2.490	1262.96	3144.78	3.253	799.63	2601.35
A_68_P21773774	chr2:156688896-156688940	NM_026124:61	1110008F13Rik	INSIDE	1.305	2.679	1489.12	3989.93	3.496	1365.87	4774.74
A_68_P30382912	chr15:82176300-82176344	NM_026914:-153	1500032L24Rik	PROMOTER	1.305	1.725	423.62	730.66	2.250	406.80	915.36
A_68_P30348811	chr15:76341995-76342039	NM_010046:232	Dgat1	INSIDE	1.305	1.592	3778.90	6017.42	2.078	2896.67	6019.19
A_68_P25328180	chr7:100229175-100229219	NM_021427:808	Fam181b	INSIDE	1.305	1.902	2855.80	5432.99	2.482	2247.40	5578.24
A_68_P30786987	chr16:57549528-57549572	NM_001177871:196	Filip1l	INSIDE	1.305	3.618	528.72	1912.77	4.721	447.30	2111.83
A_68_P24126098	chr5:137952294-137952338	NM_031408:-7791	Gigyf1	DIVERGENT_PROMOTER	1.305	2.386	3572.19	8524.98	3.115	2524.09	7861.33
A_68_P28043432	chr11:96144310-96144354	NM_010461:1114	Hoxb8	INSIDE	1.305	3.033	699.31	2121.00	3.959	652.06	2581.30
A_68_P31208325	chr17:46817475-46817519	NM_001163729:383	Klhdc3	INSIDE	1.305	2.765	2909.67	8043.92	3.607	1830.68	6602.56
A_68_P20633481	chr1:136352243-136352287	NM_153128:133	Klhl12	INSIDE	1.305	2.162	1130.03	2443.36	2.823	1098.53	3100.69
A_68_P25048198	chr7:35988774-35988818	NM_001024707:11568	Lrp3	INSIDE	1.305	1.997	577.52	1153.07	2.605	465.82	1213.33
A_68_P21600379	chr2:124949302-124949346	NM_001162417:72	Myef2	INSIDE	1.305	4.355	681.16	2966.77	5.684	653.17	3712.39

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P30939274	chr16:87354456-87354500	NM_001159331:49	N6amt1	INSIDE	1.305	2.316	635.56	1472.17	3.022	561.50	1696.68
A_68_P30506991	chr16:3884449-3884493	NM_029090:-148	Nat15	PROMOTER	1.305	1.533	1071.15	1641.57	2.000	850.70	1701.57
A_68_P23134316	chr4:97438997-97439041	NM_001122953:-5298	Nfia	PROMOTER	1.305	2.483	2469.27	6131.33	3.240	2088.40	6767.31
A_68_P27165512	chr10:58276626-58276670	NM_172788:542	Sh3rf3	INSIDE	1.305	2.964	964.44	2858.22	3.866	869.92	3363.52
A_68_P23594735	chr5:34856681-34856725	NM_139064:-74	Tnip2	PROMOTER	1.305	1.552	2390.18	3709.44	2.025	2175.02	4403.86
A_68_P29880580	chr14:106505493-106505537	NM_198601:100	Trim52	INSIDE	1.305	2.865	342.53	981.33	3.740	321.89	1203.76
A_68_P20350376	chr1:74818349-74818393	NM_009526:-95	Wnt6	PROMOTER	1.305	1.925	3236.32	6229.09	2.513	2766.33	6950.48
A_68_P29473057	chr14:25598729-25598773			Unknown	1.305	1.632	1487.98	2427.70	2.129	1240.41	2640.40
A_68_P27633575	chr11:20730716-20730761	NM_173752:373	1110067D22Rik	INSIDE	1.304	1.896	842.63	1597.74	2.472	656.57	1623.15
A_68_P23368575	chr4:141794726-141794770	NM_001109685:568	9030409G11Rik	INSIDE	1.304	1.618	3562.45	5765.55	2.111	2853.64	6023.44
A_68_P30811311	chr16:62846647-62846691	NM_026577:198	Arl13b	INSIDE	1.304	1.768	651.89	1152.46	2.305	619.91	1428.60
A_68_P24191337	chr5:151325172-151325216	NM_009765:-3	Brca2	DIVERGENT_PROMOTER	1.304	1.557	865.50	1347.75	2.030	715.03	1451.63
A_68_P30759543	chr16:52032167-52032211	NM_001033238:527	Cblb	INSIDE	1.304	1.647	1773.06	2920.06	2.148	1542.73	3313.43
A_68_P25961304	chr8:74945231-74945275	NM_007944:121	Eps15l1	INSIDE	1.304	2.169	826.17	1792.01	2.829	721.15	2039.93
A_68_P26343222	chr9:20446824-20446868	NM_013911:404	Fbxl12	INSIDE	1.304	1.988	262.22	521.24	2.593	235.93	611.76
A_68_P30631089	chr16:28564952-28564996	NM_010199:188314	Fgf12	INSIDE	1.304	1.619	711.88	1152.60	2.110	726.46	1533.19
A_68_P32704838	chrX:138156435-138156479	NM_010572:3304	Irs4	INSIDE	1.304	1.726	763.07	1317.36	2.252	405.85	913.87
A_68_P20047723	chr1:14745767-14745811	NM_010827:259	Msc	INSIDE	1.304	2.272	1295.95	2944.39	2.963	1215.99	3603.04
A_68_P30082174	chr15:25552690-25552734	NM_019472:408	Myo10	INSIDE	1.304	1.503	1828.18	2747.95	1.960	1526.06	2990.33
A_68_P27302615	chr10:83903859-83903903	NM_001004363:-664	Nuak1	PROMOTER	1.304	2.230	252.78	563.73	2.908	225.44	655.66
A_68_P23916646	chr5:98615304-98615348	NM_029947:5439	Prdm8	INSIDE	1.304	2.608	773.03	2015.71	3.401	663.87	2257.79
A_68_P25585274	chr7:148043495-148043539	NM_053194:221	Ric8	INSIDE	1.304	2.247	7898.19	17748.54	2.931	5357.36	15701.91
A_68_P31253473	chr17:56175813-56175857	NM_013664:165	Sh3gl1	INSIDE	1.304	1.522	1690.98	2574.40	1.985	1484.33	2946.12
A_68_P25412179	chr7:117365148-117365192	NM_009302:-46	Swap70	PROMOTER	1.304	2.077	1858.74	3861.00	2.708	1517.27	4108.26
A_68_P23240689	chr4:118159149-118159193	NM_011587:3284	Tie1	INSIDE	1.304	3.932	1714.91	6742.46	5.127	1394.65	7150.53
A_68_P27359835	chr10:93978114-93978158	NM_172051:535	Tmcc3	INSIDE	1.304	2.635	483.16	1273.23	3.437	593.75	2040.93
A_68_P30401287	chr15:85367949-85367993	NM_001163634:40530	Wnt7b	INSIDE	1.304	1.609	874.13	1406.16	2.098	795.35	1668.37
A_68_P24428351	chr6:48570207-48570251	NM_173429:7050	Zfp775	INSIDE	1.304	2.279	776.68	1769.92	2.971	682.04	2026.12
A_68_P23279474	chr4:125998794-125998839	NM_133883:131	Adprhl2	INSIDE	1.303	1.657	1825.59	3025.00	2.159	1555.04	3357.11
A_68_P24816768	chr6:124695641-124695685	NM_007881:10843	Atn1	INSIDE	1.303	1.954	1543.86	3016.46	2.547	1275.67	3248.71
A_68_P24104853	chr5:133019620-133019664	NM_177047:-1429	Auts2	PROMOTER	1.303	3.198	1277.02	4084.02	4.169	1095.81	4568.02
A_68_P33007787	chr4_random:127945-127989	NM_001033326:18165	Dhrsx	INSIDE	1.303	3.780	8534.81	32260.34	4.923	6191.48	30483.39
A_68_P22787931	chr4:24778185-24778229	NM_001033531:27	Klhl32	INSIDE	1.303	3.093	5015.57	15512.56	4.030	4323.68	17426.10
A_68_P25092990	chr7:52671388-52671432	NM_198190:2346	Ntf5	INSIDE	1.303	1.860	878.37	1634.07	2.424	695.84	1686.60
A_68_P27556014	chr11:4060531-4060575	NM_026175:196	Sf3a1	INSIDE	1.303	1.357	2523.46	3424.69	1.769	2025.03	3582.09
A_68_P20633021	chr1:136258633-136258677	NM_001042485:-78	Tmem183a	PROMOTER	1.303	4.529	599.66	2715.74	5.903	491.50	2901.34
A_68_P25581866	chr7:147222199-147222243	NM_133755:29	Tubgcp2	INSIDE	1.303	1.499	5556.80	8329.12	1.953	4306.14	8411.40
A_68_P21072309	chr2:25316230-25316274	NM_153557:362	BC029214	INSIDE	1.302	1.639	2301.75	3773.20	2.134	1844.86	3937.21
A_68_P26234726	chr8:125154578-125154622	NM_001109873:47475	Cbfa2t3	INSIDE	1.302	3.834	1665.13	6384.10	4.993	1459.81	7289.05
A_68_P27921467	chr11:74424565-74424610	NM_001013784:-8519	E130309D14Rik	PROMOTER	1.302	2.774	1201.41	3332.57	3.611	1111.35	4012.87
A_68_P31322349	chr17:69506595-69506639	NM_013813:467	Epb4.1l3	INSIDE	1.302	2.372	893.64	2119.76	3.089	784.38	2422.93
A_68_P32397421	chrX:53985333-53985377	NM_001077361:221	Fhl1	INSIDE	1.302	1.826	675.77	1233.67	2.378	449.65	1069.16
A_68_P21203199	chr2:49474675-49474719	NM_008449:-137	Kif5c	PROMOTER	1.302	3.019	942.50	2845.14	3.931	728.91	2865.30
A_68_P28515343	chr12:70683664-70683708	NM_001033236:329	Mettl21d	INSIDE	1.302	1.463	1751.96	2563.34	1.905	1419.61	2703.68
A_68_P23577231	chr5:31543485-31543529	NM_147201:216	Nrbp1	INSIDE	1.302	2.442	1253.65	3061.53	3.181	1041.51	3312.58
A_68_P28083321	chr11:102962810-102962854	NM_152813:140	Plcd3	INSIDE	1.302	1.563	959.01	1499.17	2.036	910.88	1854.35
A_68_P22313617	chr3:88213719-88213763	NM_025928:498	Pmf1	INSIDE	1.302	1.683	1017.38	1712.57	2.192	911.68	1998.58
A_68_P25576657	chr7:146434291-146434335	NM_001033206:-68	Pwwp2b	PROMOTER	1.302	3.305	245.94	812.92	4.305	216.44	931.77
A_68_P23896677	chr5:93327277-93327321	NM_001077596:275	Shroom3	INSIDE	1.302	0.417	1538.47	641.67	0.543	1389.54	754.44
A_68_P28050112	chr11:97223519-97223563	NM_138657:-324	Socs7	PROMOTER	1.302	2.092	955.61	1999.16	2.723	865.71	2357.67
A_68_P30572951	chr16:17278027-17278071	NM_177473:1656	Tmem191c	INSIDE	1.302	3.083	959.55	2957.86	4.012	791.47	3175.76

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31102168	chr17:25325357-25325401	NM_001197024:34	Unkl	INSIDE	1.302	1.874	17884.60	33513.20	2.439	14385.30	35092.38
A_68_P23998981	chr5:114037991-114038035	NM_177292:118546	Wscd2	INSIDE	1.302	1.884	1419.41	2673.71	2.452	1108.04	2716.51
A_68_P28872465	chr13:21454901-21454949	NM_016684:236	Zscan12	INSIDE	1.302	4.229	190.27	804.69	5.505	229.88	1265.40
A_68_P24026284	chr5:118830994-118831046			Unknown	1.302	7.064	3039.22	21468.34	9.200	2114.52	19453.68
A_68_P23756663	chr5:65884143-65884187	NM_133697:-90	1110003E01Rik	PROMOTER	1.301	1.653	1056.90	1747.18	2.151	923.78	1987.37
A_68_P25502308	chr7:133942826-133942870	NM_007438:-80	Aldoa	PROMOTER	1.301	1.675	1348.95	2259.19	2.178	1154.28	2514.55
A_68_P31125954	chr17:29235470-29235514	NM_007669:4776	Cdkn1a	INSIDE	1.301	2.115	423.86	896.58	2.751	346.27	952.67
A_68_P26779715	chr9:102255528-102255572	NM_001168296:1473	Ephb1	INSIDE	1.301	1.468	1362.93	2001.41	1.911	1140.77	2180.07
A_68_P24053334	chr5:123438191-123438235	NM_001005866:330	Kdm2b	INSIDE	1.301	1.681	534.29	898.18	2.188	420.14	919.08
A_68_P21206004	chr2:49921862-49921906	NM_177139:-97	Lypd6	PROMOTER	1.301	1.944	2140.56	4161.88	2.529	1892.45	4785.49
A_68_P27971522	chr11:83256374-83256418	NM_080453:20067	Mmp28	INSIDE	1.301	1.722	1594.45	2746.09	2.241	1420.01	3181.84
A_68_P21107808	chr2:31102041-31102085	NM_019681:620	Ncs1	INSIDE	1.301	2.203	4033.24	8886.65	2.866	2788.72	7991.54
A_68_P29322927	chr13:111184916-111184960	NM_152804:-313	Plk2	PROMOTER	1.301	2.174	1925.22	4185.78	2.828	1678.01	4746.04
A_68_P24116186	chr5:135870022-135870066	NM_148932:372	Pom121	INSIDE	1.301	2.460	1585.33	3899.91	3.201	1422.46	4553.49
A_68_P31633220	chr18:38456665-38456709	NM_001164621:228	Rnf14	INSIDE	1.301	2.208	824.12	1819.88	2.872	707.00	2030.75
A_68_P31682248	chr18:47528673-47528717	NM_018744:-172	Sema6a	PROMOTER	1.301	2.837	1347.16	3822.26	3.692	1134.67	4188.72
A_68_P31207580	chr17:46692523-46692567	NM_020493:567	Srf	INSIDE	1.301	3.279	1018.20	3338.54	4.266	800.24	3414.08
A_68_P28611534	chr12:88019825-88019869	NM_177354:197	Vash1	INSIDE	1.301	2.747	924.25	2539.26	3.575	776.70	2776.44
A_68_P21013703	chr2:12933075-12933119	NM_153155:-605	C1ql3	PROMOTER	1.300	3.616	572.94	2071.92	4.702	490.01	2303.87
A_68_P31156013	chr17:34974519-34974563	NM_001163770:577	Dom3z	INSIDE	1.300	1.778	2885.14	5128.43	2.310	2354.92	5440.15
A_68_P25051003	chr7:36539278-36539322	NM_178704:173	Dpy19l3	INSIDE	1.300	1.902	952.63	1811.46	2.472	758.51	1874.71
A_68_P29241105	chr13:96294931-96294975	NM_007974:243	F2rl1	INSIDE	1.300	1.839	4385.47	8064.38	2.391	3503.02	8375.69
A_68_P31769413	chr18:63545818-63545864	NM_001039485:997	Fam38b	INSIDE	1.300	2.155	1116.41	2406.13	2.802	928.60	2602.19
A_68_P32467043	chrX:71492064-71492108	NM_010227:-213	Flna	DIVERGENT_PROMOTER	1.300	1.615	1616.91	2611.92	2.100	692.07	1453.66
A_68_P20235844	chr1:54251715-54251759	NM_001001883:142	Hecw2	INSIDE	1.300	2.138	1070.30	2288.34	2.778	884.86	2458.49
A_68_P25995580	chr8:82162925-82162969	NM_001081164:-628	Otud4	PROMOTER	1.300	1.462	1863.58	2724.21	1.900	1652.60	3140.65
A_68_P25655776	chr8:11478793-11478843	NM_011227:-319	Rab20	PROMOTER	1.300	6.779	5575.04	37790.58	8.812	3586.03	31600.33
A_68_P25669970	chr8:13676888-13676932	NM_009025:677	Rasa3	INSIDE	1.300	3.010	1860.86	5601.74	3.912	1384.53	5416.69
A_68_P31924878	chr19:4756662-4756706	NM_025717:160	Rbm4b	INSIDE	1.300	3.042	3025.38	9203.08	3.954	2336.29	9236.68
A_68_P21117161	chr2:32597158-32597202	NM_013781:20589	Sh2d3c	INSIDE	1.300	2.954	1767.17	5219.89	3.840	1512.15	5806.58
A_68_P24940169	chr6:148393095-148393139	NM_198967:-242	Tmtc1	PROMOTER	1.300	1.421	1414.33	2010.22	1.847	1231.52	2275.00
A_68_P20886544	chr1:184339098-184339142	NM_173378:-177	Trp53bp2	PROMOTER	1.300	1.665	1389.32	2312.89	2.165	1177.55	2549.02
A_68_P28058995	chr11:98724946-98724990	NM_197940:57	Wipf2	INSIDE	1.300	4.531	809.41	3667.70	5.889	712.49	4195.57
A_68_P25008229	chr7:25861867-25861911	NM_001168506:-335	Zfp574	DIVERGENT_PROMOTER	1.300	1.489	1186.48	1766.74	1.936	937.80	1815.63
A_68_P28741431	chr12:112217094-112217138	NM_175207:115	Ankrd9	INSIDE	1.299	1.699	858.63	1458.56	2.207	827.68	1826.75
A_68_P24925471	chr6:145811847-145811891	NM_024469:1992	Bhlhe41	INSIDE	1.299	1.519	593.93	901.98	1.973	574.00	1132.46
A_68_P29698999	chr14:70474927-70474971	NM_018781:-2303	Egr3	PROMOTER	1.299	1.888	650.22	1227.78	2.453	546.97	1341.85
A_68_P22128838	chr3:51081294-51081338	NM_023502:48593	Elf2	INSIDE	1.299	3.797	7622.44	28944.50	4.934	5912.64	29171.62
A_68_P23145560	chr4:99324186-99324230	NM_010425:1219	Foxd3	INSIDE	1.299	3.025	1622.99	4910.14	3.931	1407.31	5532.08
A_68_P26245549	chr8:126958481-126958525	NM_171824:-666	Pgbd5	PROMOTER	1.299	5.258	1079.47	5675.36	6.828	826.03	5640.24
A_68_P21608665	chr2:126378771-126378815	NM_011978:33	Slc27a2	INSIDE	1.299	1.465	2040.52	2989.91	1.903	1645.65	3132.43
A_68_P22324936	chr3:90193265-90193309	NM_011988:563	Slc27a3	INSIDE	1.299	1.784	1399.12	2496.61	2.319	1273.93	2953.66
A_68_P21754953	chr2:153269988-153270032	NM_001001986:205	8430427H17Rik	INSIDE	1.298	6.644	1832.36	12174.31	8.625	1581.83	13643.01
A_68_P29940447	chr14:119104917-119104961	NM_001033336:503	Abcc4	INSIDE	1.298	0.429	1647.64	707.21	0.557	1343.33	748.52
A_68_P31341454	chr17:72953064-72953108	NM_007439:561	Alk	INSIDE	1.298	1.589	1209.55	1921.98	2.063	1060.01	2186.56
A_68_P31766433	chr18:63081950-63081994	NM_133237:-8	Apcdd1	PROMOTER	1.298	2.567	292.40	750.54	3.331	230.41	767.45
A_68_P22186543	chr3:62143850-62143894	NM_001081295:1174	Arhgef26	INSIDE	1.298	1.668	2148.51	3583.69	2.165	1814.32	3928.50
A_68_P24631553	chr6:90259469-90259513	NM_027928:15689	Chst13	INSIDE	1.298	4.268	498.04	2125.50	5.538	438.54	2428.63
A_68_P28175185	chr11:118860915-118860959	NM_001030291:11435	Enpp7	DOWNSTREAM	1.298	2.472	1553.69	3840.01	3.209	1368.30	4390.89
A_68_P20963944	chr2:3630654-3630698	NM_025626:-53	Fam107b	PROMOTER	1.298	1.903	5388.67	10253.93	2.471	4285.15	10587.07
A_68_P21113218	chr2:31940197-31940241	NM_175511:-993	Fam78a	PROMOTER	1.298	2.621	912.82	2392.38	3.401	769.12	2615.54

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P20405971	chr1:84836410-84836454	NM_025386:17	Fbxo36	INSIDE	1.298	2.008	1333.92	2679.17	2.608	1115.54	2908.78
A_68_P20187368	chr1:43220801-43220845	NM_010212:-16	Fhl2	PROMOTER	1.298	1.716	826.80	1418.44	2.226	680.97	1516.00
A_68_P26891188	chr9:122656242-122656286	NM_001199736:-199	Gm9524	PROMOTER	1.298	3.596	503.58	1810.73	4.666	499.35	2330.23
A_68_P20640026	chr1:137429314-137429358	NM_173437:52596	Nav1	INSIDE	1.298	4.238	2411.73	10220.24	5.501	1980.38	10893.07
A_68_P21527967	chr2:112106072-112106116	NM_133649:-376	Slc12a6	PROMOTER	1.298	1.451	927.01	1345.07	1.884	763.41	1437.92
A_68_P26983380	chr10:19571274-19571318	NM_029529:-31	Slc35d3	PROMOTER	1.298	1.655	1673.61	2769.15	2.148	1423.42	3057.61
A_68_P32582485	chrX:103222578-103222622	NM_001109757:-14	Atp7a	PROMOTER	1.297	2.689	2236.07	6013.78	3.487	1336.28	4659.65
A_68_P24951826	chr7:5008661-5008708	NM_146178:357	Ccdc106	INSIDE	1.297	2.334	1094.43	2554.25	3.028	940.64	2848.39
A_68_P30379091	chr15:81523948-81523992	NM_001164320:3747	Chadl	INSIDE	1.297	6.386	1931.34	12334.19	8.283	1544.16	12790.77
A_68_P22715806	chr4:8617250-8617294	NM_001081417:-795	Chd7	PROMOTER	1.297	2.698	663.02	1788.55	3.499	637.84	2232.01
A_68_P24618503	chr6:87800411-87800455	NM_001109745:668	Cnbp	INSIDE	1.297	2.147	2228.36	4784.93	2.785	1852.11	5157.96
A_68_P28920310	chr13:31065956-31066000	NM_025588:-62	Exoc2	PROMOTER	1.297	1.998	630.43	1259.64	2.592	542.21	1405.48
A_68_P31215002	chr17:48059670-48059714	NM_001110824:1889	Foxp4	INSIDE	1.297	2.173	1470.78	3196.60	2.819	1103.43	3111.00
A_68_P25892513	chr8:60130467-60130511	NM_001167981:1364	Galnt7	INSIDE	1.297	1.735	1025.27	1778.59	2.251	853.93	1921.79
A_68_P24518617	chr6:66846588-66846632	NM_001177558:-274	Gng12	PROMOTER	1.297	2.227	2008.43	4472.91	2.888	1740.11	5025.49
A_68_P28043442	chr11:96145448-96145492	NM_010461:2252	Hoxb8	INSIDE	1.297	2.629	2133.62	5608.86	3.410	1790.42	6104.62
A_68_P23415961	chr4:151383718-151383762	NM_001033352:741	Klhl21	INSIDE	1.297	2.062	866.08	1785.56	2.674	782.25	2091.51
A_68_P20883821	chr1:183772425-183772469	NM_133815:86	Lbr	INSIDE	1.297	1.416	1823.70	2581.48	1.837	1533.40	2816.29
A_68_P24591516	chr6:83065809-83065853	NM_020619:331	Mogs	INSIDE	1.297	1.518	1201.75	1824.53	1.969	1089.85	2146.46
A_68_P27890687	chr11:68505493-68505537	NM_175260:98	Myh10	INSIDE	1.297	1.651	7120.46	11758.59	2.142	5282.58	11312.67
A_68_P32240448	chrX:7419508-7419552	NM_138604:574	Otud5	INSIDE	1.297	1.990	821.81	1635.53	2.582	546.81	1411.90
A_68_P23610095	chr5:37260897-37260941	NM_172994:1110	Ppp2r2c	INSIDE	1.297	3.081	947.02	2918.08	3.996	824.42	3294.65
A_68_P23544149	chr5:24347845-24347889	NM_053075:313	Rheb	INSIDE	1.297	2.678	1112.46	2979.11	3.473	1003.77	3485.93
A_68_P28607918	chr12:87420289-87420333	NM_009368:-319	Tgfb3	DIVERGENT_PROMOTER	1.297	1.625	1813.93	2947.36	2.107	1466.67	3089.80
A_68_P25728011	chr8:26712636-26712680	NM_001001735:-119	Whsc1l1	DIVERGENT_PROMOTER	1.297	2.193	415.37	910.81	2.844	400.11	1137.72
A_68_P31147211	chr17:32966831-32966875	NM_177359:341	Zfp799	INSIDE	1.297	1.526	1016.46	1551.41	1.980	936.86	1855.30
A_68_P26721431	chr9:91250815-91250859	NM_009573:9801	Zic1	DOWNSTREAM	1.297	2.127	558.04	1186.88	2.759	439.03	1211.37
A_68_P30328927	A_68_P30328927			Unknown	1.297	3.543	1419.56	5029.41	4.594	1232.10	5660.00
A_68_P32259779	chrX:11583677-11583722			Unknown	1.297	1.445	836.56	1209.04	1.874	377.74	708.00
A_68_P21840072	chr2:168032731-168032775	NM_009628:-190	Adnp	PROMOTER	1.296	1.524	1047.99	1597.65	1.976	844.77	1669.09
A_68_P25030929	chr7:31099110-31099154	NM_198027:5361	Alkbh6	INSIDE	1.296	2.518	821.79	2069.16	3.264	711.80	2323.13
A_68_P29699202	chr14:70499993-70500037	NM_021328:63	Bin3	INSIDE	1.296	2.412	1652.74	3986.13	3.125	1445.51	4517.72
A_68_P27565933	chr11:5872063-5872107	NM_001174053:93667	Camk2b	INSIDE	1.296	1.572	1338.96	2105.01	2.037	1049.68	2138.32
A_68_P29193442	chr13:85329134-85329178	NM_023243:75	Ccnh	INSIDE	1.296	2.881	820.59	2363.73	3.734	684.11	2554.41
A_68_P26080011	chr8:97400151-97400195	NM_053246:40	Dok4	INSIDE	1.296	2.513	872.35	2191.88	3.257	725.41	2362.32
A_68_P28687870	chr12:103057567-103057611	NM_011812:-323	Fbln5	PROMOTER	1.296	1.498	2819.28	4223.31	1.941	2099.17	4074.35
A_68_P25095551	chr7:53121751-53121795	NM_008172:279	Grin2d	INSIDE	1.296	1.895	489.52	927.67	2.456	452.89	1112.39
A_68_P29628416	chr14:58143558-58143602	NM_145837:-85	Il17d	PROMOTER	1.296	4.077	1297.77	5291.50	5.286	1291.87	6828.41
A_68_P26920439	chr10:7445765-7445809	NM_011835:-11	Katna1	PROMOTER	1.296	1.732	891.38	1543.67	2.244	780.21	1750.68
A_68_P28480022	chr12:62624309-62624353	NM_178714:-1288	Lrfn5	PROMOTER	1.296	2.704	1739.40	4702.88	3.503	1494.33	5234.42
A_68_P25512277	chr7:135883845-135883889	NM_145955:77	Mcmbp	INSIDE	1.296	3.691	1193.78	4406.24	4.784	1081.71	5174.93
A_68_P23749117	chr5:64484174-64484218	NM_025700:8	Pgm1	INSIDE	1.296	1.552	2407.28	3735.03	2.011	1942.84	3906.57
A_68_P23597147	chr5:35291908-35291952	NM_173402:-166	Rgs12	PROMOTER	1.296	1.572	4666.64	7334.58	2.038	3454.23	7038.54
A_68_P22411696	chr3:108086789-108086833	NM_019972:-239	Sort1	PROMOTER	1.296	1.683	2039.03	3431.09	2.180	1716.77	3742.63
A_68_P30680165	chr16:37384543-37384587	NM_001114611:480	Stxbp5l	INSIDE	1.296	1.425	1025.40	1461.51	1.847	864.69	1597.05
A_68_P20803942	chr1:169156556-169156600	NM_030724:58680	Uck2	INSIDE	1.296	7.153	4043.17	28920.81	9.270	2672.35	24771.66
A_68_P27564781	chr11:5640818-5640862	NM_178623:339	Urgcp	INSIDE	1.296	1.533	1403.12	2150.98	1.986	1221.93	2426.95
A_68_P23396198	chr4:148116954-148116998	AK142257:4167		DOWNSTREAM	1.296	1.966	654.23	1286.44	2.548	545.79	1390.71
A_68_P23591272	chr5:34163692-34163736	ENSMUST00000168912:-590		PROMOTER	1.296	3.037	1264.98	3841.96	3.935	1218.12	4793.78
A_68_P31796719	chr18:68459858-68459902	NM_153794:107	4933403F05Rik	INSIDE	1.295	2.068	1237.67	2559.73	2.678	1164.54	3119.03
A_68_P21224222	chr2:53050731-53050775	NM_022989:-365	Arl6ip6	DIVERGENT_PROMOTER	1.295	2.236	707.67	1582.53	2.897	611.90	1772.61

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27143037	chr10:53317259-53317303	NM_025541:514	Asf1a	INSIDE	1.295	1.670	736.58	1230.13	2.163	660.03	1427.71
A_68_P23609089	chr5:37086829-37086873	NM_001081232:358	D5Ertd579e	INSIDE	1.295	2.159	1653.74	3570.45	2.796	1483.58	4147.77
A_68_P31058444	chr17:14340634-14340678	NM_172826:182	Dact2	INSIDE	1.295	2.031	1656.22	3363.44	2.630	1469.67	3865.24
A_68_P25021026	chr7:29083763-29083810	NM_007866:3018	Dll3	INSIDE	1.295	4.332	459.85	1992.26	5.613	384.31	2156.98
A_68_P28185091	chr11:120392009-120392053	NM_008101:-10	Gcgr	PROMOTER	1.295	4.453	682.96	3041.50	5.768	701.11	4044.11
A_68_P26443399	chr9:40263199-40263243	NM_172768:129	Gramd1b	INSIDE	1.295	3.536	634.59	2243.80	4.579	513.18	2349.66
A_68_P23316586	chr4:132807259-132807303	NM_016693:10548	Map3k6	INSIDE	1.295	2.203	1444.26	3181.78	2.853	1189.96	3394.98
A_68_P32767195	chrX:154036840-154036884	NM_172307:-215	Mbtps2	PROMOTER	1.295	2.882	619.68	1786.06	3.732	436.69	1629.56
A_68_P24171033	chr5:147775400-147775448	NM_029581:-74	Mtif3	PROMOTER	1.295	1.775	735.55	1305.25	2.298	603.64	1387.16
A_68_P26159422	chr8:112392225-112392269	NM_001122594:-256	Phlpp2	PROMOTER	1.295	1.681	833.82	1401.73	2.178	686.14	1494.09
A_68_P20022051	chr1:9290036-9290080	NM_027671:-247	Sntg1	PROMOTER	1.295	2.442	1826.03	4458.62	3.162	1522.51	4813.99
A_68_P31108362	chr17:26250244-26250288	NM_021793:6	Tmem8	INSIDE	1.295	2.581	1564.78	4039.30	3.344	1306.04	4367.59
A_68_P24541202	chr6:72295118-72295162	NM_138592:29	Usp39	INSIDE	1.295	1.490	1146.19	1707.91	1.930	1033.63	1995.15
A_68_P28430598	chr12:52694641-52694685	NM_001198835:335	Coch	INSIDE	1.294	2.078	1764.73	3667.86	2.690	1527.41	4109.17
A_68_P24273894	chr6:18464782-18464826	NM_080285:21	Cttnbp2	INSIDE	1.294	1.778	1181.03	2099.74	2.301	1018.93	2344.69
A_68_P22401913	chr3:106285353-106285397	NM_001093754:26	Dennd2d	INSIDE	1.294	3.081	1640.47	5054.79	3.988	1337.17	5332.95
A_68_P29310173	chr13:109004454-109004498	NM_029001:-121	Elovl7	PROMOTER	1.294	1.521	1764.64	2684.73	1.969	1532.75	3017.55
A_68_P32454246	chrX:68808773-68808817	NM_008253:-373	Hmgb3	PROMOTER	1.294	3.129	1415.47	4428.52	4.047	620.21	2510.02
A_68_P20883818	chr1:183772112-183772156	NM_133815:398	Lbr	INSIDE	1.294	1.415	1047.10	1481.24	1.831	755.53	1383.19
A_68_P31876427	chr18:82645364-82645408	NM_001025245:872	Mbp	INSIDE	1.294	3.051	1072.60	3272.01	3.947	915.05	3611.26
A_68_P25115907	chr7:57231065-57231109	NM_001037906:367	Nell1	INSIDE	1.294	1.685	891.14	1501.82	2.180	793.41	1729.68
A_68_P31112707	chr17:26976313-26976357	NM_008700:2176	Nkx2-5	INSIDE	1.294	1.806	369.56	667.57	2.338	343.85	803.90
A_68_P28072819	chr11:101107662-101107706	NM_019444:37	Ramp2	INSIDE	1.294	2.718	328.94	894.00	3.517	321.48	1130.56
A_68_P28160197	chr11:116442143-116442187	NM_173755:597	Ube2o	INSIDE	1.294	1.724	3669.26	6324.85	2.231	2951.83	6585.43
A_68_P20372370	chr1:78654845-78654889	NM_001136226:-148	Utp14b	PROMOTER	1.294	1.781	1816.14	3234.22	2.304	1502.22	3460.55
A_68_P32246203	chrX:8849653-8849697	NM_023500:-235	Xk	PROMOTER	1.294	1.906	1202.85	2292.65	2.466	709.62	1750.01
A_68_P27913320	chr11:72609515-72609559	NM_001045536:-191	Zzef1	DIVERGENT_PROMOTER	1.294	3.595	2737.74	9842.33	4.653	2173.63	10113.28
A_68_P32321492	chrX:34588621-34588665	NM_173779:-197	Ankrd58	PROMOTER	1.293	1.601	1448.89	2320.04	2.071	629.26	1303.16
A_68_P31351856	chr17:74928018-74928062	NM_007566:406	Birc6	INSIDE	1.293	2.064	1818.05	3752.79	2.669	1579.44	4216.08
A_68_P31746195	chr18:59334616-59334660	NM_001081328:-355	Chsy3	PROMOTER	1.293	6.116	886.14	5419.96	7.909	770.84	6096.84
A_68_P28003125	chr11:88835210-88835254	NM_016706:-16	Coil	PROMOTER	1.293	2.782	1351.04	3759.26	3.599	1133.47	4079.33
A_68_P29570463	chr14:46008598-46008642	NM_019425:-149	Gnpnat1	PROMOTER	1.293	1.955	3987.71	7794.83	2.528	3191.70	8069.56
A_68_P27270903	chr10:77364823-77364867	NM_145152:437	Lrrc3	INSIDE	1.293	1.944	834.13	1621.50	2.514	700.71	1761.68
A_68_P20439698	chr1:92895160-92895204	NM_001111312:-121	Lrrfip1	PROMOTER	1.293	1.583	1984.32	3141.16	2.047	1685.98	3450.53
A_68_P21206010	chr2:49922433-49922477	NM_177139:473	Lypd6	INSIDE	1.293	1.632	1611.87	2631.17	2.111	1345.53	2840.29
A_68_P23229426	chr4:116136323-116136367	NM_001042743:444	Mast2	INSIDE	1.293	2.187	4856.44	10621.51	2.827	3932.85	11119.76
A_68_P30083236	chr15:25711164-25711208	NM_019472:158882	Myo10	INSIDE	1.293	2.101	651.35	1368.72	2.717	574.21	1560.17
A_68_P21853413	chr2:170321616-170321660	NM_001013369:-289	Pfdn4	PROMOTER	1.293	1.661	1576.42	2618.61	2.148	1332.70	2862.35
A_68_P31421199	chr17:87506697-87506741	NM_019654:-300	Socs5	PROMOTER	1.293	1.366	3279.11	4479.12	1.767	2651.67	4684.64
A_68_P28307236	chr12:28024096-28024140	NM_009234:3465	Sox11	INSIDE	1.293	1.883	313.19	589.72	2.435	261.88	637.57
A_68_P20377583	chr1:79758129-79758173	NM_001111279:194	Wdfy1	INSIDE	1.293	0.392	1311.86	514.44	0.507	1043.61	529.16
A_68_P30570067	chr16:16600102-16600146	ENSMUST00000162671:-53		PROMOTER	1.293	2.661	368.27	979.95	3.440	389.81	1341.11
A_68_P25354926	chr7:105457776-105457820	NM_025408:239	Acer3	INSIDE	1.292	2.080	1948.78	4053.49	2.688	1678.46	4512.23
A_68_P24050195	chr5:122872882-122872926	NM_019805:452	Anapc7	INSIDE	1.292	1.992	532.74	1061.01	2.573	509.93	1311.83
A_68_P32533248	chrX:90540027-90540071	NM_007492:8064	Arx	INSIDE	1.292	2.283	3043.46	6947.97	2.950	1738.12	5128.00
A_68_P29338045	chr13:113778996-113779044	NM_001081062:1011	Ccno	INSIDE	1.292	3.069	801.64	2460.34	3.966	758.75	3009.01
A_68_P28575717	chr12:81535921-81535965	NM_177267:1646	Dcaf5	INSIDE	1.292	1.945	761.43	1480.71	2.512	686.74	1725.41
A_68_P32561247	chrX:97972457-97972501	NM_001177780:-131	Dlg3	PROMOTER	1.292	1.830	469.95	860.05	2.365	296.52	701.36
A_68_P26132621	chr8:107793840-107793884	NM_011939:89	Hsf4	INSIDE	1.292	2.204	951.14	2096.24	2.846	787.17	2240.60
A_68_P26348936	chr9:21599583-21599627	NM_145611:3386	Kank2	INSIDE	1.292	2.565	376.16	964.87	3.315	377.67	1251.79
A_68_P27535068	chr10:126725665-126725709	NM_033072:141	Mbd6	INSIDE	1.292	3.226	15005.23	48405.64	4.169	9062.07	37780.41

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31792975	chr18:67801303-67801347	NM_134138:72	Psmg2	INSIDE	1.292	2.938	3692.97	10849.28	3.797	3209.89	12187.58
A_68_P32567037	chrX:99266374-99266418	NM_183318:250	Rgag4	INSIDE	1.292	2.271	2620.59	5950.26	2.933	1289.14	3780.89
A_68_P23322288	chr4:133898952-133898996	NM_001039677:-10	Slc30a2	PROMOTER	1.292	2.352	2360.47	5551.59	3.038	1847.56	5612.36
A_68_P27841611	chr11:60024072-60024116	NM_011480:10012	Srebf1	INSIDE	1.292	1.462	728.78	1065.73	1.890	589.49	1114.01
A_68_P24287934	chr6:21802232-21802276	NM_173007:261	Tspan12	INSIDE	1.292	1.959	1609.18	3151.72	2.531	1361.68	3446.17
A_68_P23792610	chr5:72971627-72971672	NM_174877:674	Zar1	INSIDE	1.292	1.596	1846.35	2947.34	2.063	1567.68	3233.66
A_68_P31206539	chr17:46520782-46520826	NM_207671:90	Zfp318	INSIDE	1.292	1.937	647.28	1253.67	2.503	594.61	1488.31
A_68_P23962880	chr5:107125598-107125642	NM_026856:229	Zfp644	INSIDE	1.292	1.447	1081.50	1565.06	1.869	941.63	1760.18
A_68_P24951683	chr7:4983086-4983130	NM_001033383:11131	Zfp865	INSIDE	1.292	2.731	914.74	2498.03	3.528	838.17	2957.14
A_68_P32977601	chr12:20821877-20821921	NR_015521:-258	1700030C10Rik	PROMOTER	1.291	1.865	483.32	901.37	2.408	435.24	1047.96
A_68_P23424871	chr4:152806869-152806913	NM_001099299:50049	Ajap1	INSIDE	1.291	2.209	646.85	1428.93	2.853	532.82	1519.98
A_68_P26158883	chr8:112302603-112302647	NM_009677:85	Ap1g1	INSIDE	1.291	1.508	858.11	1294.02	1.947	719.87	1401.74
A_68_P27489850	chr10:118676304-118676348	NM_027994:785	Cand1	INSIDE	1.291	3.668	1251.31	4589.18	4.736	997.46	4723.99
A_68_P21907947	chr2:180763825-180763869	NM_015730:10036	Chrna4	INSIDE	1.291	4.584	4251.08	19486.65	5.916	2753.77	16290.43
A_68_P28156775	chr11:115866293-115866337	NM_001005608:30276	Itgb4	INSIDE	1.291	3.996	1073.42	4289.31	5.161	926.98	4783.77
A_68_P25678290	chr8:15028480-15028524	NM_029116:17478	Kbtbd11	INSIDE	1.291	10.300	1395.55	14373.56	13.299	1184.11	15747.21
A_68_P22201292	chr3:65470413-65470457	NM_001037923:278	Lekr1	INSIDE	1.291	1.788	2086.45	3729.58	2.307	1775.48	4095.78
A_68_P23244387	chr4:118905895-118905939	NM_001042411:-517	Lepre1	PROMOTER	1.291	3.108	1445.26	4491.51	4.011	1243.96	4989.48
A_68_P21006482	chr2:11423738-11423782	NM_001177752:-43	Pfkfb3	PROMOTER	1.291	1.678	388.09	651.03	2.166	300.46	650.91
A_68_P31113240	chr17:27070276-27070320	NM_009343:227	Phf1	INSIDE	1.291	2.976	1739.48	5176.56	3.841	1319.91	5069.64
A_68_P30397290	chr15:84684091-84684135	NM_001081166:2447	Phf21b	INSIDE	1.291	1.396	1057.35	1475.57	1.801	927.49	1670.49
A_68_P23767120	chr5:67698295-67698339	NM_178651:121	Slc30a9	INSIDE	1.291	1.576	868.24	1368.65	2.036	819.72	1668.74
A_68_P21221436	chr2:52601404-52601448	NM_019667:-243	Stam2	PROMOTER	1.291	2.482	1728.93	4290.50	3.205	1486.04	4762.12
A_68_P32241633	chrX:7651543-7651587	NM_011514:322	Suv39h1	INSIDE	1.291	2.502	941.04	2354.96	3.232	573.08	1852.17
A_68_P27504341	chr10:121023507-121023551	NM_019786:322	Tbk1	INSIDE	1.291	1.616	848.44	1370.73	2.086	761.54	1588.48
A_68_P26136330	chr8:108379864-108379908	NM_021513:884	Thap11	INSIDE	1.291	3.037	404.18	1227.39	3.921	424.57	1664.53
A_68_P22749332	chr4:15193464-15193508	NM_181401:520	Tmem64	INSIDE	1.291	4.049	4310.47	17453.31	5.229	3107.10	16246.49
A_68_P24425523	chr6:47997406-47997450	NM_001081382:685	Zfp777	INSIDE	1.291	4.365	1994.40	8706.21	5.635	1644.80	9267.80
A_68_P22820143	chr4:32326406-32326450	ENSMUST00000165661:-4279		PROMOTER	1.291	2.372	3698.56	8771.98	3.061	2955.79	9047.42
A_68_P31112027	chr17:26853342-26853387	NM_029870:770	A930001N09Rik	INSIDE	1.290	4.487	3324.10	14916.56	5.790	2662.85	15417.63
A_68_P31201456	chr17:45643922-45643966	NM_198608:155	Aars2	INSIDE	1.290	1.501	1304.28	1957.55	1.937	1141.63	2211.06
A_68_P29660043	chr14:63859471-63859515	NM_008092:4605	Gata4	INSIDE	1.290	5.842	1535.59	8970.55	7.535	1267.63	9551.91
A_68_P24288409	chr6:21900159-21900203	NM_023626:566	Ing3	INSIDE	1.290	1.750	947.28	1657.65	2.257	655.93	1480.32
A_68_P23154199	chr4:100937872-100937916	NM_146145:-7	Jak1	PROMOTER	1.290	1.360	3369.15	4581.96	1.754	2919.73	5121.17
A_68_P25262926	chr7:86887923-86887967	NM_011068:-33	Pex11a	DIVERGENT_PROMOTER	1.290	1.634	513.12	838.21	2.107	407.28	858.00
A_68_P31302643	chr17:66132754-66132798	NM_001114131:82	Ppp4r1	INSIDE	1.290	2.181	3218.47	7019.49	2.814	3034.14	8537.48
A_68_P20945776	chr1:194660855-194660899	NM_001177794:17065	Sertad4	DOWNSTREAM	1.290	2.106	2255.20	4749.86	2.717	1886.12	5125.42
A_68_P23768850	chr5:67999647-67999692	NM_001033415:548	Shisa3	INSIDE	1.290	2.366	1453.55	3438.65	3.052	1326.83	4049.89
A_68_P30467112	chr15:96885230-96885274	NM_027052:1135	Slc38a4	INSIDE	1.290	1.409	1492.53	2103.70	1.819	1235.31	2246.88
A_68_P20056643	chr1:16655352-16655396	NM_026392:103	Tmem70	INSIDE	1.290	2.740	389.12	1066.34	3.535	415.74	1469.49
A_68_P27635748	chr11:21138636-21138680	NM_139061:-233	Vps54	PROMOTER	1.290	1.623	1586.76	2576.07	2.095	1159.94	2429.62
A_68_P30024033	chr15:12754220-12754264	NM_029998:170	6030458C11Rik	INSIDE	1.289	2.789	479.92	1338.53	3.595	494.68	1778.54
A_68_P27977897	chr11:84326883-84326927	NM_019816:99	Aatf	INSIDE	1.289	2.065	528.48	1091.23	2.661	504.12	1341.36
A_68_P22894883	chr4:47486977-47487022	NM_019998:240	Alg2	INSIDE	1.289	0.444	1285.77	571.38	0.573	1172.33	671.43
A_68_P24816835	chr6:124705909-124705953	NM_007881:575	Atn1	INSIDE	1.289	1.789	6594.29	11798.51	2.307	4687.41	10813.01
A_68_P23637946	chr5:42235648-42235692	NM_001081422:-116	Bod1l	PROMOTER	1.289	2.274	1021.79	2323.87	2.931	906.42	2656.42
A_68_P31792971	chr18:67800851-67800895	NM_001081073:118	Cep76	INSIDE	1.289	2.042	727.58	1485.36	2.632	608.66	1602.26
A_68_P24622150	chr6:88396669-88396713	NM_023060:-157	Eefsec	PROMOTER	1.289	2.045	1396.71	2855.59	2.636	1125.78	2967.78
A_68_P28675869	chr12:100631334-100631378	NM_183186:56928	Foxn3	INSIDE	1.289	1.511	1901.73	2872.71	1.946	1651.92	3215.39
A_68_P28293531	chr12:25783897-25783941	NM_010496:-2961	Id2	PROMOTER	1.289	1.697	431.51	732.39	2.187	412.28	901.78
A_68_P25958333	chr8:74213329-74213373	NM_013564:200	Insl3	INSIDE	1.289	1.549	1098.02	1701.21	1.997	1021.72	2040.68

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31784507	chr18:66162242-66162286	NM_027400:25	Lman1	INSIDE	1.289	2.079	1219.80	2535.98	2.681	1092.13	2927.77
A_68_P23536416	chr5:22940274-22940318	NM_026984:50	Mll5	INSIDE	1.289	1.599	1101.95	1762.36	2.062	866.53	1786.43
A_68_P27282702	chr10:79819562-79819606	NM_183152:381	Plk5	INSIDE	1.289	3.503	1586.64	5558.53	4.514	1391.65	6282.17
A_68_P29055227	chr13:55573644-55573688	NM_001030296:8039	Prr7	INSIDE	1.289	1.733	780.65	1353.25	2.234	668.25	1492.81
A_68_P21808097	chr2:162486461-162486505	NM_021464:401	Ptprt	INSIDE	1.289	1.636	462.15	756.29	2.109	441.86	931.93
A_68_P23405235	chr4:149655313-149655357	NM_001085492:-690	Rere	PROMOTER	1.289	1.620	542.77	879.49	2.089	483.56	1010.13
A_68_P26684174	chr9:83442213-83442257	NM_172507:290	Sh3bgrl2	INSIDE	1.289	2.398	1482.08	3553.70	3.091	1280.38	3958.13
A_68_P27099065	chr10:42894301-42894345	NM_175407:14	Sobp	INSIDE	1.289	5.791	3868.36	22399.91	7.462	3050.32	22762.69
A_68_P31093840	chr17:23956472-23956516	NM_175229:16341	Srrm2	INSIDE	1.289	2.139	593.78	1270.33	2.757	484.74	1336.42
A_68_P26626133	chr9:71959405-71959449	NM_011544:200	Tcf12	INSIDE	1.289	2.619	913.21	2391.53	3.377	781.52	2639.11
A_68_P27812935	chr11:54769524-54769568	NM_001199275:78	Tnip1	INSIDE	1.289	1.866	1464.37	2732.85	2.406	1183.47	2847.72
A_68_P30570745	chr16:16871029-16871073	NM_011624:67	Top3b	INSIDE	1.289	1.898	1622.30	3079.60	2.446	1432.16	3503.72
A_68_P26593991	chr9:66440276-66440320	NM_144937:489	Usp3	INSIDE	1.289	3.852	611.59	2355.56	4.963	567.75	2817.64
A_68_P27504461	chr10:121043178-121043222	NM_001081056:20172	Xpot	INSIDE	1.289	2.492	2448.39	6101.70	3.213	1885.14	6056.55
A_68_P22834884	chr4:35173017-35173061	NM_001081343:91	3110043O21Rik	INSIDE	1.288	1.629	4198.56	6839.04	2.097	3555.94	7458.02
A_68_P31323856	chr17:69766821-69766865	NR_026848:1056	C030034I22Rik	INSIDE	1.288	0.539	2770.30	1492.87	0.694	2114.29	1467.09
A_68_P29613380	chr14:55250977-55251021	NM_199470:9203	Cdh24	INSIDE	1.288	1.927	487.69	939.59	2.482	393.03	975.56
A_68_P21566996	chr2:118752704-118752748	NM_028117:494	Chst14	INSIDE	1.288	1.697	809.38	1373.30	2.186	689.33	1506.57
A_68_P21100053	chr2:29745687-29745731	NM_001177662:126	Odf2	INSIDE	1.288	1.629	1415.00	2305.63	2.098	1112.08	2333.06
A_68_P23575374	chr5:31210401-31210445	NM_024460:-261	Ost4	DIVERGENT_PROMOTER	1.288	1.409	2672.42	3766.08	1.814	2171.54	3940.14
A_68_P23435280	chr4:154338579-154338623	NM_172990:359	Pank4	INSIDE	1.288	1.476	1246.41	1839.65	1.901	991.41	1885.04
A_68_P24054155	chr5:123591978-123592024	NM_175092:-9362	Rhof	PROMOTER	1.288	4.707	520.70	2450.69	6.062	425.67	2580.47
A_68_P23331867	chr4:135609136-135609180	NM_025919:128	Rpl11	INSIDE	1.288	1.717	884.91	1519.80	2.212	876.07	1938.03
A_68_P25412182	chr7:117365409-117365453	NM_009302:214	Swap70	INSIDE	1.288	1.517	1424.97	2161.70	1.954	1279.91	2500.32
A_68_P32193377	chr19:55390489-55390533	NM_001033573:12	Zdhhc6	INSIDE	1.288	2.787	1228.55	3423.75	3.591	1021.82	3668.88
A_68_P27212542	chr10:67011815-67011859	NM_001005419:-133	Ado	PROMOTER	1.287	2.556	800.10	2044.99	3.289	719.22	2365.29
A_68_P24674233	chr6:97567326-97567370	NM_145148:303	Frmd4b	INSIDE	1.287	1.396	1318.38	1840.78	1.797	1072.41	1926.75
A_68_P27278596	chr10:79198751-79198795	NM_008226:19394	Hcn2	INSIDE	1.287	3.120	1656.68	5169.41	4.014	1286.43	5164.32
A_68_P31149892	chr17:33786930-33786974	NM_001109913:35451	Hnrnpm	INSIDE	1.287	2.029	795.68	1614.10	2.611	714.21	1865.02
A_68_P23927389	chr5:100468389-100468433	NM_016690:-169	Hnrpdl	DIVERGENT_PROMOTER	1.287	2.305	549.11	1265.47	2.966	501.84	1488.28
A_68_P23323460	chr4:134107793-134107837	NM_029100:267	Sepn1	INSIDE	1.287	1.600	1384.81	2215.86	2.060	1151.32	2371.60
A_68_P22149790	chr3:54590088-54590132	NM_019483:30607	Smad9	INSIDE	1.287	3.996	3970.33	15864.16	5.142	2916.86	14999.46
A_68_P29959675	chr14:122506713-122506757	NM_080556:431	Tm9sf2	INSIDE	1.287	1.677	4349.22	7293.71	2.158	3970.40	8567.06
A_68_P25957925	chr8:74152799-74152844	NM_001029873:42835	Unc13a	INSIDE	1.287	2.711	195.03	528.66	3.488	147.91	515.87
A_68_P26884594	chr9:121551770-121551814	NM_011703:-41	Vipr1	DIVERGENT_PROMOTER	1.287	1.605	2744.98	4405.56	2.066	2386.59	4931.14
A_68_P24994117	chr7:20162610-20162654	NM_022409:-3	Zfp296	DIVERGENT_PROMOTER	1.287	1.436	1275.47	1831.12	1.848	932.61	1723.28
A_68_P23270666	chr4:124527512-124527556	NM_001142727:440	1110065P20Rik	INSIDE	1.286	1.856	516.53	958.90	2.387	469.98	1121.94
A_68_P23331196	chr4:135472765-135472809	NM_009924:21468	Cnr2	INSIDE	1.286	3.113	1739.14	5414.11	4.002	1210.68	4845.61
A_68_P27274155	chr10:77888554-77888598	NM_007793:162	Cstb	INSIDE	1.286	2.279	1337.01	3046.89	2.932	1107.48	3246.64
A_68_P31145776	chr17:32629460-32629505	NM_177307:39815	Cyp4f39	INSIDE	1.286	1.667	938.53	1564.61	2.143	826.79	1772.08
A_68_P28924067	chr13:31717371-31717415	NM_010225:-292	Foxf2	PROMOTER	1.286	1.874	3406.06	6383.19	2.410	2661.31	6413.06
A_68_P24864942	chr6:135015624-135015668	NM_181444:-33	Gprc5a	PROMOTER	1.286	2.270	1171.43	2659.29	2.919	1027.49	2999.59
A_68_P21132680	chr2:35138083-35138127	NM_146120:205	Gsn	INSIDE	1.286	2.038	662.85	1351.12	2.621	535.83	1404.57
A_68_P20267137	chr1:60100051-60100095	NM_027407:-141	Ica1l	PROMOTER	1.286	4.945	449.29	2221.94	6.359	437.87	2784.64
A_68_P20007252	chr1:4797954-4797998	NM_008866:3	Lypla1	INSIDE	1.286	2.398	898.17	2153.65	3.085	813.00	2507.85
A_68_P25089969	chr7:52147509-52147554	NM_029365:205	Med25	INSIDE	1.286	2.642	1439.58	3803.16	3.398	1241.53	4219.11
A_68_P31098020	chr17:24687629-24687673	NM_013630:756	Pkd1	INSIDE	1.286	1.763	1160.09	2045.50	2.268	908.85	2061.40
A_68_P31121256	chr17:28369519-28369563	NM_011145:-158	Ppard	PROMOTER	1.286	2.187	2258.23	4939.36	2.812	1803.11	5070.55
A_68_P28112586	chr11:108204519-108204563	NM_011101:662	Prkca	INSIDE	1.286	1.483	698.20	1035.70	1.907	649.45	1238.71
A_68_P29020469	chr13:48720658-48720702	NM_207232:262	Ptpdc1	INSIDE	1.286	1.442	1021.30	1472.37	1.853	920.53	1706.07
A_68_P32790431	chrX:159081429-159081473	NM_178256:83	Reps2	INSIDE	1.286	1.498	1210.21	1812.57	1.926	656.85	1264.84

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P21095252	chr2:28980951-28980995	NM_198033:461	Setx	INSIDE	1.286	2.330	2577.83	6006.83	2.997	2228.89	6679.52
A_68_P23896970	chr5:93371441-93371485	NM_001077596:44439	Shroom3	INSIDE	1.286	2.239	211.30	473.20	2.879	226.36	651.65
A_68_P21584534	chr2:121944006-121944050	NM_145531:94	Spg11	INSIDE	1.286	2.395	517.18	1238.88	3.081	469.57	1446.56
A_68_P25926491	chr8:67471091-67471135	NM_001163747:29	Tmem192	INSIDE	1.286	3.058	3093.79	9459.71	3.933	2762.29	10865.37
A_68_P21578171	chr2:120803024-120803068	NM_175285:249	Tmem62	INSIDE	1.286	2.537	1760.52	4466.90	3.262	1632.42	5325.09
A_68_P21622287	chr2:128793258-128793302	NM_178404:143	Zc3h6	INSIDE	1.286	1.565	1356.36	2122.77	2.013	1157.20	2329.14
A_68_P24919226	chr6:144730238-144730282	ENSMUST00000149451:179		INSIDE	1.286	2.859	569.33	1627.83	3.677	531.69	1955.14
A_68_P29098292	chr13:64414062-64414106	NM_025370:-66	1110018J18Rik	PROMOTER	1.285	1.355	2252.35	3051.57	1.741	2041.83	3554.11
A_68_P24004678	chr5:115017216-115017260	NM_001004180:-1021	BC057022	PROMOTER	1.285	2.606	457.12	1191.42	3.350	396.63	1328.67
A_68_P21569032	chr2:119148703-119148747	NM_019454:-2795	Dll4	PROMOTER	1.285	2.490	1380.47	3437.42	3.201	1138.41	3643.78
A_68_P28703499	chr12:105712671-105712715	NM_010351:-1246	Gsc	PROMOTER	1.285	3.930	554.75	2180.07	5.052	491.97	2485.21
A_68_P27289026	chr10:80809521-80809565	NM_001163165:3629	Hmg20b	INSIDE	1.285	4.034	2130.08	8592.68	5.184	1626.37	8431.46
A_68_P31381046	chr17:80461343-80461387	NM_144802:310	Hnrpll	INSIDE	1.285	2.396	1112.85	2666.55	3.080	1034.85	3187.40
A_68_P29134830	chr13:72769342-72769386	NM_010574:2939	Irx2	INSIDE	1.285	1.524	1010.13	1539.14	1.957	855.34	1674.19
A_68_P25954889	chr8:73437195-73437239	NM_173013:7344	Mtap1s	INSIDE	1.285	2.667	786.17	2096.91	3.428	606.40	2078.92
A_68_P24434513	chr6:49772917-49772962	NM_023456:212	Npy	INSIDE	1.285	2.002	1364.04	2731.28	2.573	1154.82	2970.84
A_68_P30513995	chr16:5132625-5132669	NM_008909:-72	Ppl	PROMOTER	1.285	1.706	2103.56	3589.45	2.192	1768.35	3875.98
A_68_P29612848	chr14:55136330-55136374	NM_013768:-45	Prmt5	PROMOTER	1.285	1.469	1966.21	2887.44	1.887	1657.69	3128.79
A_68_P30152573	chr15:39029866-39029910	NM_053271:11	Rims2	INSIDE	1.285	2.571	456.29	1172.97	3.304	412.49	1362.80
A_68_P30572148	chr16:17132335-17132379	NM_022324:120	Sdf2l1	INSIDE	1.285	2.570	10290.59	26442.68	3.303	8518.47	28132.55
A_68_P23283133	chr4:126698748-126698792	NM_023603:226	Sfpq	INSIDE	1.285	3.389	1636.56	5546.32	4.354	1259.70	5484.83
A_68_P27316752	chr10:86371693-86371737	NM_138673:98973	Stab2	INSIDE	1.285	4.370	8421.16	36796.62	5.617	6135.69	34464.09
A_68_P23814580	chr5:76612959-76613003	NM_011626:76	Tmem165	INSIDE	1.285	1.685	1388.10	2338.44	2.164	1228.09	2657.79
A_68_P21910958	chr2:181231832-181231876	NM_025482:-103	Tpd52l2	PROMOTER	1.285	1.674	1133.21	1897.55	2.152	1003.54	2159.55
A_68_P27992702	chr11:86940963-86941007	NM_197987:406	Trim37	INSIDE	1.285	1.772	2000.17	3544.39	2.278	1698.44	3868.21
A_68_P29220223	chr13:91881212-91881256	NM_028790:109	Acot12	INSIDE	1.284	1.849	419.07	774.72	2.373	421.38	1000.07
A_68_P31315916	chr17:68353564-68353617	NM_172964:-142	Arhgap28	PROMOTER	1.284	2.907	6597.79	19179.08	3.733	4920.44	18368.72
A_68_P20958786	chr1:196802851-196802895	NR_033564:281	C030002c11rik	INSIDE	1.284	1.870	1813.53	3391.95	2.402	1373.06	3297.79
A_68_P31160530	chr17:35837893-35837937	NM_001198833:-379	Ddr1	PROMOTER	1.284	1.753	3487.30	6111.93	2.250	2804.74	6311.79
A_68_P24138655	chr5:140448297-140448346	NM_175522:64425	Elfn1	INSIDE	1.284	6.888	2603.74	17933.33	8.841	1842.32	16287.80
A_68_P28832915	chr13:12658494-12658538	NM_026184:367	Ero1lb	INSIDE	1.284	1.726	2444.08	4218.89	2.217	2013.25	4463.20
A_68_P25025740	chr7:29956305-29956349	NM_182696:918	Ggn	INSIDE	1.284	1.402	2724.49	3818.64	1.800	2078.05	3739.60
A_68_P20226311	chr1:52289826-52289870	NM_001081081:228	Gls	INSIDE	1.284	2.898	629.51	1824.48	3.720	607.14	2258.83
A_68_P32137228	chr19:45310009-45310053	NM_010691:-304	Lbx1	PROMOTER	1.284	1.618	679.06	1098.88	2.078	597.44	1241.49
A_68_P25089971	chr7:52147810-52147854	NM_029365:-96	Med25	DIVERGENT_PROMOTER	1.284	4.218	689.10	2906.36	5.413	637.55	3451.35
A_68_P29060112	chr13:56353073-56353117	NM_010896:430	Neurog1	INSIDE	1.284	1.781	401.02	714.30	2.288	372.65	852.53
A_68_P23796836	chr5:73684343-73684387	NM_001159889:332	Ociad1	INSIDE	1.284	1.697	3145.98	5338.60	2.178	2595.73	5654.75
A_68_P30330338	chr15:73253176-73253220	NM_007982:423	Ptk2	INSIDE	1.284	1.562	2881.52	4501.91	2.006	2153.84	4320.10
A_68_P23341301	chr4:137237373-137237417	NM_001081155:-223	Rap1gap	PROMOTER	1.284	1.813	816.99	1481.18	2.328	650.14	1513.37
A_68_P26324267	chr9:15514415-15514459	NM_172289:224	Slc36a4	INSIDE	1.284	1.755	1059.09	1858.68	2.253	828.99	1867.88
A_68_P29070329	chr13:58009390-58009434	NM_001166464:281	Spock1	INSIDE	1.284	1.595	1483.77	2366.98	2.048	1279.68	2620.80
A_68_P24919225	chr6:144730091-144730135	ENSMUST00000149451:327		INSIDE	1.284	2.637	2798.00	7377.23	3.386	2432.07	8234.41
A_68_P27187160	chr10:62114175-62114219	NM_053183:-250	Ddx50	PROMOTER	1.283	1.466	2415.66	3542.06	1.881	2068.49	3890.16
A_68_P25477105	chr7:129210400-129210444	NM_026140:155	Ears2	INSIDE	1.283	1.671	938.09	1567.18	2.143	859.53	1842.21
A_68_P25503043	chr7:134072430-134072474	NM_172747:60	Kctd13	INSIDE	1.283	1.944	1767.28	3436.40	2.495	1628.44	4062.84
A_68_P23260203	chr4:122674135-122674181	NM_008506:817	Mycl1	INSIDE	1.283	1.556	1779.53	2768.55	1.997	1590.28	3175.45
A_68_P21766702	chr2:155455115-155455159	NM_001085378:18189	Myh7b	INSIDE	1.283	4.662	2897.10	13506.70	5.979	2522.48	15082.95
A_68_P21565318	chr2:118489264-118489308	NM_001033254:-26	Pak6	PROMOTER	1.283	1.421	2123.21	3017.70	1.823	1686.58	3074.60
A_68_P21775763	chr2:157030686-157030730	NM_011249:-438	Rbl1	PROMOTER	1.283	5.703	735.39	4193.93	7.318	689.12	5043.05
A_68_P28550066	chr12:76836469-76836513	NM_030750:226	Sgpp1	INSIDE	1.283	2.237	1332.38	2980.47	2.869	1135.97	3259.63
A_68_P23317228	chr4:132925954-132925998	NM_016981:290	Slc9a1	INSIDE	1.283	2.215	251.74	557.64	2.841	217.01	616.55

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P30980969	chr16:94592388-94592432	NM_009441:65	Ttc3	INSIDE	1.283	3.535	477.73	1688.68	4.536	434.97	1972.96
A_68_P26166795	chr8:113669775-113669819	ENSMUST00000143719:-416		PROMOTER	1.283	1.988	556.56	1106.28	2.549	585.55	1492.73
A_68_P26569950	chr9:62189086-62189130	NM_009672:-41	Anp32a	PROMOTER	1.282	1.417	1170.33	1657.98	1.816	953.72	1732.33
A_68_P31108558	chr17:26275751-26275795	NM_001159598:142	Axin1	INSIDE	1.282	2.387	480.12	1145.83	3.060	484.65	1483.21
A_68_P31926693	chr19:5068431-5068475	NM_054042:375	Cd248	INSIDE	1.282	1.437	1313.35	1887.33	1.842	1138.90	2097.48
A_68_P25654579	chr8:11312543-11312587	NM_009931:262	Col4a1	INSIDE	1.282	1.767	1352.72	2389.83	2.265	1125.80	2549.85
A_68_P22134618	chr3:52073824-52073868	NM_019739:1588	Foxo1	INSIDE	1.282	2.902	460.11	1335.16	3.721	417.80	1554.51
A_68_P29034746	chr13:51942012-51942056	NM_011817:-9	Gadd45g	PROMOTER	1.282	1.683	1520.19	2557.89	2.158	1305.85	2817.78
A_68_P31845028	chr18:77182898-77182942	NM_001039201:-236	Hdhd2	PROMOTER	1.282	2.623	2739.00	7183.68	3.362	2237.94	7524.61
A_68_P25678161	chr8:15011678-15011722	NM_029116:676	Kbtbd11	INSIDE	1.282	1.601	3497.59	5599.17	2.053	2773.68	5694.41
A_68_P30368805	chr15:79659228-79659272	NM_001013360:5513	Npcd	INSIDE	1.282	3.329	1213.59	4040.60	4.268	1060.34	4525.90
A_68_P24974191	chr7:13609857-13609901	NM_011588:378	Trim28	INSIDE	1.282	2.417	434.59	1050.42	3.098	404.21	1252.40
A_68_P26350760	chr9:21992704-21992748	NM_001033813:117	Zfp872	INSIDE	1.282	1.450	5185.29	7521.00	1.860	4458.97	8294.16
A_68_P22900661	chr4:48552753-48552797	NM_001145925:-43	5730528L13Rik	PROMOTER	1.281	2.663	760.51	2025.19	3.410	719.08	2452.02
A_68_P28123544	chr11:110198866-110198910	NM_147219:142	Abca5	INSIDE	1.281	6.630	420.22	2785.88	8.490	371.22	3151.78
A_68_P25601085	chr7:150646964-150647018	NM_001161624:-35	Cdkn1c	PROMOTER	1.281	2.482	817.22	2028.65	3.181	657.97	2092.98
A_68_P20149812	chr1:36748527-36748571	NM_009942:217	Cox5b	INSIDE	1.281	1.763	776.35	1368.61	2.258	718.56	1622.34
A_68_P32982444	chr5:135115258-135115302	NM_033561:-82	Eif4h	PROMOTER	1.281	2.151	1948.99	4192.90	2.757	1917.26	5285.47
A_68_P26550039	chr9:58671843-58671887	NM_001081192:546	Hcn4	INSIDE	1.281	1.486	833.96	1238.94	1.903	723.06	1375.93
A_68_P22450555	chr3:116364918-116364962	NM_008246:655	Hiat1	INSIDE	1.281	2.274	1120.72	2548.42	2.912	1009.70	2940.54
A_68_P24431597	chr6:49163986-49164030	NM_023670:945	Igf2bp3	INSIDE	1.281	2.835	532.69	1510.07	3.632	543.98	1975.72
A_68_P24993775	chr7:20108712-20108756	NM_027116:4655	Nkpd1	INSIDE	1.281	3.360	1843.00	6192.76	4.305	1558.70	6709.62
A_68_P21261721	chr2:60800858-60800902	NM_020296:381	Rbms1	INSIDE	1.281	1.939	677.62	1314.11	2.484	603.57	1499.36
A_68_P26616836	chr9:70350943-70350987	NM_033604:568	Rnf111	INSIDE	1.281	1.438	2034.62	2924.85	1.841	1835.35	3378.55
A_68_P31846338	chr18:77424406-77424450	NM_013666:-157	St8sia5	PROMOTER	1.281	1.503	1026.57	1543.38	1.926	768.49	1480.30
A_68_P25009659	chr7:26100595-26100639	NM_183311:9490	Tmem145	INSIDE	1.281	1.952	1390.26	2713.55	2.500	986.94	2467.19
A_68_P23434596	chr4:154229972-154230016	NM_172878:-314	Ttc34	PROMOTER	1.281	2.702	231.03	624.35	3.462	199.97	692.35
A_68_P28553587	chr12:77469901-77469960	NM_001172104:521	Zbtb25	INSIDE	1.281	2.065	300.12	619.89	2.646	227.00	600.72
A_68_P32977631	A_68_P32977631			Unknown	1.281	9.124	4124.59	37631.81	11.685	2407.80	28135.00
A_68_P20770397	chr1:163100998-163101042	NM_028664:28178	Ankrd45	DOWNSTREAM	1.280	1.629	896.20	1459.67	2.084	790.73	1648.05
A_68_P31793797	chr18:67959692-67959736	NM_027556:-46	Cep192	PROMOTER	1.280	2.076	1096.03	2275.59	2.657	862.87	2293.07
A_68_P25948488	chr8:72407259-72407303	NM_026818:4011	Cilp2	INSIDE	1.280	2.349	1546.96	3634.13	3.007	1315.23	3954.40
A_68_P27996721	chr11:87684998-87685044	NM_007946:4018	Epx	INSIDE	1.280	3.257	1775.56	5782.93	4.170	1261.57	5260.82
A_68_P22317571	chr3:88964184-88964228	NM_008227:-127	Hcn3	DIVERGENT_PROMOTER	1.280	1.471	2372.16	3489.68	1.882	1939.90	3651.76
A_68_P24589808	chr6:82724780-82724828	NM_013820:-356	Hk2	PROMOTER	1.280	1.737	2190.51	3805.46	2.223	1486.69	3305.12
A_68_P21777849	chr2:157385874-157385918	NM_010923:51	Nnat	INSIDE	1.280	1.704	3263.33	5561.08	2.181	2491.35	5434.40
A_68_P24785563	chr6:118146898-118146942	NM_001080780:842	Ret	INSIDE	1.280	2.030	981.12	1991.58	2.598	906.38	2354.71
A_68_P28744650	chr12:112776572-112776616	NR_033168:-2562	Snora28	PROMOTER	1.280	3.566	849.09	3028.13	4.566	712.73	3254.55
A_68_P27985534	chr11:85645565-85645609	NM_009324:-530	Tbx2	PROMOTER	1.280	1.874	1995.43	3738.55	2.399	1641.74	3937.90
A_68_P25182470	chr7:72516116-72516161	NM_001163574:-8	Tjp1	PROMOTER	1.280	2.126	612.28	1301.68	2.722	582.10	1584.61
A_68_P24449885	chr6:52266776-52266820	NR_038163:-1972	5730457N03Rik	PROMOTER	1.279	1.812	2724.97	4937.69	2.317	2335.42	5412.28
A_68_P25274224	chr7:88974543-88974587	NM_146193:-247	Btbd1	PROMOTER	1.279	2.097	1259.03	2639.57	2.682	1127.74	3024.39
A_68_P27284471	chr10:80097175-80097221	NM_001159591:4798	Csnk1g2	INSIDE	1.279	9.978	276.73	2761.19	12.765	229.00	2923.19
A_68_P31677782	chr18:46757349-46757393	NM_010120:13	Eif1a	INSIDE	1.279	1.639	3263.57	5349.50	2.096	2564.13	5374.59
A_68_P30817172	chr16:63857062-63857106	NM_010140:6899	Epha3	INSIDE	1.279	3.489	2355.73	8220.17	4.464	1910.98	8529.90
A_68_P31490816	chr18:10609789-10609833	NM_001081222:540	Esco1	INSIDE	1.279	5.594	1059.49	5927.25	7.158	936.50	6703.49
A_68_P21389688	chr2:83652981-83653025	NM_175514:118	Fam171b	INSIDE	1.279	1.837	780.83	1434.65	2.350	618.57	1453.71
A_68_P24793343	chr6:119429349-119429393	NM_133940:-315	Fbxl14	PROMOTER	1.279	2.408	444.06	1069.15	3.080	406.25	1251.09
A_68_P28419952	chr12:50484269-50484313	NM_008241:297	Foxg1	INSIDE	1.279	1.413	4166.12	5886.56	1.807	3167.10	5724.07
A_68_P28522738	chr12:71926826-71926870	NM_028127:348	Frmd6	INSIDE	1.279	2.393	600.89	1437.64	3.061	610.04	1867.43
A_68_P25307423	chr7:96553263-96553307	NM_008055:409	Fzd4	INSIDE	1.279	1.992	961.71	1916.13	2.549	900.21	2294.38

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P21722284	chr2:146909810-146909854	NM_023504:1249	Nkx2-4	INSIDE	1.279	2.098	482.85	1013.13	2.684	544.87	1462.69
A_68_P29102140	chr13:65277261-65277305	NM_175290:29742	Nlrp4f	DOWNSTREAM	1.279	1.633	1127.59	1840.90	2.089	956.29	1997.35
A_68_P26132671	chr8:107800458-107800502	NM_030152:134	Nol3	INSIDE	1.279	1.735	4572.53	7931.53	2.219	3493.10	7751.45
A_68_P31621829	chr18:36227658-36227702	NM_001167891:129134	Nrg2	INSIDE	1.279	2.408	733.99	1767.10	3.080	682.01	2100.29
A_68_P25435752	chr7:121559588-121559632	NM_011055:843	Pde3b	INSIDE	1.279	2.034	1166.03	2372.10	2.603	982.11	2556.09
A_68_P28567641	chr12:80190421-80190465	NM_029988:215	Pigh	INSIDE	1.279	2.103	1444.07	3037.03	2.690	1247.24	3354.70
A_68_P21819741	chr2:164611806-164611850	NM_133924:308	Snx21	INSIDE	1.279	1.655	1182.12	1956.02	2.116	1064.81	2252.62
A_68_P24118278	chr5:136344278-136344322	NM_021403:50325	Srrm3	INSIDE	1.279	1.738	612.85	1065.06	2.222	577.75	1283.79
A_68_P26242943	chr8:126545298-126545342	NM_133966:-111	Taf5l	DIVERGENT_PROMOTER	1.279	3.384	301.96	1021.92	4.329	350.36	1516.76
A_68_P25731030	chr8:27269296-27269340	NM_199042:678	Thap1	INSIDE	1.279	2.005	828.30	1660.65	2.565	703.16	1803.58
A_68_P20157012	chr1:38053922-38053966	NM_172054:109	Txndc9	INSIDE	1.279	1.835	1136.20	2085.46	2.348	821.10	1928.13
A_68_P32229414	A_68_P32229414			Unknown	1.279	3.806	374.96	1427.10	4.866	313.86	1527.33
A_68_P20286841	chr1:63492318-63492362	NM_001177600:-137	Adam23	PROMOTER	1.278	1.498	981.05	1469.51	1.914	832.07	1592.27
A_68_P32538581	chrX:91612170-91612214	NM_026673:-256	Apoo	PROMOTER	1.278	2.052	1710.91	3511.27	2.623	1026.75	2693.59
A_68_P24760618	chr6:113588447-113588492	NM_001113553:9	Irak2	INSIDE	1.278	3.132	575.96	1803.75	4.004	489.70	1960.68
A_68_P27887969	chr11:68026421-68026465	NM_008744:173886	Ntn1	INSIDE	1.278	2.377	1998.37	4749.87	3.036	1688.80	5128.00
A_68_P29057341	chr13:55937667-55937711	NM_011097:-4902	Pitx1	PROMOTER	1.278	1.527	1218.11	1859.65	1.950	983.27	1917.82
A_68_P23186784	chr4:106512831-106512875	ENSMUST00000151369:7673		DOWNSTREAM	1.278	1.933	747.01	1444.04	2.471	683.53	1688.67
A_68_P27179424	chr10:60708537-60708583	NM_001081127:27626	Adamts14	INSIDE	1.277	1.533	638.06	978.37	1.958	533.27	1044.15
A_68_P22376192	chr3:101407957-101408001	NM_144900:602	Atp1a1	INSIDE	1.277	3.410	530.25	1807.97	4.355	480.96	2094.48
A_68_P27914256	chr11:72774869-72774913	NM_001163336:220	Atp2a3	INSIDE	1.277	1.817	667.00	1212.17	2.321	619.08	1436.67
A_68_P27277812	chr10:79074932-79074976	NM_198614:1809	C2cd4c	INSIDE	1.277	3.920	742.15	2909.48	5.008	576.14	2885.16
A_68_P24990326	chr7:19479287-19479331	NM_001033314:16445	Ccdc61	INSIDE	1.277	2.217	1235.68	2739.02	2.831	1104.20	3126.33
A_68_P23335297	chr4:136250002-136250046	NM_010142:141826	Ephb2	INSIDE	1.277	2.121	2684.95	5694.87	2.709	1659.38	4494.55
A_68_P25420897	chr7:118923563-118923607	NM_173739:-93	Galntl4	PROMOTER	1.277	1.761	1784.11	3141.35	2.249	1590.16	3576.07
A_68_P25661161	chr8:12385043-12385087	NR_027975:-706	Gm5607	PROMOTER	1.277	1.672	686.75	1147.95	2.135	621.96	1327.66
A_68_P21345225	chr2:75497497-75497541	NR_033513:172	Gm6793	INSIDE	1.277	2.445	2267.42	5542.86	3.122	1781.65	5562.96
A_68_P26643352	chr9:75161879-75161923	NM_138719:-148	Gnb5	PROMOTER	1.277	2.194	2021.28	4434.06	2.801	1686.00	4723.04
A_68_P21766453	chr2:155418540-155418584	NM_008180:-120	Gss	PROMOTER	1.277	2.929	578.07	1693.32	3.741	527.26	1972.23
A_68_P31253724	chr17:56218702-56218746	NM_008233:-355	Hdgfrp2	DIVERGENT_PROMOTER	1.277	2.177	8173.74	17795.56	2.781	5076.44	14115.76
A_68_P24448932	chr6:52141182-52141226	NM_008265:498	Hoxa4	INSIDE	1.277	0.494	1588.96	785.36	0.631	1111.80	701.76
A_68_P31930559	chr19:5741845-5741889	NM_008520:963	Ltbp3	INSIDE	1.277	1.351	1925.91	2601.87	1.725	1473.22	2541.36
A_68_P21079215	chr2:26359143-26359187	NM_008714:178	Notch1	INSIDE	1.277	1.925	1536.95	2959.02	2.458	1356.11	3332.74
A_68_P27285560	chr10:80261376-80261420	NM_023900:-27	Plekhj1	DIVERGENT_PROMOTER	1.277	1.521	973.83	1481.23	1.942	773.64	1502.13
A_68_P25392588	chr7:112630344-112630388	NM_028444:345	Prkcdbp	INSIDE	1.277	3.374	1267.87	4278.02	4.308	1103.49	4754.16
A_68_P27915639	chr11:72990519-72990563	NM_001168470:-30	Tmem93	PROMOTER	1.277	2.941	1205.65	3546.23	3.755	942.90	3540.88
A_68_P31155253	chr17:34817071-34817115	NM_031176:9613	Tnxb	INSIDE	1.277	1.444	1128.67	1629.62	1.843	845.95	1559.44
A_68_P28003257	chr11:88861259-88861303	NM_009546:564	Trim25	INSIDE	1.277	1.678	538.09	903.17	2.144	407.52	873.71
A_68_P26822035	chr9:110020257-110020301	NM_133347:-2192	Dhx30	PROMOTER	1.276	1.621	2418.29	3919.46	2.067	2016.41	4168.91
A_68_P28221296	chr12:8305454-8305498	NM_013527:3284	Gdf7	INSIDE	1.276	1.993	1106.61	2204.97	2.542	962.99	2447.49
A_68_P25377912	chr7:109398432-109398476	NM_019566:178	Rhog	INSIDE	1.276	2.636	3077.52	8112.08	3.364	2466.75	8297.91
A_68_P28163661	chr11:117061039-117061083	NM_001113486:86	Septin9	INSIDE	1.276	6.210	1812.09	11252.51	7.923	1642.23	13011.14
A_68_P22749326	chr4:15192772-15192816	NM_181401:-172	Tmem64	PROMOTER	1.276	1.441	953.90	1374.94	1.839	883.54	1625.11
A_68_P21935175	chr3:9004387-9004431	NM_001025263:107	Tpd52	INSIDE	1.276	0.356	1955.86	695.34	0.453	1867.49	846.85
A_68_P21844347	chr2:168780711-168780761	NM_009564:351	Zfp64	INSIDE	1.276	2.304	691.58	1593.36	2.941	591.15	1738.44
A_68_P28740684	chr12:112088879-112088923	NM_001199785:412	Zfp839	INSIDE	1.276	2.023	2566.38	5190.81	2.581	2209.13	5701.65
A_68_P28055487	chr11:98156103-98156147	AK078235:9429		DOWNSTREAM	1.276	4.628	1860.55	8610.39	5.906	1531.71	9046.55
A_68_P27678672	chr11:30168407-30168451	ENSMUST00000149117:-253		PROMOTER	1.276	1.962	1405.65	2757.34	2.502	1156.17	2893.29
A_68_P20091076	chr1:24012273-24012317	NM_026503:185	1110058L19Rik	INSIDE	1.275	1.946	1250.28	2433.50	2.482	1100.40	2731.05
A_68_P24055362	chr5:123823322-123823372	NM_029850:28890	Bcl7a	INSIDE	1.275	1.672	546.43	913.64	2.132	402.49	858.18
A_68_P23280756	chr4:126234616-126234660	NM_175554:415	Clspn	INSIDE	1.275	2.118	687.12	1455.62	2.701	609.16	1645.56

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31286852	chr17:63231463-63231507	NM_010109:-818	Efna5	PROMOTER	1.275	3.126	2655.06	8298.63	3.985	1978.46	7883.59
A_68_P25151144	chr7:64764458-64764502	NM_176942:899	Gabra5	INSIDE	1.275	5.761	1529.41	8810.58	7.346	1705.22	12526.27
A_68_P30367929	chr15:79521459-79521503	NM_013818:155	Gtpbp1	INSIDE	1.275	2.134	1075.58	2295.73	2.722	858.32	2335.96
A_68_P25088121	chr7:51807262-51807306	NM_009473:2009	Nr1h2	INSIDE	1.275	2.156	1687.94	3638.48	2.747	1592.43	4375.05
A_68_P32119644	chr19:42276497-42276541	NM_018780:224	Sfrp5	INSIDE	1.275	1.789	1631.72	2919.75	2.281	1465.24	3341.72
A_68_P31711733	chr18:53336104-53336148	NM_026386:108	Snx2	INSIDE	1.275	3.207	586.78	1881.92	4.088	568.15	2322.77
A_68_P25591624	chr7:149088169-149088213	NM_023764:121	Tollip	INSIDE	1.275	1.824	1094.03	1995.89	2.327	953.64	2218.76
A_68_P32144304	chr19:46576472-46576516	NM_053100:357	Trim8	INSIDE	1.275	1.774	741.47	1315.62	2.263	685.70	1551.84
A_68_P24951043	chr7:4866972-4867016	NM_170759:176	Zfp628	INSIDE	1.275	2.191	924.82	2025.98	2.794	777.36	2172.04
A_68_P28182346	chr11:119959996-119960041	NM_183137:27	2410002I01Rik	INSIDE	1.274	1.506	2283.20	3438.72	1.919	2093.70	4016.87
A_68_P26372311	chr9:26563473-26563520	NM_029792:4350	B3gat1	INSIDE	1.274	2.541	1171.42	2976.49	3.236	910.98	2947.90
A_68_P25786792	chr8:37677018-37677062	NM_015802:-43	Dlc1	PROMOTER	1.274	1.478	1983.20	2930.27	1.883	1588.70	2991.59
A_68_P23440963	chr4:155222080-155222124	NM_010091:582	Dvl1	INSIDE	1.274	2.082	688.33	1433.32	2.652	610.03	1618.00
A_68_P31149893	chr17:33787074-33787118	NM_001109913:35307	Hnrnpm	INSIDE	1.274	1.836	515.92	947.45	2.339	472.76	1105.65
A_68_P25098815	chr7:53652229-53652273	NM_001112739:384	Kcnc1	INSIDE	1.274	3.041	1970.66	5993.53	3.876	1848.39	7164.51
A_68_P21579145	chr2:120965882-120965926	NM_177846:530	Lcmt2	INSIDE	1.274	2.513	707.60	1778.05	3.201	574.16	1837.65
A_68_P30422819	chr15:88890786-88890830	NM_001002005:653	Panx2	INSIDE	1.274	3.108	1451.93	4512.32	3.959	1241.37	4914.16
A_68_P21817620	chr2:164226294-164226338	NM_009036:-2377	Rbpjl	PROMOTER	1.274	1.849	367.57	679.62	2.355	341.97	805.51
A_68_P23542977	chr5:24108129-24108173	NM_025891:-330	Smarcd3	PROMOTER	1.274	2.707	4042.81	10944.81	3.450	3136.32	10820.35
A_68_P22900940	chr4:48598477-48598521	NM_021436:434	Tmeff1	INSIDE	1.274	2.054	1338.94	2750.62	2.616	1164.37	3046.34
A_68_P25005466	chr7:25332334-25332378	NM_009532:188	Xrcc1	INSIDE	1.274	2.463	793.15	1953.43	3.139	724.62	2274.43
A_68_P22312386	chr3:88004797-88004841	ENSMUST00000167043:274		INSIDE	1.274	2.504	747.37	1871.15	3.191	672.85	2146.76
A_68_P28266975	chr12:16818008-16818052	NM_033270:260	E2f6	INSIDE	1.273	1.452	1602.98	2327.05	1.848	1486.32	2746.33
A_68_P31117097	chr17:27692164-27692208	NM_001025427:-1332	Hmga1	PROMOTER	1.273	5.592	1103.28	6169.78	7.119	944.66	6724.58
A_68_P27887970	chr11:68026508-68026552	NM_008744:173798	Ntn1	INSIDE	1.273	2.431	1447.19	3518.00	3.096	1086.58	3363.77
A_68_P23562013	chr5:28643983-28644027	NM_028234:276	Rbm33	INSIDE	1.273	2.286	779.56	1781.76	2.909	835.37	2430.40
A_68_P21152637	chr2:39045958-39046002	NM_178778:270	Scai	INSIDE	1.273	0.419	1238.25	519.31	0.534	1175.74	627.79
A_68_P21152639	chr2:39046148-39046192	NM_178778:80	Scai	INSIDE	1.273	3.457	742.24	2566.00	4.400	708.97	3119.26
A_68_P25952924	chr8:73125225-73125269	NM_133772:6967	Ssbp4	INSIDE	1.273	0.378	1488.65	562.77	0.481	1291.55	621.35
A_68_P28048905	chr11:97000299-97000343	NM_198100:10706	Tbkbp1	INSIDE	1.273	4.083	981.94	4009.11	5.196	879.99	4572.88
A_68_P21931968	chr3:8327438-8327482			Unknown	1.273	2.348	1046.11	2456.28	2.990	988.62	2956.06
A_68_P25956908	chr8:73985491-73985535	NM_022419:2044	Abhd8	INSIDE	1.272	1.783	504.75	900.04	2.268	422.81	959.03
A_68_P25836149	chr8:47556867-47556911	NM_007981:493	Acsl1	INSIDE	1.272	2.200	593.81	1306.17	2.797	483.29	1351.89
A_68_P29223875	chr13:93196672-93196716	NM_175455:771	Ankrd34b	INSIDE	1.272	1.912	447.72	856.00	2.432	373.23	907.64
A_68_P30927978	chr16:85172880-85172924	NM_001198823:1050	App	INSIDE	1.272	3.762	848.78	3193.13	4.786	858.39	4108.41
A_68_P22019078	chr3:28680105-28680149	NM_177586:-106	Eif5a2	PROMOTER	1.272	2.442	3066.95	7490.76	3.106	2584.70	8027.02
A_68_P29626125	chr14:57723587-57723631	NM_008125:-69	Gjb2	PROMOTER	1.272	2.146	1241.35	2664.05	2.729	1111.81	3034.55
A_68_P23607764	chr5:36807549-36807593	NM_024478:-263	Grpel1	PROMOTER	1.272	1.929	2434.12	4694.94	2.454	1976.42	4849.93
A_68_P20007254	chr1:4798162-4798206	NM_008866:211	Lypla1	INSIDE	1.272	2.741	1174.82	3220.22	3.486	1072.96	3740.63
A_68_P26803474	chr9:106356284-106356328	NM_021567:119	Pcbp4	INSIDE	1.272	2.074	11582.39	24019.00	2.637	9463.05	24957.15
A_68_P29753350	chr14:80170582-80170626	NM_001042726:515	Pcdh8	INSIDE	1.272	1.360	1774.95	2413.95	1.730	1402.06	2425.54
A_68_P25908469	chr8:63703256-63703300	NM_021506:311	Sh3rf1	INSIDE	1.272	1.730	1456.07	2518.56	2.200	1204.66	2650.02
A_68_P24033996	chr5:120121006-120121050	NM_011535:351	Tbx3	INSIDE	1.272	1.906	3551.74	6769.04	2.425	2723.26	6602.77
A_68_P30422255	chr15:88785176-88785220	NM_172818:-350	Ttll8	PROMOTER	1.272	3.622	1178.37	4267.96	4.606	1106.08	5094.90
A_68_P27233861	chr10:70622146-70622190	NM_031397:214	Bicc1	INSIDE	1.271	1.907	1378.71	2629.18	2.423	1169.88	2834.63
A_68_P29024948	chr13:49478604-49478648	NM_001039179:41709	Bicd2	INSIDE	1.271	3.600	1323.63	4765.43	4.576	1283.30	5871.97
A_68_P28602202	chr12:86452173-86452217	NM_030225:412	Dlst	INSIDE	1.271	1.478	1024.73	1514.35	1.878	872.19	1637.60
A_68_P29629404	chr14:58310425-58310469	NM_015771:54514	Lats2	INSIDE	1.271	3.933	1913.49	7525.40	4.999	1497.85	7487.69
A_68_P29725075	chr14:75346986-75347030	NM_001033439:676	Lrch1	INSIDE	1.271	1.478	863.71	1276.21	1.878	742.73	1394.90
A_68_P28094412	chr11:104987932-104987976	NM_172567:216	Mettl2	INSIDE	1.271	1.590	1187.72	1887.89	2.020	992.08	2003.96
A_68_P22355466	chr3:97462027-97462071	NM_182997:-86	Prkab2	PROMOTER	1.271	2.594	4064.98	10546.53	3.297	3055.76	10074.23

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P32760547	chrX:152058267-152058311	NM_001093750:-418	Ptchd1	PROMOTER	1.271	1.505	989.25	1488.49	1.913	642.40	1228.96
A_68_P27561123	chr11:4958083-4958127	NM_145216:-26	Rasl10a	PROMOTER	1.271	1.984	1298.10	2575.37	2.522	1151.64	2904.93
A_68_P31614991	chr18:35000281-35000325	NM_001204914:60	Reep2	INSIDE	1.271	1.453	1795.60	2609.75	1.847	1457.77	2692.58
A_68_P20454240	chr1:95132647-95132691	NM_172463:195	Sned1	INSIDE	1.271	2.447	339.04	829.74	3.110	318.45	990.32
A_68_P27985620	chr11:85655489-85655533	NM_009324:9394	Tbx2	DOWNSTREAM	1.271	2.896	1775.93	5142.72	3.681	1444.85	5319.02
A_68_P21844244	chr2:168760676-168760720	NM_009564:20389	Zfp64	INSIDE	1.271	2.525	723.35	1826.43	3.208	583.75	1872.76
A_68_P31620712	chr18:36047916-36047960			Unknown	1.271	2.389	1053.04	2515.23	3.036	959.34	2912.72
A_68_P22589085	chr3:141832342-141832386	ENSMUST00000098568:-187		PROMOTER	1.271	2.817	1442.63	4064.26	3.581	1242.84	4450.79
A_68_P23197627	chr4:108453252-108453296	ENSMUST00000106658:-166		PROMOTER	1.271	1.677	767.87	1287.99	2.132	659.44	1405.91
A_68_P24173496	chr5:148211773-148211817	NM_010229:271	Flt3	INSIDE	1.270	2.280	4486.84	10227.92	2.894	3602.37	10427.02
A_68_P28189606	chr11:121121098-121121142	NM_001080932:-180	Foxk2	PROMOTER	1.270	2.014	2021.16	4070.78	2.558	1773.00	4534.45
A_68_P27835393	chr11:59005136-59005180	NM_001159410:-3915	Guk1	PROMOTER	1.270	1.522	952.61	1449.87	1.932	713.62	1378.96
A_68_P27794866	chr11:51419856-51419900	NM_001048061:505	Hnrnpab	INSIDE	1.270	1.689	1422.05	2401.77	2.145	1184.57	2541.17
A_68_P28553815	chr12:77504735-77504779	NM_001002012:-406	Hspa2	PROMOTER	1.270	3.540	2968.33	10509.26	4.495	2407.85	10823.02
A_68_P27270906	chr10:77365060-77365104	NM_145152:199	Lrrc3	INSIDE	1.270	4.664	3437.41	16030.98	5.922	2588.99	15331.64
A_68_P27282875	chr10:79849919-79849963	NM_198615:456	Mex3d	INSIDE	1.270	2.059	1297.17	2670.87	2.614	1178.37	3080.78
A_68_P28685553	chr12:102266820-102266864	NR_035421:-6839	Mir1190	PROMOTER	1.270	2.218	751.85	1667.62	2.817	742.38	2091.19
A_68_P22979365	chr4:64785845-64785889	NM_021362:659	Pappa	INSIDE	1.270	1.831	663.79	1215.23	2.326	650.64	1513.29
A_68_P21974614	chr3:19210634-19210678	NM_001122759:666	Pde7a	INSIDE	1.270	2.196	345.63	758.96	2.789	258.80	721.70
A_68_P31157969	chr17:35293395-35293439	NM_001199044:8406	Prrc2a	INSIDE	1.270	4.188	4961.32	20775.58	5.316	3725.98	19808.80
A_68_P23239476	chr4:117963343-117963387	NM_011213:638	Ptprf	INSIDE	1.270	2.880	1084.57	3123.66	3.657	906.10	3313.35
A_68_P26849149	chr9:115219514-115219558	NM_024222:3	Stt3b	INSIDE	1.270	1.386	2025.97	2807.06	1.760	1742.87	3067.12
A_68_P20016444	chr1:7387937-7387981	ENSMUST00000138711:-76		PROMOTER	1.270	1.486	1236.59	1837.32	1.887	1158.30	2186.06
A_68_P28183962	chr11:120210037-120210081	NR_038126:67	0610009L18Rik	INSIDE	1.269	4.261	999.69	4259.56	5.407	821.64	4442.33
A_68_P27277827	chr10:79076635-79076679	NM_198614:107	C2cd4c	INSIDE	1.269	2.229	611.48	1362.80	2.828	548.22	1550.58
A_68_P25272103	chr7:88598756-88598800	NM_007755:784	Cpeb1	INSIDE	1.269	1.513	1220.78	1847.29	1.920	1039.03	1995.01
A_68_P21769577	chr2:155937298-155937342	NM_170588:381	Cpne1	INSIDE	1.269	2.786	2692.57	7501.88	3.535	2306.68	8154.75
A_68_P26519504	chr9:53055815-53055859	NM_029936:381	Ddx10	INSIDE	1.269	3.135	13279.07	41625.28	3.977	8825.63	35102.54
A_68_P23471513	chr5:9161567-9161611	NM_001110327:188	Dmtf1	INSIDE	1.269	3.639	1547.19	5630.00	4.617	1269.72	5862.76
A_68_P26078518	chr8:97125424-97125468	NM_028221:180	Fam192a	INSIDE	1.269	2.561	750.10	1921.00	3.249	704.38	2288.27
A_68_P28185093	chr11:120392227-120392271	NM_008101:208	Gcgr	INSIDE	1.269	1.337	3494.02	4670.89	1.696	2710.09	4596.83
A_68_P20620518	chr1:134195183-134195227	NM_144810:2	Klhdc8a	INSIDE	1.269	3.367	1419.95	4780.62	4.274	1181.68	5050.25
A_68_P22613734	chr3:145947914-145947958	NM_022983:64012	Lpar3	INSIDE	1.269	3.037	1777.67	5398.58	3.852	1454.46	5603.19
A_68_P26983889	chr10:19653542-19653586	NM_008580:-767	Map3k5	PROMOTER	1.269	2.221	637.44	1416.06	2.820	632.97	1785.07
A_68_P27950596	chr11:79524897-79524941	NR_029579:-552	Mir193	PROMOTER	1.269	1.625	1890.18	3071.22	2.062	1514.87	3123.60
A_68_P31920646	chr19:4012495-4012539	NM_133666:209	Ndufv1	INSIDE	1.269	1.636	2741.53	4484.80	2.076	2151.81	4468.15
A_68_P26742494	chr9:95459899-95459943	NM_198414:-315	Paqr9	PROMOTER	1.269	1.829	1103.08	2017.09	2.320	951.41	2207.32
A_68_P22356139	chr3:97555701-97555745	NM_178080:16215	Pde4dip	INSIDE	1.269	2.018	798.15	1611.02	2.561	655.97	1679.97
A_68_P21417955	chr2:90420030-90420074	NM_008982:752	Ptprj	INSIDE	1.269	2.361	639.79	1510.67	2.996	596.15	1786.06
A_68_P27561122	chr11:4958001-4958045	NM_145216:-108	Rasl10a	PROMOTER	1.269	2.261	973.81	2201.50	2.868	916.47	2628.20
A_68_P24428221	chr6:48547445-48547489	NM_001079901:3585	Repin1	INSIDE	1.269	3.192	617.70	1971.72	4.051	520.03	2106.43
A_68_P30345854	chr15:75900190-75900234	NM_134089:-52	Scrib	PROMOTER	1.269	1.957	1230.03	2407.28	2.483	1055.42	2620.94
A_68_P22543381	chr3:133207644-133207688	NM_001040400:-312	Tet2	PROMOTER	1.269	1.723	1710.93	2948.59	2.188	1361.83	2979.10
A_68_P22880595	chr4:45024781-45024825	NM_001163283:482	Zbtb5	INSIDE	1.269	1.704	1217.37	2074.40	2.162	979.76	2118.20
A_68_P24994120	chr7:20162964-20163008	NM_022409:351	Zfp296	INSIDE	1.269	1.584	2185.62	3462.32	2.010	1990.34	4001.45
A_68_P29428130	A_68_P29428130			Unknown	1.269	1.979	352.01	696.65	2.511	296.85	745.48
A_68_P26399344	chr9:31019625-31019669	NM_001102455:-246	Aplp2	PROMOTER	1.268	1.899	2760.89	5242.40	2.408	2143.04	5160.90
A_68_P30281411	chr15:64213769-64213813	NM_010026:691	Asap1	INSIDE	1.268	1.697	805.58	1367.11	2.153	777.04	1672.65
A_68_P29024656	chr13:49437040-49437084	NM_001039179:145	Bicd2	INSIDE	1.268	2.566	703.80	1805.79	3.253	680.14	2212.68
A_68_P30387018	chr15:83002306-83002350	NM_029787:310	Cyb5r3	INSIDE	1.268	0.425	1347.31	572.85	0.539	1026.25	553.23
A_68_P26657027	chr9:77765735-77765781	NM_134255:587	Elovl5	INSIDE	1.268	2.553	1597.62	4078.80	3.238	1347.09	4361.69

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31936715	chr19:7000722-7000766	NM_008431:8261	Kcnk4	INSIDE	1.268	2.956	1414.46	4181.71	3.750	1184.89	4443.10
A_68_P21101982	chr2:30093777-30093821	NM_177725:510	Lrrc8a	INSIDE	1.268	5.433	963.19	5233.38	6.890	678.57	4675.64
A_68_P23588238	chr5:33678734-33678778	NM_021500:536	Maea	INSIDE	1.268	5.193	3154.45	16380.76	6.583	2359.14	15529.62
A_68_P26192683	chr8:118231489-118231533	NM_001025577:-716	Maf	PROMOTER	1.268	2.220	571.30	1268.01	2.814	440.98	1240.84
A_68_P27282831	chr10:79844492-79844536	NM_198615:5882	Mex3d	INSIDE	1.268	5.592	1593.44	8909.80	7.089	1426.84	10114.79
A_68_P22157981	chr3:55987567-55987611	NM_030595:35	Nbea	INSIDE	1.268	2.882	1223.84	3527.41	3.656	1140.24	4168.63
A_68_P25907378	chr8:63472076-63472120	NM_175089:82	Nek1	INSIDE	1.268	1.575	1075.07	1693.16	1.997	916.59	1830.27
A_68_P24622498	chr6:88450154-88450198	NM_019685:34760	Ruvbl1	DOWNSTREAM	1.268	2.081	3307.01	6881.21	2.639	2688.97	7097.30
A_68_P29578872	chr14:47502657-47502701	NM_001037221:39	Samd4	INSIDE	1.268	2.140	1800.17	3852.57	2.713	1570.51	4260.65
A_68_P20186988	chr1:43155340-43155384	NM_001013025:105	Tgfbrap1	INSIDE	1.268	0.464	1396.70	648.07	0.588	1206.06	709.74
A_68_P20858940	chr1:179252857-179252901			Unknown	1.268	1.746	1430.23	2496.48	2.213	1191.07	2636.16
A_68_P33007024	A_68_P33007024			Unknown	1.268	1.410	1148.79	1619.74	1.788	1035.37	1851.03
A_68_P21761082	chr2:154375340-154375384	NM_029305:723	1700003F12Rik	INSIDE	1.267	1.734	955.07	1656.27	2.197	932.50	2048.66
A_68_P26875484	chr9:119892493-119892537	NM_153287:1262	Csrnp1	INSIDE	1.267	1.523	716.56	1091.23	1.930	627.60	1211.26
A_68_P23342687	chr4:137469337-137469381	NM_199307:51207	Ece1	INSIDE	1.267	2.099	1339.47	2811.71	2.661	1226.65	3263.52
A_68_P21082674	chr2:26997916-26997960	NM_175427:59	Fam163b	INSIDE	1.267	1.972	961.42	1896.33	2.499	847.61	2117.81
A_68_P26612670	chr9:69607179-69607223	NM_022378:1547	Foxb1	INSIDE	1.267	1.394	7936.58	11062.42	1.766	5595.76	9882.10
A_68_P21666842	chr2:136941472-136941517	NM_013822:762	Jag1	INSIDE	1.267	2.336	447.11	1044.55	2.960	367.67	1088.24
A_68_P30148792	chr15:38229751-38229795	NM_013692:690	Klf10	INSIDE	1.267	1.480	1079.76	1598.51	1.875	980.08	1838.08
A_68_P27280137	chr10:79441295-79441339	NM_001003949:5759	ORF61	INSIDE	1.267	3.834	1323.71	5074.57	4.858	905.73	4400.18
A_68_P27265101	chr10:76424431-76424475	NM_021568:240	Pcbp3	INSIDE	1.267	2.148	4139.02	8890.74	2.722	3423.32	9318.77
A_68_P25021471	chr7:29157648-29157692	NM_001083912:11	Plekhg2	INSIDE	1.267	1.721	1857.97	3197.03	2.181	1456.21	3175.64
A_68_P21749123	chr2:152223588-152223632	NM_011438:172	Sox12	INSIDE	1.267	2.628	1477.83	3883.92	3.330	1284.04	4276.02
A_68_P30360706	chr15:78370035-78370079	NM_009218:4719	Sstr3	INSIDE	1.267	2.933	1372.50	4025.76	3.716	1157.76	4301.75
A_68_P22872456	chr4:43575371-43575415	NM_011602:63	Tln1	INSIDE	1.267	2.282	515.18	1175.45	2.892	460.83	1332.58
A_68_P21736746	chr2:149656361-149656405	NM_001085521:-136	Tmem90b	PROMOTER	1.267	1.749	1054.05	1843.43	2.215	949.44	2103.40
A_68_P23142414	chr4:98787172-98787216	NM_026082:412	Dock7	INSIDE	1.266	3.323	691.92	2299.50	4.209	656.21	2761.69
A_68_P23927390	chr5:100468503-100468547	NM_016690:-283	Hnrpdl	DIVERGENT_PROMOTER	1.266	2.734	716.05	1957.66	3.461	636.08	2201.42
A_68_P24449232	chr6:52176211-52176255	NM_010456:1137	Hoxa9	INSIDE	1.266	1.887	3973.77	7499.53	2.389	3242.61	7745.08
A_68_P27736855	chr11:40508399-40508443	NM_134017:-2236	Mat2b	PROMOTER	1.266	1.468	1336.94	1962.56	1.858	1213.79	2255.58
A_68_P27927427	chr11:75469683-75469727	NM_001080775:188	Myo1c	INSIDE	1.266	1.573	3991.67	6280.72	1.993	3457.48	6889.40
A_68_P20826591	chr1:173126357-173126401	NM_025557:21	Pcp4l1	INSIDE	1.266	1.411	1160.84	1637.64	1.786	823.83	1471.40
A_68_P20349748	chr1:74708251-74708295	NM_001014974:-55	Ttll4	PROMOTER	1.266	3.167	1384.94	4386.46	4.009	1261.58	5057.39
A_68_P26082711	chr8:97855540-97855584	NM_024467:288	Zfp319	INSIDE	1.266	5.334	2129.77	11361.27	6.755	1804.34	12188.41
A_68_P23962135	chr5:107003692-107003736	ENSMUST00000131029:20		INSIDE	1.266	1.719	1033.99	1777.88	2.176	1008.44	2194.77
A_68_P28853129	chr13:17786533-17786577	NM_138654:45	5033411D12Rik	INSIDE	1.265	2.260	9494.46	21455.77	2.859	6549.70	18722.36
A_68_P31922426	chr19:4305690-4305734	NM_130863:243	Adrbk1	INSIDE	1.265	1.678	1263.71	2120.16	2.123	1031.50	2189.55
A_68_P32139022	chr19:45616075-45616119	NM_001037758:177873	Btrc	DOWNSTREAM	1.265	2.660	605.24	1610.07	3.365	591.84	1991.53
A_68_P24268748	chr6:17586921-17586965	NM_007604:-155	Capza2	PROMOTER	1.265	2.250	679.09	1528.11	2.847	631.15	1796.93
A_68_P23397277	chr4:148274728-148274772	NM_027195:96250	Casz1	INSIDE	1.265	2.670	383.70	1024.65	3.378	360.02	1216.06
A_68_P23816915	chr5:77017837-77017881	NM_199032:-2880	Cep135	PROMOTER	1.265	2.332	329.41	768.29	2.950	295.18	870.79
A_68_P27677360	chr11:29924702-29924746	NM_146016:1309	Eml6	INSIDE	1.265	1.718	5628.08	9670.61	2.174	4630.52	10066.99
A_68_P24795429	chr6:119797862-119797906	NM_053204:284	Erc1	INSIDE	1.265	2.768	1251.71	3464.60	3.502	970.19	3397.77
A_68_P30395523	chr15:84387987-84388031	NM_177630:245	Ldoc1l	INSIDE	1.265	2.954	1386.49	4096.20	3.736	1180.54	4410.72
A_68_P31074430	chr17:17762134-17762178	NM_172827:-703	Lnpep	PROMOTER	1.265	1.373	4221.16	5796.44	1.737	3037.01	5273.79
A_68_P23296216	chr4:129012377-129012421	NM_009030:216	Rbbp4	INSIDE	1.265	1.605	1135.94	1822.82	2.030	956.85	1942.05
A_68_P31867990	chr18:81169207-81169251	NM_178280:14089	Sall3	INSIDE	1.265	1.995	1760.77	3512.89	2.524	1482.05	3741.43
A_68_P31514145	chr18:14942138-14942182	NM_001100449:407	Taf4b	INSIDE	1.265	3.463	284.18	984.01	4.379	284.97	1247.81
A_68_P26289279	chr9:7764076-7764120	NM_133739:22	Tmem123	INSIDE	1.265	2.132	1412.54	3011.59	2.696	1121.23	3023.12
A_68_P23925842	chr5:100157797-100157841	NR_030692:261	A930011G23Rik	INSIDE	1.264	1.487	1034.17	1537.35	1.879	880.36	1654.13
A_68_P32321495	chrX:34588913-34588957	NM_173779:95	Ankrd58	INSIDE	1.264	2.109	973.77	2053.51	2.666	542.37	1446.06

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28450023	chr12:56086848-56086892	NM_013815:453	Baz1a	INSIDE	1.264	1.791	538.07	963.65	2.264	489.48	1108.22
A_68_P27894659	chr11:69182111-69182155	NM_146019:796	Chd3	INSIDE	1.264	3.629	2077.29	7538.73	4.588	1704.63	7821.61
A_68_P26790788	chr9:104165092-104165136	NM_001163026:146	Dnajc13	INSIDE	1.264	4.115	2086.32	8584.19	5.201	1759.67	9152.19
A_68_P22019966	chr3:28981333-28981377	NM_001167748:-144	Egfem1	PROMOTER	1.264	2.046	1100.84	2252.74	2.587	967.63	2503.29
A_68_P32152778	chr19:47993679-47993723	NM_001001738:89	Itprip	INSIDE	1.264	2.934	633.02	1857.57	3.710	600.31	2227.22
A_68_P23120705	chr4:94717778-94717822	NM_010591:1113	Jun	INSIDE	1.264	2.591	1013.71	2626.92	3.277	901.41	2953.53
A_68_P29919366	chr14:115439544-115439588	NR_029785:-3326	Mir17	PROMOTER	1.264	3.877	1087.55	4216.78	4.902	939.26	4604.15
A_68_P25326014	chr7:99817883-99817941	NM_029078:510	Pcf11	INSIDE	1.264	2.284	1208.56	2760.68	2.886	956.98	2762.14
A_68_P31757541	chr18:61560019-61560063	NM_133249:45	Ppargc1b	INSIDE	1.264	2.927	236.47	692.04	3.698	227.81	842.44
A_68_P29507005	chr14:31438638-31438682	NM_011103:734	Prkcd	INSIDE	1.264	1.959	5453.51	10681.56	2.475	4311.23	10671.68
A_68_P28469855	chr12:60112957-60113001	NM_009147:26	Sec23a	INSIDE	1.264	2.914	818.11	2383.93	3.684	663.56	2444.38
A_68_P29011270	chr13:47138723-47138767	NM_016785:-158	Tpmt	DIVERGENT_PROMOTER	1.264	2.767	5004.81	13849.25	3.497	4026.38	14078.91
A_68_P21810978	chr2:163029877-163029921	ENSMUST00000128999:-390		PROMOTER	1.264	5.091	1077.20	5484.12	6.437	776.55	4998.35
A_68_P32050812	chr19:29122539-29122583	NM_021299:-168	Ak3	PROMOTER	1.263	1.600	3464.40	5543.36	2.022	2916.88	5896.82
A_68_P28741416	chr12:112215114-112215158	NM_175207:2095	Ankrd9	INSIDE	1.263	2.489	612.82	1525.21	3.143	561.83	1765.86
A_68_P20293018	chr1:64580121-64580165	NM_001037726:765	Creb1	INSIDE	1.263	1.928	1218.33	2348.67	2.434	1055.81	2569.78
A_68_P26317495	chr9:14305304-14305348	NM_023153:264	Cwc15	INSIDE	1.263	1.505	1330.45	2001.97	1.900	1182.32	2246.40
A_68_P27261499	chr10:75807838-75807882	NM_001081419:147	Dip2a	INSIDE	1.263	1.999	2994.62	5987.38	2.526	2628.85	6640.99
A_68_P27594246	chr11:11926108-11926153	NM_001177629:1844	Grb10	INSIDE	1.263	2.147	1896.69	4072.91	2.712	1657.21	4494.92
A_68_P25022017	chr7:29244098-29244142	NM_001141921:6864	Lrfn1	INSIDE	1.263	1.701	829.38	1411.03	2.148	639.56	1374.03
A_68_P31950794	chr19:10532257-10532301	NM_001111140:-341	Lrrc10b	PROMOTER	1.263	1.696	1186.35	2012.17	2.142	876.55	1877.28
A_68_P25187997	chr7:73532946-73532990	NM_146191:259	Lrrk1	INSIDE	1.263	2.602	2788.34	7254.89	3.285	2433.96	7995.91
A_68_P27449323	chr10:110943535-110943582	NM_009344:217	Phlda1	INSIDE	1.263	2.017	1281.53	2584.63	2.548	1117.18	2846.18
A_68_P28103447	chr11:106640770-106640814	NR_027785:37	Polg2	INSIDE	1.263	2.456	1057.25	2596.40	3.102	921.00	2857.29
A_68_P23916645	chr5:98615219-98615263	NM_029947:5353	Prdm8	INSIDE	1.263	1.519	736.27	1118.67	1.919	637.06	1222.39
A_68_P27304471	chr10:84217878-84217922	NM_001024918:-892	Rfx4	PROMOTER	1.263	2.027	838.68	1699.82	2.559	691.37	1769.49
A_68_P26142248	chr8:109459632-109459676	NM_009229:5	Sntb2	INSIDE	1.263	0.525	1169.96	614.08	0.663	1153.47	764.78
A_68_P21864915	chr2:172375828-172375872	NM_001159696:-640	Tcfap2c	PROMOTER	1.263	2.210	2070.51	4576.30	2.792	1806.04	5042.01
A_68_P28078894	chr11:102178324-102178368	NM_001044383:255	Ubtf	INSIDE	1.263	1.610	3048.58	4909.13	2.033	2742.77	5576.66
A_68_P26038357	chr8:90483082-90483126	NM_033327:390	Zfp423	INSIDE	1.263	2.604	584.93	1523.07	3.288	606.53	1994.16
A_68_P25258439	chr7:86135415-86135459			Unknown	1.263	3.364	857.39	2883.87	4.248	692.29	2941.17
A_68_P24850989	chr6:131383710-131383754			Unknown	1.263	1.623	523.16	849.24	2.051	602.17	1234.91
A_68_P24476445	chr6:56664725-56664769	NM_030235:-152	Avl9	PROMOTER	1.262	2.483	2433.00	6041.70	3.135	1876.78	5883.33
A_68_P25496228	chr7:132851532-132851576	NM_001081022:165	D430042O09Rik	INSIDE	1.262	1.711	1108.89	1897.42	2.159	972.86	2100.00
A_68_P28697529	chr12:104664017-104664061	NM_001159502:-48	Ddx24	PROMOTER	1.262	2.138	851.37	1819.85	2.697	805.34	2172.32
A_68_P28610310	chr12:87811236-87811280	NM_011934:48665	Esrrb	INSIDE	1.262	2.462	958.00	2358.63	3.108	774.94	2408.60
A_68_P23333957	chr4:135998981-135999032	NM_008309:19568	Htr1d	INSIDE	1.262	4.376	419.44	1835.45	5.522	339.79	1876.26
A_68_P21147672	chr2:38210172-38210216	NM_010710:3367	Lhx2	INSIDE	1.262	1.957	692.95	1356.06	2.470	602.11	1487.38
A_68_P22552362	chr3:135148859-135148903	NM_027288:306	Manba	INSIDE	1.262	1.413	1505.55	2127.31	1.783	1209.33	2155.79
A_68_P30345376	chr15:75828233-75828277	NM_177922:4056	Mapk15	INSIDE	1.262	1.351	2695.59	3642.36	1.705	2137.07	3644.67
A_68_P29263993	chr13:100286596-100286640	NM_008634:-61	Mtap1b	PROMOTER	1.262	2.033	1083.30	2202.21	2.566	828.90	2126.56
A_68_P28538317	chr12:74685599-74685643	NM_008856:-407	Prkch	PROMOTER	1.262	3.089	473.04	1461.31	3.898	413.37	1611.23
A_68_P26078523	chr8:97125990-97126034	NM_026274:172	Rspry1	INSIDE	1.262	3.000	1418.85	4256.87	3.787	1220.66	4622.56
A_68_P28908966	chr13:29044288-29044332	NM_009238:1241	Sox4	INSIDE	1.262	3.864	1865.85	7210.05	4.877	1550.62	7562.70
A_68_P31149740	chr17:33766012-33766058	NM_026712:-2	Zfp414	PROMOTER	1.262	1.607	934.59	1501.98	2.029	848.57	1721.55
A_68_P32180643	chr19:53216882-53216926	NM_001164100:-341	Add3	PROMOTER	1.261	1.908	2712.37	5174.71	2.406	2168.23	5216.17
A_68_P27217140	chr10:67739840-67739884	NM_023598:1612	Arid5b	INSIDE	1.261	1.572	3850.89	6052.69	1.983	2916.99	5783.27
A_68_P31103785	chr17:25571124-25571168	NM_001163691:-418	Cacna1h	PROMOTER	1.261	2.588	638.28	1652.00	3.263	581.57	1897.41
A_68_P27914667	chr11:72832981-72833025	NM_018883:493	Camkk1	INSIDE	1.261	2.415	2544.85	6146.19	3.044	1941.42	5910.36
A_68_P25537055	chr7:140005461-140005505	NM_212473:-603	Fam53b	PROMOTER	1.261	1.648	622.02	1024.98	2.078	545.76	1134.10
A_68_P27288983	chr10:80800571-80800615	NM_148951:5419	Gipc3	INSIDE	1.261	6.444	1747.06	11257.91	8.125	1635.61	13289.59

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P24182263	chr5:149739992-149740036	NM_153572:209	Katnal1	INSIDE	1.261	2.479	2306.44	5717.72	3.125	1892.74	5915.56
A_68_P22569096	chr3:138152576-138152620	NM_175224:-252	Metap1	PROMOTER	1.261	1.426	2629.55	3750.16	1.799	2263.59	4072.42
A_68_P27277569	chr10:79017872-79017916	NM_027422:-58	Mier2	PROMOTER	1.261	3.251	1824.06	5929.55	4.099	1517.89	6221.82
A_68_P23985066	chr5:111759743-111759787	NM_019640:-18	Pitpnb	PROMOTER	1.261	7.780	3564.89	27736.01	9.814	2821.85	27693.78
A_68_P28107260	chr11:107331896-107331940	NM_145823:116	Pitpnc1	INSIDE	1.261	1.509	2099.88	3168.64	1.902	1617.06	3076.05
A_68_P26747279	chr9:96379047-96379091	NM_011279:-54	Rnf7	PROMOTER	1.261	1.607	1560.64	2508.41	2.027	1285.61	2605.37
A_68_P32752149	chrX:149574498-149574542	NM_001004154:20	Rragb	INSIDE	1.261	1.419	1020.49	1447.74	1.789	467.47	836.21
A_68_P29507583	chr14:31529656-31529700	NM_001166532:878	Sfmbt1	INSIDE	1.261	1.723	762.78	1314.11	2.173	562.94	1223.06
A_68_P23896967	chr5:93371085-93371129	NM_001077596:44083	Shroom3	INSIDE	1.261	2.472	616.95	1525.12	3.116	560.31	1746.12
A_68_P23138232	chr4:98049719-98049763	NM_053157:216	Tm2d1	INSIDE	1.261	1.630	1757.28	2864.79	2.056	1281.48	2635.19
A_68_P28595367	chr12:85262475-85262519	ENSMUST00000085215:298		INSIDE	1.261	2.286	2725.85	6230.43	2.883	2169.66	6254.06
A_68_P28936243	chr13:34129600-34129644	NM_026512:113	Bphl	INSIDE	1.260	1.709	1055.28	1803.53	2.154	920.53	1982.86
A_68_P21013701	chr2:12932877-12932921	NM_153155:-407	C1ql3	PROMOTER	1.260	1.538	741.66	1140.64	1.938	641.86	1243.75
A_68_P30382333	chr15:82074905-82074949	NM_001080158:-160	Cenpm	PROMOTER	1.260	1.400	2750.92	3850.59	1.763	2354.33	4150.79
A_68_P21338895	chr2:74536395-74536439	NM_013555:597	Hoxd9	INSIDE	1.260	4.123	530.12	2185.73	5.196	528.00	2743.38
A_68_P25297068	chr7:94395278-94395322	NM_015760:-4	Nox4	PROMOTER	1.260	2.412	1693.00	4084.35	3.040	1732.65	5267.50
A_68_P31676054	chr18:46440414-46440458	NM_172627:68	Pggt1b	INSIDE	1.260	2.804	3067.69	8600.89	3.533	2521.06	8907.00
A_68_P22261355	chr3:78870478-78870522	NM_001099624:79297	Rapgef2	INSIDE	1.260	2.596	783.77	2034.66	3.271	675.06	2208.21
A_68_P25269481	chr7:88092293-88092339	NM_019951:120	Sec11a	INSIDE	1.260	1.693	937.70	1587.43	2.133	821.00	1751.35
A_68_P25952981	chr8:73133463-73133507	NM_133772:-1271	Ssbp4	DIVERGENT_PROMOTER	1.260	2.255	394.33	889.12	2.842	368.14	1046.24
A_68_P29052709	chr13:55098533-55098577	NM_153131:47762	Unc5a	INSIDE	1.260	4.337	855.43	3709.77	5.466	688.37	3762.59
A_68_P29751627	chr14:79881898-79881942	NM_018765:-845	Wbp4	PROMOTER	1.260	1.991	729.66	1452.92	2.510	807.53	2026.81
A_68_P29308211	chr13:108681537-108681581	NM_145456:-1300	Zswim6	PROMOTER	1.260	2.235	304.86	681.26	2.815	323.56	910.98
A_68_P26616432	chr9:70269348-70269392	NM_007630:-9	Ccnb2	PROMOTER	1.259	1.590	824.91	1311.72	2.003	673.55	1348.96
A_68_P23979393	chr5:110815604-110815648	NM_028596:520	Fbrsl1	INSIDE	1.259	2.320	4562.39	10586.21	2.921	3479.04	10161.39
A_68_P26886029	chr9:121766854-121766898	NM_001112668:-227	Gm9790	PROMOTER	1.259	2.366	1582.81	3745.12	2.979	1311.32	3906.59
A_68_P30252138	chr15:58912850-58912894	NM_001146180:709	Mtss1	INSIDE	1.259	2.192	1103.19	2417.70	2.758	890.65	2456.67
A_68_P28334787	chr12:32745879-32745923	NM_011158:244	Prkar2b	INSIDE	1.259	2.257	1069.46	2413.86	2.843	1028.47	2923.59
A_68_P23198163	chr4:108551696-108551740	NM_023537:44	Rab3b	INSIDE	1.259	1.785	1100.09	1963.71	2.247	927.86	2084.84
A_68_P30182585	chr15:44619330-44619374	NM_001032727:257	Sybu	INSIDE	1.259	1.505	724.39	1090.12	1.895	657.24	1245.38
A_68_P28599772	chr12:86039566-86039610	NM_001033334:169	Tmem90a	INSIDE	1.259	2.630	1669.08	4389.97	3.311	2285.92	7569.48
A_68_P22880599	chr4:45025284-45025328	NM_001163283:-22	Zbtb5	DIVERGENT_PROMOTER	1.259	1.751	453.20	793.46	2.205	395.90	872.84
A_68_P32775150	chrX:155970813-155970857	NM_001033472:235	A830080D01Rik	INSIDE	1.258	3.634	8123.73	29518.31	4.570	3538.68	16172.23
A_68_P23467740	chr5:8367848-8367892	NM_001098225:211	Adam22	INSIDE	1.258	2.932	1894.96	5555.31	3.687	1639.52	6044.47
A_68_P29487115	chr14:28242859-28242903	NM_001114879:848	D14Abb1e	INSIDE	1.258	1.500	807.19	1210.58	1.886	675.25	1273.57
A_68_P22872578	chr4:43591698-43591742	NM_172692:16	Gba2	INSIDE	1.258	1.635	796.77	1302.65	2.056	789.83	1623.99
A_68_P21579146	chr2:120965951-120965995	NM_177846:462	Lcmt2	INSIDE	1.258	1.960	333.19	653.11	2.465	310.18	764.61
A_68_P31491261	chr18:10725960-10726004	NM_144860:360	Mib1	INSIDE	1.258	3.762	332.18	1249.51	4.732	355.47	1682.11
A_68_P23279072	chr4:125933108-125933155	NM_001145970:432	Mtap7d1	INSIDE	1.258	1.636	598.76	979.55	2.058	485.96	1000.11
A_68_P22157982	chr3:55987695-55987739	NM_030595:-93	Nbea	PROMOTER	1.258	2.494	2287.63	5706.15	3.139	1915.11	6011.20
A_68_P30346603	chr15:76010310-76010354	NM_201394:15808	Plec	INSIDE	1.258	2.752	974.82	2683.00	3.463	761.69	2637.56
A_68_P30477986	chr15:98885749-98885793	NM_001163588:166	Prph	INSIDE	1.258	2.841	915.53	2600.58	3.573	788.72	2818.25
A_68_P23230625	chr4:116393777-116393821	NM_146151:239	Tesk2	INSIDE	1.258	1.767	741.54	1310.29	2.223	752.72	1673.26
A_68_P20147880	chr1:36426249-36426293	NM_172652:-244	4632411B12Rik	PROMOTER	1.257	1.900	884.01	1679.62	2.388	794.29	1896.53
A_68_P26073640	chr8:96337458-96337502	NR_026888:-25	4930488L21Rik	PROMOTER	1.257	2.599	716.81	1862.82	3.266	672.10	2195.04
A_68_P24052104	chr5:123213775-123213819	NM_001199676:15623	Camkk2	INSIDE	1.257	8.629	2862.22	24698.88	10.845	1949.78	21144.95
A_68_P32030718	chr19:25684761-25684805	NM_177360:-244	Dmrt3	PROMOTER	1.257	1.993	1456.12	2902.01	2.505	1264.38	3166.83
A_68_P26587298	chr9:65219738-65219782	NM_001111145:10894	Gm514	INSIDE	1.257	2.280	1268.80	2892.48	2.865	991.72	2840.91
A_68_P30963191	chr16:91485340-91485384	NM_010508:-97	Ifnar1	PROMOTER	1.257	0.414	1609.66	666.21	0.520	1385.83	720.98
A_68_P28748395	chr12:113413871-113413915	NM_001097621:29474	Kif26a	INSIDE	1.257	1.780	613.76	1092.79	2.238	538.02	1203.95
A_68_P21794483	chr2:160191360-160191404	NM_010658:1419	Mafb	INSIDE	1.257	1.977	2459.23	4862.52	2.485	1889.67	4694.90

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P24946819	chr7:3637588-3637632	NM_029934:7517	Mboat7	INSIDE	1.257	5.943	2786.89	16563.16	7.473	1934.76	14459.42
A_68_P21820159	chr2:164682781-164682825	NM_011125:406	Pltp	INSIDE	1.257	2.532	811.93	2056.19	3.184	652.01	2076.25
A_68_P23311885	chr4:131901472-131901516	NM_001197082:171	Rcc1	INSIDE	1.257	1.729	1212.95	2097.30	2.174	1098.83	2388.76
A_68_P32672213	chrX:131010426-131010470	NM_028958:581	Taf7l	INSIDE	1.257	1.726	747.30	1290.15	2.170	429.17	931.33
A_68_P28430594	A_68_P28430594			Unknown	1.257	1.403	1638.93	2299.68	1.764	1456.55	2568.90
A_68_P32048665	chr19:28754625-28754669	NM_175459:-79	Glis3	PROMOTER	1.256	2.912	1833.27	5338.16	3.658	1549.37	5666.85
A_68_P25957809	chr8:74135189-74135233	NM_146211:288	Glt25d1	INSIDE	1.256	2.514	1016.92	2556.94	3.159	858.36	2711.51
A_68_P27495356	chr10:119549659-119549703	NM_080446:341	Helb	INSIDE	1.256	1.806	2197.55	3968.05	2.268	1785.92	4050.29
A_68_P29612547	chr14:55083035-55083079	NM_022993:73	Lrp10	INSIDE	1.256	2.007	579.44	1163.20	2.521	550.35	1387.47
A_68_P24754176	chr6:112439420-112439464	NM_001081147:360	Oxtr	INSIDE	1.256	2.240	1047.14	2345.46	2.813	877.56	2468.65
A_68_P20121779	chr1:30929974-30930018	NM_001081080:-9895	Phf3	PROMOTER	1.256	1.671	1353.19	2260.64	2.099	1266.00	2657.44
A_68_P28042484	chr11:95985813-95985857	NM_172799:-9265	Ttll6	PROMOTER	1.256	2.473	1829.70	4525.19	3.107	1517.96	4715.79
A_68_P21739398	chr2:150296010-150296054	NM_001034900:14767	Zfp345	DOWNSTREAM	1.256	4.441	208.20	924.72	5.579	208.77	1164.72
A_68_P23622265	chr5:39075785-39075829	NM_001081144:259	Zfp518b	INSIDE	1.256	2.098	940.70	1973.56	2.636	820.78	2163.48
A_68_P27310644	chr10:85292206-85292250			Unknown	1.256	1.715	413.09	708.65	2.154	340.96	734.47
A_68_P26215030	chr8:122136802-122136846	NM_029428:178	Adad2	INSIDE	1.255	4.440	1500.69	6662.80	5.572	1316.93	7338.24
A_68_P21021381	chr2:14526447-14526491	NM_023116:536	Cacnb2	INSIDE	1.255	2.841	388.59	1103.86	3.566	401.54	1431.70
A_68_P27854485	chr11:62352688-62352732	NM_028448:53	Cenpv	INSIDE	1.255	1.768	431.71	763.10	2.218	370.78	822.39
A_68_P22317585	chr3:88968583-88968627	NM_001163432:-122	Clk2	DIVERGENT_PROMOTER	1.255	1.949	1655.57	3226.14	2.445	1458.68	3567.13
A_68_P23417714	chr4:151657357-151657401	NM_178406:8908	Gpr153	INSIDE	1.255	4.024	896.71	3608.03	5.049	725.94	3665.47
A_68_P27284931	chr10:80165309-80165353	NM_027829:-107	Izumo4	DIVERGENT_PROMOTER	1.255	2.154	3472.99	7480.59	2.703	2761.71	7465.50
A_68_P24112801	chr5:135165012-135165056	NM_010717:-574	Limk1	PROMOTER	1.255	1.398	4835.47	6759.61	1.754	3720.09	6526.85
A_68_P31074428	chr17:17761926-17761970	NM_172827:-495	Lnpep	PROMOTER	1.255	1.640	597.82	980.56	2.058	546.44	1124.66
A_68_P24322961	chr6:28783190-28783234	NM_138682:-1465	Lrrc4	PROMOTER	1.255	3.095	400.64	1239.81	3.884	343.20	1333.09
A_68_P28514078	chr12:70457923-70457967	NM_025441:209	Nemf	INSIDE	1.255	2.336	441.75	1032.10	2.932	386.83	1134.16
A_68_P31935125	chr19:6497430-6497474	NM_001205234:78715	Nrxn2	INSIDE	1.255	2.564	1052.21	2697.86	3.217	881.69	2836.68
A_68_P23308580	chr4:131392321-131392365	NM_001083119:1851	Ptpru	INSIDE	1.255	3.152	2496.09	7867.54	3.955	2080.41	8227.77
A_68_P23298059	chr4:129374001-129374045	NM_199305:60	Tmem39b	INSIDE	1.255	2.662	1338.34	3562.54	3.341	1198.59	4004.59
A_68_P21106256	chr2:30823480-30823525	NM_144884:-64	Tor1a	PROMOTER	1.255	1.826	1543.05	2817.87	2.291	1327.78	3042.61
A_68_P28225920	chr12:9037077-9037121	NM_029321:296	Ttc32	INSIDE	1.255	1.867	652.72	1218.41	2.343	555.85	1302.62
A_68_P26215029	chr8:122136700-122136744	NM_029428:76	Adad2	INSIDE	1.254	2.412	1966.12	4741.77	3.025	1515.18	4583.50
A_68_P26815973	chr9:108551515-108551559	NM_011790:175	Arih2	INSIDE	1.254	3.065	2043.35	6263.27	3.845	1670.50	6423.03
A_68_P24039810	chr5:121063118-121063162	NM_028041:2	Ddx54	INSIDE	1.254	2.009	632.99	1271.96	2.520	567.71	1430.74
A_68_P21039675	chr2:18314331-18314375	NM_001190817:105	Dnajc1	INSIDE	1.254	3.343	1735.14	5801.30	4.191	1635.49	6854.69
A_68_P31961133	chr19:12575663-12575707	NM_172442:802	Dtx4	INSIDE	1.254	2.065	1796.76	3710.69	2.589	1667.77	4318.13
A_68_P24175500	chr5:148537455-148537499	NM_010228:88	Flt1	INSIDE	1.254	1.938	2214.58	4292.48	2.431	1784.27	4337.91
A_68_P31863856	chr18:80560394-80560438	NM_001190373:577	Kcng2	INSIDE	1.254	1.962	862.04	1691.23	2.460	726.69	1787.71
A_68_P27787452	chr11:50044549-50044593	NM_145926:5734	Mgat4b	INSIDE	1.254	1.582	890.40	1408.64	1.983	815.29	1617.05
A_68_P21840225	chr2:168056474-168056518	NM_001160330:375	Mocs3	INSIDE	1.254	1.963	696.25	1366.70	2.461	626.50	1541.96
A_68_P23278957	chr4:125914290-125914334	NM_001145970:19251	Mtap7d1	INSIDE	1.254	2.255	1183.74	2669.29	2.827	1219.20	3447.18
A_68_P22063510	chr3:37318580-37318625	NM_153561:-90	Nudt6	DIVERGENT_PROMOTER	1.254	2.006	6388.36	12815.74	2.515	4755.52	11962.03
A_68_P25953913	chr8:73292527-73292571	NM_008841:8063	Pik3r2	INSIDE	1.254	2.721	1388.85	3779.08	3.413	1039.75	3548.34
A_68_P25737024	chr8:28285216-28285260	NM_001080813:-120	Rab11fip1	PROMOTER	1.254	0.424	1354.69	574.61	0.532	1125.69	598.57
A_68_P31254018	chr17:56263505-56263549	NM_013662:9749	Sema6b	INSIDE	1.254	2.636	2306.70	6081.40	3.306	2033.01	6721.59
A_68_P28613410	chr12:88331231-88331275	NM_001080943:-1626	Zdhhc22	PROMOTER	1.254	1.463	2315.29	3386.43	1.834	1850.91	3395.20
A_68_P31021101	A_68_P31021101			Unknown	1.254	2.723	1778.53	4842.27	3.414	1525.67	5208.72
A_68_P32369652	chrX:47013995-47014044	ENSMUST00000121891:-117		PROMOTER	1.254	3.826	921.42	3525.12	4.797	576.55	2765.75
A_68_P31175229	chr17:39983196-39983240	ENSMUST00000157647:-852		PROMOTER	1.254	2.739	39185.03	107319.50	3.435	30380.84	104357.00
A_68_P25983697	chr8:80041774-80041818	NM_030113:10	Arhgap10	INSIDE	1.253	3.323	12185.98	40496.24	4.165	11147.22	46430.04
A_68_P30373741	chr15:80502565-80502609	NM_145986:310	Fam83f	INSIDE	1.253	1.624	965.76	1568.18	2.034	793.11	1613.53
A_68_P26761440	chr9:98857399-98857443	NM_012020:1395	Foxl2	INSIDE	1.253	1.962	1399.72	2745.84	2.458	1150.67	2828.37

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25174077	chr7:71036413-71036457	NM_021366:47367	Klf13	INSIDE	1.253	2.627	2645.28	6948.37	3.292	2137.35	7035.35
A_68_P22843574	chr4:36897680-36897724	NM_001165999:1075	Lingo2	INSIDE	1.253	1.871	2352.98	4402.81	2.345	1851.84	4342.34
A_68_P32374346	chrX:48371757-48371801	NM_172413:-583	Rap2c	PROMOTER	1.253	3.212	955.15	3068.30	4.024	599.40	2412.03
A_68_P21071032	chr2:25127662-25127706	NM_023464:254	Ssna1	INSIDE	1.253	1.461	1609.96	2351.59	1.830	1387.39	2539.33
A_68_P25269100	chr7:88020745-88020789	NM_009553:13773	Zscan2	INSIDE	1.253	2.711	817.16	2215.20	3.396	859.95	2920.09
A_68_P22349550	chr3:96279054-96279098	AK136676:11082		DOWNSTREAM	1.253	2.531	2449.39	6200.52	3.173	1818.44	5769.75
A_68_P21320133	chr2:71383777-71383821	NM_010054:1013	Dlx2	INSIDE	1.252	2.504	2332.47	5840.69	3.136	1692.50	5306.90
A_68_P28280007	chr12:21322457-21322501	NM_026347:226	Iah1	INSIDE	1.252	1.925	2547.57	4903.56	2.410	2111.50	5089.48
A_68_P23952342	chr5:104888645-104888689	NM_008861:191	Pkd2	INSIDE	1.252	2.516	1426.52	3589.11	3.150	1279.33	4029.61
A_68_P26609884	chr9:69138237-69138281	NM_013646:636650	Rora	INSIDE	1.252	4.291	1258.44	5400.33	5.372	1049.61	5638.89
A_68_P21721819	chr2:146839148-146839192	NM_011917:375	Xrn2	INSIDE	1.252	1.811	1090.27	1974.33	2.267	938.59	2128.13
A_68_P26721481	chr9:91256506-91256550	NM_009573:4109	Zic1	INSIDE	1.252	1.563	2690.50	4205.14	1.957	2291.20	4482.97
A_68_P26020489	chr8:87082904-87082948	NM_007578:143664	Cacna1a	INSIDE	1.251	2.350	379.98	892.90	2.939	295.37	868.08
A_68_P23396572	chr4:148178339-148178383	NM_027195:-140	Casz1	PROMOTER	1.251	2.175	1480.69	3220.91	2.721	1383.52	3764.80
A_68_P26346393	chr9:21095562-21095606	NM_009878:69	Cdkn2d	INSIDE	1.251	2.226	1410.42	3139.36	2.784	1238.73	3448.90
A_68_P31565719	chr18:25645825-25645869	NM_001146292:266638	Celf4	INSIDE	1.251	1.585	4330.36	6864.65	1.983	3473.65	6888.99
A_68_P25026496	chr7:30093082-30093126	NM_013874:4081	Dpf1	INSIDE	1.251	1.387	2087.54	2895.78	1.735	1802.08	3126.91
A_68_P26804375	chr9:106553157-106553201	NM_001160353:5262	Grm2	INSIDE	1.251	2.376	806.06	1915.49	2.972	647.93	1925.83
A_68_P32507214	chrX:83022249-83022295	NM_008194:-114	Gyk	PROMOTER	1.251	2.527	7443.77	18807.17	3.162	2946.17	9315.16
A_68_P29942854	chr14:119537426-119537470	NM_015820:-38	Hs6st3	PROMOTER	1.251	2.184	1018.57	2224.87	2.734	895.53	2447.96
A_68_P26531859	chr9:55388856-55388900	NM_027397:-77	Isl2	PROMOTER	1.251	1.977	1348.32	2665.63	2.473	1058.16	2616.70
A_68_P29643581	chr14:60870353-60870397	NM_170591:-159	Nupl1	PROMOTER	1.251	1.457	1534.07	2235.00	1.822	1437.44	2619.62
A_68_P27551121	chr11:3189955-3189999	NM_019574:-483	Patz1	PROMOTER	1.251	0.267	2158.38	576.62	0.334	2034.03	679.80
A_68_P22825645	chr4:33276560-33276604	NM_001034867:130	Pm20d2	INSIDE	1.251	1.735	427.62	742.12	2.171	503.58	1093.02
A_68_P22774391	chr4:21616366-21616410	NM_001080771:-3278	Prdm13	PROMOTER	1.251	2.757	2142.24	5906.92	3.449	1784.60	6155.69
A_68_P26044785	chr8:91566664-91566708	NM_021390:1375	Sall1	INSIDE	1.251	3.706	1383.72	5127.86	4.638	1276.13	5918.42
A_68_P28685881	chr12:102321902-102321946	NM_001160214:-12	Smek1	PROMOTER	1.251	1.560	984.82	1536.02	1.951	823.90	1607.71
A_68_P30140501	chr15:36723049-36723093	NM_011740:1223	Ywhaz	INSIDE	1.251	1.936	859.32	1663.60	2.422	757.21	1834.07
A_68_P30421089	chr15:88581968-88582012	NM_181412:-150	Zbed4	PROMOTER	1.251	3.399	901.63	3064.42	4.254	786.58	3345.72
A_68_P24427165	chr6:48388397-48388441	NM_001085415:6671	Zfp467	INSIDE	1.251	1.899	904.07	1717.15	2.375	750.32	1782.38
A_68_P24359960	chr6:35084098-35084143	NM_001164412:-383	Cnot4	PROMOTER	1.250	2.009	374.97	753.48	2.512	264.96	665.48
A_68_P23361674	chr4:140581469-140581513	NM_172122:28086	Crocc	INSIDE	1.250	3.563	1418.80	5054.93	4.452	1161.68	5171.60
A_68_P21428541	chr2:92274385-92274429	NM_009963:-180	Cry2	PROMOTER	1.250	2.007	1118.40	2244.95	2.509	952.02	2389.02
A_68_P28528480	chr12:72932514-72932558	NM_026102:472	Daam1	INSIDE	1.250	1.683	773.54	1302.08	2.103	616.61	1296.98
A_68_P27756940	chr11:44431798-44431842	NM_007897:185	Ebf1	INSIDE	1.250	1.805	632.04	1140.54	2.256	557.00	1256.54
A_68_P25405197	chr7:116094538-116094582	NM_025344:16632	Eif3f	DOWNSTREAM	1.250	1.776	1707.42	3033.02	2.221	1448.00	3215.73
A_68_P23190563	chr4:107107680-107107724	NM_147221:379	Glis1	INSIDE	1.250	2.218	1538.18	3411.78	2.772	1206.59	3344.16
A_68_P21137828	chr2:35959503-35959547	NM_001083126:56	Lhx6	INSIDE	1.250	1.416	1058.01	1498.53	1.770	851.85	1507.96
A_68_P25087543	chr7:51716772-51716816	NM_198250:18938	Lrrc4b	INSIDE	1.250	2.630	1253.41	3295.97	3.286	1017.05	3342.01
A_68_P21375627	chr2:80421060-80421104	NM_016965:40	Nckap1	INSIDE	1.250	1.974	843.92	1665.98	2.467	774.98	1911.64
A_68_P28573810	chr12:81210978-81211022	NM_007564:3000	Zfp36l1	INSIDE	1.250	1.337	2953.82	3948.56	1.671	2208.98	3690.24
A_68_P30534533	chr16:8830219-8830263	NM_001081400:48	1810013L24Rik	INSIDE	1.249	3.202	933.62	2989.05	3.999	846.83	3386.17
A_68_P20425272	chr1:90599100-90599144	NM_177305:-356	Arl4c	PROMOTER	1.249	1.507	2518.27	3794.37	1.882	2142.19	4032.23
A_68_P22408448	chr3:107563100-107563144	NM_001113529:265	Csf1	INSIDE	1.249	1.689	1528.31	2581.97	2.111	1210.48	2554.77
A_68_P24123508	chr5:137357952-137357996	NM_024474:1003	Emid2	INSIDE	1.249	2.263	1647.57	3728.44	2.826	1424.76	4027.07
A_68_P31373922	chr17:79234408-79234452	NM_001081179:291	Heatr5b	INSIDE	1.249	2.023	1507.44	3050.29	2.527	1264.86	3195.69
A_68_P29863085	chr14:103381169-103381213	NM_177715:664	Kctd12	INSIDE	1.249	2.755	709.75	1955.27	3.440	586.77	2018.46
A_68_P29592278	chr14:49792394-49792438	NM_001081430:515	Naa30	INSIDE	1.249	6.468	383.49	2480.53	8.078	375.30	3031.71
A_68_P31633859	chr18:38578724-38578769	NM_022996:118	Ndfip1	INSIDE	1.249	2.818	1181.57	3329.78	3.519	1156.64	4069.83
A_68_P24643139	chr6:92041412-92041456	NM_011630:23	Nr2c2	INSIDE	1.249	2.277	202.79	461.85	2.845	225.16	640.67
A_68_P22085571	chr3:41369106-41369150	NM_001130186:327	Phf17	INSIDE	1.249	2.198	634.87	1395.22	2.745	559.02	1534.59

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P20559397	chr1:121809874-121809922	NM_175106:-153	Tmem177	PROMOTER	1.249	2.032	1437.86	2921.97	2.538	1112.11	2822.68
A_68_P30350974	chr15:76701808-76701852	NM_001007568:35	Zfp251	INSIDE	1.249	2.382	1279.27	3046.72	2.974	1171.82	3485.14
A_68_P32565198	chrX:98892284-98892328	ENSMUST00000073812:-5117		PROMOTER	1.249	4.292	7463.45	32031.83	5.362	2638.28	14146.88
A_68_P32700324	chrX:137199916-137199960	ENSMUST00000112988:328		INSIDE	1.249	3.576	838.25	2997.85	4.468	633.56	2830.49
A_68_P28050436	chr11:97277448-97277492	ENSMUST00000121799:624		INSIDE	1.249	1.790	1266.29	2266.28	2.235	1023.72	2287.88
A_68_P28708611	chr12:106575425-106575469	ENSMUST00000138649:244		INSIDE	1.249	2.424	1565.31	3794.23	3.026	1344.56	4069.29
A_68_P31408618	chr17:85490170-85490214	NM_028576:153	1700106N22Rik	INSIDE	1.248	1.567	624.98	979.26	1.956	588.22	1150.36
A_68_P27473560	chr10:115551150-115551194	NM_001161855:-199	4933416C03Rik	PROMOTER	1.248	2.323	978.87	2274.16	2.898	869.20	2519.38
A_68_P27033507	chr10:28867124-28867168	NM_026138:3345	6330407J23Rik	INSIDE	1.248	1.815	878.14	1594.23	2.266	763.35	1729.89
A_68_P20239572	chr1:54982610-54982654	NM_001081433:599	Ankrd44	INSIDE	1.248	1.767	4378.24	7738.53	2.205	3378.41	7449.77
A_68_P22609989	chr3:145316674-145316720	NM_010516:-3747	Cyr61	PROMOTER	1.248	1.523	622.12	947.61	1.900	519.34	986.94
A_68_P21874518	chr2:174125914-174125958	NM_201617:2577	Gnas	INSIDE	1.248	1.725	449.44	775.29	2.152	375.13	807.45
A_68_P25954565	chr8:73387047-73387091	NM_032397:-6161	Kcnn1	PROMOTER	1.248	1.781	637.74	1136.03	2.223	524.25	1165.42
A_68_P20127131	chr1:32229533-32229577	NM_133235:-96	Khdrbs2	PROMOTER	1.248	2.929	459.35	1345.58	3.655	463.67	1694.54
A_68_P30619231	chr16:26105726-26105770	NM_173379:122	Leprel1	INSIDE	1.248	1.960	2895.74	5676.76	2.446	2358.79	5770.00
A_68_P25279952	chr7:90016468-90016512	NM_175366:648	Mex3b	INSIDE	1.248	1.562	1292.65	2019.13	1.950	1109.58	2163.80
A_68_P26254550	chr8:128421964-128422008	NM_175561:207	Pcnxl2	INSIDE	1.248	1.925	1505.98	2898.63	2.403	1332.47	3201.93
A_68_P27911828	chr11:72303091-72303135	NM_153060:294	Spns2	INSIDE	1.248	2.134	2299.51	4906.38	2.662	1991.47	5302.04
A_68_P33005935	A_68_P33005935			Unknown	1.248	2.549	518.79	1322.28	3.181	515.51	1639.89
A_68_P27283432	chr10:79934830-79934874	ENSMUST00000158603:-4244		PROMOTER	1.248	2.273	1428.07	3245.31	2.835	1292.75	3664.93
A_68_P29335934	chr13:113442566-113442610	NM_001145885:-70	Ddx4	DIVERGENT_PROMOTER	1.247	2.866	962.97	2760.00	3.573	790.58	2824.84
A_68_P27171225	chr10:59342512-59342556	NM_019965:196	Dnajb12	INSIDE	1.247	1.650	849.75	1402.47	2.059	740.09	1523.76
A_68_P27145715	chr10:53795287-53795331	NM_008548:294	Man1a	INSIDE	1.247	2.146	2354.40	5052.54	2.676	2030.45	5432.77
A_68_P24443350	chr6:51220702-51220746	NR_029719:-815	Mir148a	PROMOTER	1.247	2.025	1306.70	2645.72	2.525	1202.64	3036.11
A_68_P26343627	chr9:20532217-20532261	NM_173777:420	Olfm2	INSIDE	1.247	5.191	2293.17	11902.71	6.471	1822.08	11789.95
A_68_P20598628	chr1:130000152-130000196	NM_181750:292	R3hdm1	INSIDE	1.247	2.327	1148.90	2673.45	2.901	966.62	2803.99
A_68_P25504562	chr7:134352166-134352210	NM_144522:-206	Tbc1d10b	DIVERGENT_PROMOTER	1.247	1.536	1015.11	1559.03	1.915	881.88	1688.82
A_68_P27416798	chr10:105011030-105011074	NM_177368:483	Tmtc2	INSIDE	1.247	1.573	1697.16	2668.91	1.960	1221.25	2394.00
A_68_P23141229	chr4:98591079-98591123	NM_146144:600	Usp1	INSIDE	1.247	1.659	1472.95	2443.54	2.068	1301.96	2692.76
A_68_P23196091	chr4:108132080-108132124	NM_175472:72	Zcchc11	INSIDE	1.247	2.526	1748.34	4416.82	3.149	1504.96	4739.78
A_68_P24783630	chr6:117791108-117791152	NM_177684:-129	Zfp637	PROMOTER	1.247	1.687	1611.83	2718.42	2.103	1410.60	2965.94
A_68_P26888895	chr9:122260872-122260916	NM_026179:161	Abhd5	INSIDE	1.246	3.749	970.64	3638.97	4.671	871.24	4069.51
A_68_P31259474	chr17:57136971-57137015	NM_025538:231	Alkbh7	INSIDE	1.246	1.713	2572.73	4408.24	2.136	2124.39	4536.82
A_68_P27897123	chr11:69609071-69609115	NM_009601:347	Chrnb1	INSIDE	1.246	1.952	1126.95	2200.28	2.432	899.88	2188.72
A_68_P25804898	chr8:41393101-41393145	NM_030110:-282	Efha2	PROMOTER	1.246	2.471	304.12	751.41	3.079	260.66	802.66
A_68_P23416685	chr4:151500131-151500175	NM_019585:2882	Espn	INSIDE	1.246	1.569	1559.72	2447.18	1.955	1150.05	2248.46
A_68_P28463194	chr12:58643991-58644035	NM_008259:3096	Foxa1	INSIDE	1.246	1.651	1395.56	2304.44	2.057	1202.32	2473.16
A_68_P23300608	chr4:129815629-129815674	NM_001163027:144	Hcrtr1	INSIDE	1.246	3.318	971.37	3223.16	4.134	849.45	3511.44
A_68_P29604766	chr14:52724118-52724162	NM_001170981:-437	Hnrnpc	DIVERGENT_PROMOTER	1.246	1.788	1184.33	2117.22	2.227	871.76	1941.82
A_68_P24051357	chr5:123064217-123064261	NM_009879:289	Ift81	INSIDE	1.246	1.726	1134.07	1956.96	2.151	967.09	2079.93
A_68_P26374351	chr9:26962634-26962678	NM_023277:350	Jam3	INSIDE	1.246	3.139	541.16	1698.71	3.912	521.35	2039.76
A_68_P28105679	chr11:107050342-107050386	NM_001161329:331	Nol11	INSIDE	1.246	2.317	3249.95	7530.63	2.888	2457.12	7095.70
A_68_P22878647	chr4:44717142-44717186	NM_008782:6148	Pax5	INSIDE	1.246	1.638	1243.00	2036.06	2.041	1224.49	2499.58
A_68_P31113239	chr17:27070188-27070232	NM_009343:139	Phf1	INSIDE	1.246	1.438	2313.67	3327.70	1.793	1950.38	3496.13
A_68_P30423673	chr15:89004061-89004105	NM_001159521:198	Plxnb2	INSIDE	1.246	3.391	1934.89	6561.95	4.225	1570.38	6635.07
A_68_P24694202	chr6:100784182-100784226	NM_182939:573	Ppp4r2	INSIDE	1.246	1.430	2138.05	3058.07	1.782	1461.44	2604.03
A_68_P26136629	chr8:108424268-108424312	NM_173432:-83	Pskh1	PROMOTER	1.246	2.322	720.89	1673.83	2.893	633.05	1831.72
A_68_P27836018	chr11:59102804-59102848	NM_009522:1427	Wnt3a	INSIDE	1.246	2.282	2968.11	6773.89	2.844	2429.64	6909.10
A_68_P28037459	chr11:95084648-95084692	ENSMUST00000150818:2276		INSIDE	1.246	5.041	2103.01	10600.95	6.282	1573.34	9884.37
A_68_P22503483	chr3:126300156-126300200	NM_001025438:288	Camk2d	INSIDE	1.245	1.465	916.26	1342.64	1.825	793.31	1447.43
A_68_P27234933	chr10:70807476-70807520	NM_134007:99	Cisd1	INSIDE	1.245	2.459	1162.36	2858.70	3.062	1080.51	3308.04

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P22614660	chr3:146113432-146113476	NM_028836:-2	Ctbs	PROMOTER	1.245	1.902	2950.13	5611.33	2.368	2334.24	5526.49
A_68_P25394427	chr7:112936384-112936433	NM_001162943:-344	Dchs1	PROMOTER	1.245	3.206	1009.19	3234.97	3.991	648.44	2587.87
A_68_P23283633	chr4:126803154-126803198	NM_001099319:-113	Gm12942	PROMOTER	1.245	1.513	956.11	1446.22	1.884	785.53	1479.87
A_68_P28577469	chr12:81858735-81858779	NM_001008423:2946	Gm1568	INSIDE	1.245	3.214	1389.69	4466.02	4.000	1106.08	4424.17
A_68_P27163122	chr10:57786302-57786346	NM_026148:111	Lims1	INSIDE	1.245	3.692	656.53	2423.74	4.598	610.74	2808.12
A_68_P25189684	chr7:73834910-73834954	NM_001191001:158	Lins	INSIDE	1.245	1.707	1319.84	2252.58	2.124	1110.91	2359.62
A_68_P25031209	chr7:31145387-31145431	NM_175478:2383	Lrfn3	INSIDE	1.245	2.575	466.90	1202.28	3.205	454.22	1455.67
A_68_P27284768	chr10:80139566-80139610	NM_021462:-4867	Mknk2	PROMOTER	1.245	1.506	1548.45	2331.61	1.874	1166.29	2185.59
A_68_P29585963	chr14:48740738-48740782	NM_033602:217	Peli2	INSIDE	1.245	1.701	1478.59	2515.67	2.118	1338.33	2834.88
A_68_P25026383	chr7:30074297-30074341	NM_026731:-20	Ppp1r14a	DIVERGENT_PROMOTER	1.245	2.661	1096.87	2918.96	3.313	907.54	3006.67
A_68_P26349533	chr9:21722608-21722652	NM_031874:-65	Rab3d	PROMOTER	1.245	1.353	3484.91	4713.97	1.685	3009.85	5070.84
A_68_P30575874	chr16:17815530-17815575	NM_153790:18178	Scarf2	DOWNSTREAM	1.245	4.568	1222.80	5585.25	5.685	1053.27	5987.68
A_68_P29421305	chr14:15535746-15535790	NM_001033270:230	Slc4a7	INSIDE	1.245	2.894	1173.65	3397.03	3.603	974.75	3512.40
A_68_P21749133	chr2:152224628-152224672	NM_011438:-868	Sox12	PROMOTER	1.245	1.800	485.24	873.51	2.241	443.37	993.47
A_68_P32672216	chrX:131010833-131010877	NM_028958:175	Taf7l	INSIDE	1.245	1.871	582.99	1090.56	2.328	337.70	786.28
A_68_P28536526	chr12:74387399-74387443	NM_029580:278	Trmt5	INSIDE	1.245	0.452	1178.56	532.24	0.562	1006.04	565.85
A_68_P29950628	A_68_P29950628			Unknown	1.245	2.174	1561.10	3393.72	2.706	1412.12	3820.79
A_68_P28725239	chr12:109244424-109244468	NM_001079883:-2822	Bcl11b	PROMOTER	1.244	1.391	1623.33	2257.30	1.730	1382.98	2392.33
A_68_P20456920	chr1:95583181-95583225	NM_016778:932	Bok	INSIDE	1.244	2.225	647.81	1441.29	2.768	599.15	1658.48
A_68_P31620309	chr18:35990795-35990839	NM_133687:1345	Cxxc5	INSIDE	1.244	1.769	1890.23	3343.00	2.201	1524.20	3354.40
A_68_P27281217	chr10:79602092-79602136	NR_036582:-2	Dos	DIVERGENT_PROMOTER	1.244	1.549	1805.92	2797.64	1.927	1438.56	2772.35
A_68_P26132769	chr8:107814164-107814208	NM_177788:5812	Exoc3l	INSIDE	1.244	1.571	1164.82	1829.53	1.954	1012.60	1978.53
A_68_P28080758	chr11:102526866-102526910	NM_001127576:-13	Gm1564	PROMOTER	1.244	2.990	2089.75	6248.75	3.719	1642.64	6108.78
A_68_P27812448	chr11:54680388-54680432	NM_008248:471	Hint1	INSIDE	1.244	1.744	1484.50	2588.72	2.170	1308.37	2838.89
A_68_P20739612	chr1:157589907-157589951	NM_010712:-771	Lhx4	PROMOTER	1.244	2.251	1070.22	2408.98	2.801	998.26	2795.74
A_68_P29725076	chr14:75347080-75347124	NM_001033439:582	Lrch1	INSIDE	1.244	5.256	911.20	4789.64	6.541	752.47	4922.20
A_68_P32266420	chrX:13063059-13063103	NM_173415:18283	Nyx	INSIDE	1.244	1.668	1069.58	1784.24	2.076	619.59	1286.00
A_68_P31655270	chr18:42554978-42555022	NM_138945:750	Pou4f3	INSIDE	1.244	0.483	1446.10	698.58	0.601	1248.73	750.64
A_68_P31735662	chr18:57522846-57522891	NM_028447:8482	Prrc1	INSIDE	1.244	3.999	2807.67	11228.79	4.976	1990.29	9904.65
A_68_P29518735	chr14:33411263-33411307	NM_001001796:-1828	Prrxl1	PROMOTER	1.244	2.059	2013.62	4146.23	2.562	1813.30	4645.67
A_68_P30375546	chr15:80808340-80808384	NM_134091:168	Sgsm3	INSIDE	1.244	2.090	1155.13	2414.38	2.599	1148.50	2985.52
A_68_P24009033	chr5:115777444-115777488	NM_025573:281	Srsf9	INSIDE	1.244	0.487	1268.23	617.57	0.606	974.10	589.95
A_68_P20880193	chr1:183141557-183141601	NM_145514:531	Wdr26	INSIDE	1.244	3.488	599.71	2091.94	4.339	550.61	2389.35
A_68_P30571778	chr16:17070255-17070299	NM_023249:-127	Ypel1	PROMOTER	1.244	2.528	5306.44	13416.66	3.145	3892.40	12240.73
A_68_P24098211	chr5:131915292-131915336	NM_177047:1102899	Auts2	INSIDE	1.243	2.259	711.67	1607.87	2.809	697.07	1957.96
A_68_P31092908	chr17:23803677-23803721	NM_153784:6209	Ccdc64b	INSIDE	1.243	2.159	309.19	667.51	2.683	266.22	714.13
A_68_P29957984	chr14:122197004-122197048	NM_134074:-70	Dock9	PROMOTER	1.243	2.182	628.20	1370.81	2.712	531.98	1442.63
A_68_P23363269	chr4:140864959-140865003	NM_010139:7826	Epha2	INSIDE	1.243	4.222	3321.64	14025.22	5.249	2268.17	11906.38
A_68_P21315048	chr2:70499769-70499813	NM_027352:225	Gorasp2	INSIDE	1.243	5.489	1053.46	5782.87	6.822	936.99	6391.96
A_68_P27210043	chr10:66590012-66590056	NM_207221:29	Jmjd1c	INSIDE	1.243	1.880	720.26	1353.78	2.337	648.50	1515.27
A_68_P28744817	chr12:112812887-112812931	NM_021516:188	Mark3	INSIDE	1.243	2.508	904.56	2268.92	3.119	748.34	2333.79
A_68_P27281296	chr10:79612763-79612807	NM_021565:1750	Midn	INSIDE	1.243	3.371	2199.07	7414.03	4.191	1821.78	7635.18
A_68_P25025268	chr7:29871232-29871276	NR_035489:-2541	Mir1963	PROMOTER	1.243	2.310	386.85	893.59	2.871	287.15	824.27
A_68_P28055691	chr11:98188926-98188970	NM_010895:2011	Neurod2	INSIDE	1.243	1.630	673.71	1098.28	2.027	617.22	1250.96
A_68_P22509731	chr3:127336864-127336908	NM_009718:824	Neurog2	INSIDE	1.243	1.829	1273.66	2329.76	2.274	1064.78	2421.49
A_68_P23792520	chr5:72950217-72950261	NM_133921:646	Nfxl1	INSIDE	1.243	1.775	1114.16	1977.16	2.206	1059.70	2337.52
A_68_P22946060	chr4:57580871-57580915	NM_172868:-227	Palm2	PROMOTER	1.243	1.953	2016.46	3937.84	2.428	1923.99	4672.15
A_68_P22031102	chr3:30868233-30868277	NM_001165954:83	Phc3	INSIDE	1.243	1.598	2356.87	3767.43	1.987	1957.54	3889.76
A_68_P21351534	chr2:76485547-76485591	NM_011871:483	Prkra	INSIDE	1.243	1.991	753.34	1500.29	2.476	620.54	1536.70
A_68_P26826272	chr9:110760480-110760524	NM_146227:32	Prss50	INSIDE	1.243	1.802	1509.79	2720.03	2.239	1273.09	2850.40
A_68_P30213989	chr15:51823378-51823422	NM_009009:-94	Rad21	PROMOTER	1.243	2.424	512.24	1241.62	3.012	568.55	1712.35

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27695163	chr11:33413461-33413505	NM_023146:264	Ranbp17	INSIDE	1.243	1.689	724.83	1224.46	2.100	720.91	1514.26
A_68_P26240713	chr8:126177658-126177702	NM_133955:-148	Rhou	PROMOTER	1.243	1.957	2592.72	5073.24	2.432	2129.31	5178.14
A_68_P30489267	chr15:100876705-100876749	NM_011323:110025	Scn8a	DOWNSTREAM	1.243	1.454	952.86	1385.49	1.808	754.50	1363.75
A_68_P22829976	chr4:34136877-34136921	NM_026293:144	Spaca1	INSIDE	1.243	2.106	273.16	575.34	2.617	269.97	706.62
A_68_P23325212	chr4:134408532-134408576	NM_025382:706	Tmem57	INSIDE	1.243	1.885	1913.71	3606.48	2.343	1637.27	3836.66
A_68_P29478600	chr14:26427576-26427620	NM_183208:148928	Zmiz1	INSIDE	1.243	1.722	442.38	761.73	2.140	380.10	813.50
A_68_P20625946	chr1:135060523-135060567			Unknown	1.243	4.473	841.22	3762.62	5.561	676.78	3763.47
A_68_P25591880	chr7:149136294-149136338	NM_001009929:326	Brsk2	INSIDE	1.242	5.492	589.54	3237.99	6.822	507.97	3465.37
A_68_P24980672	chr7:16871856-16871900	NM_172297:-1870	Ccdc9	PROMOTER	1.242	2.206	5364.89	11837.58	2.740	3756.48	10293.89
A_68_P24052807	chr5:123349777-123349821	NM_013910:561	Kdm2b	INSIDE	1.242	3.035	237.11	719.64	3.768	237.92	896.55
A_68_P22601418	chr3:143865112-143865156	NM_001161770:162	Lmo4	INSIDE	1.242	1.792	3344.93	5992.95	2.226	2452.77	5459.35
A_68_P27931782	chr11:76212095-76212139	NM_008750:527	Nxn	INSIDE	1.242	1.396	2403.92	3356.63	1.734	2185.04	3789.94
A_68_P31958230	chr19:11943487-11943531	NM_001011775:2196	Olfr1419	DOWNSTREAM	1.242	2.053	903.37	1854.28	2.550	799.94	2039.68
A_68_P26587151	chr9:65194360-65194404	NM_016688:508	Pdcd7	INSIDE	1.242	4.360	439.00	1914.24	5.417	406.00	2199.31
A_68_P24206536	chr6:4697665-4697715	NM_001040611:385	Peg10	INSIDE	1.242	1.805	383.28	691.98	2.242	450.16	1009.31
A_68_P24949867	chr7:4610509-4610553	NM_172894:22	Ppp6r1	INSIDE	1.242	1.439	2039.58	2935.55	1.788	1631.68	2917.31
A_68_P29605620	chr14:52877501-52877545	NM_172601:21548	Rab2b	DOWNSTREAM	1.242	2.516	539.52	1357.42	3.125	467.97	1462.18
A_68_P27054670	chr10:33739429-33739473	NM_025614:-28	Rwdd1	PROMOTER	1.242	1.898	692.21	1314.01	2.358	694.41	1637.11
A_68_P30463773	chr15:96291502-96291546	NM_028148:-250	Scaf11	PROMOTER	1.242	1.863	1099.28	2047.92	2.314	971.70	2248.83
A_68_P32144298	chr19:46575400-46575444	NM_053100:-715	Trim8	PROMOTER	1.242	3.957	1474.95	5836.50	4.916	1317.92	6478.51
A_68_P30665016	chr16:34573818-34573862	ENSMUST00000114961:-222		PROMOTER	1.242	1.649	616.46	1016.40	2.048	500.75	1025.41
A_68_P32237967	chrX:6895968-6896012	ENSMUST00000132126:306		INSIDE	1.242	2.576	431.86	1112.67	3.199	303.68	971.44
A_68_P24686642	chr6:99471242-99471286	ENSMUST00000155466:145527		INSIDE	1.242	2.325	566.03	1315.96	2.888	436.63	1260.97
A_68_P28612730	chr12:88224807-88224851	NM_145836:936	6430527G18Rik	INSIDE	1.241	1.521	1897.55	2886.17	1.887	1505.53	2841.36
A_68_P27282652	chr10:79811999-79812043	NM_001113548:-829	Adamtsl5	DIVERGENT_PROMOTER	1.241	2.558	1695.30	4335.84	3.175	1465.16	4651.50
A_68_P30281416	chr15:64214267-64214311	NM_010026:193	Asap1	INSIDE	1.241	2.017	1051.04	2120.28	2.503	1004.74	2515.13
A_68_P25503172	chr7:134093232-134093276	NM_001039645:-159	Asphd1	DIVERGENT_PROMOTER	1.241	1.574	3098.78	4876.18	1.953	2367.27	4623.35
A_68_P25371475	chr7:108256912-108256956	NM_001146010:-354	Fchsd2	PROMOTER	1.241	2.611	1581.60	4129.11	3.239	1347.12	4362.84
A_68_P24501238	chr6:63207151-63207195	NM_008167:322	Grid2	INSIDE	1.241	1.559	899.11	1401.34	1.934	817.59	1580.99
A_68_P20897050	chr1:186542380-186542424	NM_008250:13970	Hlx	DOWNSTREAM	1.241	2.146	1253.58	2690.62	2.664	1034.80	2757.03
A_68_P20864309	chr1:180460129-180460173	NM_001161665:895	Kif26b	INSIDE	1.241	1.727	437.24	755.19	2.143	415.39	890.07
A_68_P21615602	chr2:127614486-127614530	NM_016902:82	Nphp1	INSIDE	1.241	1.532	1048.58	1606.01	1.901	976.74	1856.37
A_68_P22325404	chr3:90269294-90269338	NM_008727:472	Npr1	INSIDE	1.241	2.781	1212.93	3373.39	3.453	1057.74	3652.19
A_68_P28397148	chr12:45370156-45370200	NM_026164:38	Pnpla8	INSIDE	1.241	1.617	1845.78	2984.75	2.007	1449.14	2908.38
A_68_P24152257	chr5:143026729-143026773	NM_178702:281	Radil	INSIDE	1.241	2.493	1926.80	4803.14	3.093	1706.90	5279.37
A_68_P23618265	chr5:38611458-38611503	NM_029162:187	Zbtb49	INSIDE	1.241	1.465	1245.44	1824.82	1.818	1165.60	2119.63
A_68_P23588821	chr5:33773068-33773112	ENSMUST00000030994:754		DOWNSTREAM	1.241	1.561	1828.78	2855.12	1.938	1536.19	2977.50
A_68_P27339936	chr10:90545573-90545617	NM_001042558:-106	Apaf1	DIVERGENT_PROMOTER	1.240	2.561	670.67	1717.48	3.176	634.13	2013.89
A_68_P32233091	chrX:5660358-5660402	NM_001033211:158	AU022751	INSIDE	1.240	2.810	373.95	1050.64	3.484	219.06	763.29
A_68_P21324623	chr2:72124103-72124147	NM_178084:367	B230120H23Rik	INSIDE	1.240	1.622	433.08	702.37	2.011	419.95	844.59
A_68_P28183231	chr11:120096349-120096393	NM_198423:2110	Bahcc1	INSIDE	1.240	1.576	463.59	730.80	1.954	443.92	867.52
A_68_P23260770	chr4:122782660-122782704	NM_007559:275	Bmp8b	INSIDE	1.240	1.667	1952.32	3254.69	2.067	1560.75	3225.52
A_68_P29289426	chr13:105018966-105019010	NM_181061:-46	Cenpk	DIVERGENT_PROMOTER	1.240	2.914	265.54	773.76	3.613	266.41	962.60
A_68_P23609093	chr5:37087355-37087399	NM_001081232:-168	D5Ertd579e	PROMOTER	1.240	4.486	2650.67	11889.93	5.561	2185.60	12154.40
A_68_P28525540	chr12:72419394-72419438	NM_001190466:8546	Dact1	INSIDE	1.240	2.243	909.41	2040.06	2.781	713.15	1983.48
A_68_P28705232	chr12:105990506-105990550	NM_148948:-366	Dicer1	PROMOTER	1.240	1.712	1413.42	2420.17	2.123	1292.42	2744.31
A_68_P31694858	chr18:49992481-49992525	NM_001081371:-164	Dmxl1	PROMOTER	1.240	4.242	273.20	1158.83	5.261	260.32	1369.40
A_68_P21052793	chr2:20891228-20891272	NR_033225:750	Gm13375	INSIDE	1.240	1.514	1545.28	2339.43	1.878	1297.01	2435.35
A_68_P26220843	chr8:123060419-123060463	NM_001145896:-868	Gse1	PROMOTER	1.240	2.353	2561.25	6026.72	2.918	2050.43	5983.03
A_68_P28452663	chr12:56701421-56701465	NM_020287:1539	Insm2	INSIDE	1.240	1.746	2136.04	3729.95	2.166	1950.16	4223.07
A_68_P20925497	chr1:191167558-191167602	NM_001159850:-348	Kcnk2	PROMOTER	1.240	1.742	1493.38	2602.05	2.160	1321.58	2854.22

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26537382	chr9:56483766-56483810	NM_181074:49272	Lingo1	INSIDE	1.240	3.194	3619.85	11560.74	3.960	3342.47	13236.53
A_68_P24796449	chr6:119987179-119987223	NR_030487:-2871	Mir706	PROMOTER	1.240	2.561	1001.63	2564.95	3.175	901.57	2862.28
A_68_P27222783	chr10:68732909-68732953	NM_001081347:57526	Rhobtb1	INSIDE	1.240	1.956	1458.67	2853.35	2.426	1110.64	2694.65
A_68_P31383398	chr17:80879916-80879960	NM_009231:-145	Sos1	PROMOTER	1.240	1.703	1343.08	2287.37	2.111	1149.16	2425.95
A_68_P27915637	chr11:72990334-72990378	NM_001168470:154	Tmem93	INSIDE	1.240	2.253	981.87	2211.77	2.793	842.99	2354.21
A_68_P20023923	chr1:9738247-9738291	NM_173443:195	Vcpip1	INSIDE	1.240	0.494	1117.23	551.58	0.612	914.46	559.92
A_68_P27287685	chr10:80606918-80606962	NM_010731:7925	Zbtb7a	INSIDE	1.240	2.668	269.30	718.38	3.308	250.24	827.84
A_68_P26199435	chr8:119387454-119387498			Unknown	1.240	1.721	748.78	1288.47	2.133	648.06	1382.53
A_68_P23542162	chr5:23991041-23991085	NM_139153:33068	Agap3	INSIDE	1.239	1.481	1333.93	1975.65	1.836	1228.96	2255.86
A_68_P28025136	chr11:92960730-92960774	NM_028296:149	Car10	INSIDE	1.239	1.670	1646.14	2749.64	2.069	1290.25	2669.70
A_68_P22340619	chr3:94583028-94583072	NM_001037711:7387	Cgn	INSIDE	1.239	3.622	428.70	1552.64	4.489	360.99	1620.52
A_68_P28150128	chr11:114713294-114713338	NM_147217:-27	Gprc5c	PROMOTER	1.239	1.601	3772.47	6039.25	1.984	2980.61	5912.21
A_68_P29059426	chr13:56236410-56236454	NM_001159513:479	H2afy	INSIDE	1.239	1.965	697.29	1370.08	2.434	566.58	1378.97
A_68_P26142251	chr8:109460182-109460226	NM_009229:555	Sntb2	INSIDE	1.239	1.946	3526.37	6863.93	2.411	2992.61	7214.83
A_68_P24951724	chr7:4989811-4989856	NM_001039532:215	Zfp784	INSIDE	1.239	1.886	8734.42	16475.17	2.336	6341.85	14817.50
A_68_P29056514	chr13:55794315-55794359	NM_181278:-148	B230219D22Rik	PROMOTER	1.238	2.236	890.15	1990.52	2.767	799.64	2212.84
A_68_P27258520	chr10:75226966-75227010	NM_172549:114	Cabin1	INSIDE	1.238	0.516	1214.82	627.29	0.639	973.45	622.34
A_68_P31834477	chr18:75178883-75178927	NM_027727:479	Dym	INSIDE	1.238	4.146	1322.65	5483.98	5.131	1121.13	5752.82
A_68_P29928905	chr14:117325692-117325736	NM_001079844:1178	Gpc6	INSIDE	1.238	2.202	269.73	593.81	2.726	255.58	696.83
A_68_P20877961	chr1:182743984-182744028	NM_008210:-272	H3f3a	PROMOTER	1.238	2.192	1350.01	2958.78	2.714	1176.66	3193.29
A_68_P29097470	chr13:64263694-64263738	NM_019986:543	Habp4	INSIDE	1.238	0.435	1755.82	764.58	0.539	1625.97	876.25
A_68_P23540977	chr5:23830831-23830875	NM_013569:26570	Kcnh2	INSIDE	1.238	1.856	726.25	1347.81	2.298	508.36	1168.28
A_68_P20620520	chr1:134195429-134195473	NM_144810:248	Klhdc8a	INSIDE	1.238	1.485	630.48	936.52	1.839	596.56	1096.87
A_68_P31600354	chr18:32098983-32099027	NM_144862:7844	Lims2	INSIDE	1.238	3.081	745.99	2298.21	3.813	623.46	2377.42
A_68_P30004455	chr15:9070632-9070676	NM_177178:329	Lmbrd2	INSIDE	1.238	1.985	935.03	1855.86	2.457	836.88	2056.07
A_68_P23134366	chr4:97445300-97445344	NM_001122953:1006	Nfia	INSIDE	1.238	2.670	535.17	1429.03	3.307	462.23	1528.55
A_68_P21565421	chr2:118502775-118502819	NM_001145854:-185	Pak6	PROMOTER	1.238	1.450	3479.05	5043.21	1.795	2846.84	5110.26
A_68_P31023590	chr17:7182740-7182784	NM_026611:-446	Rnaset2b	PROMOTER	1.238	7.390	18851.93	139315.30	9.147	12639.12	115612.90
A_68_P30671369	chr16:35651290-35651334	NM_013661:109865	Sema5b	INSIDE	1.238	2.393	399.51	956.14	2.963	374.12	1108.49
A_68_P32149065	chr19:47388402-47388446	NM_001164717:150477	Sh3pxd2a	INSIDE	1.238	2.786	576.32	1605.88	3.451	449.39	1550.75
A_68_P27851930	chr11:61890326-61890370	NM_001029936:-250	Specc1	PROMOTER	1.238	1.892	6923.25	13101.79	2.342	5444.28	12750.40
A_68_P32136814	chr19:45230529-45230573	NM_021901:5346	Tlx1	INSIDE	1.238	0.447	1308.50	585.31	0.554	1010.63	559.58
A_68_P26292116	chr9:8544357-8544401	NM_013838:237	Trpc6	INSIDE	1.238	2.452	394.17	966.68	3.036	400.80	1216.79
A_68_P25715449	chr8:24318844-24318888	NM_018743:59	Agpat6	INSIDE	1.237	1.793	699.64	1254.42	2.218	634.63	1407.82
A_68_P29675826	chr14:66456589-66456633	NM_145944:472	Ccdc25	INSIDE	1.237	1.602	921.96	1477.40	1.983	914.05	1812.27
A_68_P28177060	chr11:119161422-119161466	NM_138669:-87	Eif4a3	PROMOTER	1.237	1.870	1394.98	2609.17	2.313	1155.28	2672.57
A_68_P23973616	chr5:109124200-109124244	NM_001164259:975	Fgfrl1	INSIDE	1.237	1.930	4703.58	9079.96	2.388	3704.93	8846.37
A_68_P21338950	chr2:74542960-74543004	NM_008276:-563	Hoxd8	PROMOTER	1.237	3.289	792.64	2606.66	4.067	771.79	3139.04
A_68_P21103437	chr2:30328220-30328264	NM_030244:1477	Ier5l	INSIDE	1.237	1.783	969.41	1728.04	2.206	873.63	1926.91
A_68_P26348964	chr9:21603129-21603173	NM_145611:-160	Kank2	PROMOTER	1.237	2.092	1105.14	2311.91	2.588	917.52	2374.59
A_68_P25022020	chr7:29244408-29244453	NM_001141921:7174	Lrfn1	INSIDE	1.237	2.756	999.80	2755.87	3.410	851.80	2904.46
A_68_P29226007	chr13:93614754-93614798	NM_001162945:35	Mtx3	INSIDE	1.237	5.397	1440.29	7772.75	6.675	1232.82	8229.37
A_68_P30458581	chr15:95359007-95359051	NM_016743:109	Nell2	INSIDE	1.237	0.414	1492.61	618.14	0.512	1266.69	648.80
A_68_P25370976	chr7:108160468-108160512	NM_008773:15	P2ry2	INSIDE	1.237	4.261	1849.73	7881.62	5.271	1535.93	8095.53
A_68_P30423565	chr15:88991328-88991372	NM_001159521:12930	Plxnb2	INSIDE	1.237	2.121	368.90	782.47	2.624	282.04	739.96
A_68_P20740069	chr1:157660136-157660180	NM_001024945:-129	Qsox1	PROMOTER	1.237	1.817	479.57	871.24	2.247	523.68	1176.62
A_68_P28956973	chr13:37949256-37949300	NM_001039188:30017	Rreb1	INSIDE	1.237	1.816	446.55	811.04	2.248	426.08	957.66
A_68_P28830403	chr13:12198675-12198719	NM_023868:516	Ryr2	INSIDE	1.237	2.275	854.64	1944.66	2.815	839.04	2362.14
A_68_P20945911	chr1:194681059-194681103	NM_001177794:-3139	Sertad4	PROMOTER	1.237	2.947	1351.92	3984.15	3.645	1205.19	4392.81
A_68_P26710064	chr9:88333383-88333427	NM_172926:385	Snx14	INSIDE	1.237	2.074	1749.58	3628.84	2.566	1420.74	3645.36
A_68_P26626138	chr9:71959964-71960008	NM_011544:-360	Tcf12	PROMOTER	1.237	2.531	2042.50	5168.92	3.132	1681.02	5264.45

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26544600	A_68_P26544600			Unknown	1.237	3.490	1101.16	3843.33	4.316	987.12	4260.49
A_68_P31215274	chr17:48112426-48112470			Unknown	1.237	1.731	789.53	1366.32	2.141	690.46	1478.42
A_68_P32670206	chrX:130593674-130593718	NM_133196:-191	Cstf2	PROMOTER	1.236	2.152	871.71	1875.76	2.660	632.77	1683.00
A_68_P24449035	chr6:52153690-52153734	NM_010453:874	Hoxa5	INSIDE	1.236	1.981	1294.73	2564.25	2.449	1072.42	2625.86
A_68_P28043567	chr11:96160575-96160619	NM_008269:112	Hoxb6	INSIDE	1.236	1.992	1521.36	3030.19	2.463	1248.37	3074.14
A_68_P26640632	chr9:74711201-74711245	NM_008262:1495	Onecut1	INSIDE	1.236	2.985	3357.89	10022.92	3.690	2778.40	10253.04
A_68_P20241610	chr1:55463210-55463254	NM_001114663:443	Plcl1	INSIDE	1.236	1.632	915.80	1494.27	2.016	850.74	1715.41
A_68_P31600225	chr18:32070729-32070773	NM_026006:807	Sft2d3	INSIDE	1.236	1.597	914.21	1460.16	1.973	872.48	1721.73
A_68_P27966237	chr11:82248208-82248252	NM_023438:45829	Tmem132e	INSIDE	1.236	3.714	1503.42	5583.86	4.591	1268.33	5822.68
A_68_P28261138	chr12:15822842-15822886	NM_144551:727	Trib2	INSIDE	1.236	3.276	625.97	2050.90	4.049	686.49	2779.48
A_68_P27910151	chr11:72020571-72020617	NM_026559:-461	Txndc17	DIVERGENT_PROMOTER	1.236	1.705	607.46	1035.89	2.108	526.85	1110.75
A_68_P26948225	chr10:12642644-12642688	NR_038027:259	B230208H11Rik	INSIDE	1.235	1.796	495.93	890.72	2.219	441.49	979.68
A_68_P28153095	chr11:115228977-115229021	NM_175454:35	C630004H02Rik	INSIDE	1.235	3.505	877.03	3073.74	4.329	1029.77	4457.52
A_68_P28170165	chr11:118110109-118110153	NM_001112699:-224	Cyth1	PROMOTER	1.235	2.764	1221.01	3375.34	3.413	997.16	3403.27
A_68_P30590962	chr16:21204783-21204827	NM_010143:-63	Ephb3	PROMOTER	1.235	3.268	710.78	2322.96	4.035	565.11	2280.23
A_68_P29996508	chr15:7763780-7763824	NM_010275:2792	Gdnf	INSIDE	1.235	1.708	684.74	1169.37	2.108	599.98	1265.04
A_68_P32767190	chrX:154036239-154036283	NM_172307:387	Mbtps2	INSIDE	1.235	1.745	631.98	1102.73	2.155	329.06	709.18
A_68_P28052184	chr11:97561645-97561689	NM_001163308:-704	Pcgf2	PROMOTER	1.235	1.718	1571.01	2698.74	2.122	1284.56	2726.03
A_68_P28055914	chr11:98219976-98220020	NM_021547:301	Stard3	INSIDE	1.235	1.966	797.08	1566.71	2.428	635.47	1542.91
A_68_P23317937	chr4:133054043-133054087	NM_001081156:401	Trnp1	INSIDE	1.235	3.366	947.42	3188.70	4.157	842.58	3502.95
A_68_P24874652	chr6:136776509-136776553	NM_021714:207	Wbp11	INSIDE	1.235	1.527	3699.15	5646.81	1.884	2809.48	5294.46
A_68_P25600929	chr7:150624243-150624287			Unknown	1.235	3.584	722.05	2587.69	4.426	654.92	2898.72
A_68_P21565885	chr2:118571382-118571426	NR_030716:-93	5430417L22Rik	PROMOTER	1.234	1.916	1461.77	2800.90	2.364	1291.48	3053.51
A_68_P27033510	chr10:28867430-28867474	NM_026138:3651	6330407J23Rik	INSIDE	1.234	1.641	1994.17	3273.28	2.025	1639.25	3319.61
A_68_P24469556	chr6:55402442-55402486	NM_001025372:491	Adcyap1r1	INSIDE	1.234	1.418	837.79	1187.83	1.749	722.95	1264.50
A_68_P29342444	chr13:114585071-114585115	NM_172595:377	Arl15	INSIDE	1.234	1.500	3228.18	4840.67	1.850	2735.40	5061.43
A_68_P21324621	chr2:72123755-72123799	NM_178084:19	B230120H23Rik	INSIDE	1.234	1.529	797.45	1219.18	1.886	690.20	1301.67
A_68_P27100735	chr10:43231159-43231203	NM_199028:32235	Bend3	INSIDE	1.234	2.682	750.18	2012.34	3.311	643.42	2130.22
A_68_P21040743	chr2:18593952-18593996	NM_147778:-114	Commd3	PROMOTER	1.234	1.603	2488.35	3988.75	1.978	2335.94	4621.12
A_68_P27286404	chr10:80392789-80392833	NM_008655:-25	Gadd45b	PROMOTER	1.234	1.669	2540.30	4238.98	2.059	2173.09	4473.86
A_68_P27794864	chr11:51419555-51419599	NM_001048061:807	Hnrnpab	INSIDE	1.234	1.411	1693.90	2390.86	1.741	1472.33	2563.46
A_68_P20241001	chr1:55294058-55294102	NM_175439:60	Mars2	INSIDE	1.234	1.581	695.13	1099.14	1.951	638.40	1245.25
A_68_P21240022	chr2:56969332-56969376	NM_013613:-1905	Nr4a2	PROMOTER	1.234	2.574	1506.44	3877.61	3.175	1177.32	3738.28
A_68_P20937889	chr1:193221406-193221450	NM_144880:-508	Ppp2r5a	PROMOTER	1.234	2.008	1221.32	2452.48	2.478	1000.57	2479.18
A_68_P20793343	chr1:167124694-167124739	NM_145512:-152	Sft2d2	PROMOTER	1.234	2.186	836.65	1829.18	2.699	732.23	1975.97
A_68_P21820991	chr2:164823054-164823098	NM_020333:29589	Slc12a5	INSIDE	1.234	1.746	1633.82	2852.86	2.156	1806.18	3893.38
A_68_P32196168	chr19:55816042-55816086	NM_001142918:-235	Tcf7l2	PROMOTER	1.234	1.752	1637.11	2867.52	2.161	1401.68	3029.05
A_68_P29733543	chr14:76814437-76814481	NM_207652:-1169	Tsc22d1	PROMOTER	1.234	1.886	1653.09	3117.66	2.327	1401.61	3261.57
A_68_P31982218	chr19:16855459-16855503	NM_173028:-63	Vps13a	PROMOTER	1.234	3.153	470.62	1483.96	3.892	432.33	1682.66
A_68_P24954137	chr7:6083887-6083931	NM_001013012:23665	Zfp787	INSIDE	1.234	3.739	3994.65	14935.73	4.614	3130.49	14442.68
A_68_P20162421	chr1:38892803-38892847	ENSMUST00000147695:111		INSIDE	1.234	2.999	484.34	1452.42	3.700	522.16	1931.96
A_68_P23268972	chr4:124252405-124252449	ENSMUST00000164308:5994		INSIDE	1.234	1.647	863.46	1421.78	2.033	734.34	1492.62
A_68_P25713873	chr8:24085890-24085934	NM_001110783:559	Ank1	INSIDE	1.233	1.576	1016.08	1601.02	1.943	838.45	1629.00
A_68_P21080072	chr2:26484180-26484224	NM_019833:226	Fam69b	INSIDE	1.233	3.820	381.45	1457.15	4.709	331.17	1559.50
A_68_P28043916	chr11:96202147-96202192	NM_010458:-2913	Hoxb3	PROMOTER	1.233	1.393	1248.94	1739.30	1.717	1151.69	1976.87
A_68_P22080609	chr3:40439835-40439879	NM_175515:168	Intu	INSIDE	1.233	2.460	373.11	917.90	3.034	356.07	1080.28
A_68_P31100484	chr17:25073844-25073888	NM_001163447:56	Mapk8ip3	INSIDE	1.233	1.565	808.90	1266.33	1.931	789.98	1525.30
A_68_P22357697	chr3:97817451-97817495	NM_010928:12	Notch2	INSIDE	1.233	2.887	1140.75	3293.65	3.560	1010.67	3598.29
A_68_P25601377	chr7:150688210-150688254	NM_009434:197	Phlda2	INSIDE	1.233	1.626	608.67	989.95	2.006	542.58	1088.51
A_68_P31599575	chr18:31948663-31948707	NM_027002:-128	Polr2d	PROMOTER	1.233	2.408	4034.10	9714.80	2.969	3275.83	9724.90
A_68_P30477989	chr15:98886157-98886201	NM_001163588:574	Prph	INSIDE	1.233	1.503	1733.54	2605.56	1.853	1555.19	2881.91

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28042231	chr11:95926737-95926781	NM_172300:-80	Ube2z	PROMOTER	1.233	2.073	281.69	584.05	2.556	392.09	1002.33
A_68_P27947946	chr11:79068163-79068207	NM_019653:13	Wsb1	INSIDE	1.233	2.154	2856.62	6154.39	2.657	2088.05	5547.64
A_68_P21067995	chr2:24618544-24618589	NM_001042528:1	Cacna1b	INSIDE	1.232	1.428	1148.66	1640.72	1.759	1047.72	1843.10
A_68_P32111328	chr19:40905903-40905947	NM_172839:156	Ccnj	INSIDE	1.232	2.153	771.12	1660.53	2.652	689.25	1828.14
A_68_P23448647	chr5:4104421-4104465	NM_020010:255	Cyp51	INSIDE	1.232	2.400	1632.82	3918.57	2.957	1271.28	3759.14
A_68_P22288625	chr3:83843924-83843968	NM_172681:137	D930015E06Rik	INSIDE	1.232	1.536	1161.00	1783.82	1.893	946.27	1791.52
A_68_P23081271	chr4:86394332-86394376	NM_001081014:-104	Dennd4c	PROMOTER	1.232	1.610	1405.26	2262.23	1.983	1205.91	2391.42
A_68_P23142413	chr4:98786997-98787041	NM_026082:588	Dock7	INSIDE	1.232	2.294	716.58	1644.00	2.826	638.27	1804.07
A_68_P21113255	chr2:31944229-31944273	NM_175511:-5025	Fam78a	DIVERGENT_PROMOTER	1.232	1.563	852.24	1331.80	1.925	804.68	1548.84
A_68_P26458699	chr9:42752539-42752583	NM_175481:-106	Grik4	PROMOTER	1.232	2.405	357.87	860.78	2.963	360.24	1067.29
A_68_P24868562	chr6:135682934-135682978	NM_008171:440573	Grin2b	INSIDE	1.232	1.918	500.98	960.81	2.363	403.88	954.55
A_68_P32152395	chr19:47939790-47939835	NM_030051:-222	Gsto2	PROMOTER	1.232	3.284	741.51	2434.96	4.047	623.46	2523.27
A_68_P32095551	chr19:37509175-37509219	NM_008245:-134	Hhex	PROMOTER	1.232	1.399	1105.66	1546.39	1.723	1015.80	1750.62
A_68_P30477336	chr15:98748107-98748151	NM_029098:401	Lmbr1l	INSIDE	1.232	2.239	1327.10	2971.37	2.758	1218.06	3359.49
A_68_P23896966	chr5:93370979-93371023	NM_001077596:43977	Shroom3	INSIDE	1.232	3.027	621.66	1881.46	3.729	603.54	2250.80
A_68_P26031095	chr8:89269939-89269983	NM_009172:-55	Siah1a	PROMOTER	1.232	2.392	492.98	1179.08	2.946	436.18	1284.95
A_68_P27365031	chr10:94878605-94878649	NM_001168656:-508	Socs2	PROMOTER	1.232	1.955	1850.53	3617.23	2.409	1495.91	3602.94
A_68_P28745892	A_68_P28745892			Unknown	1.232	4.201	312.61	1313.32	5.178	301.70	1562.09
A_68_P21594122	chr2:123915605-123915649	ENSMUST00000137172:-78		PROMOTER	1.232	1.652	1954.46	3229.10	2.036	1701.34	3463.88
A_68_P31619430	chr18:35813598-35813642	NM_027222:-4599	2010001M09Rik	PROMOTER	1.231	2.219	312.19	692.64	2.732	275.04	751.27
A_68_P24430829	chr6:49023914-49023958	NM_029353:143	2410003K15Rik	INSIDE	1.231	1.648	426.66	703.25	2.029	398.52	808.62
A_68_P25952414	chr8:73046706-73046750	NM_029366:351	2810422J05Rik	INSIDE	1.231	1.634	3089.90	5050.44	2.013	2292.98	4615.03
A_68_P27282604	chr10:79805724-79805768	NM_025629:5411	Adamtsl5	INSIDE	1.231	1.712	736.33	1260.42	2.107	684.01	1441.16
A_68_P26741570	chr9:95307111-95307155	NM_018763:557	Chst2	INSIDE	1.231	1.791	453.81	812.60	2.204	372.06	820.11
A_68_P27475788	chr10:115911221-115911265	NM_021452:-663	Kcnmb4	PROMOTER	1.231	3.008	1683.22	5062.79	3.704	1542.11	5711.26
A_68_P25022022	chr7:29244663-29244707	NM_001141921:7428	Lrfn1	INSIDE	1.231	2.420	534.11	1292.35	2.979	495.36	1475.77
A_68_P21822913	chr2:165113069-165113113	NM_144893:237	Slc35c2	INSIDE	1.231	0.446	1241.72	553.31	0.549	946.93	519.56
A_68_P24820215	chr6:125311848-125311892	NM_011609:12130	Tnfrsf1a	INSIDE	1.231	2.922	753.59	2201.62	3.597	607.65	2185.54
A_68_P24951680	chr7:4982714-4982758	NM_001033383:10759	Zfp865	INSIDE	1.231	2.091	297.20	621.40	2.573	274.77	706.99
A_68_P21797522	chr2:160698309-160698353	NM_177263:396	Zhx3	INSIDE	1.231	1.339	3465.47	4639.79	1.648	2675.65	4409.78
A_68_P21833422	chr2:166888209-166888253	NM_001081005:-203	1500012F01Rik	PROMOTER	1.230	2.330	544.13	1267.81	2.866	487.60	1397.67
A_68_P30468157	chr15:97078001-97078045	NM_001164563:-304	Amigo2	PROMOTER	1.230	1.493	1005.64	1501.01	1.835	1008.90	1851.63
A_68_P30502976	chr15:103070313-103070357	NM_001076789:-87	Cbx5	DIVERGENT_PROMOTER	1.230	0.450	1455.01	655.15	0.554	1164.57	645.05
A_68_P31157311	chr17:35195952-35195996	NM_001190449:-5	Ddah2	PROMOTER	1.230	1.507	3276.84	4938.01	1.854	2586.63	4794.62
A_68_P29361885	chr13:118009364-118009408	NM_010330:7	Emb	INSIDE	1.230	2.294	840.00	1927.26	2.822	735.72	2076.20
A_68_P28171532	chr11:118338109-118338153	NM_172573:-143	Engase	PROMOTER	1.230	1.412	1846.85	2607.24	1.736	1476.00	2562.76
A_68_P22071607	chr3:38786088-38786133	NM_183221:249	Fat4	INSIDE	1.230	2.228	694.26	1546.83	2.740	525.85	1440.62
A_68_P25007848	chr7:25795874-25795918	NM_008168:61492	Grik5	INSIDE	1.230	2.823	3495.69	9868.19	3.473	2584.16	8974.15
A_68_P25196753	chr7:75097151-75097195	NM_010513:30	Igf1r	INSIDE	1.230	4.008	1503.59	6027.14	4.931	1262.54	6225.99
A_68_P29952578	chr14:121310982-121311026	NM_023579:589	Ipo5	INSIDE	1.230	1.677	963.91	1616.15	2.062	792.05	1633.04
A_68_P28271091	chr12:17551967-17552011	NM_013614:310	Odc1	INSIDE	1.230	2.162	2582.31	5583.53	2.660	2122.93	5647.21
A_68_P31066146	chr17:15663980-15664024	NM_008799:263	Pdcd2	INSIDE	1.230	2.695	857.19	2310.36	3.316	750.54	2488.78
A_68_P30578589	chr16:18248400-18248444	NM_011239:365	Ranbp1	INSIDE	1.230	1.705	2260.66	3854.55	2.097	1923.63	4034.56
A_68_P21706316	chr2:144096174-144096218	NR_030762:-4258	Snord17	PROMOTER	1.230	2.303	904.99	2083.99	2.832	801.34	2269.41
A_68_P26455637	chr9:42280374-42280418	NM_173038:-87	Tbcel	PROMOTER	1.230	1.651	824.04	1360.52	2.031	733.44	1489.33
A_68_P27900651	chr11:70245942-70245986	NM_145429:-190	Arrb2	PROMOTER	1.229	1.546	1553.06	2400.75	1.900	1488.33	2827.45
A_68_P21285104	chr2:65076845-65076889	NM_027225:-183	Cobll1	PROMOTER	1.229	0.412	1598.81	658.86	0.506	1269.58	642.91
A_68_P27183508	chr10:61441806-61441850	NM_007731:28	Col13a1	INSIDE	1.229	1.704	2705.65	4610.97	2.094	2021.23	4232.27
A_68_P24620288	chr6:88140437-88140481	NM_008090:-8199	Gata2	PROMOTER	1.229	3.065	3155.55	9672.95	3.768	2633.69	9923.04
A_68_P31624332	chr18:36675376-36675420	NM_010415:61	Hbegf	INSIDE	1.229	2.145	1199.99	2573.73	2.637	1439.23	3794.92
A_68_P20228742	chr1:52784064-52784108	NM_133829:76	Mfsd6	INSIDE	1.229	1.361	2780.57	3783.89	1.673	2266.05	3790.85

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group Relative methylation (Cy5/Cy3)	Sham group Cy3 signal (Input)	Sham group Cy5 signal (MeDIP)	TiO_2-H group Relative methylation (Cy5/Cy3)	TiO_2-H group Cy3 signal (Input)	TiO_2-H group Cy5 signal (MeDIP)
A_68_P30368847	chr15:79664630-79664674	NM_001013360:111	Npcd	INSIDE	1.229	1.521	3801.75	5782.91	1.869	3069.43	5738.13
A_68_P30961945	chr16:91270311-91270355	NM_016968:319	Olig1	INSIDE	1.229	1.423	866.91	1233.81	1.749	745.77	1304.37
A_68_P25730820	chr8:27229765-27229809	NM_029965:-65	Rnf170	DIVERGENT_PROMOTER	1.229	1.842	464.17	854.77	2.263	362.99	821.45
A_68_P24630040	chr6:89785772-89785816	NM_053221:9737	Vmn1r42	DOWNSTREAM	1.229	2.967	1374.81	4078.92	3.646	1256.51	4581.76
A_68_P27568222	chr11:6289791-6289835	NM_001005867:-5315	Zmiz2	PROMOTER	1.229	2.068	685.07	1416.68	2.541	569.82	1447.76
A_68_P20718903	chr1:153936776-153936820	NM_197990:652	1700025G04Rik	INSIDE	1.228	2.036	4522.29	9208.00	2.501	3098.69	7750.10
A_68_P22905957	chr4:49610300-49610344	NM_025944:420	2810432L12Rik	INSIDE	1.228	1.681	1179.40	1982.04	2.063	985.94	2033.96
A_68_P22151288	chr3:54859609-54859653	NM_007628:-653	Ccna1	PROMOTER	1.228	2.400	1122.33	2693.33	2.947	1034.44	3048.09
A_68_P20910365	chr1:188791961-188792005	NM_033077:688	D1Pas1	INSIDE	1.228	3.475	1136.98	3950.91	4.268	881.33	3761.77
A_68_P24133866	chr5:139626612-139626656	NM_001081265:458	Heatr2	INSIDE	1.228	2.083	766.79	1596.99	2.557	608.20	1555.28
A_68_P25031211	chr7:31145626-31145670	NM_175478:2143	Lrfn3	INSIDE	1.228	2.437	1319.81	3216.65	2.993	1079.76	3231.79
A_68_P30343816	chr15:75578159-75578203	NM_194350:172	Mafa	INSIDE	1.228	2.750	2383.80	6555.74	3.378	2098.13	7087.88
A_68_P28671530	chr12:99927621-99927665	NM_011877:45213	Ptpn21	INSIDE	1.228	3.152	2204.42	6948.39	3.870	1444.78	5591.59
A_68_P22826130	chr4:33397227-33397271	NM_011884:-37	Rngtt	PROMOTER	1.228	3.959	1538.77	6091.71	4.862	1236.26	6010.36
A_68_P22286846	chr3:83570454-83570498	NM_009144:234	Sfrp2	INSIDE	1.228	1.617	940.06	1520.06	1.986	795.89	1580.52
A_68_P28781896	chr12:120087840-120087884	NM_177082:3061	Sp8	INSIDE	1.228	3.215	1362.52	4380.64	3.949	1219.70	4816.19
A_68_P27787326	chr11:50024305-50024349	NM_011018:-34	Sqstm1	PROMOTER	1.228	2.761	550.75	1520.66	3.390	434.71	1473.52
A_68_P21864909	chr2:172375260-172375304	NM_001159696:-1208	Tcfap2c	PROMOTER	1.228	2.180	691.57	1507.33	2.676	597.23	1597.91
A_68_P21610504	chr2:126701750-126701794	NM_001164325:225	Trpm7	INSIDE	1.228	2.123	1630.06	3460.12	2.607	1496.67	3902.35
A_68_P29604340	chr14:52639614-52639658	NM_027248:772	Zfp219	INSIDE	1.228	1.544	499.19	770.83	1.897	451.01	855.39
A_68_P25098516	chr7:53604272-53604316	AK015435:95		INSIDE	1.228	2.251	1736.49	3908.75	2.764	1378.33	3809.61
A_68_P30462687	chr15:96117084-96117128	NM_175251:-846	Arid2	PROMOTER	1.227	1.901	933.88	1775.24	2.333	872.69	2035.94
A_68_P32071736	chr19:32786770-32786814	NM_026487:-4	Atad1	PROMOTER	1.227	0.522	1477.87	770.94	0.640	1242.71	795.14
A_68_P25503356	chr7:134119822-134119866	NM_026638:-18	Cdipt	PROMOTER	1.227	1.884	912.21	1718.37	2.312	756.91	1749.82
A_68_P22954049	chr4:59016297-59016341	NM_001033165:254	Dnajc25	INSIDE	1.227	2.696	701.18	1890.34	3.308	642.03	2123.55
A_68_P27003034	chr10:23070344-23070388	NM_010167:-657	Eya4	PROMOTER	1.227	1.943	1594.66	3098.56	2.384	1430.38	3410.50
A_68_P22369563	chr3:100293548-100293593	NM_001142952:-455	Fam46c	PROMOTER	1.227	1.472	667.29	981.98	1.806	519.22	937.91
A_68_P25504682	chr7:134376720-134376764	NR_030674:-98	Gm4532	DIVERGENT_PROMOTER	1.227	2.153	993.33	2138.67	2.642	824.46	2178.34
A_68_P29982185	chr15:5093533-5093577	NM_001013367:-306	Prkaa1	PROMOTER	1.227	2.084	601.67	1254.00	2.558	518.63	1326.80
A_68_P30463770	chr15:96290889-96290933	NM_028148:364	Scaf11	INSIDE	1.227	2.041	1279.57	2611.67	2.503	1313.24	3287.52
A_68_P30348909	chr15:76354254-76354298	NM_130893:-1717	Scrt1	PROMOTER	1.227	2.435	854.93	2081.43	2.987	702.24	2097.31
A_68_P23403484	chr4:149329133-149329178	NM_029035:-40	Spsb1	PROMOTER	1.227	1.543	1454.34	2244.66	1.894	1259.78	2386.46
A_68_P22323362	chr3:89884192-89884236	NM_022314:7599	Tpm3	INSIDE	1.227	2.084	4837.23	10081.20	2.556	3971.26	10152.08
A_68_P31301680	chr17:65962034-65962078	NM_013933:839	Vapa	INSIDE	1.227	1.753	516.65	905.61	2.151	511.07	1099.12
A_68_P24049903	chr5:122804592-122804636	NM_019780:193	Vps29	INSIDE	1.227	1.577	1546.24	2438.78	1.936	1363.23	2638.68
A_68_P23195376	chr4:107973405-107973449	NM_001033634:269	Zyg11b	INSIDE	1.227	1.496	4893.35	7321.19	1.835	3773.54	6924.85
A_68_P22322663	chr3:89764566-89764610	NM_001081182:2842	Atp8b2	INSIDE	1.226	2.640	457.10	1206.63	3.236	449.16	1453.58
A_68_P27903678	chr11:70796278-70796322	NM_007573:228	C1qbp	INSIDE	1.226	2.295	1922.10	4410.66	2.814	1771.75	4986.10
A_68_P20166302	chr1:39593044-39593088	NM_028043:420	D1Bwg0212e	INSIDE	1.226	2.595	718.46	1864.56	3.183	706.12	2247.34
A_68_P23365990	chr4:141346639-141346683	NM_172338:-101	Dnajc16	DIVERGENT_PROMOTER	1.226	1.835	1744.87	3201.47	2.250	1531.30	3444.89
A_68_P23613128	chr5:37729744-37729788	NM_145920:50	Evc2	INSIDE	1.226	2.168	750.76	1627.35	2.657	585.43	1555.35
A_68_P23927135	chr5:100407424-100407468	NM_001077265:511	Hnrnpd	INSIDE	1.226	0.432	1994.52	862.44	0.530	1578.39	836.56
A_68_P30342689	chr15:75396844-75396888	NM_001135689:212	Ly6h	INSIDE	1.226	2.454	1590.39	3903.43	3.008	1369.01	4118.41
A_68_P27500270	chr10:120335605-120335649	NM_177092:401	Msrb3	INSIDE	1.226	2.705	1388.11	3755.11	3.316	1316.25	4365.29
A_68_P28514079	chr12:70458006-70458050	NM_025441:125	Nemf	INSIDE	1.226	2.550	1071.88	2733.09	3.127	986.98	3086.25
A_68_P31867986	chr18:81168668-81168712	NM_178280:14627	Sall3	INSIDE	1.226	2.009	721.32	1449.13	2.462	616.64	1518.47
A_68_P32672211	chrX:131010176-131010220	NM_028958:831	Taf7l	INSIDE	1.226	2.102	3097.66	6512.06	2.577	1611.16	4151.38
A_68_P27507137	chr10:121534278-121534322	NM_153059:-142	Tmem5	PROMOTER	1.226	2.309	2895.69	6687.54	2.832	2106.24	5964.45
A_68_P27287684	chr10:80606810-80606854	NM_010731:7817	Zbtb7a	INSIDE	1.226	1.856	369.15	684.96	2.275	346.56	788.41
A_68_P28050434	chr11:97277178-97277222	ENSMUST00000121799:354		INSIDE	1.226	1.575	872.23	1374.09	1.932	737.13	1424.27
A_68_P21138537	chr2:36066471-36066515	ENSMUST00000128242:201		INSIDE	1.226	1.921	686.54	1319.17	2.356	618.62	1457.47

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28183237	chr11:120096983-120097028	NM_198423:2745	Bahcc1	INSIDE	1.225	2.444	219.70	536.84	2.992	196.95	589.36
A_68_P28160638	chr11:116515525-116515569	NM_030206:81	Cygb	INSIDE	1.225	1.769	2344.97	4147.39	2.167	1835.19	3976.36
A_68_P27992419	chr11:86887561-86887605	NM_025638:57	Gdpd1	INSIDE	1.225	2.144	824.01	1766.68	2.627	735.40	1932.04
A_68_P31929500	chr19:5567652-5567696	NM_001033448:-399	Gm962	DIVERGENT_PROMOTER	1.225	1.689	1417.64	2394.41	2.069	1199.60	2482.25
A_68_P30540355	chr16:9994229-9994273	NM_008170:-1624	Grin2a	PROMOTER	1.225	1.693	1423.74	2410.40	2.074	1225.16	2540.53
A_68_P29247522	chr13:97440489-97440533	NM_008255:381	Hmgcr	INSIDE	1.225	1.577	1808.36	2852.06	1.932	1518.68	2933.52
A_68_P28997661	chr13:44826453-44826497	NM_001205043:-165	Jarid2	PROMOTER	1.225	1.839	1510.37	2777.67	2.252	1365.55	3075.17
A_68_P32218824	chr19:59420634-59420678	NM_001033222:-386	Pdzd8	PROMOTER	1.225	1.969	962.38	1895.01	2.412	839.52	2025.30
A_68_P29479231	chr14:26513717-26513761	NM_134084:83	Ppif	INSIDE	1.225	1.353	3010.47	4073.36	1.658	2550.60	4228.16
A_68_P24092504	chr5:130647587-130647631	NM_001199059:-80	Rabgef1	PROMOTER	1.225	2.954	1188.45	3510.89	3.618	968.47	3504.16
A_68_P21920095	chr3:5219581-5219625	NM_030708:1049	Zfhx4	INSIDE	1.225	1.664	914.63	1521.85	2.039	800.95	1632.75
A_68_P20872225	chr1:181733706-181733750	NM_026375:418	Ahctf1	INSIDE	1.224	1.839	948.71	1744.62	2.251	850.17	1914.11
A_68_P28576088	chr12:81620372-81620416	NM_001081421:418	Galntl1	INSIDE	1.224	2.315	1570.96	3637.15	2.835	1387.99	3934.54
A_68_P20432981	chr1:91825501-91825545	NM_010262:2229	Gbx2	INSIDE	1.224	1.784	1245.97	2222.38	2.183	1048.73	2289.06
A_68_P30659188	chr16:33684818-33684862	NM_175256:289	Heg1	INSIDE	1.224	1.761	634.91	1117.88	2.156	557.05	1200.85
A_68_P31834167	chr18:75120830-75120874	NM_010720:65	Lipg	INSIDE	1.224	1.785	2507.39	4475.37	2.185	2116.70	4625.96
A_68_P31099061	chr17:24833259-24833303	NM_027988:102	Noxo1	INSIDE	1.224	1.704	3566.40	6076.17	2.085	2770.54	5776.03
A_68_P20354546	chr1:75502170-75502214	NM_178884:835	Obsl1	INSIDE	1.224	1.496	1182.11	1767.89	1.830	1036.25	1896.50
A_68_P29618379	chr14:56159407-56159453	NM_028994:328	Pck2	INSIDE	1.224	2.157	292.61	631.02	2.640	313.77	828.25
A_68_P21250387	chr2:58999594-58999638	NM_026361:710	Pkp4	INSIDE	1.224	3.545	527.38	1869.54	4.339	529.44	2297.29
A_68_P28746794	chr12:113146363-113146407	NM_011625:-118	Ppp1r13b	PROMOTER	1.224	2.010	433.82	871.86	2.460	428.59	1054.41
A_68_P31106620	chr17:25974088-25974132	NM_144816:-38	Rhbdl1	PROMOTER	1.224	2.405	2457.35	5909.73	2.944	1910.25	5623.49
A_68_P23699213	chr5:53604822-53604866	NM_172710:-153	Sel1l3	PROMOTER	1.224	1.517	2365.84	3590.14	1.858	2017.93	3748.93
A_68_P23440102	chr4:155079253-155079297	NM_026899:351	Ssu72	INSIDE	1.224	4.098	850.86	3486.75	5.017	726.50	3644.95
A_68_P20998558	chr2:9969914-9969958	NM_027748:300	Taf3	INSIDE	1.224	1.790	1109.09	1985.04	2.191	884.61	1938.57
A_68_P28176626	chr11:119089661-119089705	NM_172443:131	Tbc1d16	INSIDE	1.224	2.327	1982.20	4612.60	2.849	1677.17	4778.38
A_68_P31213969	chr17:47875277-47875321	NM_001161723:419	Tcfeb	INSIDE	1.224	2.946	345.45	1017.55	3.607	288.05	1038.93
A_68_P31386730	chr17:81464149-81464193	NM_028138:255	Thumpd2	INSIDE	1.224	1.716	1027.58	1763.14	2.100	991.87	2082.99
A_68_P30963823	chr16:91597831-91597875	NM_030018:73	Tmem50b	INSIDE	1.224	1.669	1208.84	2017.90	2.043	1008.54	2060.89
A_68_P26644964	chr9:75459172-75459216	NM_016711:-62	Tmod2	PROMOTER	1.224	2.097	2242.67	4703.79	2.567	1736.67	4458.86
A_68_P31542075	chr18:21054261-21054305	NM_177038:297	Trappc8	INSIDE	1.224	1.757	687.06	1207.20	2.151	636.80	1369.72
A_68_P20551186	chr1:120207831-120207875	NM_011650:-143	Tsn	PROMOTER	1.224	1.743	552.94	963.58	2.132	480.37	1024.28
A_68_P22630557	chr3:148650752-148650796	ENSMUST00000098518:1506		INSIDE	1.224	1.768	9995.66	17669.51	2.163	6813.05	14739.70
A_68_P30671880	chr16:35735579-35735623	NM_153550:33842	Dirc2	INSIDE	1.223	2.148	1465.32	3147.91	2.626	1190.41	3126.37
A_68_P30981934	chr16:94748127-94748171	NM_007834:88	Dscr3	INSIDE	1.223	1.877	1063.38	1995.83	2.295	956.24	2194.75
A_68_P21585581	chr2:122124764-122124808	NM_025777:151	Duoxa2	INSIDE	1.223	14.281	862.74	12320.62	17.466	674.94	11788.86
A_68_P24142816	chr5:141178207-141178251	NM_028833:104	Iqce	INSIDE	1.223	2.460	793.10	1950.80	3.009	623.60	1876.61
A_68_P24112797	chr5:135164410-135164454	NM_010717:28	Limk1	INSIDE	1.223	3.946	1189.66	4694.60	4.826	1031.39	4977.17
A_68_P23588234	chr5:33678349-33678393	NM_021500:150	Maea	INSIDE	1.223	2.187	3783.12	8272.60	2.674	3137.32	8388.58
A_68_P29116722	chr13:69750305-69750349	NM_175283:15	Srd5a1	INSIDE	1.223	1.700	2550.30	4335.32	2.079	1885.09	3918.71
A_68_P21579355	chr2:120997099-120997143	NM_153387:179	Tubgcp4	INSIDE	1.223	1.905	1073.76	2045.52	2.330	891.10	2076.03
A_68_P32326600	chrX:35542695-35542742	NM_001079513:-251	Zbtb33	PROMOTER	1.223	2.961	616.99	1826.62	3.621	430.10	1557.23
A_68_P28741418	chr12:112215432-112215476	NM_175207:1777	Ankrd9	INSIDE	1.222	2.621	1325.34	3473.50	3.204	1058.32	3390.41
A_68_P21425706	chr2:91805641-91805685	NM_138306:-1942	Dgkz	PROMOTER	1.222	1.905	683.84	1302.55	2.327	598.46	1392.86
A_68_P32743940	chrX:147482252-147482296	NM_008001:499	Fgd1	INSIDE	1.222	2.341	449.34	1051.74	2.861	291.76	834.66
A_68_P20455651	chr1:95342033-95342077	NM_133808:33331	Hdlbp	INSIDE	1.222	1.584	1424.42	2256.09	1.936	1236.06	2393.27
A_68_P29717288	chr14:73784719-73784763	NM_008410:338	Itm2b	INSIDE	1.222	4.968	7211.91	35827.01	6.068	5508.43	33427.36
A_68_P20510207	chr1:108656347-108656391	NM_027534:-49	Kdsr	PROMOTER	1.222	1.514	1734.11	2625.89	1.851	1781.69	3297.17
A_68_P22171315	chr3:58809811-58809855	NM_177855:-1067	Med12l	PROMOTER	1.222	2.528	570.34	1442.07	3.091	511.31	1580.24
A_68_P31208519	chr17:46848833-46848877	NM_145488:443	Pex6	INSIDE	1.222	3.867	962.67	3722.62	4.726	920.14	4348.54
A_68_P32142309	chr19:46222327-46222371	NM_008852:467	Pitx3	INSIDE	1.222	2.179	2169.91	4727.81	2.662	1695.21	4512.46

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25091653	chr7:52437711-52437755	NM_053256:1368	Pth2	DOWNSTREAM	1.222	3.688	630.07	2323.72	4.506	511.43	2304.57
A_68_P24061235	chr5:124875362-124875406	NM_001081203:539	Sbno1	INSIDE	1.222	4.184	1675.42	7009.98	5.115	1312.24	6711.56
A_68_P27926563	chr11:75328969-75329013	NM_001004157:1948	Scarf1	INSIDE	1.222	2.748	594.63	1634.26	3.359	535.87	1799.89
A_68_P22169673	chr3:58495733-58495777	NM_009174:556	Siah2	INSIDE	1.222	2.583	943.81	2438.21	3.156	914.83	2887.66
A_68_P28781791	chr12:120075046-120075090	NM_177082:-9733	Sp8	PROMOTER	1.222	1.748	2047.32	3578.11	2.136	1760.30	3760.04
A_68_P31479221	chr18:7868637-7868681	NR_027465:-197	Wac	PROMOTER	1.222	2.412	621.15	1498.38	2.947	593.00	1747.85
A_68_P22408056	chr3:107499381-107499425	NM_145542:64	Ahcyl1	INSIDE	1.221	3.804	604.76	2300.36	4.643	582.18	2702.99
A_68_P21068910	chr2:24790687-24790731	NM_001162485:93	Arrdc1	INSIDE	1.221	1.760	1978.72	3481.87	2.148	1658.76	3563.63
A_68_P21566800	chr2:118728429-118728473	NM_001045523:1100	Bahd1	INSIDE	1.221	1.529	1105.76	1691.24	1.867	1087.07	2030.10
A_68_P25661488	chr8:12430745-12430789	NR_027975:44996	Gm5607	INSIDE	1.221	1.440	3591.20	5170.10	1.758	2564.52	4508.14
A_68_P21283784	chr2:64860481-64860525	NM_016719:321	Grb14	INSIDE	1.221	1.616	2437.16	3939.07	1.974	2045.12	4037.12
A_68_P32215806	chr19:58935621-58935665	NM_175199:-168	Hspa12a	PROMOTER	1.221	1.792	1191.09	2134.23	2.188	1002.16	2192.71
A_68_P24818876	chr6:125081706-125081750	NM_138747:-172	Nop2	PROMOTER	1.221	1.805	1792.87	3236.23	2.204	1450.08	3195.48
A_68_P26011767	chr8:85388102-85388146	NM_177378:870	Rnf150	INSIDE	1.221	1.556	700.95	1090.48	1.900	616.87	1172.03
A_68_P28167721	chr11:117734583-117734627	NM_027919:236	Tha1	INSIDE	1.221	1.577	609.44	961.04	1.926	572.04	1101.77
A_68_P29260367	chr13:99696244-99696288	NM_178716:73	Tnpo1	INSIDE	1.221	2.206	1171.67	2585.16	2.694	958.39	2582.00
A_68_P21836563	chr2:167456985-167457029	NM_023230:499	Ube2v1	INSIDE	1.221	2.095	1821.01	3814.31	2.557	1477.22	3776.89
A_68_P31625689	chr18:36920123-36920167	NM_026464:252	Wdr55	INSIDE	1.221	1.417	2263.84	3206.83	1.730	1740.24	3010.16
A_68_P31408615	chr17:85489810-85489854	NM_028576:-207	1700106N22Rik	DIVERGENT_PROMOTER	1.220	1.724	2932.18	5055.40	2.103	2255.24	4741.77
A_68_P31331955	chr17:71351299-71351343	NM_026064:553	2900073G15Rik	INSIDE	1.220	2.185	2941.98	6429.19	2.667	2397.31	6393.55
A_68_P32957258	chr17:8476452-8476496	NM_018819:-203	Brp44l	PROMOTER	1.220	1.425	1595.27	2273.87	1.739	1415.48	2461.45
A_68_P24798986	chr6:120481161-120481205	NM_144815:135	Cecr5	INSIDE	1.220	1.599	1030.33	1647.33	1.950	902.76	1760.81
A_68_P21477095	chr2:102291921-102291965	NM_010218:7	Fjx1	INSIDE	1.220	1.914	597.28	1143.08	2.334	524.22	1223.61
A_68_P25087550	chr7:51717698-51717742	NM_198250:19864	Lrrc4b	INSIDE	1.220	1.787	967.20	1728.71	2.181	847.95	1849.50
A_68_P23334088	chr4:136025956-136026001	NM_024452:303	Luzp1	INSIDE	1.220	3.249	216.59	703.69	3.964	185.84	736.66
A_68_P26041378	chr8:91045300-91045344	NM_001163660:-6209	Nkd1	PROMOTER	1.220	3.426	457.24	1566.51	4.181	391.00	1634.88
A_68_P30542114	chr16:10411911-10411955	NM_011955:-98	Nubp1	PROMOTER	1.220	2.917	1464.43	4272.17	3.559	1146.64	4081.18
A_68_P32240644	chrX:7455750-7455794	NM_138606:341	Pim2	INSIDE	1.220	1.739	2037.48	3542.39	2.122	956.24	2028.70
A_68_P31253472	chr17:56175685-56175729	NM_013664:293	Sh3gl1	INSIDE	1.220	2.499	680.59	1700.67	3.048	629.49	1918.47
A_68_P26644962	chr9:75459020-75459064	NM_016711:90	Tmod2	INSIDE	1.220	2.056	1367.80	2811.58	2.509	1144.93	2872.09
A_68_P23111973	chr4:93001689-93001733	NM_026954:492	Tusc1	INSIDE	1.220	3.702	429.98	1591.87	4.517	408.78	1846.61
A_68_P27181846	chr10:61159115-61159159	NM_027912:875	Tysnd1	INSIDE	1.220	2.673	839.86	2244.68	3.262	782.79	2553.38
A_68_P20827837	chr1:173341785-173341830	NM_009480:-4	Usf1	PROMOTER	1.220	1.481	1011.33	1497.82	1.807	846.49	1529.96
A_68_P30378286	chr15:81353764-81353808			Unknown	1.220	2.355	872.83	2055.76	2.875	813.49	2338.46
A_68_P20874334	chr1:182126153-182126197	NM_023341:-23	Adck3	PROMOTER	1.219	2.146	957.16	2053.87	2.616	802.24	2098.32
A_68_P25370481	chr7:108079952-108079996	NM_001081116:701	Arhgef17	INSIDE	1.219	3.161	666.69	2107.10	3.852	562.87	2168.40
A_68_P32260375	chrX:11668929-11668973	NM_001168321:68531	Bcor	INSIDE	1.219	1.666	453.85	756.20	2.031	284.92	578.67
A_68_P21565620	chr2:118529638-118529682	NM_001081971:39	Gm1337	INSIDE	1.219	3.180	825.42	2625.01	3.876	759.57	2944.15
A_68_P28041811	chr11:95852863-95852907	NM_009951:14374	Igf2bp1	INSIDE	1.219	1.554	1463.15	2274.31	1.895	1125.11	2132.18
A_68_P32082882	chr19:34996734-34996778	NM_183046:-91	Kif20b	PROMOTER	1.219	1.637	663.28	1085.95	1.996	570.64	1139.14
A_68_P27624062	chr11:18927325-18927369	NM_001193271:-8374	Meis1	PROMOTER	1.219	2.226	514.50	1145.18	2.714	467.18	1268.00
A_68_P23278955	chr4:125914068-125914112	NM_001145970:19473	Mtap7d1	INSIDE	1.219	2.742	1776.84	4872.62	3.343	1522.05	5087.55
A_68_P23236917	chr4:117540757-117540801	NM_008135:32916	Slc6a9	INSIDE	1.219	2.076	2217.44	4602.91	2.530	1955.98	4949.45
A_68_P27966235	chr11:82248010-82248054	NM_023438:45631	Tmem132e	INSIDE	1.219	1.387	1092.69	1515.42	1.690	798.51	1349.42
A_68_P31620889	chr18:36079889-36079933	AK021191:7125		DOWNSTREAM	1.219	2.143	940.11	2014.98	2.613	879.30	2297.45
A_68_P27971499	chr11:83253762-83253806	NM_025492:2589	1700020L24Rik	INSIDE	1.218	2.503	284.99	713.23	3.049	277.22	845.18
A_68_P23545744	chr5:24606762-24606806	NR_027851:-8	2900005J15Rik	DIVERGENT_PROMOTER	1.218	1.546	1476.11	2281.50	1.882	1334.20	2511.10
A_68_P27257131	chr10:75022752-75022796	NM_198860:301	AI646023	INSIDE	1.218	1.899	1136.89	2158.93	2.312	950.89	2198.63
A_68_P26234305	chr8:125100749-125100793	NM_009698:37	Aprt	INSIDE	1.218	3.940	10683.97	42096.27	4.798	6517.13	31271.70
A_68_P28153160	chr11:115243190-115243234	NM_001080929:-17	Cdr2l	PROMOTER	1.218	1.777	1294.07	2299.80	2.165	1141.67	2471.44
A_68_P29618487	chr14:56179252-56179296	NM_001199009:-485	Dcaf11	PROMOTER	1.218	1.689	1309.25	2211.35	2.057	867.90	1784.85

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27572316	chr11:7113730-7113774	NM_008343:174	Igfbp3	INSIDE	1.218	1.530	1434.05	2193.49	1.863	1104.16	2057.00
A_68_P22934420	chr4:55543726-55543770	NM_010637:1599	Klf4	INSIDE	1.218	1.693	1092.36	1849.56	2.062	990.88	2043.25
A_68_P26537258	chr9:56467405-56467449	NM_181074:65634	Lingo1	INSIDE	1.218	5.982	3327.82	19905.82	7.288	1983.17	14453.23
A_68_P27542076	chr10:128003183-128003227	NM_011119:-214	Pa2g4	PROMOTER	1.218	2.281	653.65	1491.04	2.778	574.51	1596.07
A_68_P22081520	chr3:40603976-40604020	NM_011495:126	Plk4	INSIDE	1.218	3.028	394.07	1193.38	3.690	370.14	1365.71
A_68_P32227660	chr19:60950291-60950335	NM_007452:129	Prdx3	INSIDE	1.218	1.888	3592.01	6780.73	2.300	2633.46	6057.23
A_68_P31868119	chr18:81184645-81184689	NM_178280:-1349	Sall3	PROMOTER	1.218	1.827	659.62	1205.02	2.225	516.93	1150.13
A_68_P26084861	chr8:98239992-98240036	NM_001035123:202	Setd6	INSIDE	1.218	2.990	3190.57	9539.16	3.641	2531.08	9214.92
A_68_P25957631	chr8:74108344-74108388	NM_011977:15541	Slc27a1	INSIDE	1.218	1.556	575.66	895.51	1.894	408.88	774.58
A_68_P32147463	chr19:47142891-47142935	NM_177342:675	Taf5	INSIDE	1.218	1.585	565.84	897.04	1.931	511.88	988.40
A_68_P32557245	chrX:97016277-97016321	NM_001081283:-109	Tmem28	PROMOTER	1.218	2.729	424.89	1159.72	3.325	264.69	880.23
A_68_P24777345	chr6:116578587-116578631	NM_026057:387	Zfp422	INSIDE	1.218	1.363	1560.09	2127.07	1.661	1178.73	1958.03
A_68_P23611946	chr5:37554326-37554370	AK036147:261		INSIDE	1.218	3.156	715.66	2258.85	3.844	653.45	2511.74
A_68_P22312389	chr3:88005037-88005081	ENSMUST00000167043:514		INSIDE	1.218	3.674	920.17	3380.42	4.476	866.24	3876.91
A_68_P29249239	chr13:97841732-97841776	NM_001100458:157	Fam169a	INSIDE	1.217	1.529	544.84	832.80	1.860	511.23	950.80
A_68_P26809635	chr9:107473258-107473302	NM_010489:1787	Hyal2	INSIDE	1.217	2.344	959.28	2248.38	2.852	703.05	2005.23
A_68_P24804559	chr6:121423187-121423231	NM_001033354:488	Iqsec3	INSIDE	1.217	2.100	466.46	979.71	2.557	493.04	1260.74
A_68_P31863853	chr18:80560016-80560060	NM_001190373:955	Kcng2	INSIDE	1.217	1.620	1215.45	1968.48	1.970	1088.15	2144.11
A_68_P26144747	chr8:109949061-109949105	NM_026277:-144	Nob1	PROMOTER	1.217	2.368	1208.29	2860.91	2.882	1033.59	2978.72
A_68_P27357768	chr10:93610732-93610776	NM_011629:79	Nr2c1	INSIDE	1.217	1.752	1829.57	3205.03	2.132	1420.83	3029.79
A_68_P27924779	chr11:75008788-75008832	NM_177708:1316	Rtn4rl1	INSIDE	1.217	1.578	570.41	900.06	1.920	488.48	937.69
A_68_P25024912	chr7:29805278-29805322	NM_009109:104870	Ryr1	INSIDE	1.217	2.133	767.95	1638.34	2.596	699.79	1816.35
A_68_P27552578	chr11:3435772-3435816	NM_001159284:3501	Smtn	INSIDE	1.217	2.168	853.02	1849.67	2.640	794.44	2097.06
A_68_P26696148	chr9:85737347-85737391	NM_001164792:910	Tpbg	INSIDE	1.217	2.215	911.09	2017.91	2.694	839.94	2263.20
A_68_P23763266	chr5:67067724-67067768	NM_011670:387	Uchl1	INSIDE	1.217	4.045	1721.59	6962.99	4.921	1280.87	6303.08
A_68_P27563477	chr11:5344468-5344513	NM_001080924:360	Znrf3	INSIDE	1.217	1.546	1341.80	2074.88	1.881	1209.54	2275.51
A_68_P25097408	chr7:53435337-53435381	NM_011510:45	Abcc8	INSIDE	1.216	1.856	2952.84	5480.32	2.257	2330.10	5258.56
A_68_P26665701	chr9:79566357-79566401	NM_007730:107	Col12a1	INSIDE	1.216	1.596	2430.74	3880.54	1.942	1980.78	3846.77
A_68_P30579148	chr16:18343878-18343922	NM_138583:125	D16H22S680E	INSIDE	1.216	1.339	2497.85	3343.59	1.628	2201.48	3583.74
A_68_P31227863	chr17:50432140-50432184	NM_010021:762	Dazl	INSIDE	1.216	1.362	4813.80	6558.69	1.657	3976.66	6588.76
A_68_P32119984	chr19:42330495-42330539	NM_027694:288	Golga7b	INSIDE	1.216	0.494	1290.49	638.10	0.601	1069.39	642.92
A_68_P30021000	chr15:12251385-12251429	NM_025673:156	Golph3	INSIDE	1.216	1.905	727.77	1386.64	2.316	729.80	1690.18
A_68_P29363819	chr13:118391652-118391696	NM_010408:548	Hcn1	INSIDE	1.216	1.927	1040.13	2004.48	2.343	997.56	2337.07
A_68_P24137556	chr5:140251303-140251347	NM_026748:308	Ints1	INSIDE	1.216	0.473	2140.77	1012.17	0.575	1721.04	989.59
A_68_P27922696	chr11:74645200-74645244	NM_010813:797	Mnt	INSIDE	1.216	2.877	680.70	1958.34	3.499	740.74	2591.54
A_68_P23523153	chr5:20387713-20387757	NM_172992:208	Phtf2	INSIDE	1.216	1.648	1303.91	2149.11	2.004	1272.49	2549.94
A_68_P32118987	chr19:42164891-42164935	NM_145501:-12	Pi4k2a	DIVERGENT_PROMOTER	1.216	1.502	1258.15	1889.56	1.827	1113.07	2033.48
A_68_P29648701	chr14:61792097-61792141	NM_172809:34825	Sacs	INSIDE	1.216	1.769	1343.37	2376.27	2.151	1227.85	2641.07
A_68_P25090603	chr7:52263124-52263168	NM_001008422:8473	Scaf1	INSIDE	1.216	2.144	741.55	1589.61	2.608	576.21	1502.49
A_68_P26887823	chr9:122075943-122075987	NM_001164572:49581	Snrk	INSIDE	1.216	1.852	1244.00	2304.39	2.252	962.59	2167.89
A_68_P30019344	chr15:11925168-11925212	NM_011294:572	Sub1	INSIDE	1.216	1.948	1157.79	2255.22	2.369	959.97	2273.81
A_68_P31209393	chr17:47027920-47027964	NM_178385:373	Tbcc	INSIDE	1.216	2.067	705.06	1457.22	2.514	584.66	1469.91
A_68_P24459355	chr6:53770847-53770891	NM_025817:-49	Tril	PROMOTER	1.216	1.561	2820.71	4403.22	1.898	2033.29	3858.81
A_68_P22142065	chr3:53282814-53282858	NM_173382:15098	2810046L04Rik	INSIDE	1.215	4.242	6919.45	29351.52	5.153	5009.68	25813.97
A_68_P29049838	chr13:54605642-54605686	NM_176987:499	4732471D19Rik	INSIDE	1.215	2.243	677.44	1519.76	2.726	635.08	1731.27
A_68_P23154903	chr4:101092599-101092643	NM_009647:313	Ak4	INSIDE	1.215	2.763	3503.47	9678.66	3.358	3174.14	10657.39
A_68_P30357052	chr15:77825727-77825771	NM_007583:123962	Cacng2	INSIDE	1.215	1.776	826.86	1468.79	2.159	594.32	1283.06
A_68_P24040307	chr5:121144585-121144629	NM_008052:17072	Dtx1	INSIDE	1.215	1.943	542.80	1054.74	2.360	448.67	1058.88
A_68_P31928722	chr19:5448027-5448071	NM_010235:351	Fosl1	INSIDE	1.215	1.594	1667.83	2659.35	1.937	1372.21	2658.55
A_68_P24226580	chr6:8460315-8460359	NM_133236:741	Glcci1	INSIDE	1.215	2.075	1530.55	3175.74	2.522	1327.77	3348.11
A_68_P26467075	chr9:44143629-44143673	NM_010436:853	H2afx	INSIDE	1.215	2.114	1285.43	2717.19	2.568	1028.36	2640.43

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P22603829	chr3:144232802-144232849	NM_011828:355	Hs2st1	INSIDE	1.215	1.906	1245.14	2373.51	2.316	1107.93	2565.60
A_68_P32465997	chrX:71268691-71268735	NM_001177975:545	Irak1	INSIDE	1.215	1.954	516.82	1009.72	2.374	346.10	821.78
A_68_P28099128	chr11:105880140-105880184	NM_001037712:10646	Kcnh6	INSIDE	1.215	1.598	808.37	1291.42	1.942	662.97	1287.23
A_68_P31259699	chr17:57171306-57171350	NM_010613:-398	Khsrp	PROMOTER	1.215	1.414	3773.68	5335.16	1.718	2951.95	5072.48
A_68_P27558539	chr11:4494769-4494813	NM_028860:28	Mtmr3	INSIDE	1.215	2.817	925.25	2606.01	3.423	893.53	3058.31
A_68_P29654922	chr14:62951071-62951115	NM_026001:151	Rnaseh2b	INSIDE	1.215	1.929	1085.90	2094.21	2.342	927.31	2172.07
A_68_P21311406	chr2:69699566-69699610	NM_001110145:-30	Ssb	PROMOTER	1.215	1.657	1330.55	2204.31	2.014	1081.60	2177.89
A_68_P20804307	chr1:169213914-169213958	NM_030724:1322	Uck2	INSIDE	1.215	1.487	2282.46	3393.54	1.806	2003.04	3617.56
A_68_P25728007	chr8:26712095-26712139	NM_001001735:-661	Whsc1l1	DIVERGENT_PROMOTER	1.215	2.175	764.67	1662.89	2.643	689.20	1821.55
A_68_P32369655	chrX:47014344-47014388	ENSMUST00000121891:230		INSIDE	1.215	1.793	411.42	737.83	2.179	257.78	561.62
A_68_P29147535	chr13:74946041-74946085	NM_009817:-693	Cast	PROMOTER	1.214	2.119	2732.05	5789.63	2.572	2368.41	6090.97
A_68_P31186625	chr17:43013785-43013829	NM_009847:-433	Cd2ap	PROMOTER	1.214	1.709	1088.08	1859.39	2.074	913.37	1894.27
A_68_P26844378	chr9:114293915-114293959	NM_019922:5894	Crtap	INSIDE	1.214	2.702	590.24	1594.85	3.280	494.84	1623.18
A_68_P29628539	chr14:58161485-58161529	NM_145837:17841	Il17d	INSIDE	1.214	2.918	1027.70	2998.40	3.542	990.17	3506.85
A_68_P20168281	chr1:39958327-39958371	NM_008696:591	Map4k4	INSIDE	1.214	1.487	1182.43	1758.56	1.805	992.43	1791.73
A_68_P29330292	chr13:112515172-112515216	NM_172593:38809	Mier3	DOWNSTREAM	1.214	1.384	1262.53	1747.10	1.680	969.96	1629.70
A_68_P25809390	chr8:42218830-42218874	NM_001005863:228	Mtus1	INSIDE	1.214	1.551	2016.19	3126.23	1.883	1817.19	3421.10
A_68_P23322026	chr4:133842693-133842737	NM_001163794:454	Pdik1l	INSIDE	1.214	1.965	938.36	1844.12	2.385	967.74	2308.52
A_68_P30861550	chr16:72663819-72663863	NM_019413:447	Robo1	INSIDE	1.214	1.608	1630.32	2621.63	1.952	1304.27	2545.63
A_68_P21095249	chr2:28980679-28980724	NM_198033:190	Setx	INSIDE	1.214	1.550	557.70	864.59	1.882	546.02	1027.61
A_68_P24083090	chr5:128938897-128938941	NM_172885:19	Tmem132d	INSIDE	1.214	2.527	910.69	2301.06	3.069	914.61	2806.50
A_68_P31292453	chr17:64213171-64213215	ENSMUST00000050753:-52		DIVERGENT_PROMOTER	1.214	2.671	1169.59	3123.83	3.241	1007.04	3264.13
A_68_P21741661	chr2:150730134-150730178	NM_024465:311	Abhd12	INSIDE	1.213	2.015	1271.67	2562.23	2.444	1093.83	2672.89
A_68_P21438435	chr2:93851039-93851083	NM_026944:-173	Alkbh3	PROMOTER	1.213	2.163	764.64	1653.54	2.624	605.84	1589.68
A_68_P30925872	chr16:84835744-84835788	NM_016755:53	Atp5j	INSIDE	1.213	1.839	525.84	966.88	2.231	557.29	1243.15
A_68_P21419476	chr2:90729680-90729724	NM_026161:3760	C1qtnf4	INSIDE	1.213	0.463	1193.16	551.85	0.561	1003.74	563.11
A_68_P26426473	chr9:36533774-36533818	NM_007691:447	Chek1	INSIDE	1.213	1.364	1897.82	2589.22	1.655	1527.98	2529.17
A_68_P29060387	chr13:56397406-56397450	NM_019568:484	Cxcl14	INSIDE	1.213	1.686	1021.51	1722.57	2.045	971.78	1987.59
A_68_P21374004	chr2:80155781-80155825	NM_024181:180	Dnajc10	INSIDE	1.213	1.756	2330.78	4092.81	2.130	2039.39	4342.95
A_68_P31097233	chr17:24563466-24563510	NM_010023:-139	Eci1	PROMOTER	1.213	2.568	898.95	2308.29	3.115	793.32	2471.08
A_68_P24908778	chr6:143116037-143116081	NM_029250:309	Etnk1	INSIDE	1.213	2.765	730.28	2018.90	3.352	614.99	2061.52
A_68_P27930555	chr11:76015561-76015605	NM_027773:25	Fam57a	INSIDE	1.213	1.859	3970.10	7381.69	2.256	3291.20	7424.16
A_68_P31106390	chr17:25946464-25946508	NM_001164225:457	Fbxl16	INSIDE	1.213	1.667	3314.97	5525.25	2.021	2685.30	5427.25
A_68_P29257124	chr13:99124764-99124808	NM_008242:587	Foxd1	INSIDE	1.213	1.803	2041.75	3680.27	2.186	1641.97	3588.96
A_68_P24112561	chr5:134789297-134789341	NM_001080746:1298	Gtf2i	INSIDE	1.213	0.550	1194.65	657.02	0.667	1019.57	680.40
A_68_P26020983	chr8:87186771-87186818	NM_010499:-43	Ier2	PROMOTER	1.213	1.382	1896.58	2621.84	1.677	1520.49	2549.89
A_68_P27284096	chr10:80039600-80039644	NM_078477:419	Klf16	INSIDE	1.213	2.167	1393.30	3019.67	2.629	1153.65	3033.17
A_68_P23657851	chr5:46061284-46061329	NM_019438:143	Ncapg	INSIDE	1.213	1.742	566.02	985.83	2.113	476.62	1007.31
A_68_P33012160	chr9_random:55072-55116	NM_011154:-62	Ppp2r3d	PROMOTER	1.213	3.675	3654.69	13431.85	4.460	2786.60	12427.65
A_68_P30478003	chr15:98887633-98887677	NM_001163588:2050	Prph	INSIDE	1.213	1.957	730.48	1429.75	2.374	537.81	1276.62
A_68_P24061317	chr5:124895849-124895893	NM_030241:5932	Setd8	INSIDE	1.213	1.415	1452.31	2055.36	1.717	1198.19	2057.02
A_68_P27466129	chr10:114238135-114238179	NM_146241:270	Trhde	INSIDE	1.213	1.844	807.67	1489.00	2.237	817.83	1829.36
A_68_P27969172	chr11:82744813-82744857	NM_178680:20080	Unc45b	INSIDE	1.213	2.008	3402.11	6832.57	2.436	2986.49	7276.05
A_68_P28677276	chr12:100866117-100866161	ENSMUST00000137842:64088		DOWNSTREAM	1.213	2.071	457.34	947.17	2.512	418.69	1051.83
A_68_P20876218	chr1:182413556-182413600	NM_001081227:57	6330403A02Rik	INSIDE	1.212	2.568	721.17	1852.23	3.112	593.47	1846.75
A_68_P26595206	chr9:66643069-66643113	NM_177583:140	Aph1b	INSIDE	1.212	1.438	1281.51	1842.73	1.743	1122.10	1955.36
A_68_P28050945	chr11:97362080-97362124	NM_021493:50629	Arhgap23	INSIDE	1.212	2.861	701.92	2008.51	3.467	634.80	2201.14
A_68_P28724521	chr12:109154706-109154750	NM_001079883:86896	Bcl11b	INSIDE	1.212	2.803	415.06	1163.41	3.398	400.50	1361.00
A_68_P31161463	chr17:36016977-36017021	NM_026987:276	Dhx16	INSIDE	1.212	2.333	789.17	1840.98	2.828	812.59	2298.12
A_68_P23342692	chr4:137469822-137469866	NM_199307:51693	Ece1	INSIDE	1.212	1.580	696.00	1099.95	1.915	588.29	1126.84
A_68_P27181452	chr10:61088878-61088922	NM_001177511:30669	Npffr1	INSIDE	1.212	1.575	804.23	1266.92	1.909	662.94	1265.87

						Sham group			TiO$_2$-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P29589458	chr14:49293418-49293462	NR_029384:4478	Otx2os1	INSIDE	1.212	1.884	611.37	1151.77	2.283	544.58	1243.36
A_68_P32113657	chr19:41281416-41281460	NM_011904:-174	Tll2	PROMOTER	1.212	1.720	1625.52	2795.99	2.085	1519.56	3167.62
A_68_P28593635	chr12:84937847-84937891	NM_183154:229	Zfyve1	INSIDE	1.212	1.458	1015.85	1480.99	1.768	874.06	1544.95
A_68_P31103786	chr17:25571232-25571276	NM_001163691:-526	Cacna1h	PROMOTER	1.211	2.155	1772.87	3820.35	2.610	1475.59	3851.48
A_68_P26822034	chr9:110020069-110020113	NM_133347:-2004	Dhx30	PROMOTER	1.211	1.750	677.52	1185.81	2.119	545.30	1155.61
A_68_P31099856	chr17:24987535-24987579	NM_001159626:-55	Hagh	PROMOTER	1.211	2.844	1136.89	3233.30	3.444	948.52	3266.92
A_68_P25264890	chr7:87259796-87259840	NM_173011:418	Idh2	INSIDE	1.211	2.221	7254.05	16113.71	2.690	5105.30	13733.74
A_68_P20285216	chr1:63160901-63160945	NM_001081436:-81	Ino80d	PROMOTER	1.211	2.238	1355.93	3034.20	2.709	1215.97	3294.23
A_68_P24053338	chr5:123438550-123438594	NM_001005866:-30	Kdm2b	PROMOTER	1.211	1.770	15591.49	27603.73	2.145	10896.96	23371.47
A_68_P20641807	chr1:137715358-137715402	NM_133664:206	Lad1	INSIDE	1.211	1.868	456.66	853.19	2.263	426.36	965.01
A_68_P26134881	chr8:108138096-108138140	NR_035492:-1247	Mir1966	PROMOTER	1.211	2.300	1524.62	3507.30	2.786	1216.70	3389.50
A_68_P21006475	chr2:11423041-11423085	NM_001177752:655	Pfkfb3	INSIDE	1.211	2.120	2292.87	4860.41	2.567	1992.15	5114.79
A_68_P27287755	chr10:80616237-80616281	NM_021501:14207	Pias4	DOWNSTREAM	1.211	3.414	959.62	3276.19	4.133	777.76	3214.36
A_68_P27469298	chr10:114821572-114821616	NM_025780:-103	Thap2	DIVERGENT_PROMOTER	1.211	1.721	4851.98	8349.37	2.084	4025.04	8389.94
A_68_P26217893	A_68_P26217893			Unknown	1.211	2.282	1996.67	4556.17	2.763	1930.64	5334.78
A_68_P28031039	chr11:94010311-94010355	ENSMUST00000155965:15517		INSIDE	1.211	1.452	1984.94	2881.26	1.757	1590.97	2795.89
A_68_P21565892	chr2:118572266-118572310	NR_030716:791	5430417L22Rik	INSIDE	1.210	0.404	2818.48	1139.86	0.489	1636.87	801.03
A_68_P30434244	chr15:91030048-91030092	NM_011994:-7832	Abcd2	PROMOTER	1.210	2.404	1423.99	3423.11	2.908	1133.33	3295.15
A_68_P20241456	chr1:55420453-55420497	NM_029267:-161	Boll	PROMOTER	1.210	1.560	515.69	804.43	1.887	491.67	927.74
A_68_P24980698	chr7:16881008-16881052	NM_001136471:-8886	Ccdc9	PROMOTER	1.210	2.242	1518.35	3403.93	2.713	1309.25	3552.51
A_68_P22889575	chr4:46614883-46614927	NM_001164804:-103	Coro2a	PROMOTER	1.210	3.004	1884.05	5659.50	3.636	1331.83	4841.95
A_68_P25842219	chr8:48618727-48618771	NM_177240:76	D030016E14Rik	INSIDE	1.210	2.187	1753.26	3834.54	2.647	1577.35	4175.02
A_68_P30364005	chr15:78873228-78873272	NM_015738:936	Galr3	INSIDE	1.210	2.816	647.24	1822.33	3.408	585.40	1995.13
A_68_P27087303	chr10:40791899-40791943	NM_199058:-530	Gpr6	PROMOTER	1.210	1.633	992.17	1620.21	1.976	872.03	1722.94
A_68_P24156175	chr5:144119353-144119397	NM_133355:-6212	Grid2ip	PROMOTER	1.210	5.490	5258.33	28868.55	6.646	5041.27	33502.05
A_68_P29138629	chr13:73397900-73397944	NM_018885:-22	Irx4	PROMOTER	1.210	2.940	1412.02	4151.56	3.556	1281.35	4557.11
A_68_P21902329	chr2:179960496-179960540	NM_001081171:46	Lama5	INSIDE	1.210	2.391	1073.73	2567.44	2.893	912.09	2639.11
A_68_P28154416	chr11:115473786-115473830	NM_027162:9	Mif4gd	INSIDE	1.210	2.950	1262.79	3725.77	3.569	1068.60	3814.23
A_68_P31227302	chr17:50329542-50329586	NM_181397:258	Rftn1	INSIDE	1.210	3.297	1539.25	5075.30	3.991	1407.06	5615.56
A_68_P22317135	chr3:88894988-88895032	NM_001083808:-1057	Rusc1	PROMOTER	1.210	1.574	2138.77	3365.96	1.905	1700.57	3238.87
A_68_P25090607	chr7:52263642-52263686	NM_001008422:7955	Scaf1	INSIDE	1.210	1.532	774.04	1185.85	1.853	605.87	1122.84
A_68_P21707841	chr2:144382255-144382299	NM_019787:264	Sec23b	INSIDE	1.210	3.903	1293.78	5049.14	4.724	963.28	4550.43
A_68_P30651947	chr16:32333125-32333169	NM_177633:809	Ubxn7	INSIDE	1.210	3.221	437.20	1408.30	3.897	433.52	1689.37
A_68_P32039606	chr19:27293512-27293556	NM_001161420:2025	Vldlr	INSIDE	1.210	1.516	1207.62	1830.62	1.834	894.67	1640.91
A_68_P23938661	chr5:102498072-102498116	NM_172882:846	Wdfy3	INSIDE	1.210	1.857	557.00	1034.33	2.246	478.19	1074.16
A_68_P25844871	chr8:49075873-49075917	NM_133791:11	Wwc2	INSIDE	1.210	1.721	828.75	1425.91	2.081	699.20	1455.14
A_68_P33005807	A_68_P33005807			Unknown	1.210	3.543	902.80	3198.78	4.287	789.06	3382.59
A_68_P31019377	A_68_P31019377			Unknown	1.210	2.532	255.63	647.25	3.064	242.82	743.88
A_68_P29848865	chr14:100684720-100684764	AK021307:-1136		PROMOTER	1.210	1.771	1294.44	2292.44	2.143	1027.10	2200.77
A_68_P28275058	chr12:19181894-19181939	BC012645:412612		INSIDE	1.210	2.183	28311.06	61795.69	2.642	22174.70	58588.32
A_68_P23435929	chr4:154417040-154417084	ENSMUST00000135665:201		INSIDE	1.210	1.651	723.71	1194.90	1.998	663.70	1326.21
A_68_P27473559	chr10:115551010-115551054	NM_001161855:-59	4933416C03Rik	PROMOTER	1.209	2.550	1628.90	4153.49	3.084	1336.31	4121.08
A_68_P27804987	chr11:53292850-53292894	NM_183173:825	Ankrd43	INSIDE	1.209	5.455	270.63	1476.23	6.595	264.40	1743.64
A_68_P27083519	chr10:40068940-40068984	NM_001168304:-151	Cdk19	PROMOTER	1.209	1.484	1031.52	1530.91	1.794	818.88	1468.75
A_68_P29060392	chr13:56397929-56397973	NM_019568:-38	Cxcl14	PROMOTER	1.209	3.247	15148.05	49182.02	3.926	10128.64	39765.74
A_68_P23541891	chr5:23951016-23951060	NM_023229:15	Fastk	INSIDE	1.209	2.456	822.35	2019.51	2.970	758.13	2251.79
A_68_P25265269	chr7:87343641-87343685	NM_013659:11936	Sema4b	INSIDE	1.209	2.280	2248.75	5126.41	2.755	1818.43	5010.02
A_68_P29512056	chr14:32249107-32249151	NM_011894:91	Sh3bp5	INSIDE	1.209	1.919	380.32	729.82	2.321	318.48	739.05
A_68_P32775569	chrX:156065756-156065800	NM_001135727:439	Sh3kbp1	INSIDE	1.209	1.410	1561.88	2202.85	1.705	702.29	1197.31
A_68_P27138493	chr10:52410426-52410470	NM_178675:142	Slc35f1	INSIDE	1.209	3.200	2916.10	9331.08	3.869	2239.55	8664.61
A_68_P23801182	chr5:74489320-74489364	NR_031758:-212	Snora26	PROMOTER	1.209	1.452	2144.70	3113.99	1.755	1872.65	3285.93

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P21900382	chr2:179666703-179666747	NM_001081092:44627	Taf4a	INSIDE	1.209	3.692	580.06	2141.42	4.464	546.36	2438.88
A_68_P29919369	A_68_P29919369			Unknown	1.209	2.929	205.40	601.66	3.542	138.16	489.39
A_68_P24513207	chr6:65622605-65622649	NM_172399:1022	A930038C07Rik	INSIDE	1.208	1.483	2336.85	3466.32	1.792	1795.97	3219.23
A_68_P23897550	chr5:93473495-93473539	NM_175270:532	Ankrd56	INSIDE	1.208	1.720	1966.63	3381.90	2.077	1634.43	3394.44
A_68_P24172968	chr5:148116746-148116790	NM_007673:2057	Cdx2	INSIDE	1.208	1.434	1086.45	1558.01	1.733	932.64	1616.02
A_68_P31694860	chr18:49992722-49992766	NM_001081371:78	Dmxl1	INSIDE	1.208	1.585	483.46	766.18	1.914	673.09	1288.30
A_68_P24334780	chr6:30908766-30908810	NM_001135093:202	Klf14	INSIDE	1.208	4.077	338.89	1381.55	4.924	339.69	1672.63
A_68_P24443356	chr6:51221246-51221290	NR_029719:-1359	Mir148a	PROMOTER	1.208	2.358	470.13	1108.49	2.848	435.21	1239.41
A_68_P31157234	chr17:35183191-35183235	NM_013600:339	Msh5	INSIDE	1.208	2.753	972.47	2676.94	3.327	834.02	2774.41
A_68_P30363152	chr15:78744712-78744756	NM_020271:386	Pdxp	INSIDE	1.208	4.206	844.10	3550.39	5.081	772.17	3923.59
A_68_P29055223	chr13:55573203-55573247	NM_001030296:7597	Prr7	INSIDE	1.208	1.695	3482.14	5903.44	2.048	3195.29	6544.11
A_68_P31227303	chr17:50329691-50329735	NM_181397:110	Rftn1	INSIDE	1.208	1.540	1156.27	1780.47	1.861	1041.43	1937.95
A_68_P26823386	chr9:110283633-110283677	NM_001001144:47858	Scap	INSIDE	1.208	2.701	3742.13	10105.67	3.263	2934.74	9574.77
A_68_P30425918	chr15:89388530-89388574	NM_021423:58265	Shank3	INSIDE	1.208	1.421	945.84	1344.26	1.716	779.53	1337.99
A_68_P26822092	chr9:110034844-110034888	NM_009211:339	Smarcc1	INSIDE	1.208	1.539	1277.09	1964.84	1.858	1241.54	2307.05
A_68_P29937468	chr14:118633821-118633865	NM_177753:2410	Sox21	INSIDE	1.208	1.399	4476.06	6261.92	1.689	3426.76	5789.21
A_68_P22825734	chr4:33296280-33296324	NM_177774:337	Srsf12	INSIDE	1.208	3.249	1547.76	5029.04	3.925	1319.07	5177.96
A_68_P27187528	chr10:62188471-62188515	NM_001033260:355	Stox1	INSIDE	1.208	3.141	1315.43	4132.20	3.795	1190.73	4519.24
A_68_P31260743	chr17:57390196-57390242	NM_134125:1345	Trip10	INSIDE	1.208	1.805	318.17	574.32	2.180	310.56	676.97
A_68_P30453204	chr15:94420006-94420050	NM_008971:227	Twf1	INSIDE	1.208	2.659	2003.30	5327.44	3.214	1751.51	5628.69
A_68_P25411548	chr7:117205451-117205495	NM_009281:257	Zfp143	INSIDE	1.208	1.727	440.26	760.22	2.087	352.21	734.98
A_68_P20184572	chr1:42741537-42741581	NR_027826:10112	2610017I09Rik	INSIDE	1.207	1.596	4694.31	7490.19	1.926	3365.88	6482.10
A_68_P28432829	chr12:53107422-53107466	NM_029545:44	6530401N04Rik	INSIDE	1.207	1.922	2211.06	4250.74	2.320	1858.65	4311.98
A_68_P26617800	chr9:70526556-70526600	NM_007399:-229	Adam10	PROMOTER	1.207	1.603	884.87	1418.57	1.935	833.21	1612.13
A_68_P27282385	chr10:79775990-79776034	NM_011789:11448	Apc2	INSIDE	1.207	3.154	1399.50	4414.39	3.808	1096.28	4174.19
A_68_P20456915	chr1:95582543-95582587	NM_016778:294	Bok	INSIDE	1.207	0.410	1341.70	549.63	0.494	1081.27	534.44
A_68_P24000794	chr5:114358647-114358691	NM_011779:47	Coro1c	INSIDE	1.207	2.767	1982.64	5485.08	3.339	1802.46	6017.90
A_68_P20383169	chr1:80754785-80754829	NM_175291:322	Dock10	INSIDE	1.207	0.430	1340.73	575.89	0.519	1067.11	553.45
A_68_P21113209	chr2:31939133-31939177	NM_175511:71	Fam78a	INSIDE	1.207	1.740	1448.64	2520.25	2.101	1131.20	2376.28
A_68_P27286395	chr10:80391635-80391679	NM_008655:-1179	Gadd45b	PROMOTER	1.207	0.490	1172.23	574.50	0.592	1005.25	594.86
A_68_P28989506	chr13:43399105-43399149	NM_001033399:415	Gfod1	INSIDE	1.207	2.520	390.30	983.69	3.043	356.18	1083.82
A_68_P27279738	chr10:79384372-79384416	NM_053244:4679	Kiss1r	INSIDE	1.207	1.419	1165.95	1655.02	1.714	909.30	1558.27
A_68_P31475770	chr18:7004914-7004958	NM_177595:-159	Mkx	PROMOTER	1.207	1.835	1192.33	2188.08	2.216	1074.98	2381.95
A_68_P24990783	chr7:19576629-19576673	NM_145579:57	Mypop	INSIDE	1.207	1.422	1419.62	2018.55	1.717	1119.76	1922.35
A_68_P24428193	chr6:48544163-48544207	NM_001079901:303	Repin1	INSIDE	1.207	2.575	964.64	2484.34	3.107	904.20	2809.72
A_68_P26129565	chr8:107154553-107154597	NM_019662:647	Rrad	INSIDE	1.207	1.390	1404.33	1952.16	1.678	1122.45	1883.78
A_68_P28187710	chr11:120810691-120810735	NM_001038653:332	Slc16a3	INSIDE	1.207	1.707	1225.51	2092.38	2.061	974.29	2008.14
A_68_P28550363	chr12:76919145-76919189	NM_001005510:-138	Syne2	PROMOTER	1.207	1.708	609.14	1040.52	2.061	561.50	1157.31
A_68_P24061812	chr5:124990693-124990737	NM_019770:-85	Tmed2	DIVERGENT_PROMOTER	1.207	2.616	542.07	1417.98	3.158	522.03	1648.36
A_68_P24951465	chr7:4946322-4946366	NM_026741:1359	Zfp579	INSIDE	1.207	4.924	2513.06	12375.01	5.946	1889.30	11233.07
A_68_P25947784	chr8:72240592-72240636	NM_181274:-229	Zfp869	PROMOTER	1.207	1.837	1966.78	3612.26	2.217	1810.30	4012.74
A_68_P24050007	chr5:122822159-122822211	NM_026883:-212	1500011H22Rik	DIVERGENT_PROMOTER	1.206	2.053	780.57	1602.90	2.476	681.98	1688.26
A_68_P30478228	chr15:98928659-98928703	NM_176835:-1234	Dnajc22	PROMOTER	1.206	2.299	897.95	2064.41	2.773	824.16	2285.22
A_68_P23796632	chr5:73647376-73647420	NM_028194:459	Fryl	INSIDE	1.206	1.984	841.94	1670.48	2.392	839.41	2008.04
A_68_P27271932	chr10:77532109-77532153	NM_015790:18	Icosl	INSIDE	1.206	1.418	1348.92	1912.53	1.709	1009.89	1726.26
A_68_P32028431	chr19:25312079-25312123	NM_181404:409	Kank1	INSIDE	1.206	1.823	499.82	910.94	2.198	409.07	899.05
A_68_P24333873	chr6:30688134-30688178	NR_029900:-3142	Mir335	PROMOTER	1.206	1.587	712.42	1130.79	1.914	629.86	1205.73
A_68_P30681786	chr16:37654577-37654621	NM_026610:-144	Ndufb4	PROMOTER	1.206	1.454	1249.36	1816.82	1.754	1077.66	1889.79
A_68_P26137546	chr8:108583679-108583723	NM_010901:198	Nfatc3	INSIDE	1.206	1.683	375.65	632.26	2.030	367.52	746.12
A_68_P29350211	chr13:115880342-115880386	NM_134058:2	Pelo	INSIDE	1.206	2.189	1298.94	2842.80	2.639	1143.00	3015.91
A_68_P24046797	chr5:122286984-122287028	NM_008507:-196	Sh2b3	PROMOTER	1.206	2.268	937.38	2125.58	2.734	884.39	2417.72

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P23991346	chr5:112737009-112737053	NM_009419:31304	Tpst2	INSIDE	1.206	1.844	2178.30	4017.56	2.224	1731.64	3850.95
A_68_P30176278	chr15:43309169-43309213	NM_025736:416	Ttc35	INSIDE	1.206	11.506	2959.95	34057.52	13.876	2316.18	32140.01
A_68_P21047273	chr2:19831293-19831337	ENSMUST00000114610:-92		PROMOTER	1.206	4.426	4936.41	21846.20	5.335	3571.91	19057.88
A_68_P23364695	chr4:141101558-141101602	NR_030695:-496	B330016D10Rik	DIVERGENT_PROMOTER	1.205	1.858	1020.09	1895.39	2.239	931.31	2084.81
A_68_P24120336	chr5:136750661-136750705	NM_198602:292593	Cux1	INSIDE	1.205	2.752	433.57	1193.27	3.317	439.37	1457.35
A_68_P20660113	chr1:140860423-140860467	NM_181347:-3853	Dennd1b	PROMOTER	1.205	3.266	647.57	2114.75	3.934	629.41	2476.36
A_68_P21319994	chr2:71367531-71367575	NM_010053:51	Dlx1	INSIDE	1.205	1.660	7033.80	11673.78	2.000	6150.28	12300.98
A_68_P28577471	chr12:81858975-81859019	NM_001008423:2706	Gm1568	INSIDE	1.205	2.435	413.84	1007.83	2.935	368.66	1082.17
A_68_P22565467	chr3:137527631-137527675	NM_016750:90	H2afz	INSIDE	1.205	2.434	971.95	2365.24	2.932	805.68	2362.05
A_68_P27495310	chr10:119542700-119542745	NM_080446:7299	Helb	INSIDE	1.205	2.602	278.34	724.37	3.137	280.18	878.96
A_68_P21908761	chr2:180869735-180869779	NM_001003824:174	Kcnq2	INSIDE	1.205	1.570	496.64	779.92	1.893	465.00	880.09
A_68_P24333876	chr6:30688404-30688448	NR_029900:-2872	Mir335	PROMOTER	1.205	3.232	1916.77	6194.18	3.895	1405.29	5473.62
A_68_P25588916	chr7:148641001-148641045	NM_001163689:-64	Pnpla2	PROMOTER	1.205	1.681	1026.23	1725.53	2.026	791.87	1604.40
A_68_P23921376	chr5:99466286-99466330	NM_008926:-210	Prkg2	PROMOTER	1.205	1.426	1398.71	1994.05	1.718	1254.18	2154.94
A_68_P31868010	chr18:81171392-81171436	NM_178280:11903	Sall3	INSIDE	1.205	3.097	1061.96	3289.01	3.733	1010.19	3771.19
A_68_P25805590	chr8:41509132-41509176	NM_178395:-14	Zdhhc2	PROMOTER	1.205	4.513	663.48	2994.06	5.436	694.49	3775.25
A_68_P24973911	chr7:13556484-13556528	NM_178732:5294	Zfp324	INSIDE	1.205	5.259	2625.33	13807.29	6.336	2500.36	15842.21
A_68_P31939719	chr19:7496867-7496911	NM_175381:4774	2700081O15Rik	INSIDE	1.204	3.596	2149.64	7729.16	4.330	1843.47	7981.71
A_68_P26158882	chr8:112302510-112302554	NM_009677:-7	Ap1g1	PROMOTER	1.204	2.368	1138.42	2695.58	2.851	981.29	2797.89
A_68_P23979252	chr5:110792613-110792657	NM_028596:23512	Fbrsl1	INSIDE	1.204	1.543	1002.79	1547.66	1.859	859.18	1596.97
A_68_P23248723	chr4:119705546-119705590	NM_010657:218286	Hivep3	INSIDE	1.204	2.857	1045.25	2986.40	3.440	953.42	3279.53
A_68_P30511776	chr16:4726510-4726554	NM_001136066:172	Hmox2	INSIDE	1.204	1.684	875.43	1474.02	2.027	709.15	1437.15
A_68_P30956553	chr16:90386404-90386448	NM_015755:-215	Hunk	PROMOTER	1.204	1.462	1047.74	1531.37	1.759	927.71	1632.30
A_68_P27109368	chr10:44786970-44787014	NM_011156:-27	Prep	PROMOTER	1.204	1.724	1058.95	1826.06	2.076	912.49	1893.90
A_68_P32583451	chrX:103414842-103414886	NM_001001176:317	Taf9b	INSIDE	1.204	1.674	577.58	966.85	2.016	326.37	657.81
A_68_P31936612	chr19:6984205-6984249	NM_001166370:39	Trmt112	INSIDE	1.204	1.955	1393.20	2723.52	2.353	1313.17	3090.40
A_68_P26885417	chr9:121672235-121672279	NM_001166644:3106	Zfp651	INSIDE	1.204	1.875	480.33	900.61	2.258	441.82	997.64
A_68_P25579476	chr7:146846040-146846084	ENSMUST00000118750:-8		PROMOTER	1.204	2.417	2631.11	6360.44	2.909	2065.82	6010.26
A_68_P21079933	chr2:26459306-26459350	NM_026212:402	Agpat2	INSIDE	1.203	1.892	656.03	1241.32	2.277	605.01	1377.37
A_68_P20975262	chr2:5635173-5635217	NM_177343:516	Camk1d	INSIDE	1.203	5.198	1437.93	7474.26	6.253	1158.72	7245.33
A_68_P28745355	chr12:112910496-112910540	NM_021273:31	Ckb	INSIDE	1.203	2.306	1940.40	4474.67	2.773	1519.96	4215.19
A_68_P20258855	chr1:58480898-58480942	NM_001042634:12	Clk1	INSIDE	1.203	1.725	1869.07	3224.53	2.076	1666.37	3458.95
A_68_P25268092	chr7:87833284-87833328	NM_173863:457	Crtc3	INSIDE	1.203	2.888	1369.27	3954.51	3.475	1189.59	4133.44
A_68_P23415470	chr4:151308129-151308173	NM_172704:322	Dnajc11	INSIDE	1.203	2.195	442.74	971.92	2.641	370.30	978.07
A_68_P25596358	chr7:149845220-149845264	NR_002855:-355	Igf2as	DIVERGENT_PROMOTER	1.203	2.933	1135.39	3330.63	3.528	965.24	3405.49
A_68_P25952869	chr8:73118953-73118997	NM_023627:595	Isyna1	INSIDE	1.203	2.305	1975.31	4554.06	2.773	1604.48	4450.01
A_68_P23588237	chr5:33678644-33678688	NM_021500:446	Maea	INSIDE	1.203	4.465	1242.80	5549.32	5.371	1051.07	5645.77
A_68_P23978674	chr5:110698757-110698801	NM_001163538:140	Pgam5	INSIDE	1.203	2.077	828.18	1720.26	2.500	694.43	1735.81
A_68_P31254024	chr17:56264131-56264175	NM_013662:9123	Sema6b	INSIDE	1.203	2.478	2592.56	6425.25	2.981	1974.26	5884.48
A_68_P27095211	chr10:42222280-42222324	NM_017472:443	Snx3	INSIDE	1.203	2.859	1344.03	3842.41	3.439	1300.70	4472.92
A_68_P26163688	chr8:113142314-113142358	NM_146216:-201	Vac14	PROMOTER	1.203	2.251	1513.09	3406.72	2.709	1273.76	3451.24
A_68_P25499302	chr7:133343826-133343870	NM_028816:74	Xpo6	INSIDE	1.203	1.465	777.14	1138.55	1.763	858.23	1513.19
A_68_P31144038	A_68_P31144038			Unknown	1.203	2.582	568.68	1468.28	3.105	478.04	1484.52
A_68_P31159052	chr17:35496088-35496132	M19687:92295		INSIDE	1.203	3.619	3325.24	12035.17	4.353	2816.53	12261.71
A_68_P28573972	chr12:81233698-81233742	NR_033514:111	2310015A10Rik	INSIDE	1.202	2.767	587.25	1624.69	3.327	515.19	1713.80
A_68_P28181737	chr11:119873242-119873286	NM_001198787:29831	Aatk	INSIDE	1.202	2.499	988.52	2469.91	3.003	803.88	2414.16
A_68_P22411290	chr3:108013838-108013882	NM_175183:-8	Atxn7l2	PROMOTER	1.202	2.468	1955.92	4827.76	2.966	1551.88	4602.91
A_68_P27275481	chr10:78215248-78215292	NM_027630:542	Ccdc105	INSIDE	1.202	2.253	489.86	1103.46	2.708	424.64	1149.89
A_68_P26674982	chr9:81526714-81526758	NM_010482:-577	Htr1b	PROMOTER	1.202	1.528	944.96	1443.82	1.837	822.85	1511.50
A_68_P28161572	chr11:116704633-116704677	NM_033398:109	Jmjd6	INSIDE	1.202	2.083	2133.37	4443.18	2.503	1716.89	4298.09
A_68_P30114903	chr15:31460728-31460772	NM_172606:42	Marchf6	INSIDE	1.202	1.560	2000.26	3121.15	1.876	1724.98	3236.31

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27279615	chr10:79365943-79365988	NM_001163276:5718	Med16	INSIDE	1.202	2.420	2154.97	5214.57	2.908	1617.33	4703.97
A_68_P25957228	chr8:74035689-74035737	NM_032398:-44	Plvap	PROMOTER	1.202	2.105	429.88	905.07	2.531	413.76	1047.38
A_68_P24538898	chr6:71858964-71859010	NM_009088:-60	Polr1a	DIVERGENT_PROMOTER	1.202	1.929	539.01	1039.80	2.319	435.79	1010.74
A_68_P27287000	chr10:80494188-80494232	NM_134135:2447	Slc39a3	INSIDE	1.202	4.007	1550.65	6213.92	4.818	1290.24	6216.36
A_68_P23185610	chr4:106311623-106311667	NM_177667:16591	Ttc22	INSIDE	1.202	2.320	1270.77	2948.47	2.788	1024.68	2856.75
A_68_P27255926	chr10:74779688-74779732	NM_009630:23	Adora2a	INSIDE	1.201	1.376	3824.63	5261.75	1.653	2937.97	4855.30
A_68_P26888669	chr9:122203192-122203236	NM_133979:278	Ano10	INSIDE	1.201	1.714	2282.07	3911.22	2.058	1951.61	4016.58
A_68_P27869724	chr11:64976171-64976215	NM_001099288:271	Arhgap44	INSIDE	1.201	1.935	1509.74	2921.23	2.324	1336.19	3105.08
A_68_P26544129	chr9:57684523-57684567	NM_019689:-2503	Arid3b	PROMOTER	1.201	1.934	472.62	913.96	2.322	389.11	903.36
A_68_P28732762	chr12:110698103-110698147	NM_001190703:6460	Dlk1	INSIDE	1.201	1.565	508.18	795.43	1.879	438.73	824.48
A_68_P28842025	chr13:15555334-15555378	NM_008130:-199	Gli3	PROMOTER	1.201	2.068	1512.51	3128.27	2.483	1353.34	3360.74
A_68_P31978250	chr19:16207196-16207240	NM_008139:-102	Gnaq	PROMOTER	1.201	2.136	1515.67	3237.78	2.566	1259.86	3233.00
A_68_P28156587	chr11:115836535-115836579	NM_001005608:518	Itgb4	INSIDE	1.201	1.793	951.18	1705.87	2.154	799.94	1722.72
A_68_P24052806	chr5:123349603-123349647	NM_013910:735	Kdm2b	INSIDE	1.201	1.905	668.87	1274.50	2.289	594.00	1359.42
A_68_P31614616	chr18:34937211-34937255	NM_001081256:571	Kdm3b	INSIDE	1.201	3.930	2091.99	8222.40	4.721	1702.98	8039.95
A_68_P30345383	chr15:75829147-75829191	NM_177922:4970	Mapk15	INSIDE	1.201	2.222	3250.31	7222.26	2.669	2395.77	6395.16
A_68_P30512463	chr16:4886291-4886335	NM_029657:61	Mgrn1	INSIDE	1.201	0.492	1704.49	839.26	0.591	1353.17	800.34
A_68_P23391037	chr4:147242647-147242691	NM_001025365:160	Miip	INSIDE	1.201	1.505	804.89	1211.57	1.808	594.37	1074.79
A_68_P32383984	chrX:50097577-50097621	NR_029657:-1854	Mir106a	PROMOTER	1.201	1.595	826.61	1318.74	1.916	481.03	921.51
A_68_P23893298	chr5:92706005-92706049	NM_001163687:1181	Naaa	INSIDE	1.201	3.103	919.71	2854.17	3.726	788.33	2937.06
A_68_P29694800	chr14:69793093-69793137	NM_010920:3256	Nkx2-6	INSIDE	1.201	1.401	1432.03	2005.64	1.682	1249.73	2101.65
A_68_P21239896	chr2:56954902-56954946	NM_013613:12525	Nr4a2	DOWNSTREAM	1.201	2.020	672.20	1357.99	2.427	561.07	1361.53
A_68_P23950024	chr5:104475955-104475999	NM_028794:-53	Nudt9	PROMOTER	1.201	2.443	749.67	1831.59	2.934	647.10	1898.32
A_68_P27542078	chr10:128003336-128003380	NM_011119:-368	Pa2g4	PROMOTER	1.201	1.971	4498.71	8868.12	2.367	3408.54	8067.44
A_68_P25587733	chr7:148445537-148445581	NM_001081118:30872	Phrf1	INSIDE	1.201	4.271	960.13	4101.12	5.129	862.30	4422.98
A_68_P21044973	chr2:19367231-19367275	NM_018809:-37	Ptf1a	PROMOTER	1.201	1.546	753.98	1165.95	1.857	632.19	1174.06
A_68_P22378033	chr3:101728452-101728496	NM_001039371:-98	Slc22a15	PROMOTER	1.201	1.422	1112.23	1581.70	1.708	910.47	1555.27
A_68_P30137263	chr15:36140403-36140447	NM_012031:31140	Spag1	INSIDE	1.201	4.975	1552.37	7722.78	5.976	1363.33	8147.36
A_68_P28740618	chr12:112078936-112078980	NM_011973:191	Stk30	INSIDE	1.201	1.460	1162.40	1697.03	1.753	998.21	1749.57
A_68_P21431327	chr2:92755255-92755299	NM_030725:19	Syt13	INSIDE	1.201	2.702	815.33	2203.34	3.246	732.49	2377.70
A_68_P26447523	chr9:40965396-40965440	NM_176860:159	Ubash3b	INSIDE	1.201	1.514	1986.08	3007.57	1.819	1579.76	2873.94
A_68_P28765898	chr12:117316198-117316242	NM_009511:25	Vipr2	INSIDE	1.201	2.137	1336.38	2855.37	2.565	1051.81	2698.41
A_68_P25947915	chr8:72298581-72298625	NM_177899:208	Zfp866	INSIDE	1.201	1.730	1494.48	2584.81	2.076	1491.94	3097.87
A_68_P25106560	chr7:55392877-55392921			Unknown	1.201	1.374	1979.16	2718.52	1.650	1660.38	2740.15
A_68_P27977898	chr11:84326983-84327029	NM_019816:-3	Aatf	PROMOTER	1.200	1.495	986.76	1475.63	1.795	842.45	1511.81
A_68_P21007911	chr2:11699878-11699922	NM_177268:521	Ankrd16	INSIDE	1.200	1.428	2346.46	3351.49	1.714	1802.10	3089.34
A_68_P23887087	chr5:91568591-91568635	NM_009704:-28	Areg	PROMOTER	1.200	1.490	1128.74	1681.98	1.789	1004.59	1796.85
A_68_P31013734	chr17:4994384-4994428	NM_001085355:-667	Arid1b	PROMOTER	1.200	1.402	1052.67	1475.81	1.682	1016.82	1710.06
A_68_P26078866	chr8:97190855-97190900	NM_024269:-128	Arl2bp	PROMOTER	1.200	1.657	1141.95	1892.25	1.989	936.67	1862.85
A_68_P28685559	chr12:102267503-102267547	NM_026681:-331	Ccdc88c	PROMOTER	1.200	1.599	676.07	1081.01	1.919	550.69	1057.01
A_68_P27921612	chr11:74452062-74452106	NM_001013784:18978	E130309D14Rik	INSIDE	1.200	2.223	724.51	1610.30	2.667	632.73	1687.51
A_68_P31121752	chr17:28450748-28450792	NM_001163819:296	Fance	INSIDE	1.200	1.754	642.77	1127.42	2.105	622.22	1309.88
A_68_P27288984	chr10:80800721-80800765	NM_148951:5269	Gipc3	INSIDE	1.200	2.025	1090.07	2207.29	2.429	963.35	2340.28
A_68_P30777939	chr16:55822496-55822540	NM_001159394:-267	Nfkbiz	PROMOTER	1.200	1.556	764.68	1189.63	1.866	685.66	1279.72
A_68_P30424834	chr15:89204309-89204353	NM_001111288:-81	Sco2	PROMOTER	1.200	2.430	3102.64	7540.79	2.915	2493.70	7270.00
A_68_P20354816	chr1:75543154-75543198	NM_009208:336	Slc4a3	INSIDE	1.200	1.830	869.00	1590.61	2.196	677.53	1487.88
A_68_P27542561	chr10:128106235-128106279	NM_173733:4718	Suox	DOWNSTREAM	1.200	1.712	1991.25	3408.27	2.055	1665.84	3422.59
A_68_P23594736	chr5:34856754-34856798	NM_139064:-148	Tnip2	PROMOTER	1.200	1.639	992.62	1626.68	1.966	873.30	1716.85
A_68_P21774854	chr2:156865842-156865886	NM_001164663:39137	9830001H06Rik	INSIDE	1.199	2.038	437.35	891.42	2.443	395.35	965.81
A_68_P30747802	chr16:49855795-49855839	NM_010581:50	Cd47	INSIDE	1.199	2.040	634.47	1294.02	2.445	551.19	1347.74
A_68_P27303131	chr10:83997120-83997164	NM_175451:-509	Ckap4	PROMOTER	1.199	1.871	836.19	1564.72	2.243	735.25	1649.43

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P32126462	chr19:43515774-43515818	NM_031396:871	Cnnm1	INSIDE	1.199	2.659	1402.10	3728.82	3.189	1245.96	3973.03
A_68_P31715735	chr18:54022118-54022162	NM_152809:374	Csnk1g3	INSIDE	1.199	2.101	1200.08	2521.09	2.519	994.27	2504.13
A_68_P24593883	chr6:83447756-83447800	NM_001162521:9185	Dguok	INSIDE	1.199	1.520	847.49	1288.42	1.823	674.59	1229.91
A_68_P24156003	chr5:144076609-144076653	NM_172726:409	E130309D02Rik	INSIDE	1.199	1.446	1100.55	1591.31	1.733	993.09	1721.15
A_68_P26804376	chr9:106553310-106553354	NM_001160353:5108	Grm2	INSIDE	1.199	1.780	492.34	876.19	2.135	373.69	797.69
A_68_P26430295	chr9:37192346-37192390	NM_175189:17178	Hepacam	INSIDE	1.199	1.859	1049.45	1951.42	2.230	889.29	1983.10
A_68_P29942857	chr14:119537874-119537918	NM_015820:410	Hs6st3	INSIDE	1.199	1.657	555.66	920.94	1.988	508.63	1011.00
A_68_P26772687	chr9:100978284-100978328	NM_001100451:-144	Msl2	PROMOTER	1.199	6.874	1267.60	8713.53	8.242	749.65	6178.30
A_68_P29075365	chr13:58909956-58910000	NM_001025074:785	Ntrk2	INSIDE	1.199	2.290	1856.49	4250.45	2.744	1528.82	4195.30
A_68_P32114803	chr19:41459691-41459735	NM_031376:-152	Pik3ap1	PROMOTER	1.199	2.753	2209.03	6082.22	3.302	1929.94	6372.56
A_68_P31925249	chr19:4811087-4811131	NM_019869:526	Rbm14	INSIDE	1.199	3.061	2761.21	8452.75	3.671	2371.79	8707.75
A_68_P24153528	chr5:143576639-143576683	NM_001122730:2406	Tnrc18	INSIDE	1.199	1.632	671.58	1095.86	1.956	607.97	1189.09
A_68_P33004939	A_68_P33004939			Unknown	1.199	2.169	215.84	468.23	2.600	309.92	805.91
A_68_P22348135	chr3:96001508-96001552	NM_026975:-21	Bola1	PROMOTER	1.198	1.846	874.79	1614.54	2.211	705.40	1559.71
A_68_P24268751	chr6:17587317-17587361	NM_007604:241	Capza2	INSIDE	1.198	1.965	973.94	1914.05	2.354	819.49	1928.91
A_68_P23397601	chr4:148312774-148312818	NM_027195:134296	Casz1	INSIDE	1.198	2.111	2234.17	4717.09	2.530	1612.59	4079.45
A_68_P26761428	chr9:98856199-98856243	NM_012020:195	Foxl2	INSIDE	1.198	3.325	1323.32	4400.14	3.985	1143.24	4555.85
A_68_P21375629	chr2:80421545-80421589	NM_016965:-444	Nckap1	PROMOTER	1.198	2.202	1385.35	3051.00	2.637	1195.45	3152.93
A_68_P21100049	chr2:29745376-29745420	NM_001177662:-184	Odf2	PROMOTER	1.198	0.535	1223.75	654.86	0.641	977.58	626.78
A_68_P20506809	chr1:108069287-108069331	NM_133821:863	Phlpp1	INSIDE	1.198	0.362	2336.90	846.47	0.434	1997.62	867.09
A_68_P21928446	chr3:7366713-7366757	NM_008862:131	Pkia	INSIDE	1.198	1.586	1508.69	2392.07	1.899	1393.98	2646.76
A_68_P21149538	chr2:38499224-38499268	NM_011187:180	Psmb7	INSIDE	1.198	1.479	3601.32	5327.07	1.772	3034.55	5377.73
A_68_P26044790	chr8:91567290-91567334	NM_021390:749	Sall1	INSIDE	1.198	1.794	2770.37	4969.06	2.149	2217.58	4766.64
A_68_P24640499	chr6:91634367-91634411	NM_009320:328	Slc6a6	INSIDE	1.198	1.647	1530.11	2519.63	1.973	1271.29	2507.95
A_68_P26228070	chr8:124175318-124175362	NM_080855:493	Zcchc14	INSIDE	1.198	2.972	1405.77	4177.65	3.560	1250.98	4453.92
A_68_P24424843	chr6:47855408-47855452	NM_146175:27877	Zfp282	INSIDE	1.198	2.585	2972.27	7683.04	3.098	2282.90	7071.57
A_68_P24155214	chr5:143919270-143919314	ENSMUST00000157346:-2486		PROMOTER	1.198	2.470	724.17	1788.53	2.960	700.45	2073.15
A_68_P22953595	chr4:58924697-58924741	NM_172381:879	AI314180	INSIDE	1.197	1.747	2148.60	3754.12	2.092	1726.90	3611.82
A_68_P25524391	chr7:137910411-137910455	NM_001081038:-7150	Btbd16	PROMOTER	1.197	2.439	1590.49	3878.90	2.919	1337.47	3903.97
A_68_P22822456	chr4:32702176-32702220	NM_001122978:-249	Casp8ap2	PROMOTER	1.197	1.979	2193.11	4340.85	2.370	1706.66	4044.52
A_68_P31715220	chr18:53904386-53904430	NM_178686:-207	Cep120	PROMOTER	1.197	0.511	1571.24	802.47	0.611	1284.34	785.03
A_68_P33008827	chr4_random:110161-110205	NM_001033326:381	Dhrsx	INSIDE	1.197	2.014	2401.18	4836.73	2.412	2218.64	5350.53
A_68_P28577477	chr12:81859800-81859844	NM_001008423:1880	Gm1568	INSIDE	1.197	3.137	857.75	2690.73	3.756	782.02	2937.65
A_68_P32245741	chrX:8777677-8777721	NM_173414:600	Lancl3	INSIDE	1.197	2.141	1388.26	2972.43	2.564	798.82	2048.01
A_68_P23156221	chr4:101320393-101320437	NM_175036:27	Leprot	INSIDE	1.197	1.563	1363.66	2131.28	1.871	1274.77	2384.91
A_68_P28565714	chr12:79850102-79850146	NM_019579:191	Mpp5	INSIDE	1.197	1.828	1176.34	2150.33	2.188	1086.67	2377.44
A_68_P21150017	chr2:38567253-38567297	NM_139051:2788	Nr5a1	INSIDE	1.197	2.582	1941.44	5012.63	3.091	1513.12	4677.30
A_68_P31442544	chr17:91487486-91487530	NM_020252:4634	Nrxn1	INSIDE	1.197	3.043	312.05	949.49	3.641	342.10	1245.62
A_68_P27542073	chr10:128002710-128002754	NM_011119:258	Pa2g4	INSIDE	1.197	1.424	7265.17	10347.92	1.705	5235.63	8928.44
A_68_P29246773	chr13:97312251-97312295	NM_012048:168	Polk	INSIDE	1.197	2.587	1124.61	2909.53	3.098	983.35	3046.21
A_68_P31157970	chr17:35293556-35293603	NM_001199044:8243	Prrc2a	INSIDE	1.197	2.537	350.79	889.93	3.037	289.97	880.53
A_68_P30489328	chr15:100884313-100884357	NM_011323:117633	Scn8a	DOWNSTREAM	1.197	2.815	1023.14	2880.41	3.371	918.95	3097.88
A_68_P26574111	chr9:62993729-62993773	NM_172446:1037	Skor1	INSIDE	1.197	1.821	586.46	1067.98	2.180	467.76	1019.77
A_68_P28889208	chr13:24923670-24923714	NM_019551:165	Tdp2	INSIDE	1.197	1.784	4814.88	8590.57	2.135	4055.02	8658.86
A_68_P30363491	chr15:78798091-78798135	NM_001039155:19959	Triobp	INSIDE	1.197	3.848	3215.14	12370.25	4.607	2187.53	10078.29
A_68_P27895906	chr11:69395043-69395087	NM_001127233:1204	Trp53	INSIDE	1.197	3.025	950.02	2874.19	3.622	838.58	3037.04
A_68_P24630036	chr6:89785323-89785367	NM_053221:10187	Vmn1r42	DOWNSTREAM	1.197	3.380	1101.90	3724.54	4.047	882.11	3570.12
A_68_P24951463	chr7:4946096-4946140	NM_026741:1585	Zfp579	INSIDE	1.197	2.466	699.81	1725.54	2.951	533.42	1574.09
A_68_P28737719	chr12:111558035-111558079	AK200124:417495		INSIDE	1.197	3.062	1165.11	3567.74	3.665	932.54	3417.82
A_68_P21133893	chr2:35347074-35347118	ENSMUST00000121664:-57		PROMOTER	1.197	3.254	622.32	2025.07	3.896	566.77	2208.36
A_68_P24460750	chr6:53989374-53989418	NM_001163640:-529	Chn2	PROMOTER	1.196	2.194	803.20	1762.22	2.624	792.44	2079.40

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P29841645	chr14:99499049-99499093	NM_028315:-81	Dis3	PROMOTER	1.196	2.390	679.87	1624.88	2.859	520.43	1488.11
A_68_P32030095	chr19:25581366-25581410	NM_015826:1193	Dmrt1	INSIDE	1.196	3.020	447.64	1351.77	3.611	400.99	1447.95
A_68_P25537310	chr7:140050852-140050896	NM_198017:-33	Fam175b	DIVERGENT_PROMOTER	1.196	2.728	877.71	2394.66	3.264	839.35	2739.59
A_68_P23246064	chr4:119212892-119212936	NM_172699:622	Foxj3	INSIDE	1.196	1.754	832.79	1460.53	2.098	764.35	1603.68
A_68_P28529995	chr12:73171043-73171090	NM_181752:912	Gpr135	INSIDE	1.196	3.578	898.42	3214.43	4.281	786.93	3368.51
A_68_P31125155	chr17:29089634-29089678	NM_025888:-504	Kctd20	PROMOTER	1.196	1.802	1349.17	2431.22	2.155	1174.92	2532.27
A_68_P22674476	chr3:156223832-156223876	NM_001039094:-903	Negr1	PROMOTER	1.196	1.802	6783.26	12224.22	2.155	5207.52	11222.95
A_68_P22774296	chr4:21605518-21605562	NM_001080771:7570	Prdm13	INSIDE	1.196	1.873	556.18	1041.73	2.241	491.28	1100.81
A_68_P31713995	chr18:53712057-53712101	NM_001033281:87879	Prdm6	INSIDE	1.196	1.476	662.09	977.41	1.766	603.83	1066.11
A_68_P23164321	chr4:102786815-102786859	NM_146254:68	Wdr78	INSIDE	1.196	1.367	1752.93	2395.52	1.635	1521.03	2486.26
A_68_P22217918	chr3:68673912-68673956	NM_001167996:427	1110032F04Rik	INSIDE	1.195	6.444	642.03	4137.02	7.697	847.75	6525.18
A_68_P32579167	chrX:102274990-102275034	NM_026312:-101	2610029G23Rik	DIVERGENT_PROMOTER	1.195	3.215	226.15	727.06	3.843	194.91	749.06
A_68_P24091172	chr5:130384666-130384710	NM_026916:279	4930579G22Rik	INSIDE	1.195	1.904	685.49	1305.42	2.275	571.90	1301.08
A_68_P28752162	chr12:113974838-113974882	NM_001024602:14476	AW555464	INSIDE	1.195	3.181	4019.01	12786.48	3.801	3145.97	11959.15
A_68_P24735108	chr6:108610209-108610253	NM_011498:-392	Bhlhe40	PROMOTER	1.195	2.015	812.46	1637.30	2.409	752.79	1813.19
A_68_P20827298	chr1:173259152-173259196	NM_001128609:-101	Dedd	PROMOTER	1.195	1.451	1647.59	2390.77	1.734	1221.32	2117.55
A_68_P32219569	chr19:59533670-59533714	NM_010132:513	Emx2	INSIDE	1.195	2.136	668.95	1428.72	2.553	525.69	1342.02
A_68_P23363268	chr4:140864869-140864913	NM_010139:7736	Epha2	INSIDE	1.195	2.445	1188.37	2905.43	2.923	1078.11	3151.13
A_68_P26134297	chr8:108042949-108042993	NM_008289:325	Hsd11b2	INSIDE	1.195	3.040	568.80	1728.95	3.631	533.68	1937.83
A_68_P27804079	chr11:53113636-53113680	NM_008300:323	Hspa4	INSIDE	1.195	1.552	1285.21	1994.36	1.855	1131.28	2098.55
A_68_P26500007	chr9:49605368-49605412	NM_001081445:1784	Ncam1	INSIDE	1.195	3.028	1201.60	3638.90	3.618	954.29	3452.15
A_68_P29237468	chr13:95638619-95638663	NM_011021:-6941	Otp	PROMOTER	1.195	2.010	508.94	1022.87	2.402	443.75	1065.93
A_68_P29619051	chr14:56262543-56262587	NM_028780:79	Tm9sf1	INSIDE	1.195	2.774	351.60	975.50	3.316	288.82	957.78
A_68_P21084626	chr2:27282675-27282719	NM_009500:-351	Vav2	PROMOTER	1.195	3.594	984.63	3538.43	4.296	828.94	3560.77
A_68_P26511312	A_68_P26511312			Unknown	1.195	3.374	516.49	1742.85	4.032	434.75	1752.71
A_68_P20872224	chr1:181733633-181733677	NM_026375:492	Ahctf1	INSIDE	1.194	2.197	998.52	2193.43	2.622	861.46	2258.66
A_68_P21144181	chr2:37649266-37649310	NM_001163566:17520	Crb2	INSIDE	1.194	3.612	2212.31	7990.61	4.313	1562.42	6738.56
A_68_P29241525	chr13:96374455-96374499	NM_010169:13912	F2r	INSIDE	1.194	2.824	420.10	1186.56	3.373	383.43	1293.37
A_68_P28071798	chr11:100941289-100941333	NM_010475:1586	Hsd17b1	INSIDE	1.194	1.542	2070.49	3193.21	1.841	1700.89	3132.07
A_68_P27894856	chr11:69213335-69213379	NM_001017426:13821	Kdm6b	INSIDE	1.194	2.139	1525.97	3263.77	2.555	1189.26	3038.14
A_68_P20659550	chr1:140738110-140738154	NM_001025565:889	Lhx9	INSIDE	1.194	1.416	2120.04	3002.21	1.690	1611.22	2723.76
A_68_P25587562	chr7:148414623-148414668	NM_001081118:-41	Phrf1	DIVERGENT_PROMOTER	1.194	2.212	755.34	1670.63	2.640	589.72	1556.85
A_68_P28164255	chr11:117151945-117151989	NM_001113487:24407	Septin9	INSIDE	1.194	2.321	353.04	819.56	2.771	327.48	907.53
A_68_P21836029	chr2:167364249-167364293	NM_011427:544	Snai1	INSIDE	1.194	1.894	2099.09	3976.36	2.262	1770.36	4005.22
A_68_P25983693	chr8:80041310-80041354	NR_028125:378	0610038B21Rik	INSIDE	1.193	2.324	912.20	2119.71	2.771	812.28	2250.88
A_68_P29419197	chr14:14844919-14844966	NM_139227:-62	Atxn7	PROMOTER	1.193	2.249	1293.71	2909.69	2.684	1082.05	2903.93
A_68_P21094146	chr2:28771793-28771837	NM_019446:127	Barhl1	INSIDE	1.193	1.706	1434.26	2447.18	2.036	1360.93	2770.20
A_68_P21969034	chr3:17954954-17954998	NM_021560:652	Bhlhe22	INSIDE	1.193	1.926	666.69	1284.08	2.298	597.03	1372.19
A_68_P26880501	chr9:120842440-120842484	NM_007614:-55	Ctnnb1	PROMOTER	1.193	1.575	743.11	1170.28	1.878	744.78	1398.97
A_68_P27311664	chr10:85484474-85484519	NM_153195:-177	Fbxo7	DIVERGENT_PROMOTER	1.193	1.731	2136.20	3696.93	2.065	1924.36	3974.43
A_68_P28675866	chr12:100630793-100630837	NM_183186:57470	Foxn3	INSIDE	1.193	0.534	1414.50	755.58	0.637	1164.91	742.37
A_68_P26248332	chr8:127421933-127421977	NM_001111141:169	Gm505	INSIDE	1.193	2.011	358.67	721.22	2.400	303.45	728.20
A_68_P25958332	chr8:74213234-74213278	NM_013564:106	Insl3	INSIDE	1.193	2.543	406.36	1033.31	3.033	388.94	1179.47
A_68_P30575359	chr16:17722895-17722939	NM_001040683:107	Med15	INSIDE	1.193	1.761	1883.39	3316.02	2.100	1585.20	3329.50
A_68_P22317891	chr3:89018021-89018065	NM_001161824:215	Mtx1	INSIDE	1.193	3.137	1233.42	3869.11	3.741	972.58	3638.84
A_68_P27560497	chr11:4847206-4847250	NM_010904:839	Nefh	INSIDE	1.193	2.497	338.55	845.38	2.979	365.52	1088.94
A_68_P23134368	chr4:97445476-97445520	NM_001122953:1182	Nfia	INSIDE	1.193	2.120	2538.36	5380.76	2.530	2274.70	5754.40
A_68_P27980110	chr11:84693182-84693228	NM_027388:493	Pigw	INSIDE	1.193	3.518	381.69	1342.88	4.197	397.58	1668.78
A_68_P31201639	chr17:45672060-45672104	NM_013688:11700	Tcte1	INSIDE	1.193	2.517	1119.73	2818.45	3.003	934.86	2807.65
A_68_P29560593	chr14:41780203-41780247	NM_145928:-128	Tspan14	PROMOTER	1.193	1.339	2742.41	3670.95	1.597	2420.12	3865.19
A_68_P32320541	chrX:34414442-34414486	NM_019668:104	Ube2a	INSIDE	1.193	2.080	850.63	1769.42	2.482	613.74	1523.27

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P30133052	chr15:35301302-35301346	NM_177151:24	Vps13b	INSIDE	1.193	2.685	540.21	1450.48	3.202	524.15	1678.44
A_68_P28706884	chr12:106248180-106248224	NM_172500:-183	4831426I19Rik	PROMOTER	1.192	1.893	1837.17	3477.10	2.256	1579.06	3561.97
A_68_P26920198	chr10:7400931-7400975	NR_033219:4	BC020402	INSIDE	1.192	2.316	925.05	2142.05	2.760	836.31	2307.98
A_68_P22412543	chr3:108218968-108219012	NM_001004177:-578	Celsr2	PROMOTER	1.192	3.067	731.38	2243.17	3.655	618.00	2259.06
A_68_P26816896	chr9:108735008-108735052	NM_080437:6380	Celsr3	INSIDE	1.192	0.489	1330.34	649.95	0.583	956.08	556.91
A_68_P27941268	chr11:77893553-77893597	NM_022313:311	Eral1	INSIDE	1.192	1.418	2251.05	3192.11	1.691	1829.04	3092.02
A_68_P26458361	chr9:42705530-42705574	NM_175481:46902	Grik4	INSIDE	1.192	4.344	2887.47	12541.93	5.176	2200.02	11387.69
A_68_P23197991	chr4:108520598-108520642	NM_029571:159	Kti12	INSIDE	1.192	0.580	1232.03	714.76	0.692	1317.47	911.39
A_68_P28246268	chr12:12944044-12944088	NM_008709:4576	Mycn	INSIDE	1.192	3.402	588.88	2003.09	4.055	585.54	2374.45
A_68_P30961948	chr16:91270536-91270580	NM_016968:545	Olig1	INSIDE	1.192	2.525	1532.09	3867.92	3.010	1309.77	3942.72
A_68_P21626037	chr2:129514047-129514091	NM_018863:1536	Pdyn	INSIDE	1.192	5.092	2907.65	14805.35	6.069	2024.43	12285.94
A_68_P22825644	chr4:33276387-33276431	NM_001034867:304	Pm20d2	INSIDE	1.192	2.991	766.50	2292.29	3.566	706.84	2520.66
A_68_P22825900	chr4:33334938-33334982	NM_001033225:802	Pnrc1	INSIDE	1.192	1.788	1579.02	2822.94	2.131	1408.37	3001.07
A_68_P21604779	chr2:125608569-125608613	NM_177608:16	Secisbp2l	INSIDE	1.192	1.335	3704.89	4946.48	1.591	3098.16	4930.71
A_68_P25504896	chr7:134417212-134417256	NM_009266:339	Sephs2	INSIDE	1.192	3.351	485.04	1625.54	3.995	417.65	1668.70
A_68_P31093838	chr17:23956287-23956338	NM_175229:16159	Srrm2	INSIDE	1.192	2.276	367.58	836.48	2.713	295.98	802.86
A_68_P27466138	chr10:114239189-114239233	NM_146241:-784	Trhde	PROMOTER	1.192	2.823	1122.41	3169.11	3.365	972.02	3270.88
A_68_P25951333	chr8:72877019-72877063	NM_001122829:132	Upf1	INSIDE	1.192	3.104	613.15	1903.27	3.699	563.05	2082.45
A_68_P20319167	chr1:69423580-69423624			Unknown	1.192	1.903	657.24	1251.01	2.269	646.37	1466.36
A_68_P21533269	chr2:113057403-113057447	ENSMUST00000128192:-171		PROMOTER	1.192	2.249	1327.52	2985.22	2.681	1192.00	3195.92
A_68_P30927981	chr16:85173236-85173280	NM_001198823:694	App	INSIDE	1.191	2.061	1193.89	2460.99	2.455	1120.86	2751.57
A_68_P28074534	chr11:101413318-101413362	NM_009764:-71	Brca1	DIVERGENT_PROMOTER	1.191	1.978	790.37	1563.53	2.356	631.98	1489.22
A_68_P26423439	chr9:35366246-35366290	NM_013932:-213	Ddx25	DIVERGENT_PROMOTER	1.191	0.397	1534.71	609.30	0.473	1395.67	659.85
A_68_P24991559	chr7:19703647-19703691	NM_175530:-1539	Fbxo46	PROMOTER	1.191	2.506	1033.56	2590.50	2.985	781.12	2331.61
A_68_P20187366	chr1:43220621-43220665	NM_010212:164	Fhl2	INSIDE	1.191	1.713	659.20	1129.27	2.040	561.46	1145.29
A_68_P24135227	chr5:139856761-139856805	NM_001038703:-9075	Gpr146	PROMOTER	1.191	1.806	1308.77	2363.14	2.151	1151.99	2477.47
A_68_P26039231	chr8:90662304-90662348	NM_172757:543	Heatr3	INSIDE	1.191	1.426	1290.16	1839.73	1.699	1073.19	1822.86
A_68_P23331512	chr4:135528527-135528571	NM_011942:-39	Lypla2	PROMOTER	1.191	1.682	872.93	1468.63	2.004	736.21	1475.27
A_68_P27278629	chr10:79202122-79202166	NM_172551:7182	Polrmt	INSIDE	1.191	2.210	1590.85	3515.45	2.632	1177.78	3099.80
A_68_P31863198	chr18:80453249-80453293	NM_001164423:226	Pqlc1	INSIDE	1.191	1.555	491.19	763.82	1.853	392.29	726.80
A_68_P28523608	chr12:72076024-72076068	NM_011184:437	Psma3	INSIDE	1.191	2.132	680.54	1451.09	2.540	587.20	1491.59
A_68_P30401591	chr15:85408071-85408115	NM_001163634:408	Wnt7b	INSIDE	1.191	1.743	605.16	1054.96	2.077	590.37	1225.99
A_68_P24054285	chr5:123610907-123610951	ENSMUST00000162839:-2462		PROMOTER	1.191	2.607	1978.07	5156.25	3.106	1583.43	4917.43
A_68_P32145406	chr19:46764395-46764439	NM_025563:21	2010012O05Rik	INSIDE	1.190	1.643	671.21	1102.64	1.954	621.95	1215.38
A_68_P25394423	chr7:112935862-112935906	NM_001162943:180	Dchs1	INSIDE	1.190	1.440	1037.34	1494.04	1.713	954.00	1634.50
A_68_P26286958	chr9:7184623-7184667	NM_029775:79	Dcun1d5	INSIDE	1.190	4.112	566.12	2328.00	4.893	516.28	2526.06
A_68_P20294256	chr1:64783172-64783216	NM_001042659:1130	Fzd5	INSIDE	1.190	1.474	929.98	1371.07	1.754	749.64	1315.21
A_68_P20644881	chr1:138157260-138157304	NM_001101516:168	Gpr25	INSIDE	1.190	2.591	1119.21	2899.74	3.083	1048.01	3231.41
A_68_P27995148	chr11:87430476-87430520	NM_001045527:-167	Hsf5	PROMOTER	1.190	2.895	616.40	1784.54	3.446	559.56	1928.25
A_68_P25086723	chr7:51568193-51568237	NM_001034115:2581	Shank1	INSIDE	1.190	2.230	648.03	1444.80	2.653	497.98	1321.24
A_68_P32427541	chrX:61528987-61529031	NM_178740:1163	Slitrk4	INSIDE	1.190	2.126	2222.11	4724.22	2.529	1123.55	2841.52
A_68_P28155493	chr11:115676194-115676238	NM_029557:164	Tsen54	INSIDE	1.190	1.749	1975.10	3455.21	2.081	1574.95	3277.99
A_68_P23185485	chr4:106295363-106295407	NM_177667:331	Ttc22	INSIDE	1.190	3.357	249.85	838.66	3.995	242.24	967.81
A_68_P24425394	chr6:47974652-47974696	NM_001081382:23439	Zfp777	INSIDE	1.190	1.804	1045.36	1886.35	2.148	969.37	2082.10
A_68_P21105114	chr2:30626927-30626971			Unknown	1.190	2.951	569.73	1681.23	3.512	533.67	1873.98
A_68_P20046438	chr1:14496853-14496897			Unknown	1.190	2.234	898.78	2008.12	2.658	826.49	2196.89
A_68_P24856098	chr6:133055497-133055541	NM_001163445:262	2700089E24Rik	INSIDE	1.189	2.511	1150.75	2889.25	2.986	998.02	2980.26
A_68_P22953596	chr4:58924953-58924997	NM_172381:623	AI314180	INSIDE	1.189	3.328	283.12	942.33	3.958	280.63	1110.79
A_68_P24059412	chr5:124571591-124571635	NM_011256:94815	Pitpnm2	INSIDE	1.189	3.406	921.50	3138.28	4.049	794.11	3215.65
A_68_P28164070	chr11:117127735-117127779	NM_001113487:197	Septin9	INSIDE	1.189	1.800	1115.46	2008.19	2.140	1035.90	2216.58
A_68_P28751511	chr12:113882861-113882905	NM_001161737:-156	Siva1	PROMOTER	1.189	1.556	4921.13	7657.49	1.849	3920.30	7250.40

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P24155692	chr5:144016313-144016357	NM_017467:15367	Zfp316	INSIDE	1.189	2.120	724.33	1535.30	2.519	615.54	1550.65
A_68_P24837689	chr6:128150353-128150397	ENSMUST00000071101:267		INSIDE	1.189	0.443	1350.21	598.63	0.527	1159.05	610.93
A_68_P27508735	chr10:121885914-121885958	NM_016847:382	Avpr1a	INSIDE	1.188	1.766	1349.40	2383.62	2.099	1122.68	2356.89
A_68_P20561474	chr1:122237586-122237630	NM_207233:450	C1ql2	INSIDE	1.188	1.979	1061.38	2100.76	2.351	921.90	2167.00
A_68_P25948475	chr8:72405501-72405545	NM_026818:5769	Cilp2	INSIDE	1.188	2.696	442.98	1194.29	3.202	421.83	1350.75
A_68_P21877294	chr2:174586233-174586277	NM_007903:-19	Edn3	PROMOTER	1.188	7.053	834.30	5884.22	8.380	743.66	6231.99
A_68_P21339409	chr2:74600922-74600966	NM_010467:-92	Hoxd1	PROMOTER	1.188	2.063	905.17	1867.31	2.450	780.69	1912.95
A_68_P21809984	chr2:162843268-162843312	NM_172150:83	Ift52	INSIDE	1.188	2.270	792.72	1799.20	2.695	724.18	1951.98
A_68_P24759668	chr6:113419933-113419977	NM_001034029:11066	Il17re	INSIDE	1.188	2.014	1210.10	2436.55	2.391	1148.67	2746.92
A_68_P24053123	chr5:123401996-123402040	NM_001005866:36524	Kdm2b	INSIDE	1.188	1.526	4698.48	7171.64	1.814	3737.51	6779.76
A_68_P20726276	chr1:155179693-155179737	NM_010683:202	Lamc1	INSIDE	1.188	3.524	1316.97	4641.04	4.186	1311.92	5491.91
A_68_P25266278	chr7:87508116-87508160	NM_172903:8123	Man2a2	INSIDE	1.188	2.501	995.22	2488.95	2.972	678.20	2015.69
A_68_P28052461	chr11:97605654-97605698	NM_054051:342	Pip4k2b	INSIDE	1.188	1.696	5214.13	8844.54	2.016	3995.07	8053.93
A_68_P24007303	chr5:115460994-115461038	NM_029012:-516	Sppl3	PROMOTER	1.188	2.151	1644.55	3538.22	2.556	1442.32	3686.58
A_68_P28755239	chr12:114425974-114426018	NM_153776:1883	Tmem121	INSIDE	1.188	1.731	675.00	1168.54	2.056	594.31	1221.78
A_68_P23984847	chr5:111706473-111706517	NM_024477:397673	Ttc28	INSIDE	1.188	2.347	483.10	1133.91	2.789	440.81	1229.29
A_68_P22878937	chr4:44769646-44769690	NM_138590:238	Zcchc7	INSIDE	1.188	1.381	1864.27	2575.32	1.641	1623.92	2664.81
A_68_P31623248	chr18:36479879-36479923	AK015580:1246		DOWNSTREAM	1.188	1.538	1715.45	2638.67	1.827	1513.76	2765.96
A_68_P31939720	chr19:7496955-7496999	NM_175381:4862	2700081O15Rik	INSIDE	1.187	1.668	5836.06	9734.12	1.981	3783.49	7493.24
A_68_P26351648	chr9:22193305-22193349	NM_028390:324	Anln	INSIDE	1.187	2.217	622.15	1379.04	2.631	581.35	1529.81
A_68_P21078053	chr2:26208046-26208090	NM_001037747:6999	Card9	INSIDE	1.187	2.198	861.78	1894.55	2.609	694.89	1812.96
A_68_P27278709	chr10:79217725-79217769	NM_023304:-117	Fgf22	DIVERGENT_PROMOTER	1.187	1.474	6133.92	9039.58	1.750	4083.47	7146.00
A_68_P31214873	chr17:48041518-48041563	NM_001110824:20041	Foxp4	INSIDE	1.187	5.301	3964.68	21018.71	6.292	2851.71	17943.38
A_68_P22864174	chr4:41702682-41702730	NM_016658:581	Galt	INSIDE	1.187	1.593	1093.96	1742.69	1.890	730.83	1381.41
A_68_P20769691	chr1:162965037-162965081	NR_002840:-238	Gas5	DIVERGENT_PROMOTER	1.187	3.134	1806.28	5660.63	3.721	1652.58	6149.38
A_68_P32240896	chrX:7499453-7499497	NM_013892:2527	Pcsk1n	INSIDE	1.187	1.443	2129.59	3072.44	1.713	1105.82	1893.79
A_68_P24992917	chr7:19955431-19955475	NM_001010836:8888	Ppp1r13l	INSIDE	1.187	1.593	1452.51	2313.95	1.891	1275.53	2412.50
A_68_P23545737	chr5:24606038-24606082	NM_145401:400	Prkag2	INSIDE	1.187	3.249	392.97	1276.68	3.857	367.32	1416.68
A_68_P26983364	chr10:19569406-19569450	NM_029529:1837	Slc35d3	INSIDE	1.187	1.625	1304.20	2118.67	1.928	1016.82	1960.91
A_68_P31163430	chr17:36408687-36408731	NM_178281:-330	Trim39	PROMOTER	1.187	1.483	962.34	1427.45	1.761	804.56	1416.46
A_68_P22129169	chr3:51144329-51144373	ENSMUST00000091144:138		INSIDE	1.187	2.044	1327.56	2713.40	2.426	1121.58	2720.45
A_68_P20286429	chr1:63411957-63412001	ENSMUST00000120413:-39		PROMOTER	1.187	2.465	915.34	2256.42	2.925	833.13	2437.20
A_68_P23467743	chr5:8368197-8368241	NM_001098225:-137	Adam22	PROMOTER	1.186	2.060	1137.28	2343.04	2.444	1056.57	2581.90
A_68_P26234239	chr8:125091584-125091628	NM_026014:-308	Cdt1	PROMOTER	1.186	1.887	1759.05	3319.18	2.238	1454.65	3254.82
A_68_P32769557	chrX:154481653-154481697	NM_177751:-632	Cnksr2	PROMOTER	1.186	2.112	1061.37	2242.13	2.505	635.68	1592.39
A_68_P24388781	chr6:40385401-40385445	NM_175528:710	E330009J07Rik	INSIDE	1.186	2.071	3956.35	8192.25	2.455	3097.27	7604.23
A_68_P21680290	chr2:139503712-139503756	NM_001126490:-179	Ism1	PROMOTER	1.186	1.578	802.04	1265.39	1.871	681.97	1275.83
A_68_P21206006	chr2:49922023-49922067	NM_177139:63	Lypd6	INSIDE	1.186	2.356	1095.68	2581.11	2.793	980.41	2738.11
A_68_P29919368	chr14:115439764-115439808	NR_029785:-3106	Mir17	PROMOTER	1.186	2.291	831.94	1905.57	2.718	868.55	2360.38
A_68_P25981542	chr8:79709972-79710016	NM_001083906:283588	Nr3c2	INSIDE	1.186	1.934	415.77	804.02	2.294	319.17	732.29
A_68_P22356140	chr3:97555778-97555823	NM_178080:16137	Pde4dip	INSIDE	1.186	2.617	519.58	1359.96	3.104	402.47	1249.13
A_68_P26744223	chr9:95745481-95745525	NM_001033210:196	Pls1	INSIDE	1.186	2.495	2416.27	6029.45	2.960	2154.27	6375.87
A_68_P21843419	chr2:168591449-168591493	NM_175303:1231	Sall4	INSIDE	1.186	1.774	1288.52	2285.22	2.104	1112.90	2340.99
A_68_P20945912	chr1:194681174-194681218	NM_001177794:-3255	Sertad4	PROMOTER	1.186	3.961	384.23	1521.92	4.697	425.63	1999.37
A_68_P27947942	chr11:79067536-79067580	NM_019653:639	Wsb1	INSIDE	1.186	2.064	1868.53	3856.69	2.448	1572.98	3850.16
A_68_P21721815	chr2:146838797-146838841	NM_011917:23	Xrn2	INSIDE	1.186	1.589	1574.55	2502.68	1.884	1402.54	2642.84
A_68_P30402203	chr15:85502100-85502144	AK038224:-5049		PROMOTER	1.186	1.807	304.07	549.58	2.144	261.43	560.43
A_68_P22941605	chr4:56814945-56814989	NM_001081420:-234	BC026590	PROMOTER	1.185	1.675	1300.10	2177.03	1.985	1042.38	2069.03
A_68_P23607906	chr5:36827371-36827415	NM_025725:156	Ccdc96	INSIDE	1.185	1.484	749.61	1112.23	1.758	597.66	1050.89
A_68_P31921839	chr19:4214705-4214749	NM_019952:335	Clcf1	INSIDE	1.185	2.233	1026.28	2291.78	2.647	902.86	2389.76
A_68_P21752059	chr2:152769043-152769087	NM_001159376:8254	Dusp15	INSIDE	1.185	2.077	342.13	710.58	2.461	358.37	881.85

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P22957376	chr4:59638970-59639014	NM_153158:-100	E130308A19Rik	PROMOTER	1.185	2.119	1021.97	2165.07	2.511	939.08	2357.65
A_68_P27640630	chr11:22186736-22186780	NM_153078:-917	Ehbp1	PROMOTER	1.185	2.496	1389.99	3469.37	2.958	1241.61	3672.92
A_68_P27180609	chr10:60915255-60915299	NM_010124:141	Eif4ebp2	INSIDE	1.185	1.630	1554.18	2534.08	1.932	1249.09	2413.82
A_68_P31927969	chr19:5307468-5307512	NM_001024717:9160	Gal3st3	INSIDE	1.185	3.004	403.44	1212.03	3.559	387.39	1378.67
A_68_P29072859	chr13:58460443-58460487	NM_175214:-4241	Kif27	PROMOTER	1.185	1.384	2947.81	4079.93	1.641	2500.69	4102.47
A_68_P31930563	chr19:5742280-5742324	NM_008520:1399	Ltbp3	INSIDE	1.185	2.833	929.09	2632.34	3.358	853.78	2866.75
A_68_P30340463	chr15:74785980-74786024	NM_001164040:467	Ly6e	INSIDE	1.185	2.730	21731.91	59321.27	3.234	14707.19	47568.69
A_68_P32266424	chrX:13063560-13063604	NM_173415:18785	Nyx	INSIDE	1.185	4.530	363.54	1646.94	5.366	262.53	1408.85
A_68_P20782634	chr1:165242803-165242847	NM_011127:957	Prrx1	INSIDE	1.185	2.155	542.24	1168.54	2.553	451.77	1153.34
A_68_P25588867	chr7:148633309-148633353	NM_026020:-218	Rplp2	DIVERGENT_PROMOTER	1.185	1.692	1470.19	2486.98	2.004	1106.43	2217.30
A_68_P26887821	chr9:122075732-122075776	NM_001164572:49371	Snrk	INSIDE	1.185	1.881	1028.17	1934.07	2.228	775.75	1728.57
A_68_P31421396	chr17:87534273-87534317	NM_019654:27276	Socs5	INSIDE	1.185	3.050	2188.27	6674.15	3.615	1812.63	6553.10
A_68_P21864919	chr2:172376460-172376504	NM_001159696:-8	Tcfap2c	PROMOTER	1.185	1.716	507.49	870.94	2.033	376.61	765.74
A_68_P24819777	chr6:125236044-125236088	NM_009446:-6	Tuba3a	PROMOTER	1.185	1.612	739.24	1191.95	1.911	570.68	1090.31
A_68_P20977354	chr2:6022037-6022081	NM_001159657:29173	5430407P10Rik	INSIDE	1.184	2.323	409.44	950.97	2.749	347.66	955.67
A_68_P24010911	chr5:116112644-116112688	NM_001080808:68902	Ccdc64	INSIDE	1.184	3.239	3818.08	12366.38	3.833	3197.66	12257.70
A_68_P27934411	chr11:76660318-76660362	NM_007754:170	Cpd	INSIDE	1.184	0.507	1023.03	519.18	0.601	907.53	545.40
A_68_P25949731	chr8:72608268-72608312	NM_177900:863	Hapln4	INSIDE	1.184	1.438	804.93	1157.12	1.703	651.75	1109.70
A_68_P27315613	chr10:86168167-86168211	NM_011631:1	Hsp90b1	INSIDE	1.184	1.564	4080.66	6382.68	1.853	3268.24	6054.53
A_68_P21420371	chr2:90894443-90894487	NM_008948:292	Psmc3	INSIDE	1.184	3.449	2662.54	9182.12	4.083	2021.47	8254.26
A_68_P32019129	chr19:23762386-23762431	NM_028208:519	Ptar1	INSIDE	1.184	2.079	290.24	603.33	2.462	254.60	626.81
A_68_P25025138	chr7:29849498-29849542	NM_009109:60650	Ryr1	INSIDE	1.184	2.703	1634.30	4417.20	3.199	1327.01	4245.69
A_68_P26750366	chr9:96896367-96896411	NM_145134:22386	Spsb4	INSIDE	1.184	2.871	457.80	1314.36	3.400	410.59	1395.93
A_68_P28678695	chr12:101122821-101122865	NM_028354:118	Tdp1	INSIDE	1.184	3.712	433.79	1610.22	4.397	383.01	1683.92
A_68_P31092442	chr17:23713394-23713438	NM_011747:23038	Zfp13	INSIDE	1.184	1.502	1815.08	2726.65	1.779	1364.63	2427.39
A_68_P32674749	chrX:131543372-131543416	NM_175446:354	Zmat1	INSIDE	1.184	2.635	546.21	1438.99	3.118	325.94	1016.40
A_68_P28752686	chr12:114047096-114047140	NM_145450:-67	BC022687	PROMOTER	1.183	1.855	823.29	1526.84	2.193	617.78	1354.87
A_68_P28313704	chr12:29237167-29237211	NM_001177964:-3986	Dcdc2c	PROMOTER	1.183	2.331	826.07	1925.55	2.759	692.29	1909.80
A_68_P21819504	chr2:164571506-164571550	NM_133763:14	Dnttip1	INSIDE	1.183	2.527	1027.54	2596.88	2.991	918.72	2747.56
A_68_P29703988	chr14:71289674-71289718	NM_008115:-240	Gfra2	PROMOTER	1.183	1.804	546.38	985.88	2.134	428.67	914.97
A_68_P24133864	chr5:139626346-139626390	NM_001081265:192	Heatr2	INSIDE	1.183	2.951	1728.63	5102.00	3.490	1598.98	5580.66
A_68_P31244136	chr17:53706802-53706846	NM_020005:529	Kat2b	INSIDE	1.183	2.247	692.47	1556.13	2.657	577.68	1535.14
A_68_P30795699	chr16:59471732-59471776	NM_025910:154	Mina	INSIDE	1.183	1.667	1395.38	2326.12	1.972	1287.78	2538.87
A_68_P27708454	chr11:35583064-35583108	NM_145962:90	Pank3	INSIDE	1.183	2.247	5735.70	12885.78	2.658	4833.75	12850.05
A_68_P21612440	chr2:127096105-127096149	NM_139308:162	Stard7	INSIDE	1.183	4.366	1182.72	5163.27	5.165	911.91	4710.40
A_68_P28074032	chr11:101327214-101327258	NM_012037:277	Vat1	INSIDE	1.183	1.883	287.23	540.81	2.227	251.38	559.85
A_68_P20859688	chr1:179372159-179372203	NM_001012330:-2611	Zfp238	PROMOTER	1.183	0.499	1499.90	748.11	0.590	1220.01	719.64
A_68_P21104695	chr2:30549015-30549059	ENSMUST00000146702:63862		DOWNSTREAM	1.183	2.707	639.24	1730.46	3.203	529.32	1695.54
A_68_P24864121	chr6:134848481-134848525	NR_029441:524	2810454H06Rik	INSIDE	1.182	1.563	488.17	763.02	1.848	498.94	922.13
A_68_P31331958	chr17:71351874-71351918	NM_026064:-23	2900073G15Rik	PROMOTER	1.182	1.855	858.64	1592.84	2.193	746.12	1636.45
A_68_P26019649	chr8:86938288-86938332	NM_007578:-952	Cacna1a	PROMOTER	1.182	2.444	815.37	1992.98	2.888	781.70	2257.55
A_68_P27764452	chr11:45665495-45665539	NM_001045520:51	Clint1	INSIDE	1.182	1.525	772.74	1178.77	1.804	801.22	1445.12
A_68_P23192160	chr4:107356153-107356197	NM_019872:593	Dmrtb1	INSIDE	1.182	3.323	619.94	2059.90	3.929	545.95	2144.78
A_68_P20825164	chr1:172815355-172815399	NM_023173:295	Dusp12	INSIDE	1.182	1.396	1760.97	2457.70	1.649	1559.16	2571.46
A_68_P27893912	chr11:69049971-69050015	NM_008192:532	Gucy2e	INSIDE	1.182	2.340	772.44	1807.42	2.767	710.63	1966.12
A_68_P25274810	chr7:89078740-89078784	NM_013886:583	Hdgfrp3	INSIDE	1.182	2.374	1065.61	2529.93	2.806	985.69	2765.69
A_68_P31558687	chr18:24280026-24280070	NM_172625:272	Ino80c	INSIDE	1.182	2.458	2861.81	7033.48	2.905	2881.99	8371.38
A_68_P27828613	chr11:57822962-57823006	NM_028451:419	Larp1	INSIDE	1.182	5.529	528.11	2919.82	6.538	413.35	2702.39
A_68_P24159776	chr5:144934512-144934556	NM_001081109:73230	Lmtk2	INSIDE	1.182	2.453	632.54	1551.69	2.900	510.60	1480.78
A_68_P21240085	chr2:56976720-56976764	NM_001139509:-328	Nr4a2	PROMOTER	1.182	2.356	1070.53	2521.96	2.784	963.40	2682.54
A_68_P32147398	chr19:47125047-47125091	NM_027654:267	Pcgf6	INSIDE	1.182	1.655	499.17	825.88	1.956	465.54	910.51

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P22518661	chr3:128907456-128907500	NM_001042502:-9376	Pitx2	PROMOTER	1.182	2.649	2229.61	5905.84	3.131	1841.62	5765.92
A_68_P31802711	chr18:69505644-69505688	NM_001083967:292	Tcf4	INSIDE	1.182	1.646	747.31	1230.06	1.946	626.15	1218.63
A_68_P22510646	chr3:127492950-127492994	NM_145133:142	Tifa	INSIDE	1.182	1.546	1220.98	1887.04	1.828	1104.80	2019.08
A_68_P25411545	chr7:117205191-117205235	NM_009281:-3	Zfp143	PROMOTER	1.182	3.087	10187.97	31449.07	3.649	7588.74	27692.57
A_68_P24800508	chr6:120786336-120786380	NM_153516:111	Bcl2l13	INSIDE	1.181	3.461	2660.20	9207.73	4.089	1988.63	8131.17
A_68_P28944866	chr13:35832734-35832778	NM_001123386:-514	Cdyl	PROMOTER	1.181	2.282	1083.90	2473.82	2.696	879.59	2371.61
A_68_P25313627	chr7:97591983-97592027	NM_145151:714	Crebzf	INSIDE	1.181	2.402	1157.23	2779.37	2.835	1094.65	3103.85
A_68_P24951534	chr7:4960187-4960231	NM_001110330:4636	Fiz1	INSIDE	1.181	2.640	762.45	2012.68	3.116	749.75	2336.50
A_68_P31075179	chr17:17987266-17987310	NM_008215:4864	Has1	INSIDE	1.181	2.604	1723.66	4488.49	3.075	1390.40	4275.85
A_68_P23192848	chr4:107475278-107475322	NM_001080926:437	Lrp8	INSIDE	1.181	1.593	933.55	1487.56	1.883	822.84	1549.00
A_68_P32181745	chr19:53388277-53388321	NM_001008542:3303	Mxi1	INSIDE	1.181	1.535	823.75	1264.39	1.813	757.53	1373.06
A_68_P22875663	chr4:44181273-44181317	NM_001038993:-139	Rnf38	PROMOTER	1.181	2.728	478.17	1304.55	3.221	446.94	1439.71
A_68_P27923093	chr11:74710538-74710582	NM_197943:22	Sgsm2	INSIDE	1.181	1.988	1772.45	3524.28	2.348	1486.53	3490.62
A_68_P28071034	chr11:100800458-100800502	NM_011486:345	Stat3	INSIDE	1.181	1.405	1214.34	1706.46	1.659	1050.90	1743.59
A_68_P23966229	chr5:107717967-107718011	NM_011578:626	Tgfbr3	INSIDE	1.181	2.620	1501.38	3933.04	3.093	1306.12	4040.12
A_68_P21739582	chr2:150351755-150351799	ENSMUST00000119514:4948		DOWNSTREAM	1.181	1.374	1832.06	2517.64	1.623	1698.13	2755.29
A_68_P27899783	chr11:70068622-70068666	NM_007440:199	Alox12	INSIDE	1.180	1.346	2549.15	3430.63	1.588	1853.75	2943.08
A_68_P30990992	chr16:96303585-96303629	NM_145125:429	Brwd1	INSIDE	1.180	2.371	2169.95	5145.85	2.797	2021.10	5653.66
A_68_P32316566	chrX:33565537-33565581	NM_001009947:136732	Dock11	INSIDE	1.180	3.352	858.77	2878.78	3.956	606.25	2398.36
A_68_P28051738	chr11:97490235-97490279	NM_175332:774	E130012A19Rik	INSIDE	1.180	1.988	1857.30	3691.41	2.345	1690.47	3964.67
A_68_P30478816	chr15:99054388-99054432	NM_010601:-996	Kcnh3	PROMOTER	1.180	1.554	2388.94	3713.30	1.833	1842.63	3378.35
A_68_P32396635	chrX:53850948-53850992	NM_146234:126	Mmgt1	INSIDE	1.180	1.481	866.96	1284.08	1.748	415.55	726.20
A_68_P24992504	chr7:19878717-19878763	NM_001025364:2293	Rtn2	INSIDE	1.180	3.278	1027.12	3366.73	3.868	788.62	3050.45
A_68_P27340134	chr10:90586370-90586414	NM_133668:316	Slc25a3	INSIDE	1.180	0.543	1031.27	559.70	0.640	899.50	575.84
A_68_P28052666	chr11:97643069-97643113	NR_028078:-10	Snora21	PROMOTER	1.180	3.549	623.28	2212.08	4.189	494.91	2072.95
A_68_P20353686	chr1:75384915-75384959	NM_001085370:2752	Speg	INSIDE	1.180	1.553	1206.68	1874.30	1.833	1135.92	2082.23
A_68_P31335315	chr17:71965807-71965851	NM_175639:274	Wdr43	INSIDE	1.180	2.560	1507.13	3858.32	3.022	1328.52	4014.40
A_68_P23195378	chr4:107973651-107973695	NM_001033634:23	Zyg11b	INSIDE	1.180	1.535	3893.30	5977.24	1.811	2816.66	5101.46
A_68_P33005897	A_68_P33005897			Unknown	1.180	2.981	617.20	1839.84	3.518	536.57	1887.64
A_68_P31620715	chr18:36048154-36048198			Unknown	1.180	2.156	932.07	2009.85	2.545	857.65	2182.47
A_68_P21839558	chr2:167942901-167942945			Unknown	1.180	6.706	1506.48	10102.30	7.911	1155.79	9143.71
A_68_P32373281	chrX:48194954-48194998	NM_133729:364	2610018G03Rik	INSIDE	1.179	1.657	911.24	1509.50	1.953	537.77	1050.16
A_68_P29523397	chr14:34133413-34133457	NM_153800:103426	Arhgap22	INSIDE	1.179	1.504	1672.24	2514.42	1.773	1478.82	2621.22
A_68_P20753946	chr1:160292678-160292722	NM_001205204:266	Astn1	INSIDE	1.179	4.381	602.88	2640.95	5.163	524.62	2708.50
A_68_P21814762	chr2:163679681-163679725	NM_001030292:217	Kcnk15	INSIDE	1.179	2.991	712.02	2129.53	3.528	623.69	2200.14
A_68_P22201243	chr3:65463433-65463477	NM_001166659:-6695	Lekr1	PROMOTER	1.179	3.237	796.34	2577.44	3.815	737.08	2811.72
A_68_P31923503	chr19:4509996-4510046	NM_001162946:-451	Pcx	PROMOTER	1.179	1.900	1097.27	2085.11	2.241	755.88	1694.03
A_68_P30650135	chr16:31932946-31932990	NM_172822:-968	Pigz	PROMOTER	1.179	2.748	258.77	711.14	3.240	282.25	914.61
A_68_P21110366	chr2:31493479-31493523	NM_001123362:-2056	Prdm12	PROMOTER	1.179	1.786	1397.58	2496.15	2.105	1209.03	2545.39
A_68_P29605617	chr14:52877185-52877229	NM_172601:21864	Rab2b	DOWNSTREAM	1.179	1.397	2622.90	3663.30	1.647	2105.01	3466.29
A_68_P20011684	chr1:6205145-6205189	NM_009826:424	Rb1cc1	INSIDE	1.179	1.886	402.52	759.02	2.224	360.74	802.11
A_68_P28957533	chr13:38023055-38023099	NM_001177869:42337	Rreb1	INSIDE	1.179	2.465	1137.56	2804.27	2.907	957.77	2784.12
A_68_P21820793	chr2:164793533-164793577	NM_020333:67	Slc12a5	INSIDE	1.179	1.665	3206.47	5337.49	1.963	2511.42	4930.66
A_68_P27848100	chr11:61191430-61191474	NM_026183:125	Slc47a1	INSIDE	1.179	2.168	675.67	1464.89	2.556	640.54	1637.46
A_68_P29955473	chr14:121778112-121778156	NM_145465:318	Stk24	INSIDE	1.179	1.922	942.99	1812.06	2.265	894.12	2024.94
A_68_P32562270	chrX:98255164-98255208	NM_031384:-208	Tex11	PROMOTER	1.179	2.236	1378.80	3082.92	2.637	576.46	1520.01
A_68_P23991123	chr5:112705779-112705823	NM_009419:74	Tpst2	INSIDE	1.179	2.513	759.96	1909.76	2.963	687.45	2037.12
A_68_P25663078	chr8:12672178-12672222	NM_198031:-100	Tubgcp3	PROMOTER	1.179	1.896	290.89	551.43	2.236	246.83	551.84
A_68_P32237968	chrX:6896043-6896087	ENSMUST00000132126:232		INSIDE	1.179	1.936	528.59	1023.57	2.283	379.29	865.96
A_68_P30567433	chr16:15887647-15887691	NM_007679:290	Cebpd	INSIDE	1.178	0.523	1530.76	800.83	0.617	1133.01	698.52
A_68_P25827831	chr8:46095191-46095238	NM_001081286:59653	Fat1	INSIDE	1.178	2.745	210.19	577.07	3.233	197.04	637.04

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26572465	chr9:62659122-62659166	NM_010193:311	Fem1b	INSIDE	1.178	1.743	2653.03	4623.82	2.054	2281.84	4686.31
A_68_P32745698	chrX:147955401-147955445	NM_177201:208	Phf8	INSIDE	1.178	2.814	562.00	1581.30	3.315	362.33	1201.23
A_68_P21431994	chr2:92855345-92855389	NM_001177536:30935	Prdm11	INSIDE	1.178	1.386	1167.56	1618.76	1.633	1102.41	1800.08
A_68_P28096908	chr11:105451551-105451595	NM_181071:273	Tanc2	INSIDE	1.178	2.084	3086.66	6433.49	2.455	2486.33	6103.63
A_68_P27798805	chr11:52175093-52175137	NM_011694:498	Vdac1	INSIDE	1.178	0.536	1313.28	703.50	0.631	1043.15	658.33
A_68_P31599638	chr18:31963974-31964018	NM_001170966:286	Wdr33	INSIDE	1.178	1.648	866.41	1427.64	1.942	817.58	1587.44
A_68_P28577649	chr12:81891588-81891632	NM_178682:65	4933426M11Rik	INSIDE	1.177	1.454	1063.69	1546.33	1.712	989.54	1693.60
A_68_P24160788	chr5:145119007-145119051	NM_025833:-47	Baiap2l1	PROMOTER	1.177	2.903	2923.69	8488.36	3.417	2530.79	8647.03
A_68_P27170203	chr10:59165375-59165419	NM_144822:14	Cbara1	INSIDE	1.177	1.810	2896.74	5244.33	2.131	2134.20	4548.60
A_68_P21853424	chr2:170322747-170322791	NM_009996:-130	Cyp24a1	PROMOTER	1.177	1.871	4193.27	7846.27	2.202	3098.94	6822.80
A_68_P20831242	chr1:174078262-174078306	NM_153555:139	Dcaf8	INSIDE	1.177	2.111	2711.99	5725.63	2.485	2520.61	6262.84
A_68_P31106387	chr17:25946215-25946259	NM_001164225:207	Fbxl16	INSIDE	1.177	3.750	590.90	2215.86	4.414	538.78	2378.10
A_68_P31936769	chr19:7008810-7008854	NM_008431:173	Kcnk4	INSIDE	1.177	1.592	2284.28	3637.05	1.874	1926.29	3610.47
A_68_P21077008	chr2:26058081-26058125	NM_001039653:3974	Lhx3	INSIDE	1.177	1.999	1203.82	2406.55	2.352	1068.07	2512.45
A_68_P27551861	chr11:3309133-3309177	NM_010718:84	Limk2	INSIDE	1.177	1.784	2180.04	3888.87	2.100	1716.91	3606.21
A_68_P24027257	chr5:119011484-119011528	NM_172424:779	Med13l	INSIDE	1.177	1.739	1121.26	1949.53	2.047	866.97	1774.75
A_68_P20240461	chr1:55187949-55187993	NM_025283:-118	Mobkl3	PROMOTER	1.177	1.892	1017.01	1924.51	2.227	902.22	2009.10
A_68_P23430797	chr4:153715735-153715779	NM_001177995:295226	Prdm16	INSIDE	1.177	4.816	4127.11	19877.44	5.671	3108.68	17628.89
A_68_P25089827	chr7:52125023-52125067	NM_133949:114	Ptov1	INSIDE	1.177	2.339	1331.25	3114.42	2.753	1224.34	3370.60
A_68_P24464123	chr6:54516358-54516402	NM_027268:-4	Scrn1	PROMOTER	1.177	1.939	1267.41	2457.38	2.282	1200.89	2739.99
A_68_P26983373	chr10:19570476-19570520	NM_029529:767	Slc35d3	INSIDE	1.177	5.374	1943.91	10446.65	6.327	1830.25	11580.90
A_68_P30479870	chr15:99223391-99223435	NM_001171035:-237	Tmbim6	PROMOTER	1.177	2.258	2572.45	5808.41	2.657	1754.23	4660.94
A_68_P27286198	chr10:80360560-80360604	NM_001081688:18022	Tmprss9	INSIDE	1.177	2.091	1863.20	3896.65	2.462	1467.24	3612.94
A_68_P27636577	chr11:21270655-21270699	NM_139297:206	Ugp2	INSIDE	1.177	18.291	4294.76	78553.37	21.521	3151.00	67811.32
A_68_P30351142	chr15:76742082-76742126	NM_001168276:13774	Zfp647	INSIDE	1.177	2.112	683.51	1443.70	2.487	546.51	1359.20
A_68_P28724518	chr12:109154385-109154429	NM_001079883:87218	Bcl11b	INSIDE	1.176	2.405	3047.11	7327.36	2.828	2396.16	6775.97
A_68_P21821742	chr2:164941702-164941746	NM_174988:118513	Cdh22	INSIDE	1.176	2.712	2489.47	6752.49	3.189	1734.16	5529.61
A_68_P24818636	chr6:125046050-125046094	NM_145979:-108	Chd4	PROMOTER	1.176	2.328	6303.65	14674.87	2.737	4637.39	12692.72
A_68_P26519505	chr9:53055899-53055943	NM_029936:297	Ddx10	INSIDE	1.176	3.135	8812.13	27625.80	3.687	6282.21	23162.20
A_68_P28925109	chr13:31900260-31900304	NM_008592:1768	Foxc1	INSIDE	1.176	0.490	2394.15	1172.73	0.576	2210.88	1273.86
A_68_P24052688	chr5:123330338-123330382	NM_013910:19999	Kdm2b	INSIDE	1.176	2.162	2575.04	5567.15	2.543	2090.33	5315.33
A_68_P28513753	chr12:70397631-70397675	NM_027117:-15	Klhdc2	PROMOTER	1.176	1.827	1015.23	1854.31	2.147	926.60	1989.82
A_68_P22210771	chr3:67386632-67386676	NM_025813:-35	Mfsd1	PROMOTER	1.176	3.689	840.82	3102.06	4.337	618.77	2683.79
A_68_P21904884	chr2:180324017-180324061	NM_031373:-73	Ogfr	PROMOTER	1.176	1.986	1002.71	1991.18	2.336	858.38	2005.34
A_68_P24053485	chr5:123465296-123465340	NM_175423:236	Orai1	INSIDE	1.176	3.759	660.33	2482.04	4.421	653.26	2887.93
A_68_P32326382	chrX:35474320-35474364	NM_001185002:326	Rhox13	INSIDE	1.176	2.115	738.67	1562.32	2.487	388.24	965.44
A_68_P22324939	chr3:90193494-90193538	NM_011988:333	Slc27a3	INSIDE	1.176	2.058	965.88	1988.26	2.421	937.30	2269.29
A_68_P31056399	chr17:13898251-13898295	NM_022311:129	Tcte2	INSIDE	1.176	2.522	2553.85	6439.65	2.967	2185.59	6483.62
A_68_P25032389	chr7:31373349-31373393	NM_029274:375	Wbp7	INSIDE	1.176	1.721	5578.90	9599.10	2.024	4074.99	8248.28
A_68_P28593636	chr12:84937949-84937993	NM_183154:127	Zfyve1	INSIDE	1.176	1.501	3434.07	5155.41	1.766	3008.02	5312.60
A_68_P21071713	chr2:25228424-25228468	NM_001081085:606	2010317E24Rik	INSIDE	1.175	3.315	480.47	1592.85	3.895	435.00	1694.37
A_68_P23391467	chr4:147315560-147315604	NM_029841:579	2510039O18Rik	INSIDE	1.175	2.276	1203.32	2738.18	2.674	1099.53	2940.23
A_68_P21900711	chr2:179711603-179711647	NR_033782:67	4921531C22Rik	INSIDE	1.175	1.834	3091.93	5670.25	2.154	2597.42	5596.03
A_68_P21346286	chr2:75670175-75670220	NM_172666:-36	Agps	PROMOTER	1.175	4.022	1651.64	6643.53	4.726	1444.21	6825.85
A_68_P24816767	chr6:124695514-124695558	NM_007881:10969	Atn1	INSIDE	1.175	2.735	1605.21	4389.64	3.214	1331.81	4280.50
A_68_P31794502	chr18:68093477-68093521	NM_172631:588	D18Ertd653e	INSIDE	1.175	1.654	2675.89	4424.72	1.942	2205.60	4283.81
A_68_P24123516	chr5:137358920-137358964	NM_024474:35	Emid2	INSIDE	1.175	1.492	1062.72	1585.22	1.753	973.25	1706.07
A_68_P31544268	chr18:21458551-21458595	NM_001033445:68	Fam59a	INSIDE	1.175	1.876	993.04	1862.59	2.204	813.80	1793.40
A_68_P26761427	chr9:98856071-98856115	NM_012020:67	Foxl2	INSIDE	1.175	2.878	1162.33	3345.53	3.382	974.36	3294.88
A_68_P22248625	chr3:75760605-75760649	NM_175193:127	Golim4	INSIDE	1.175	1.576	1553.47	2448.55	1.851	1182.10	2188.51
A_68_P31425150	chr17:88196845-88196889	NM_199251:468	Kcnk12	INSIDE	1.175	2.834	594.01	1683.27	3.329	584.56	1945.98

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26811597	chr9:107790348-107790392	NM_028369:-89	Mon1a	PROMOTER	1.175	1.496	674.87	1009.67	1.758	556.77	979.04
A_68_P21351542	chr2:76486311-76486355	NM_011871:-281	Prkra	DIVERGENT_PROMOTER	1.175	2.351	3629.28	8530.82	2.762	2854.07	7882.19
A_68_P22405721	chr3:107137047-107137091	NM_001045807:-861	Rbm15	PROMOTER	1.175	1.853	658.70	1220.27	2.177	654.33	1424.52
A_68_P21078764	chr2:26300667-26300711	NM_153125:48	Sec16a	INSIDE	1.175	3.699	2327.97	8611.71	4.347	1921.31	8352.09
A_68_P32320134	chrX:34335518-34335562	NM_007451:-106	Slc25a5	PROMOTER	1.175	1.383	1384.81	1915.45	1.625	857.68	1393.69
A_68_P31058955	chr17:14417592-14417636	NM_022315:1102	Smoc2	INSIDE	1.175	1.933	1349.92	2609.07	2.271	1247.15	2832.86
A_68_P24663948	chr6:95668305-95668349	NM_011507:505	Suclg2	INSIDE	1.175	1.811	758.30	1372.99	2.128	625.67	1331.39
A_68_P30595261	chr16:21947632-21947676	NM_025693:-29	Tmem41a	PROMOTER	1.175	2.319	1071.51	2484.48	2.724	928.62	2529.91
A_68_P30023613	chr15:12669624-12669668	ENSMUST00000096893:33		INSIDE	1.175	4.322	408.86	1767.12	5.079	375.46	1907.07
A_68_P26225640	chr8:123797224-123797270	ENSMUST00000127664:1362506		INSIDE	1.175	3.168	620.19	1964.88	3.724	516.68	1924.10
A_68_P22082007	chr3:40698419-40698463	NM_026622:242	3110057O12Rik	INSIDE	1.174	1.574	597.20	939.78	1.847	535.28	988.92
A_68_P25354430	chr7:105342884-105342928	NM_001081167:5079	B3gnt6	INSIDE	1.174	2.240	405.30	907.91	2.629	372.63	979.71
A_68_P20329006	chr1:71149346-71149390	NM_007525:178	Bard1	INSIDE	1.174	1.798	999.83	1797.81	2.111	995.65	2102.21
A_68_P26236468	chr8:125388849-125388893	NM_007662:16597	Cdh15	INSIDE	1.174	1.539	844.80	1299.78	1.806	749.67	1354.25
A_68_P25009389	chr7:26063544-26063588	NM_001110131:-3631	Cic	PROMOTER	1.174	2.985	1331.06	3972.77	3.505	1095.19	3839.02
A_68_P29455231	chr14:22667975-22668019	NM_026965:136	Comtd1	INSIDE	1.174	2.696	15959.49	43034.38	3.165	13321.09	42167.36
A_68_P23203754	chr4:109653015-109653059	NM_172296:2407	Dmrta2	INSIDE	1.174	1.562	2790.54	4358.82	1.834	2191.03	4019.43
A_68_P31343015	chr17:73268700-73268744	NM_029999:1078	Lbh	INSIDE	1.174	1.550	1411.15	2187.14	1.820	1173.68	2135.68
A_68_P31601518	chr18:32322635-32322679	NM_011946:-86	Map3k2	PROMOTER	1.174	2.837	510.27	1447.68	3.330	529.79	1764.37
A_68_P22898222	chr4:48064747-48064791	NM_015743:649	Nr4a3	INSIDE	1.174	2.191	2419.99	5301.69	2.571	1900.45	4886.03
A_68_P22309969	chr3:87587605-87587650	NM_001033124:11457	Ntrk1	INSIDE	1.174	2.652	400.59	1062.18	3.114	355.54	1107.04
A_68_P29471619	chr14:25306273-25306317	NM_001081247:-26	Polr3a	DIVERGENT_PROMOTER	1.174	1.551	624.42	968.48	1.820	553.74	1007.87
A_68_P26044775	chr8:91565596-91565640	NM_021390:2443	Sall1	INSIDE	1.174	1.454	2192.95	3188.24	1.706	1881.28	3210.37
A_68_P22338877	chr3:94217455-94217499	NM_028307:237	Tdrkh	INSIDE	1.174	1.939	5021.73	9735.26	2.275	3385.58	7702.92
A_68_P24776845	chr6:116411172-116411216	NM_009662:2	Alox5	INSIDE	1.173	2.585	1718.19	4441.70	3.033	1492.39	4526.74
A_68_P25756352	chr8:32261404-32261448	NM_144927:639	BC019943	INSIDE	1.173	2.060	437.02	900.07	2.416	377.37	911.55
A_68_P26346396	chr9:21095892-21095936	NM_009878:-261	Cdkn2d	PROMOTER	1.173	2.361	291.74	688.84	2.769	256.26	709.62
A_68_P24817997	chr6:124915301-124915345	NM_012003:93	Cops7a	INSIDE	1.173	1.540	3010.61	4637.26	1.806	2495.11	4506.97
A_68_P30082169	chr15:25552086-25552130	NM_019472:-196	Myo10	PROMOTER	1.173	3.038	16835.81	51145.46	3.564	9923.02	35369.00
A_68_P30094309	chr15:27677579-27677623	NM_001081302:278003	Trio	INSIDE	1.173	3.190	1948.03	6215.01	3.742	1440.71	5391.71
A_68_P23692818	chr5:52505349-52505393	AK076709:-3181		PROMOTER	1.173	1.986	1069.74	2124.12	2.330	1094.81	2550.44
A_68_P23819409	chr5:77445107-77445151	NM_027970:81	1700023E05Rik	INSIDE	1.172	2.182	1709.35	3729.44	2.558	1432.96	3665.36
A_68_P27996046	chr11:87578150-87578194	NM_172449:4130	Bzrap1	INSIDE	1.172	1.607	903.83	1452.83	1.884	843.58	1589.08
A_68_P27315614	chr10:86168270-86168314	NM_011631:-103	Hsp90b1	DIVERGENT_PROMOTER	1.172	1.377	4402.15	6062.93	1.614	3113.80	5025.96
A_68_P28099477	chr11:105946015-105946059	NM_011947:-179	Map3k3	PROMOTER	1.172	2.104	800.72	1685.03	2.467	712.88	1758.86
A_68_P25957202	chr8:74031641-74031685	NM_032398:4006	Plvap	INSIDE	1.172	1.827	338.17	617.81	2.140	306.47	656.00
A_68_P30479249	chr15:99125815-99125859	NM_018786:-3	Prpf40b	DIVERGENT_PROMOTER	1.172	2.164	4875.43	10549.88	2.535	3676.80	9321.97
A_68_P20410046	chr1:87961433-87961477	NM_027357:261	Psmd1	INSIDE	1.172	1.858	1165.07	2164.95	2.179	1015.82	2213.19
A_68_P29507209	chr14:31467715-31467759	NM_177815:176	Rft1	INSIDE	1.172	2.007	760.90	1527.20	2.352	731.05	1719.45
A_68_P22871711	chr4:43454970-43455014	NM_011571:-156	Tesk1	PROMOTER	1.172	1.521	1802.41	2741.86	1.782	1492.29	2659.59
A_68_P30657576	chr16:33380868-33380912	NM_011749:30	Zfp148	INSIDE	1.172	1.592	553.78	881.68	1.866	507.34	946.92
A_68_P31156110	A_68_P31156110			Unknown	1.172	2.907	307.77	894.64	3.406	290.75	990.41
A_68_P24043268	chr5:121670665-121670709	ENSMUST00000119892:459		INSIDE	1.172	2.367	886.12	2097.88	2.775	735.38	2040.82
A_68_P24798987	chr6:120481227-120481271	NM_144815:69	Cecr5	INSIDE	1.171	2.505	1351.25	3384.32	2.933	1147.76	3366.51
A_68_P27281433	chr10:79630600-79630644	NM_007705:37	Cirbp	INSIDE	1.171	2.359	1774.83	4186.77	2.763	1355.97	3746.92
A_68_P26841770	chr9:113650921-113650965	NM_001114347:352	Clasp2	INSIDE	1.171	1.780	575.59	1024.84	2.085	553.87	1154.56
A_68_P28185233	chr11:120410651-120410695	NM_001033231:369	Fam195b	INSIDE	1.171	5.275	2908.91	15344.37	6.175	2105.91	13004.68
A_68_P28054695	chr11:98011746-98011790	NM_028149:-838	Fbxl20	PROMOTER	1.171	2.520	907.52	2286.60	2.950	885.19	2611.29
A_68_P21339003	chr2:74549994-74550038	NM_010468:-33	Hoxd3	PROMOTER	1.171	4.305	423.13	1821.49	5.043	413.21	2083.60
A_68_P27470617	chr10:115024975-115025019	NM_010195:-160	Lgr5	PROMOTER	1.171	2.026	1166.86	2364.64	2.374	965.12	2291.21
A_68_P26580973	chr9:64101378-64101422	NM_008927:12	Map2k1	INSIDE	1.171	2.516	653.51	1644.18	2.947	653.18	1924.87

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31158451	chr17:35371961-35372005	NM_010909:778	Nfkbil1	INSIDE	1.171	6.490	6156.92	39955.50	7.596	4445.24	33768.05
A_68_P30343472	chr15:75534891-75534935	NM_001163465:195	Rhpn1	INSIDE	1.171	1.559	1227.30	1913.77	1.826	991.26	1810.51
A_68_P27284271	chr10:80069708-80069752	NM_019575:4104	Scamp4	INSIDE	1.171	2.566	1122.20	2879.64	3.004	872.37	2620.38
A_68_P25092755	chr7:52631986-52632030	NM_009224:19009	Snrnp70	INSIDE	1.171	5.045	1420.34	7165.66	5.906	1160.11	6851.10
A_68_P24974188	chr7:13609447-13609491	NM_011588:-32	Trim28	PROMOTER	1.171	10.235	957.80	9803.35	11.981	634.32	7599.91
A_68_P21781777	chr2:158055194-158055238	NM_001131021:-258	D630003M21Rik	PROMOTER	1.170	1.945	911.27	1772.15	2.276	924.04	2102.71
A_68_P31065253	chr17:15511986-15512030	NM_007865:779	Dll1	INSIDE	1.170	2.302	597.27	1375.18	2.695	534.13	1439.26
A_68_P29247524	chr13:97440758-97440802	NM_008255:111	Hmgcr	INSIDE	1.170	1.987	621.79	1235.56	2.324	585.32	1360.45
A_68_P21309976	chr2:69423831-69423875	NM_001081088:272	Lrp2	INSIDE	1.170	1.522	547.70	833.67	1.781	478.90	852.87
A_68_P32385500	chrX:50410153-50410197	NR_029756:-2648	Mir322	PROMOTER	1.170	4.313	8848.37	38161.07	5.048	4339.45	21905.66
A_68_P22209749	chr3:67178298-67178342	NM_001039543:302	Mlf1	INSIDE	1.170	3.526	1301.46	4589.44	4.126	912.46	3765.06
A_68_P27708457	chr11:35583330-35583374	NM_145962:356	Pank3	INSIDE	1.170	2.292	488.97	1120.79	2.682	449.18	1204.82
A_68_P25908468	chr8:63703117-63703161	NM_021506:171	Sh3rf1	INSIDE	1.170	2.328	1964.55	4573.12	2.723	1756.40	4783.53
A_68_P30366259	chr15:79233437-79233481	NM_172608:275	Tmem184b	INSIDE	1.170	1.995	1749.87	3491.67	2.335	1513.75	3534.59
A_68_P22856569	chr4:40215391-40215435	NM_134097:1462	Topors	INSIDE	1.170	2.390	438.18	1047.15	2.796	526.87	1472.93
A_68_P22372024	chr3:100726413-100726457	NM_001165953:19	Trim45	INSIDE	1.170	1.685	1086.90	1831.42	1.971	855.83	1687.00
A_68_P20820922	chr1:172105070-172105114	NM_133806:-15	Uap1	PROMOTER	1.170	2.249	1284.18	2888.59	2.632	1193.52	3141.16
A_68_P27287713	chr10:80611280-80611324	NM_010731:12287	Zbtb7a	INSIDE	1.170	3.948	3896.85	15386.58	4.619	2916.87	13473.78
A_68_P24951459	chr7:4945480-4945524	NM_026741:2201	Zfp579	INSIDE	1.170	2.055	1189.59	2445.08	2.404	912.48	2193.44
A_68_P27282448	chr10:79783216-79783260	NM_025521:55	2310011J03Rik	INSIDE	1.169	1.578	1045.47	1649.40	1.845	762.14	1405.83
A_68_P28724526	chr12:109155259-109155303	NM_001079883:86344	Bcl11b	INSIDE	1.169	2.975	2007.04	5971.63	3.477	1626.65	5655.68
A_68_P24735103	chr6:108609619-108609663	NM_011498:-982	Bhlhe40	PROMOTER	1.169	1.528	1307.76	1998.29	1.786	1253.00	2237.58
A_68_P22019968	chr3:28981553-28981597	NM_001167748:76	Egfem1	INSIDE	1.169	2.778	604.99	1680.69	3.248	488.45	1586.50
A_68_P22843581	chr4:36898671-36898715	NM_001165999:85	Lingo2	INSIDE	1.169	1.717	4110.15	7055.25	2.007	3340.56	6704.30
A_68_P24117100	chr5:136108637-136108681	NM_146002:135	Rhbdd2	INSIDE	1.169	1.574	1408.35	2216.47	1.841	1233.96	2271.16
A_68_P26745887	chr9:96096585-96096629	NM_001184706:-87	Tfdp2	PROMOTER	1.169	2.006	1202.81	2412.23	2.344	1018.95	2388.52
A_68_P29225757	chr13:93564876-93564920	NM_011582:-125	Thbs4	PROMOTER	1.169	1.814	2878.95	5221.48	2.120	2240.45	4750.73
A_68_P29052393	chr13:55057473-55057517	NM_153131:6702	Unc5a	INSIDE	1.169	1.916	2710.68	5193.47	2.240	2155.21	4827.54
A_68_P27281235	chr10:79605180-79605224	NM_025313:143	Atp5d	INSIDE	1.168	1.399	2343.57	3277.90	1.634	1722.01	2813.61
A_68_P26528581	chr9:54798811-54798855	NM_145229:-71	AY074887	PROMOTER	1.168	3.821	432.71	1653.22	4.464	375.19	1674.78
A_68_P21906145	chr2:180511577-180511621	NM_080641:7	Bhlhe23	INSIDE	1.168	3.176	1016.80	3228.86	3.709	938.50	3480.51
A_68_P31103375	chr17:25522729-25522773	NM_001163691:47978	Cacna1h	INSIDE	1.168	7.111	2787.64	19822.74	8.305	2027.47	16837.58
A_68_P31106875	chr17:26005655-26005699	NM_026633:7	Fam195a	INSIDE	1.168	1.552	1377.19	2137.56	1.813	1187.50	2153.50
A_68_P20819671	chr1:171899591-171899635	NM_010476:-276	Hsd17b7	PROMOTER	1.168	1.597	633.28	1011.18	1.866	492.61	919.04
A_68_P27806466	chr11:53583987-53584031	NM_001159396:34	Irf1	INSIDE	1.168	3.227	649.35	2095.55	3.768	517.44	1949.59
A_68_P28036508	chr11:94937511-94937555	NM_013565:496	Itga3	INSIDE	1.168	2.307	406.22	936.96	2.695	311.03	838.11
A_68_P25362046	chr7:106617483-106617527	NM_028145:2991	Klhl35	INSIDE	1.168	6.002	474.79	2849.66	7.011	377.26	2645.16
A_68_P21826984	chr2:165818646-165818690	NM_008679:532	Ncoa3	INSIDE	1.168	6.635	13235.85	87819.52	7.746	8271.53	64074.80
A_68_P24119777	chr5:136646370-136646414	NM_178751:134	Orai2	INSIDE	1.168	2.450	2503.77	6134.38	2.861	2280.77	6526.27
A_68_P31626159	chr18:37091821-37091865	NM_198117:-7016	Pcdha2	PROMOTER	1.168	2.249	717.03	1612.58	2.627	574.12	1508.33
A_68_P31207759	chr17:46728766-46728810	NM_175168:37665	Ptk7	INSIDE	1.168	6.175	701.98	4334.54	7.211	650.35	4689.63
A_68_P20871442	chr1:181598207-181598251	NM_178653:-133	Sccpdh	PROMOTER	1.168	3.031	1098.04	3327.82	3.540	980.73	3472.20
A_68_P28726325	chr12:109417342-109417386	NM_028262:130	Setd3	INSIDE	1.168	4.935	671.05	3311.79	5.765	904.36	5213.30
A_68_P23437238	chr4:154596264-154596308	NM_011385:358	Ski	INSIDE	1.168	0.435	1575.44	684.98	0.508	1205.52	612.25
A_68_P27286997	chr10:80493927-80493971	NM_134135:2709	Slc39a3	INSIDE	1.168	2.052	1488.23	3054.04	2.396	1327.30	3180.33
A_68_P23694282	chr5:52759804-52759848	NM_011435:4784	Sod3	INSIDE	1.168	1.736	506.10	878.76	2.028	389.37	789.52
A_68_P25183831	chr7:72789891-72789935	NM_172310:129	Tarsl2	INSIDE	1.168	1.987	379.50	753.98	2.320	347.16	805.30
A_68_P25049869	chr7:36322564-36322608	NM_028034:177	Tdrd12	INSIDE	1.168	2.954	1133.07	3346.67	3.451	966.03	3333.35
A_68_P21394207	chr2:84555063-84555107	NM_144887:237	Zdhhc5	INSIDE	1.168	1.569	2698.58	4235.31	1.834	2214.63	4061.16
A_68_P26154270	chr8:111471142-111471186	NM_007496:232621	Zfhx3	INSIDE	1.168	2.752	1731.08	4763.11	3.214	1537.66	4941.51
A_68_P21844345	chr2:168780474-168780518	NM_009564:591	Zfp64	INSIDE	1.168	1.868	1000.90	1869.68	2.181	927.33	2022.89

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P24428352	chr6:48570342-48570386	NM_173429:7186	Zfp775	INSIDE	1.168	2.564	241.84	619.97	2.995	209.69	628.03
A_68_P26240063	A_68_P26240063			Unknown	1.168	2.955	629.58	1860.64	3.451	522.78	1804.31
A_68_P29625000	chr14:57484103-57484147	AK209334:-600		PROMOTER	1.168	1.832	1452.19	2660.45	2.140	1092.17	2337.65
A_68_P29090576	chr13:63066071-63066115	ENSMUST00000170896:-160		PROMOTER	1.168	5.055	1004.60	5078.19	5.903	870.98	5141.53
A_68_P22311243	chr3:87803866-87803910	NM_007529:390	Bcan	INSIDE	1.167	1.480	1001.50	1482.50	1.728	839.77	1451.22
A_68_P20561482	chr1:122238470-122238514	NM_207233:1334	C1ql2	INSIDE	1.167	2.067	2220.70	4589.35	2.412	1710.42	4125.26
A_68_P32670209	chrX:130594062-130594106	NM_133196:197	Cstf2	INSIDE	1.167	2.180	771.48	1681.60	2.545	479.05	1218.98
A_68_P28069094	chr11:100480931-100480975	NM_019795:530	Dnajc7	INSIDE	1.167	1.629	2233.29	3637.65	1.901	1724.85	3278.49
A_68_P26885391	chr9:121669059-121669103	NR_033503:-19	E530011L22Rik	DIVERGENT_PROMOTER	1.167	1.499	684.62	1026.23	1.749	664.94	1162.84
A_68_P21071367	chr2:25174641-25174685	NM_001177656:21	Grin1	INSIDE	1.167	0.389	1355.28	527.85	0.454	1194.69	542.84
A_68_P28152361	chr11:115119374-115119418	NM_010350:9161	Grin2c	INSIDE	1.167	2.191	1420.38	3111.90	2.557	1285.03	3285.26
A_68_P30339717	chr15:74630092-74630141	NM_029627:282	Ly6k	INSIDE	1.167	4.372	698.14	3052.55	5.103	564.33	2879.52
A_68_P24613352	chr6:86959758-86959802	NM_001170591:-49	Nfu1	PROMOTER	1.167	4.595	2845.89	13077.41	5.363	2377.80	12751.89
A_68_P28058395	chr11:98629793-98629837	NM_145434:6742	Nr1d1	INSIDE	1.167	3.396	1062.87	3609.55	3.962	842.93	3340.04
A_68_P28802627	chr13:6547373-6547417	NM_145131:-8	Pitrm1	PROMOTER	1.167	1.505	2063.02	3105.60	1.757	1640.16	2882.03
A_68_P26079046	chr8:97219612-97219656	NM_026385:508	Pllp	INSIDE	1.167	2.656	870.94	2313.17	3.099	776.48	2406.25
A_68_P25089777	chr7:52119118-52119162	NM_133949:6018	Ptov1	INSIDE	1.167	1.956	2459.03	4808.72	2.282	2127.62	4854.25
A_68_P28159202	chr11:116274533-116274577	NM_027258:-208	Rnf157	PROMOTER	1.167	1.474	1007.94	1485.30	1.720	877.84	1510.09
A_68_P31738728	chr18:58037843-58037887	NM_009194:-467	Slc12a2	PROMOTER	1.167	2.167	1231.22	2668.08	2.528	1280.23	3236.80
A_68_P24771682	chr6:115494959-115495004	NM_199033:260	Tsen2	INSIDE	1.167	2.768	405.89	1123.44	3.231	315.88	1020.68
A_68_P23334946	chr4:136194010-136194054	ENSMUST00000146123:15526		DOWNSTREAM	1.167	1.990	610.95	1215.51	2.322	582.43	1352.40
A_68_P22169031	chr3:58381260-58381314	NM_001040396:707	2810407C02Rik	INSIDE	1.166	1.598	622.06	993.85	1.863	477.32	889.12
A_68_P28182974	chr11:120050877-120050921	NR_030682:272	2810410L24Rik	INSIDE	1.166	7.043	915.25	6446.36	8.209	767.59	6301.25
A_68_P31925522	chr19:4867768-4867812	NM_013456:10094	Actn3	INSIDE	1.166	2.112	1914.48	4044.22	2.462	1467.45	3613.51
A_68_P24994775	chr7:20282050-20282094	NM_009696:2443	Apoe	INSIDE	1.166	2.448	987.41	2416.97	2.854	862.79	2461.98
A_68_P21754299	chr2:153171488-153171547	NM_001039939:-357	Asxl1	PROMOTER	1.166	3.197	254.38	813.28	3.726	235.13	876.21
A_68_P20740948	chr1:157820278-157820322	NM_001039184:85	Cep350	INSIDE	1.166	2.097	890.49	1866.95	2.444	902.34	2205.19
A_68_P25368311	chr7:107685728-107685772	NM_183270:137	Chchd8	INSIDE	1.166	2.320	1049.99	2435.87	2.704	1152.50	3116.64
A_68_P20166303	chr1:39593180-39593224	NM_028043:556	D1Bwg0212e	INSIDE	1.166	3.176	494.81	1571.64	3.703	461.40	1708.52
A_68_P20600406	chr1:130314008-130314052	NM_177445:-37	Dars	PROMOTER	1.166	2.678	1238.05	3315.33	3.122	990.98	3093.92
A_68_P33015610	chr1_random:49416-49460	NM_026866:135900	Disp1	INSIDE	1.166	2.435	569.47	1386.91	2.841	520.89	1479.79
A_68_P22872021	chr4:43512609-43512653	NM_001013377:-98	E130306D19Rik	DIVERGENT_PROMOTER	1.166	2.778	918.02	2550.20	3.240	772.64	2503.26
A_68_P27921506	chr11:74432896-74432940	NM_001013784:-188	E130309D14Rik	PROMOTER	1.166	1.844	1715.91	3164.87	2.150	1387.26	2982.81
A_68_P23278481	chr4:125826881-125826925	NM_172145:1656	Fam176b	INSIDE	1.166	1.424	2365.06	3367.83	1.660	1762.93	2926.81
A_68_P24544189	chr6:72848961-72849005	NM_019715:991	Kcmf1	INSIDE	1.166	1.930	716.29	1382.63	2.251	665.98	1498.86
A_68_P22344954	chr3:95463365-95463409	NM_008562:744	Mcl1	INSIDE	1.166	3.785	665.65	2519.18	4.411	643.65	2839.10
A_68_P31866306	chr18:80905336-80905380	NM_001164111:-446	Nfatc1	PROMOTER	1.166	2.099	1000.58	2100.11	2.448	951.49	2329.55
A_68_P29620064	chr14:56444394-56444438	NM_001168346:785	Nfatc4	INSIDE	1.166	1.624	956.60	1553.90	1.893	843.96	1597.94
A_68_P31442543	chr17:91487324-91487368	NM_020252:4796	Nrxn1	INSIDE	1.166	2.653	902.84	2395.25	3.093	789.77	2442.60
A_68_P27280128	chr10:79440201-79440245	NM_001003949:6853	ORF61	INSIDE	1.166	2.892	514.13	1486.75	3.371	469.56	1582.83
A_68_P23523156	chr5:20387967-20388011	NM_172992:-46	Phtf2	DIVERGENT_PROMOTER	1.166	2.800	509.68	1427.33	3.265	465.37	1519.46
A_68_P31375073	chr17:79420257-79420301	NM_001171004:-122	Prkd3	PROMOTER	1.166	1.924	901.90	1735.33	2.243	985.30	2210.25
A_68_P23308456	chr4:131375306-131375350	NM_001083119:18865	Ptpru	INSIDE	1.166	2.395	1070.24	2563.65	2.792	849.34	2371.43
A_68_P23301754	chr4:130219409-130219453	NM_001159603:157	Pum1	INSIDE	1.166	1.593	2943.81	4688.97	1.857	2433.48	4518.09
A_68_P27971356	chr11:83232242-83232286	NM_001013386:8691	Rasl10b	INSIDE	1.166	1.888	560.46	1058.16	2.202	505.04	1112.08
A_68_P23269838	chr4:124386319-124386363	NM_029157:-5764	Sf3a3	PROMOTER	1.166	2.270	1051.12	2385.68	2.645	923.29	2442.51
A_68_P28469868	chr12:60114568-60114612	NM_025656:211	Sip1	INSIDE	1.166	3.562	947.64	3375.86	4.154	750.96	3119.53
A_68_P23437240	chr4:154596449-154596493	NM_011385:174	Ski	INSIDE	1.166	3.145	1421.01	4469.39	3.668	1317.50	4832.49
A_68_P31190360	chr17:43766712-43766757	NM_001161366:514	Tdrd6	INSIDE	1.166	3.015	1388.38	4186.14	3.517	1101.66	3874.57
A_68_P29733539	chr14:76814024-76814068	NM_207652:-1581	Tsc22d1	PROMOTER	1.166	1.597	1582.73	2527.26	1.862	1241.80	2312.65
A_68_P21365113	chr2:78708721-78708765	NM_009454:-461	Ube2e3	PROMOTER	1.166	1.490	728.34	1085.41	1.737	674.61	1171.98

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27804989	chr11:53293020-53293064	NM_183173:655	Ankrd43	INSIDE	1.165	1.588	776.88	1233.52	1.849	718.72	1329.25
A_68_P26813124	chr9:108017763-108017807	NM_007567:74930	Bsn	INSIDE	1.165	2.238	593.78	1328.85	2.606	504.27	1314.23
A_68_P29265995	chr13:100670678-100670722	NM_001081493:-62	Cartpt	PROMOTER	1.165	1.491	1525.60	2274.37	1.736	1340.60	2327.63
A_68_P20148459	chr1:36529023-36529067	NM_033570:603	Cnnm4	INSIDE	1.165	1.785	745.44	1330.67	2.080	617.23	1283.54
A_68_P25394242	chr7:112911135-112911179	NM_001162943:24908	Dchs1	INSIDE	1.165	2.578	2574.72	6638.59	3.005	1994.20	5992.69
A_68_P26656976	chr9:77758360-77758404	NM_134255:-6789	Elovl5	PROMOTER	1.165	2.843	775.36	2204.73	3.313	719.40	2383.17
A_68_P26919702	chr10:7310204-7310248	NM_172784:629	Lrp11	INSIDE	1.165	2.684	499.30	1340.24	3.126	444.91	1390.92
A_68_P28744821	chr12:112813339-112813383	NM_021516:640	Mark3	INSIDE	1.165	0.486	1189.00	578.41	0.567	1016.12	575.83
A_68_P31827985	chr18:73975089-73975133	NM_145494:-64	Me2	PROMOTER	1.165	6.271	892.85	5598.90	7.304	890.11	6500.97
A_68_P28071734	chr11:100931359-100931403	NM_013792:-27	Naglu	PROMOTER	1.165	2.415	1017.05	2456.08	2.813	926.57	2606.71
A_68_P25953245	chr8:73183706-73183750	NM_023217:-148	Pgpep1	PROMOTER	1.165	1.716	7569.75	12989.11	1.998	5233.01	10458.06
A_68_P25265268	chr7:87343468-87343512	NM_013659:11764	Sema4b	INSIDE	1.165	4.737	898.99	4258.33	5.516	879.43	4851.20
A_68_P22963535	chr4:61947389-61947433	NM_025286:-68	Slc31a2	PROMOTER	1.165	2.140	906.91	1940.79	2.494	893.96	2229.65
A_68_P21556057	chr2:116947191-116947235	NM_033524:27	Spred1	INSIDE	1.165	3.570	303.39	1083.24	4.158	285.58	1187.43
A_68_P32775152	chrX:155971013-155971057	NM_001033472:435	A830080D01Rik	INSIDE	1.164	2.538	1217.05	3088.99	2.953	922.06	2722.95
A_68_P27285629	chr10:80269928-80269972	NM_007445:1958	Amh	INSIDE	1.164	1.844	717.78	1323.69	2.146	631.50	1355.50
A_68_P25372490	chr7:108450530-108450574	NM_001111111:50	Atg16l2	INSIDE	1.164	1.840	694.52	1277.58	2.141	577.71	1236.66
A_68_P22871971	chr4:43506143-43506188	NM_001037913:-71	Ccdc107	DIVERGENT_PROMOTER	1.164	3.292	448.35	1475.76	3.832	370.94	1421.41
A_68_P27303130	chr10:83997039-83997083	NM_175451:-427	Ckap4	PROMOTER	1.164	1.563	983.03	1536.56	1.820	841.91	1532.39
A_68_P29335933	chr13:113442449-113442493	NM_001145885:48	Ddx4	INSIDE	1.164	3.803	895.02	3403.52	4.425	799.64	3538.47
A_68_P25776099	chr8:35872603-35872647	NM_176933:1961	Dusp4	INSIDE	1.164	2.837	620.70	1760.80	3.303	563.63	1861.79
A_68_P26983899	chr10:19654713-19654757	NM_008580:403	Map3k5	INSIDE	1.164	2.398	3140.19	7531.51	2.792	2610.10	7287.64
A_68_P25025267	chr7:29871114-29871158	NR_035489:-2423	Mir1963	PROMOTER	1.164	3.748	884.50	3315.12	4.364	694.22	3029.26
A_68_P28790400	chr13:3892775-3892819	NM_001047159:28	Net1	INSIDE	1.164	1.641	540.23	886.63	1.911	477.41	912.36
A_68_P25846475	chr8:49362088-49362132	NM_001145937:397934	Odz3	INSIDE	1.164	2.003	587.65	1176.83	2.332	528.97	1233.48
A_68_P26018119	chr8:86618743-86618787	NM_009055:28030	Rfx1	INSIDE	1.164	2.584	763.92	1973.77	3.008	717.04	2156.87
A_68_P30425657	chr15:89354548-89354592	NM_021423:24283	Shank3	INSIDE	1.164	2.008	560.78	1126.20	2.337	621.33	1451.99
A_68_P28332009	chr12:32243915-32243959	NM_011867:898	Slc26a4	INSIDE	1.164	2.034	667.24	1356.89	2.366	587.76	1390.74
A_68_P28047897	chr11:96838592-96838636	NM_001080964:388	Sp2	INSIDE	1.164	4.326	886.05	3833.34	5.036	857.14	4316.19
A_68_P20886547	chr1:184339477-184339521	NM_173378:201	Trp53bp2	INSIDE	1.164	1.427	1103.43	1574.76	1.662	1022.68	1699.44
A_68_P24874649	chr6:136776165-136776209	NM_021714:551	Wbp11	INSIDE	1.164	1.634	1191.71	1947.50	1.902	999.15	1900.43
A_68_P20412363	chr1:88383877-88383921			Unknown	1.164	2.015	1185.95	2389.44	2.345	1015.60	2381.90
A_68_P32101745	chr19:38555886-38555930	ENSMUST00000158315:-8216		PROMOTER	1.164	1.605	1073.85	1723.43	1.869	895.69	1673.74
A_68_P24045560	chr5:122068966-122069010	NM_178799:-41	Acad12	PROMOTER	1.163	1.860	372.25	692.22	2.163	353.93	765.45
A_68_P21021376	chr2:14525863-14525907	NM_023116:-48	Cacnb2	PROMOTER	1.163	1.602	1155.81	1851.38	1.863	1025.78	1911.28
A_68_P32315763	chrX:33428723-33428767	NM_001009947:-82	Dock11	PROMOTER	1.163	2.910	459.91	1338.39	3.385	251.06	849.78
A_68_P26896523	chr9:123626629-123626673	NM_033322:25	Lztfl1	INSIDE	1.163	1.494	1426.66	2131.75	1.738	1060.48	1843.48
A_68_P24132966	chr5:139470282-139470326	NM_008808:603	Pdgfa	INSIDE	1.163	1.573	5580.03	8775.96	1.829	4162.00	7610.81
A_68_P28159703	chr11:116360161-116360205	NM_026364:-8522	Prpsap1	PROMOTER	1.163	1.550	1351.56	2094.93	1.802	1066.40	1922.01
A_68_P27045328	chr10:31328333-31328377	NM_001146349:1177	Rnf217	INSIDE	1.163	2.238	510.93	1143.60	2.604	475.56	1238.40
A_68_P25408486	chr7:116662855-116662899	NR_028079:-769	Snora3	PROMOTER	1.163	1.854	1941.16	3599.16	2.156	1582.30	3412.06
A_68_P21265074	chr2:61431520-61431564	NM_001164071:389	Tank	INSIDE	1.163	1.521	851.53	1295.35	1.768	729.75	1290.55
A_68_P25056438	chr7:37480533-37480577	NM_172298:-2582	Tshz3	PROMOTER	1.163	1.583	4047.07	6407.55	1.841	3162.14	5820.64
A_68_P29072113	chr13:58317002-58317046	NM_026842:-10	Ubqln1	PROMOTER	1.163	2.057	600.52	1235.01	2.391	547.77	1309.98
A_68_P28152749	chr11:115179633-115179677	NM_176847:3578	Ush1g	INSIDE	1.163	1.541	3067.01	4726.19	1.792	2464.29	4416.65
A_68_P21583235	chr2:121692691-121692735	NM_001205371:-728	Casc4	PROMOTER	1.162	2.770	373.35	1034.29	3.219	360.94	1162.01
A_68_P25672257	chr8:14096396-14096440	NM_001145965:544	Dlgap2	INSIDE	1.162	3.953	809.97	3202.12	4.595	729.25	3350.76
A_68_P28958812	chr13:38243505-38243549	NM_023842:364	Dsp	INSIDE	1.162	2.133	585.73	1249.13	2.478	505.13	1251.96
A_68_P20192817	chr1:44204965-44205009	NM_011729:398	Ercc5	INSIDE	1.162	2.004	1968.31	3943.75	2.328	1667.14	3880.40
A_68_P21582987	chr2:121632660-121632704	NM_172673:111	Frmd5	INSIDE	1.162	1.775	4081.34	7245.41	2.063	3367.87	6947.58
A_68_P28107590	chr11:107409081-107409125	NM_198298:-171	Helz	PROMOTER	1.162	1.765	2408.20	4251.53	2.051	2018.51	4139.88

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P20633482	chr1:136352339-136352383	NM_153128:229	Klhl12	INSIDE	1.162	1.746	576.39	1006.33	2.029	540.89	1097.33
A_68_P27284766	chr10:80139373-80139417	NM_021462:-4673	Mknk2	PROMOTER	1.162	0.489	1718.43	839.46	0.568	1357.70	770.68
A_68_P31478454	chr18:7626883-7626927	NM_001081287:-43	Mpp7	PROMOTER	1.162	1.478	1676.34	2477.40	1.717	1396.87	2398.57
A_68_P30083235	chr15:25711092-25711136	NM_019472:158810	Myo10	INSIDE	1.162	2.489	663.44	1651.06	2.892	565.16	1634.44
A_68_P24084799	chr5:129242041-129242085	NM_021311:-58	Piwil1	PROMOTER	1.162	2.744	1410.40	3870.44	3.188	1125.43	3587.53
A_68_P30513996	chr16:5132766-5132810	NM_008909:-214	Ppl	PROMOTER	1.162	1.562	909.88	1421.00	1.815	807.16	1464.79
A_68_P23538313	chr5:23289297-23289341	NM_178403:161	Pus7	INSIDE	1.162	1.354	1984.53	2687.86	1.574	1618.98	2548.35
A_68_P23993051	chr5:113005885-113005929	NM_019982:299	Sez6l	INSIDE	1.162	1.662	832.98	1384.55	1.932	762.18	1472.36
A_68_P23576449	chr5:31395933-31395977	NM_011773:-54	Slc30a3	PROMOTER	1.162	1.333	4714.24	6282.60	1.549	3547.57	5495.42
A_68_P27287686	chr10:80607070-80607114	NM_010731:8077	Zbtb7a	INSIDE	1.162	2.345	1634.05	3831.22	2.726	1251.88	3412.07
A_68_P25261702	chr7:86680581-86680625	ENSMUST00000141822:35600		DOWNSTREAM	1.162	2.394	1222.47	2926.70	2.783	1069.30	2975.58
A_68_P32538580	chrX:91612075-91612119	NM_026673:-352	Apoo	PROMOTER	1.161	1.776	931.76	1654.73	2.063	493.39	1017.63
A_68_P23350169	chr4:138748940-138748984	NM_001037761:69	Capzb	INSIDE	1.161	0.498	2606.24	1296.94	0.578	2247.46	1298.31
A_68_P26127991	chr8:106864790-106864834	NM_024217:319	Cmtm3	INSIDE	1.161	2.268	1053.71	2389.46	2.633	885.32	2331.31
A_68_P29578364	chr14:47407974-47408018	NM_009919:36	Cnih	INSIDE	1.161	0.594	2979.49	1769.89	0.690	2436.84	1681.31
A_68_P24158342	chr5:144578471-144578515	NM_013557:-168	Eif2ak1	PROMOTER	1.161	1.445	4526.62	6541.93	1.678	3554.32	5963.62
A_68_P26612669	chr9:69607113-69607157	NM_022378:1613	Foxb1	INSIDE	1.161	1.745	5516.67	9628.09	2.026	4452.61	9019.66
A_68_P26224602	chr8:123640403-123640447	NM_013519:354	Foxc2	INSIDE	1.161	1.785	647.47	1155.93	2.073	590.03	1223.19
A_68_P32823843	chrX:166435357-166435401	NM_183151:117825	Mid1	DOWNSTREAM	1.161	1.952	20431.29	39877.87	2.267	17302.79	39218.31
A_68_P21742433	chr2:150864640-150864699	NM_026086:446	Nanp	INSIDE	1.161	1.808	605.21	1094.50	2.100	547.92	1150.48
A_68_P32266421	chrX:13063192-13063236	NM_173415:18417	Nyx	INSIDE	1.161	1.926	755.79	1455.54	2.236	365.90	818.02
A_68_P21775756	chr2:157029918-157029962	NM_011249:330	Rbl1	INSIDE	1.161	1.688	1073.55	1812.10	1.960	892.77	1750.20
A_68_P23405236	chr4:149655404-149655448	NM_001085492:-598	Rere	PROMOTER	1.161	3.151	649.22	2045.76	3.659	603.89	2209.74
A_68_P25050061	chr7:36370407-36370451	NM_145840:173	Rgs9bp	INSIDE	1.161	1.472	671.23	988.26	1.710	564.62	965.42
A_68_P30465077	chr15:96529839-96529883	NM_175121:269	Slc38a2	INSIDE	1.161	1.661	1754.43	2914.12	1.929	1551.69	2992.48
A_68_P20005795	chr1:4482172-4482216	NM_011441:4300	Sox17	INSIDE	1.161	1.784	876.78	1564.43	2.072	771.57	1598.41
A_68_P31752325	chr18:60755946-60755990	NM_177340:27991	Synpo	INSIDE	1.161	1.988	453.13	900.73	2.308	358.69	827.98
A_68_P23416140	chr4:151406689-151406733	NM_031867:5889	Tas1r1	INSIDE	1.161	2.454	1721.04	4222.81	2.848	1236.85	3523.10
A_68_P29048726	chr13:54398661-54398705	AK086128:102013		DOWNSTREAM	1.161	2.343	1399.89	3279.85	2.719	1321.84	3594.11
A_68_P23425242	chr4:152856847-152856891	NM_001099299:71	Ajap1	INSIDE	1.160	1.544	554.00	855.46	1.791	480.57	860.66
A_68_P23210414	chr4:111087603-111087647	NM_026279:14	Bend5	INSIDE	1.160	2.318	2336.90	5416.06	2.688	1735.98	4665.75
A_68_P24093838	chr5:130925235-130925279	NM_021371:595	Caln1	INSIDE	1.160	1.977	954.06	1886.18	2.294	859.31	1971.33
A_68_P30459324	chr15:95485068-95485112	NM_207533:112	Dbx2	INSIDE	1.160	1.935	1460.66	2826.98	2.245	1208.85	2714.17
A_68_P32651795	chrX:126284318-126284362	NM_172493:63	Diap2	INSIDE	1.160	1.606	1484.43	2384.13	1.864	720.63	1343.02
A_68_P29250235	chr13:98010886-98010930	NM_007930:-151	Enc1	PROMOTER	1.160	2.613	1346.21	3517.81	3.032	1206.68	3659.00
A_68_P20441864	chr1:93242302-93242346	NM_001033292:23673	Espnl	INSIDE	1.160	1.865	373.50	696.57	2.163	298.95	646.52
A_68_P26617706	chr9:70505115-70505159	NM_172772:-155	Fam63b	PROMOTER	1.160	4.001	1407.09	5629.81	4.640	1348.15	6256.02
A_68_P31936818	chr19:7015888-7015932	NM_001177360:-227	Gpr137	PROMOTER	1.160	0.476	1920.49	914.03	0.552	1627.59	898.76
A_68_P21680297	chr2:139504517-139504561	NM_001126490:625	Ism1	INSIDE	1.160	2.306	530.37	1223.07	2.675	493.09	1318.92
A_68_P21074761	chr2:25733684-25733728	NM_175462:326	Kcnt1	INSIDE	1.160	1.958	764.40	1496.40	2.270	584.33	1326.47
A_68_P27767869	chr11:46250544-46250588	NM_001104556:104	Med7	INSIDE	1.160	1.894	1120.01	2121.24	2.198	862.62	1895.61
A_68_P27922353	chr11:74584217-74584261	NM_026197:-126	Mettl16	PROMOTER	1.160	1.855	2512.12	4659.88	2.153	1995.23	4294.96
A_68_P32774619	chrX:155852596-155852640	NM_001081124:109	Mtap7d2	INSIDE	1.160	2.861	1001.79	2866.21	3.319	714.12	2369.83
A_68_P24992918	chr7:19955528-19955572	NM_001010836:8986	Ppp1r13l	INSIDE	1.160	1.914	985.22	1885.39	2.220	877.85	1948.64
A_68_P28058848	chr11:98698706-98698750	NM_001080925:630	Rapgefl1	INSIDE	1.160	1.437	1326.86	1906.16	1.666	1019.99	1699.69
A_68_P28037688	chr11:95120636-95120680	NM_053093:-2184	Tac4	PROMOTER	1.160	1.579	845.68	1335.31	1.831	730.18	1337.12
A_68_P29095533	chr13:63916826-63916870	NM_023507:207	0610007P08Rik	INSIDE	1.159	2.493	997.04	2485.63	2.888	929.73	2685.42
A_68_P30404613	chr15:85862950-85862994	NM_009886:1235	Celsr1	INSIDE	1.159	3.177	1485.04	4717.54	3.680	1245.53	4584.13
A_68_P22649277	chr3:151872936-151872980	NM_027287:305	Dnajb4	INSIDE	1.159	2.736	1124.88	3077.72	3.171	1025.47	3252.22
A_68_P26137129	chr8:108503182-108503226	NM_027960:115	Dpep3	INSIDE	1.159	6.067	6485.20	39344.93	7.029	4215.29	29628.86
A_68_P25592947	chr7:149281374-149281418	NM_008748:-207	Dusp8	PROMOTER	1.159	1.443	3302.17	4763.96	1.672	2564.44	4286.69

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P24131504	chr5:139231132-139231176	NM_030565:120	Fam20c	INSIDE	1.159	1.484	1863.85	2765.61	1.719	1547.42	2660.61
A_68_P28940417	chr13:34839281-34839325	NM_138746:7792	Fam50b	INSIDE	1.159	2.694	1092.47	2942.64	3.122	872.89	2725.40
A_68_P28558330	chr12:78339604-78339648	NM_016893:-381	Fut8	PROMOTER	1.159	1.710	622.26	1064.14	1.982	558.95	1107.99
A_68_P23417713	chr4:151657232-151657276	NM_178406:8784	Gpr153	INSIDE	1.159	1.729	995.04	1720.92	2.005	855.70	1715.49
A_68_P26991381	chr10:20879458-20879502	NM_001198914:1310	Myb	INSIDE	1.159	2.304	1496.69	3448.80	2.672	2098.36	5605.77
A_68_P25088768	chr7:51924794-51924838	NM_028021:-3943	Myh14	PROMOTER	1.159	3.492	1828.66	6386.37	4.048	1540.49	6236.61
A_68_P32147200	chr19:47089737-47089781	NM_001164363:-79	Nt5c2	PROMOTER	1.159	4.456	652.74	2908.64	5.164	608.74	3143.35
A_68_P24464318	chr6:54545243-54545287	NM_001001335:-7876	Plekha8	PROMOTER	1.159	3.022	388.51	1174.15	3.503	345.22	1209.42
A_68_P27646888	chr11:23565964-23566008	NM_028304:11	Pus10	INSIDE	1.159	1.528	906.17	1384.92	1.771	795.22	1408.44
A_68_P23538314	chr5:23289429-23289473	NM_178403:29	Pus7	INSIDE	1.159	0.492	2412.81	1186.80	0.570	1999.98	1139.89
A_68_P31096075	chr17:24345873-24345917	NM_001163847:-3387	Tbc1d24	PROMOTER	1.159	2.273	1696.78	3856.21	2.633	1542.43	4061.20
A_68_P23416613	chr4:151490095-151490139	NM_033042:-335	Tnfrsf25	PROMOTER	1.159	2.088	1440.34	3006.97	2.420	1165.13	2819.27
A_68_P24153998	chr5:143668502-143668546	NM_007393:-121	Actb	PROMOTER	1.158	1.736	1188.70	2063.87	2.011	986.52	1983.81
A_68_P27899598	chr11:70044019-70044063	NM_007528:-740	Bcl6b	DIVERGENT_PROMOTER	1.158	2.917	691.45	2016.72	3.378	604.63	2042.55
A_68_P30567430	chr16:15887377-15887421	NM_007679:20	Cebpd	INSIDE	1.158	1.751	3930.87	6882.25	2.028	3060.61	6207.85
A_68_P30981937	chr16:94748428-94748472	NM_007834:-214	Dscr3	PROMOTER	1.158	1.942	755.82	1467.54	2.248	708.23	1591.80
A_68_P25565283	chr7:144514346-144514390	NM_001113414:-8240	Ebf3	PROMOTER	1.158	1.540	850.97	1310.83	1.784	787.12	1404.50
A_68_P30345479	chr15:75839800-75839844	NM_001168253:106	Fam83h	INSIDE	1.158	4.882	1616.96	7894.66	5.655	1461.34	8264.06
A_68_P31099059	chr17:24832929-24832973	NM_023040:151	Gfer	INSIDE	1.158	2.092	392.30	820.80	2.423	319.25	773.47
A_68_P29138631	chr13:73398065-73398109	NM_018885:142	Irx4	INSIDE	1.158	2.495	449.44	1121.21	2.889	488.88	1412.60
A_68_P31936764	chr19:7008234-7008278	NM_008431:749	Kcnk4	INSIDE	1.158	2.114	2046.22	4325.38	2.449	1656.81	4057.10
A_68_P27897675	chr11:69694588-69694632	NM_153143:-123	Kctd11	PROMOTER	1.158	1.503	1277.15	1919.13	1.740	1213.74	2112.29
A_68_P32281788	chrX:17740669-17740713	NM_009483:898	Kdm6a	INSIDE	1.158	0.413	1681.79	694.05	0.478	773.20	369.41
A_68_P26017626	chr8:86535448-86535492	NR_035431:62	Mir1199	INSIDE	1.158	3.710	1220.15	4526.23	4.295	1066.78	4581.71
A_68_P26610634	chr9:69245687-69245731	NM_145618:-96	Narg2	PROMOTER	1.158	3.492	373.65	1304.78	4.044	363.11	1468.53
A_68_P31938622	chr19:7280556-7280600	NM_134150:196	Otub1	INSIDE	1.158	1.461	1112.23	1625.01	1.692	1141.24	1931.34
A_68_P22774300	chr4:21606032-21606076	NM_001080771:7056	Prdm13	INSIDE	1.158	3.298	558.32	1841.30	3.818	482.94	1844.03
A_68_P21086001	chr2:27532393-27532437	NM_011305:-306	Rxra	PROMOTER	1.158	0.528	1452.89	766.40	0.611	1215.90	742.78
A_68_P32126392	chr19:43502033-43502077			Unknown	1.158	3.022	746.70	2256.29	3.500	628.86	2200.90
A_68_P32473671	chrX:73211910-73211954	ENSMUST00000121090:-7625		PROMOTER	1.158	2.230	1777.83	3965.40	2.582	726.23	1875.48
A_68_P23195470	chr4:108000920-108000964	NM_027250:186	2010305A19Rik	INSIDE	1.157	1.465	5344.99	7832.16	1.696	3928.29	6662.37
A_68_P30475044	chr15:98364664-98364708	NM_133714:-34	2310037I24Rik	PROMOTER	1.157	1.404	1906.96	2678.06	1.625	1780.35	2893.71
A_68_P31103782	chr17:25570573-25570617	NM_001163691:134	Cacna1h	INSIDE	1.157	2.787	623.68	1737.90	3.225	543.74	1753.39
A_68_P21021384	chr2:14526701-14526745	NM_023116:790	Cacnb2	INSIDE	1.157	1.420	2744.64	3898.10	1.644	2168.95	3564.77
A_68_P30978138	chr16:93883923-93883967	NM_028083:-201	Chaf1b	PROMOTER	1.157	2.705	2183.38	5906.71	3.131	1634.23	5116.40
A_68_P22729161	chr4:11249125-11249169	NM_001081201:132	Dpy19l4	INSIDE	1.157	1.628	735.55	1197.84	1.884	634.65	1195.85
A_68_P31252967	chr17:56095790-56095834	NM_015766:3767	Ebi3	INSIDE	1.157	2.913	618.38	1801.32	3.369	543.91	1832.44
A_68_P25328176	chr7:100228697-100228741	NM_021427:330	Fam181b	INSIDE	1.157	2.624	2630.72	6902.01	3.035	2185.13	6631.03
A_68_P23546246	chr5:24728813-24728857	NM_144908:124	Galnt11	INSIDE	1.157	2.125	443.46	942.42	2.459	446.08	1096.73
A_68_P28091896	chr11:104469667-104469711	NM_016780:375	Itgb3	INSIDE	1.157	2.102	2504.57	5263.47	2.432	2020.52	4913.52
A_68_P22686351	chr3:158224713-158224757	NM_001081358:451	Lrrc7	INSIDE	1.157	0.399	1406.49	561.65	0.462	1064.24	491.81
A_68_P25169129	chr7:69564808-69564852	NM_011746:195	Mkrn3	INSIDE	1.157	2.341	1013.95	2373.88	2.710	832.69	2256.34
A_68_P32266423	chrX:13063488-13063532	NM_173415:18713	Nyx	INSIDE	1.157	4.248	599.53	2546.75	4.914	483.60	2376.30
A_68_P24832848	chr6:127403924-127403968	NM_181402:206	Parp11	INSIDE	1.157	1.601	1326.84	2124.07	1.851	1212.37	2244.69
A_68_P22101766	chr3:45184223-45184267	NM_011043:1925	Pcdh10	INSIDE	1.157	1.610	981.14	1579.28	1.862	738.83	1375.94
A_68_P24479719	chr6:57641697-57641742	NM_025574:353	Pigy	INSIDE	1.157	2.388	1735.35	4144.24	2.763	1623.52	4485.24
A_68_P30377510	chr15:81191319-81191363	NM_011399:-145	Slc25a17	PROMOTER	1.157	0.517	1028.75	532.34	0.599	806.35	482.61
A_68_P25016939	chr7:28149566-28149610	NM_001199235:29937	Spnb4	INSIDE	1.157	2.209	701.16	1548.84	2.556	605.31	1546.98
A_68_P31175211	A_68_P31175211			Unknown	1.157	6.601	10784.75	71187.93	7.637	7274.03	55553.92
A_68_P31498901	chr18:12279785-12279829	NM_178801:156	6030446N20Rik	INSIDE	1.156	2.003	2839.72	5686.95	2.315	2295.22	5313.65
A_68_P22682766	chr3:157610204-157610248	NM_001013806:-203	Ankrd13c	PROMOTER	1.156	2.091	542.69	1134.73	2.416	546.11	1319.62

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P30533733	chr16:8672342-8672386	NM_025821:-118	Carhsp1	PROMOTER	1.156	2.730	1314.80	3588.98	3.155	1185.90	3741.36
A_68_P29976942	chr15:3929549-3929593	NM_134099:3	Fbxo4	INSIDE	1.156	3.256	1137.38	3703.72	3.764	950.74	3578.57
A_68_P32104291	chr19:39005160-39005205	NM_008234:-297	Hells	PROMOTER	1.156	1.515	759.51	1150.45	1.751	671.56	1175.95
A_68_P21339338	chr2:74590901-74590945	NM_010468:40873	Hoxd3	DOWNSTREAM	1.156	2.826	221.94	627.30	3.268	213.91	699.14
A_68_P27971658	chr11:83276246-83276290	NM_080453:195	Mmp28	INSIDE	1.156	2.247	567.02	1274.19	2.597	502.23	1304.47
A_68_P20237359	chr1:54614549-54614593	NM_001163314:-44	Pgap1	PROMOTER	1.156	1.681	1484.85	2495.30	1.942	1145.74	2225.53
A_68_P23794549	chr5:73305228-73305272	NM_001113423:-305	Slain2	PROMOTER	1.156	1.579	1282.97	2025.55	1.825	1051.06	1918.03
A_68_P23278183	chr4:125781499-125781543	NM_001145827:320	Stk40	INSIDE	1.156	0.471	1316.57	619.55	0.544	1027.19	558.54
A_68_P22039928	chr3:32716452-32716496	NM_001013024:-73	Usp13	PROMOTER	1.156	1.465	870.46	1274.93	1.693	669.07	1132.52
A_68_P26257412	chr8:128946745-128946789	NM_174987:366	1810063B05Rik	INSIDE	1.155	2.405	681.37	1638.65	2.777	568.60	1578.98
A_68_P28534553	chr12:74018698-74018742	NM_029444:32	4930447C04Rik	INSIDE	1.155	3.989	7108.18	28356.46	4.609	5976.23	27542.38
A_68_P23542800	chr5:24082936-24082980	NM_001190443:327	Abcf2	INSIDE	1.155	0.589	1560.59	919.10	0.680	1203.93	818.89
A_68_P28745653	chr12:112951441-112951485	NM_027404:5	Bag5	INSIDE	1.155	1.726	982.62	1696.40	1.994	868.71	1731.79
A_68_P28731506	chr12:110272427-110272471	NM_001163175:33979	Begain	INSIDE	1.155	2.366	1683.56	3983.20	2.733	1420.80	3883.43
A_68_P29056138	chr13:55724621-55724665	NM_007596:277	Caml	INSIDE	1.155	2.478	1255.29	3110.73	2.862	1096.60	3138.88
A_68_P21958960	chr3:14886530-14886574	NM_009801:127	Car2	INSIDE	1.155	1.353	2604.46	3524.53	1.563	2263.90	3537.82
A_68_P24818640	chr6:125046428-125046472	NM_145979:270	Chd4	INSIDE	1.155	1.801	701.15	1263.00	2.080	738.31	1535.56
A_68_P26885385	chr9:121668453-121668497	NR_033503:587	E530011L22Rik	INSIDE	1.155	1.646	856.34	1409.34	1.900	669.58	1272.38
A_68_P32397419	chrX:53984962-53985006	NM_001077361:-149	Fhl1	PROMOTER	1.155	3.065	1977.99	6062.99	3.541	1065.91	3773.98
A_68_P28099479	chr11:105946314-105946358	NM_011947:121	Map3k3	INSIDE	1.155	1.514	1454.11	2200.96	1.749	1247.97	2182.65
A_68_P21630447	chr2:130390003-130390047	NM_207207:532	Mrps26	INSIDE	1.155	3.831	1830.39	7011.35	4.426	1511.55	6690.00
A_68_P32066442	chr19:31838948-31838992	NM_001013833:553	Prkg1	INSIDE	1.155	2.084	5310.62	11069.05	2.408	3956.50	9525.71
A_68_P31256043	chr17:56567276-56567320	NM_011218:48605	Ptprs	INSIDE	1.155	3.724	3535.54	13167.54	4.301	2675.37	11505.97
A_68_P27165504	chr10:58275815-58275859	NM_172788:-270	Sh3rf3	PROMOTER	1.155	0.536	969.40	519.69	0.619	859.35	532.21
A_68_P25409835	chr7:116895803-116895847	NM_020050:-47	Tmem9b	PROMOTER	1.155	1.829	513.43	938.86	2.111	423.64	894.50
A_68_P21936415	chr3:9251283-9251327	NM_177660:738	Zbtb10	INSIDE	1.155	3.331	869.86	2897.25	3.848	782.06	3009.73
A_68_P31841471	chr18:76305627-76305671	NM_145356:325817	Zbtb7c	INSIDE	1.155	2.249	566.33	1273.67	2.598	495.76	1288.20
A_68_P23416422	chr4:151460754-151460798	ENSMUST00000118648:-190		PROMOTER	1.155	2.205	765.62	1688.31	2.548	701.03	1786.12
A_68_P32410982	chrX:56820979-56821023	ENSMUST00000145767:-2		PROMOTER	1.155	1.591	1587.32	2525.98	1.839	819.86	1507.50
A_68_P31791928	chr18:67609055-67609099	NM_027130:-286	Afg3l2	PROMOTER	1.154	5.143	12828.58	65972.89	5.933	8047.74	47750.72
A_68_P23763013	chr5:67009680-67009724	NM_009686:208	Apbb2	INSIDE	1.154	2.668	730.51	1948.79	3.079	625.01	1924.45
A_68_P23237353	chr4:117599338-117599382	NM_009711:3008	Artn	INSIDE	1.154	2.737	650.07	1779.35	3.159	563.57	1780.24
A_68_P32397416	chrX:53984482-53984526	NM_010211:-459	Fhl1	PROMOTER	1.154	2.692	598.90	1612.02	3.106	371.04	1152.36
A_68_P25189681	chr7:73834635-73834679	NM_001191001:-118	Lins	DIVERGENT_PROMOTER	1.154	2.834	1821.77	5162.80	3.271	1294.19	4233.66
A_68_P24444194	chr6:51382876-51382920	NM_010903:230	Nfe2l3	INSIDE	1.154	1.555	2333.32	3627.26	1.794	1802.04	3233.76
A_68_P30346600	chr15:76010013-76010057	NM_201394:16106	Plec	INSIDE	1.154	3.116	695.31	2166.92	3.597	533.84	1920.38
A_68_P31152721	chr17:34341412-34341456	NM_011530:11	Tap2	INSIDE	1.154	1.589	558.74	887.67	1.833	495.39	907.98
A_68_P21084955	chr2:27331406-27331450	NM_001113573:-235	Brd3	PROMOTER	1.153	2.112	683.68	1444.11	2.435	654.59	1593.77
A_68_P26317082	chr9:14185179-14185223	NM_028013:486	Endod1	INSIDE	1.153	1.726	1018.61	1757.62	1.989	889.30	1769.04
A_68_P24154218	chr5:143723570-143723614	NM_007984:1559	Fscn1	INSIDE	1.153	1.589	527.00	837.53	1.832	385.81	706.67
A_68_P27280645	chr10:79516852-79516896	NM_001037741:93	Gpx4	INSIDE	1.153	6.485	420.35	2725.92	7.474	416.77	3115.07
A_68_P25770032	chr8:34763961-34764005	NM_010344:273	Gsr	INSIDE	1.153	4.055	2576.34	10447.66	4.676	2207.67	10323.87
A_68_P32820568	chrX:165758296-165758340	NM_008222:-43	Hccs	PROMOTER	1.153	2.079	470.76	978.51	2.397	273.15	654.67
A_68_P31876422	chr18:82644757-82644801	NM_001025245:264	Mbp	INSIDE	1.153	2.947	1321.25	3894.28	3.398	1102.20	3744.89
A_68_P20354530	chr1:75500243-75500287	NM_178884:2763	Obsl1	INSIDE	1.153	2.068	1461.22	3022.31	2.384	1186.06	2827.44
A_68_P30346578	chr15:76007226-76007270	NM_201394:18892	Plec	INSIDE	1.153	2.602	1583.85	4121.26	3.001	1283.60	3852.48
A_68_P25586915	chr7:148317107-148317151	NM_013782:-56	Ptdss2	PROMOTER	1.153	1.639	1023.62	1678.04	1.891	823.34	1556.71
A_68_P27190661	chr10:62801691-62801735	NM_001159590:31	Sirt1	INSIDE	1.153	1.703	1161.69	1978.28	1.963	884.11	1735.58
A_68_P30580600	chr16:18586533-18586577	NM_011532:508	Tbx1	INSIDE	1.153	1.395	1737.24	2423.83	1.608	1351.56	2173.74
A_68_P20228140	chr1:52687403-52687448	NM_001142647:-123	Tmem194b	PROMOTER	1.153	1.901	1178.02	2239.49	2.192	1077.49	2362.21
A_68_P23440602	chr4:155158465-155158509	NM_001033394:1497	Tmem88b	INSIDE	1.153	1.632	988.17	1612.51	1.881	909.92	1711.80

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P23984844	chr5:111706164-111706208	NM_024477:397365	Ttc28	INSIDE	1.153	2.010	1297.30	2606.94	2.317	987.23	2287.64
A_68_P23409800	chr4:150431562-150431606	NM_009498:478	Vamp3	INSIDE	1.153	1.425	1745.14	2486.69	1.643	1553.07	2551.70
A_68_P27863350	chr11:63892884-63892928	NM_178379:68	Cox10	INSIDE	1.152	0.551	1745.95	962.02	0.635	1551.37	985.07
A_68_P30106581	chr15:30102269-30102313	NM_008729:-57	Ctnnd2	PROMOTER	1.152	1.929	560.44	1080.84	2.221	541.42	1202.42
A_68_P31830235	chr18:74376174-74376218	NM_028868:331	Cxxc1	INSIDE	1.152	0.571	1521.91	868.85	0.658	1252.81	824.05
A_68_P28075716	chr11:101646089-101646133	NM_008815:514	Etv4	INSIDE	1.152	1.778	1326.32	2358.77	2.049	1114.10	2282.99
A_68_P31129059	chr17:29797809-29797853	NM_028791:285	Ftsjd2	INSIDE	1.152	8.814	1656.89	14604.27	10.155	1605.52	16303.57
A_68_P28080759	chr11:102527010-102527054	NM_001127576:131	Gm1564	INSIDE	1.152	2.624	1077.03	2825.96	3.023	1089.15	3292.33
A_68_P31114981	chr17:27340635-27340679	NM_146075:727	Lemd2	INSIDE	1.152	1.503	615.33	924.93	1.732	482.80	836.27
A_68_P21147646	chr2:38207402-38207446	NM_010710:597	Lhx2	INSIDE	1.152	1.841	1141.04	2100.71	2.121	958.31	2032.12
A_68_P27787407	chr11:50038771-50038815	NM_145926:-44	Mgat4b	PROMOTER	1.152	3.262	814.85	2658.43	3.757	726.36	2728.77
A_68_P22747170	chr4:14753655-14753699	NM_152812:58	Otud6b	INSIDE	1.152	1.698	514.41	873.62	1.957	368.39	720.91
A_68_P22825737	chr4:33296673-33296717	NM_177774:729	Srsf12	INSIDE	1.152	1.580	1188.05	1876.62	1.820	924.49	1682.97
A_68_P31206911	chr17:46582449-46582493	NM_001162864:42154	Ttbk1	INSIDE	1.152	2.193	1789.25	3924.04	2.526	1399.77	3536.41
A_68_P21839206	chr2:167875978-167876022			Unknown	1.152	1.581	1258.23	1989.21	1.821	1086.28	1978.20
A_68_P26215510	chr8:122223902-122223946	NM_026922:16	Atp2c2	INSIDE	1.151	2.071	535.12	1108.12	2.383	438.83	1045.53
A_68_P27534326	chr10:126603018-126603062	NM_027739:154	B4galnt1	INSIDE	1.151	3.016	1466.51	4423.32	3.473	1157.42	4019.34
A_68_P28198046	chr12:3982083-3982127	NM_001082483:56811	Efr3b	INSIDE	1.151	3.068	3248.42	9965.24	3.532	2458.78	8684.08
A_68_P21874508	chr2:174124774-174124818	NM_201617:1437	Gnas	INSIDE	1.151	3.335	2389.18	7967.92	3.838	1975.22	7580.59
A_68_P28529997	chr12:73171347-73171391	NM_181752:610	Gpr135	INSIDE	1.151	1.732	1530.24	2650.15	1.994	1318.66	2629.36
A_68_P23812527	chr5:76374231-76374275	NM_010612:201	Kdr	INSIDE	1.151	1.548	795.11	1231.04	1.782	694.36	1237.52
A_68_P30127461	chr15:34168406-34168450	NM_033521:648	Laptm4b	INSIDE	1.151	2.387	1148.37	2741.12	2.747	1087.40	2987.28
A_68_P23264337	chr4:123364300-123364344	NM_001199136:-2719	Macf1	PROMOTER	1.151	2.167	353.42	765.78	2.494	283.89	708.15
A_68_P27287761	chr10:80616838-80616882	NM_021501:13605	Pias4	INSIDE	1.151	3.003	2071.67	6220.81	3.458	1748.95	6047.29
A_68_P27385038	chr10:98569722-98569766	NM_027740:-60	Poc1b	PROMOTER	1.151	1.788	601.13	1075.03	2.059	609.33	1254.53
A_68_P23440604	chr4:155158617-155158661	NM_001033394:1345	Tmem88b	INSIDE	1.151	1.362	2051.50	2794.00	1.568	1740.74	2729.08
A_68_P25842775	chr8:48732135-48732179			Unknown	1.151	2.042	369.10	753.62	2.350	367.87	864.34
A_68_P22150498	chr3:54719703-54719747	NM_177854:85	6030405A18Rik	INSIDE	1.150	1.446	1113.81	1610.68	1.663	916.62	1524.09
A_68_P20241449	chr1:55419481-55419525	NM_001113367:49	Boll	INSIDE	1.150	1.747	682.79	1193.15	2.010	583.53	1172.82
A_68_P24046889	chr5:122302699-122302743	NM_175474:3684	Fam109a	INSIDE	1.150	2.068	362.88	750.40	2.379	270.56	643.62
A_68_P27088635	chr10:41023104-41023148	NM_133999:-79	Fig4	PROMOTER	1.150	1.517	1590.68	2413.02	1.744	1381.33	2408.82
A_68_P23968414	chr5:108150872-108150916	NM_010278:2469	Gfi1	INSIDE	1.150	2.940	832.39	2447.48	3.382	726.42	2456.58
A_68_P26891187	chr9:122656143-122656187	NM_001199736:-299	Gm9524	PROMOTER	1.150	2.222	872.48	1938.92	2.555	708.56	1810.08
A_68_P26345743	chr9:20966106-20966150	NM_183408:-4029	Pde4a	PROMOTER	1.150	2.230	951.45	2121.40	2.565	804.78	2064.01
A_68_P30369712	chr15:79843045-79843089	NM_011057:2172	Pdgfb	INSIDE	1.150	2.543	1051.94	2674.89	2.924	878.09	2567.18
A_68_P30346548	chr15:76003699-76003743	NM_201394:22420	Plec	INSIDE	1.150	2.013	1564.84	3150.25	2.315	1141.32	2642.48
A_68_P24085130	chr5:129287884-129287928	NM_001081388:171331	Rimbp2	INSIDE	1.150	1.834	1114.28	2043.87	2.110	882.95	1863.05
A_68_P26845374	chr9:114472361-114472405	NM_001042503:1105	Trim71	INSIDE	1.150	1.412	1198.14	1691.77	1.624	945.59	1536.07
A_68_P23297753	chr4:129318253-129318297	NM_001005506:-225	Txlna	PROMOTER	1.150	0.526	2103.56	1106.73	0.605	1736.42	1050.79
A_68_P24540295	chr6:72139369-72139413			Unknown	1.150	2.265	2184.93	4948.60	2.605	1735.39	4520.00
A_68_P28183973	chr11:120211378-120211422	NR_038126:1409	0610009L18Rik	INSIDE	1.149	1.619	434.50	703.53	1.861	401.51	747.19
A_68_P25505914	chr7:134656178-134656222	NR_024331:183	1700008J07Rik	INSIDE	1.149	1.740	2414.76	4202.83	1.999	1954.02	3906.12
A_68_P21706322	chr2:144096823-144096872	NM_028984:77	8430406I07Rik	INSIDE	1.149	1.735	745.56	1293.37	1.993	638.65	1273.05
A_68_P28075091	chr11:101527015-101527059	NM_025404:182	Arl4d	INSIDE	1.149	1.538	1562.43	2402.64	1.767	1382.73	2443.16
A_68_P21907945	chr2:180763668-180763712	NM_015730:10192	Chrna4	INSIDE	1.149	4.048	1725.01	6982.32	4.649	1162.89	5406.42
A_68_P23200238	chr4:108953316-108953360	NM_007943:459	Eps15	INSIDE	1.149	2.136	675.25	1442.32	2.454	644.64	1581.66
A_68_P30988899	chr16:95923500-95923544	NM_011809:-491	Ets2	PROMOTER	1.149	2.001	716.67	1434.05	2.298	614.74	1412.93
A_68_P20553862	chr1:120733925-120733969	NM_001081125:216250	Gli2	INSIDE	1.149	3.651	1064.38	3885.94	4.196	797.16	3344.76
A_68_P27278161	chr10:79132524-79132568	NM_148934:392	Gm16517	INSIDE	1.149	1.454	1137.15	1653.78	1.671	961.73	1607.37
A_68_P31829405	chr18:74223815-74223859	NM_172632:767	Mapk4	INSIDE	1.149	1.704	1577.83	2689.19	1.959	1325.20	2596.28
A_68_P28058593	chr11:98657535-98657579	NM_028722:474	Msl1	INSIDE	1.149	0.547	1212.22	662.73	0.628	1001.63	629.01

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P22278907	chr3:82162344-82162388	NM_001081230:373	Mtap9	INSIDE	1.149	1.687	2298.93	3877.82	1.939	1837.89	3562.99
A_68_P24758829	chr6:113276600-113276644	NM_010957:-347	Ogg1	PROMOTER	1.149	0.467	1435.35	669.83	0.536	1065.39	571.35
A_68_P25354129	chr7:105293827-105293871	NM_011010:109	Omp	INSIDE	1.149	2.062	480.69	991.22	2.370	372.61	882.90
A_68_P30346547	chr15:76003595-76003639	NM_201394:22524	Plec	INSIDE	1.149	2.174	969.23	2107.08	2.498	679.40	1696.82
A_68_P25406005	chr7:116226702-116226746	NM_001038624:114	Ric3	INSIDE	1.149	1.974	926.07	1827.95	2.267	797.64	1808.44
A_68_P23467999	chr5:8423016-8423060	NM_178766:189	Slc25a40	INSIDE	1.149	1.835	449.82	825.36	2.108	413.55	871.65
A_68_P20172913	chr1:40738293-40738337	NM_001033289:-242	Slc9a2	PROMOTER	1.149	2.329	495.35	1153.59	2.677	517.14	1384.28
A_68_P21330558	chr2:73115586-73115630	NM_001005343:5626	Sp9	DOWNSTREAM	1.149	2.730	397.69	1085.74	3.136	382.48	1199.60
A_68_P24760943	chr6:113647199-113647243	NM_001033463:-272	Tatdn2	PROMOTER	1.149	1.568	642.60	1007.29	1.801	571.71	1029.74
A_68_P20405960	chr1:84835061-84835105	NM_133975:797	Trip12	INSIDE	1.149	1.573	1164.17	1830.72	1.807	964.18	1741.94
A_68_P24066624	chr5:125869903-125869947	NM_019639:463	Ubc	INSIDE	1.149	1.614	2006.21	3237.36	1.854	1637.33	3035.47
A_68_P28992608	chr13:43960038-43960082	ENSMUST00000158482:-8110		PROMOTER	1.149	1.561	596.13	930.69	1.794	545.88	979.56
A_68_P32373279	chrX:48194718-48194762	NM_133729:128	2610018G03Rik	INSIDE	1.148	2.034	1137.10	2312.60	2.336	595.41	1390.72
A_68_P26158735	chr8:112261518-112261562	NM_001080930:99	Atxn1l	INSIDE	1.148	0.501	3757.68	1882.24	0.575	3104.61	1785.73
A_68_P26920733	chr10:7500333-7500377	NM_145418:361	BC013529	INSIDE	1.148	0.424	2350.01	996.08	0.487	1973.35	960.28
A_68_P27796930	chr11:51817853-51817897	NM_001166655:152	Cdkl3	INSIDE	1.148	1.460	1417.02	2069.52	1.677	1171.54	1965.02
A_68_P26585433	chr9:64880240-64880284	NM_028906:-2	Dpp8	PROMOTER	1.148	2.027	697.06	1413.25	2.328	589.23	1371.96
A_68_P30540365	chr16:9995470-9995514	NM_008170:-2866	Grin2a	PROMOTER	1.148	1.424	4960.74	7064.25	1.635	3680.85	6018.02
A_68_P26954153	chr10:13685444-13685488	NM_010437:-718	Hivep2	PROMOTER	1.148	1.784	1339.21	2388.49	2.047	1110.57	2273.65
A_68_P21890549	chr2:178142357-178142402	NM_177191:-16	Sycp2	PROMOTER	1.148	4.637	255.79	1186.08	5.325	222.49	1184.80
A_68_P31385965	chr17:81344280-81344324	NM_026516:331	Tmem178	INSIDE	1.148	2.017	796.65	1606.93	2.316	677.17	1568.23
A_68_P32467741	chrX:71613538-71613585	NM_145405:305	Ubl4	INSIDE	1.148	1.561	1085.93	1694.69	1.792	587.05	1052.18
A_68_P22715608	chr4:8574757-8574801	AK084737:-179		PROMOTER	1.148	1.951	3467.41	6763.96	2.240	3093.96	6931.47
A_68_P26055738	chr8:93432239-93432283	NM_177224:79527	Chd9	INSIDE	1.147	1.525	696.37	1062.00	1.748	661.38	1156.43
A_68_P32219657	chr19:59543612-59543656	NM_010132:10455	Emx2	DOWNSTREAM	1.147	2.613	671.78	1755.50	2.998	603.73	1809.84
A_68_P26234160	chr8:125074869-125074913	NM_001037298:339	Fam38a	INSIDE	1.147	2.912	744.90	2168.89	3.339	648.66	2166.20
A_68_P27278594	chr10:79198492-79198536	NM_008226:19136	Hcn2	INSIDE	1.147	2.836	798.73	2265.34	3.254	714.36	2324.19
A_68_P25656208	chr8:11555566-11555610	NM_011919:-477	Ing1	DIVERGENT_PROMOTER	1.147	1.485	1406.37	2088.15	1.703	968.52	1649.07
A_68_P30660050	chr16:33829808-33829852	NM_001145884:80	Itgb5	INSIDE	1.147	0.524	1221.84	640.16	0.601	1071.45	643.74
A_68_P20725327	chr1:155033029-155033073	NM_008485:527	Lamc2	INSIDE	1.147	1.443	2155.58	3109.55	1.655	1888.68	3126.03
A_68_P24817390	chr6:124807543-124807587	NM_013534:141	Leprel2	INSIDE	1.147	2.965	603.53	1789.17	3.401	555.26	1888.39
A_68_P30086030	chr15:26239396-26239440	NM_177597:592	Marchf11	INSIDE	1.147	1.701	1533.20	2607.97	1.951	1305.56	2547.75
A_68_P26824824	chr9:110532605-110532649	NM_183276:24039	Nbeal2	INSIDE	1.147	2.999	4559.26	13673.66	3.441	3199.65	11009.77
A_68_P25507199	chr7:134913679-134913723	NM_198424:372	Orai3	INSIDE	1.147	1.420	1173.39	1666.07	1.629	908.09	1478.88
A_68_P30369639	chr15:79832333-79832377	NM_011057:12884	Pdgfb	INSIDE	1.147	2.403	314.82	756.55	2.757	274.89	757.78
A_68_P22727584	chr4:10935394-10935438	NM_175175:-650	Plekhf2	PROMOTER	1.147	4.620	3714.69	17162.09	5.301	2901.09	15379.18
A_68_P27997510	chr11:87861570-87861615	NM_001078167:420	Srsf1	INSIDE	1.147	1.352	4076.03	5511.77	1.551	2952.90	4579.51
A_68_P24539866	chr6:72047427-72047471	NM_001035228:-158	St3gal5	PROMOTER	1.147	1.742	1402.30	2443.15	1.999	1239.77	2478.14
A_68_P24951681	chr7:4982839-4982883	NM_001033383:10883	Zfp865	INSIDE	1.147	3.014	1643.98	4955.44	3.459	1375.69	4758.27
A_68_P32579462	chrX:102347389-102347433	AK136781:-2300		PROMOTER	1.147	2.156	1328.61	2864.61	2.473	723.39	1788.92
A_68_P31122888	chr17:28655312-28655356	ENSMUST00000114792:-865		DIVERGENT_PROMOTER	1.147	2.051	1694.27	3475.54	2.353	1360.97	3201.97
A_68_P27371447	chr10:96079236-96079280	NM_007569:-376	Btg1	PROMOTER	1.146	1.747	651.75	1138.68	2.002	568.25	1137.36
A_68_P29413813	chr14:13654802-13654846	NM_001042617:769	Cadps	INSIDE	1.146	2.063	495.72	1022.87	2.365	395.06	934.44
A_68_P23881742	chr5:90652641-90652685	NM_001033310:359	Cox18	INSIDE	1.146	2.644	1093.43	2891.44	3.030	953.31	2888.81
A_68_P30597632	chr16:22439432-22439476	NM_023794:189	Etv5	INSIDE	1.146	1.540	1122.92	1729.36	1.765	1004.04	1772.61
A_68_P23417715	chr4:151657468-151657512	NM_178406:9020	Gpr153	INSIDE	1.146	3.479	875.71	3046.49	3.985	765.58	3051.19
A_68_P31927058	chr19:5118339-5118383	NM_008451:48	Klc2	INSIDE	1.146	2.108	920.18	1939.91	2.415	874.32	2111.86
A_68_P31304303	chr17:66450941-66450985	NM_028388:-131	Ndufv2	DIVERGENT_PROMOTER	1.146	2.833	293.43	831.27	3.246	309.33	1004.13
A_68_P29516148	chr14:33015159-33015203	NM_011960:24	Parg	INSIDE	1.146	1.848	1409.37	2604.50	2.117	1204.44	2550.01
A_68_P28159662	chr11:116351581-116351625	NM_026364:58	Prpsap1	INSIDE	1.146	0.562	1876.10	1054.65	0.644	1526.63	983.73
A_68_P31256044	chr17:56567422-56567466	NM_011218:48459	Ptprs	INSIDE	1.146	2.105	728.87	1534.11	2.411	633.36	1527.06

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27278801	chr10:79229322-79229366	NM_144528:322	Rnf126	INSIDE	1.146	1.758	1376.94	2420.31	2.014	1173.18	2362.58
A_68_P28267488	chr12:16902116-16902160	NM_009072:355	Rock2	INSIDE	1.146	1.705	1265.22	2157.44	1.954	1185.50	2316.01
A_68_P31857883	chr18:79306004-79306048	NM_053099:104	Setbp1	INSIDE	1.146	2.809	318.05	893.29	3.219	277.81	894.35
A_68_P31335036	chr17:71901525-71901569	NM_001142631:146	Spdya	INSIDE	1.146	1.884	1423.82	2682.70	2.159	1190.81	2571.49
A_68_P26495378	chr9:48863573-48863617	NM_012039:-91	Zw10	PROMOTER	1.146	0.584	1322.24	772.49	0.669	1055.85	706.74
A_68_P31157494	chr17:35226276-35226320	NM_178592:63	Abhd16a	INSIDE	1.145	2.161	1166.14	2519.81	2.473	1036.03	2562.23
A_68_P26595208	chr9:66643280-66643324	NM_177583:-72	Aph1b	PROMOTER	1.145	1.349	2023.61	2730.84	1.545	1609.91	2486.73
A_68_P20910361	chr1:188791550-188791594	NM_033077:278	D1Pas1	INSIDE	1.145	2.999	898.09	2693.55	3.434	737.92	2534.04
A_68_P27995151	chr11:87430824-87430868	NM_001045527:181	Hsf5	INSIDE	1.145	2.852	1092.69	3116.31	3.265	914.23	2984.58
A_68_P25176744	chr7:71536910-71536954	NM_026483:190	Mphosph10	INSIDE	1.145	1.415	1901.07	2690.74	1.621	1565.50	2536.98
A_68_P21766706	chr2:155455507-155455551	NM_001085378:18581	Myh7b	INSIDE	1.145	1.445	2078.49	3002.81	1.654	1648.52	2727.10
A_68_P21826985	chr2:165818808-165818852	NM_008679:694	Ncoa3	INSIDE	1.145	9.319	16574.18	154453.60	10.673	9712.30	103662.90
A_68_P26143993	chr8:109817338-109817382	NM_018823:-9	Nfat5	PROMOTER	1.145	2.190	1725.82	3780.06	2.509	1593.99	3998.84
A_68_P27638841	chr11:21893689-21893733	NM_011023:7944	Otx1	DOWNSTREAM	1.145	1.951	665.39	1298.11	2.234	529.96	1184.10
A_68_P30422883	chr15:88898977-88899021	NM_001002005:8843	Panx2	INSIDE	1.145	1.689	1262.48	2131.96	1.933	965.63	1866.86
A_68_P24424497	chr6:47780471-47780515	NM_177882:12	Zfp786	INSIDE	1.145	2.292	1671.68	3831.11	2.624	1432.27	3757.89
A_68_P22202961	chr3:65778787-65778831	AK133062:4973		DOWNSTREAM	1.145	1.377	1272.11	1751.64	1.577	1114.13	1757.07
A_68_P26686357	chr9:83818668-83818712	ENSMUST00000034801:-66		PROMOTER	1.145	1.667	2198.69	3665.55	1.909	1807.73	3450.68
A_68_P23349887	chr4:138686949-138686993	NR_033745:-18	2310028O11Rik	PROMOTER	1.144	1.610	668.37	1076.29	1.842	629.81	1160.18
A_68_P23470075	chr5:8893888-8893932	NM_008830:190	Abcb4	INSIDE	1.144	1.832	1594.06	2919.94	2.096	1304.42	2733.61
A_68_P24098220	chr5:131916295-131916339	NM_177047:1101897	Auts2	INSIDE	1.144	1.938	599.95	1162.40	2.217	724.89	1606.87
A_68_P30379107	chr15:81525500-81525544	NM_001164320:2195	Chadl	INSIDE	1.144	1.708	2331.94	3983.76	1.954	1946.06	3803.48
A_68_P26756439	chr9:97933339-97933383	NM_022319:226	Clstn2	INSIDE	1.144	2.092	2083.53	4358.32	2.393	1768.44	4231.25
A_68_P22874796	chr4:44025897-44025941	NM_001080384:404	Clta	INSIDE	1.144	0.539	2883.94	1554.15	0.616	2250.60	1387.39
A_68_P28732761	chr12:110697987-110698031	NM_001190703:6344	Dlk1	INSIDE	1.144	1.561	1106.10	1726.58	1.786	1061.40	1895.27
A_68_P22483665	chr3:122322229-122322273	NM_001114665:335	Fnbp1l	INSIDE	1.144	3.310	856.91	2836.36	3.787	766.56	2903.14
A_68_P22448210	chr3:115955054-115955098	NM_022427:1326	Gpr88	INSIDE	1.144	1.863	1132.96	2110.22	2.131	969.20	2065.07
A_68_P20897164	chr1:186556642-186556686	NM_008250:-292	Hlx	PROMOTER	1.144	1.773	462.95	820.70	2.027	460.42	933.37
A_68_P28068270	chr11:100333380-100333424	NM_172565:694	Klhl11	INSIDE	1.144	1.816	2440.30	4431.08	2.077	1895.71	3937.90
A_68_P21548580	chr2:115686166-115686210	NM_001159569:204169	Meis2	DOWNSTREAM	1.144	0.554	1024.15	567.65	0.634	825.09	523.27
A_68_P20293515	chr1:64663797-64663841	NM_025964:-76	Mettl21a	PROMOTER	1.144	1.729	429.27	742.27	1.979	394.61	780.78
A_68_P21339747	chr2:74663863-74663907	NM_016804:16	Mtx2	INSIDE	1.144	2.190	327.21	716.61	2.505	306.73	768.40
A_68_P28523604	chr12:72075575-72075619	NM_011184:-13	Psma3	PROMOTER	1.144	2.010	631.63	1269.65	2.299	596.95	1372.34
A_68_P21261141	chr2:60719359-60719403	NM_001141931:115	Rbms1	INSIDE	1.144	2.191	282.47	618.89	2.505	256.38	642.33
A_68_P22336391	chr3:93247585-93247629	NM_001163098:1355	Tchh	INSIDE	1.144	2.137	1454.63	3109.17	2.446	1219.93	2983.87
A_68_P21070954	chr2:25118703-25118747	NM_175286:607	Tprn	INSIDE	1.144	1.533	1113.00	1705.69	1.753	983.21	1723.33
A_68_P27473556	chr10:115550730-115550774	NM_001161855:221	4933416C03Rik	INSIDE	1.143	2.052	496.92	1019.64	2.344	432.89	1014.90
A_68_P28609993	chr12:87762632-87762676	NM_011934:61	Esrrb	INSIDE	1.143	1.759	916.15	1611.57	2.010	795.42	1598.60
A_68_P22888253	chr4:46356368-46356412	NM_183298:-675	Foxe1	PROMOTER	1.143	1.645	770.29	1267.12	1.881	699.15	1314.76
A_68_P20556971	chr1:121318266-121318310	NM_008381:537	Inhbb	INSIDE	1.143	1.555	965.48	1501.06	1.777	918.01	1630.88
A_68_P26258418	chr8:129116571-129116616	NM_001164598:743	Irf2bp2	INSIDE	1.143	2.685	391.89	1052.05	3.069	353.53	1084.99
A_68_P31936712	chr19:7000456-7000500	NM_008431:8527	Kcnk4	INSIDE	1.143	1.595	1158.65	1847.83	1.822	1029.44	1876.10
A_68_P24045149	chr5:121995337-121995381	NM_010765:543	Mapkapk5	INSIDE	1.143	2.283	490.57	1119.86	2.608	472.92	1233.48
A_68_P20935797	chr1:192849641-192849685	NM_001081259:407	Mfsd7b	INSIDE	1.143	1.410	1694.90	2389.78	1.612	1293.74	2085.69
A_68_P22944674	chr4:57313119-57313163	NM_011207:1569	Ptpn3	INSIDE	1.143	1.537	1616.30	2484.45	1.756	1493.44	2622.79
A_68_P26748152	chr9:96531410-96531454	NM_053268:490	Rasa2	INSIDE	1.143	1.840	1099.73	2022.97	2.103	944.73	1986.30
A_68_P28301682	chr12:27100225-27100269	NM_001081977:-125	Rnf144a	PROMOTER	1.143	1.674	1893.27	3169.01	1.913	1653.53	3163.47
A_68_P27284240	chr10:80065867-80065911	NM_019575:262	Scamp4	INSIDE	1.143	0.461	1258.91	580.86	0.527	848.67	447.41
A_68_P22031739	chr3:30993591-30993635	NM_001039090:-370	Skil	PROMOTER	1.143	2.519	873.02	2198.71	2.878	780.35	2245.49
A_68_P32036072	chr19:26679451-26679495	NM_011416:-177	Smarca2	PROMOTER	1.143	1.648	1021.62	1683.35	1.883	841.48	1584.64
A_68_P31962490	chr19:12869772-12869816	NR_024093:819	U05342	INSIDE	1.143	2.436	901.28	2195.20	2.784	866.72	2413.08

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P21779874	chr2:157740919-157740963	NM_198627:552	Vstm2l	INSIDE	1.143	3.186	3156.91	10059.25	3.643	2160.54	7870.49
A_68_P21076583	chr2:25994281-25994325	ENSMUST00000163836:20		INSIDE	1.143	2.486	5233.91	13009.34	2.842	4058.83	11535.03
A_68_P27281469	chr10:79634617-79634661	NM_027207:-1050	1600002K03Rik	PROMOTER	1.142	3.140	1389.69	4363.61	3.586	1101.78	3950.74
A_68_P20416762	chr1:89161364-89161408	NM_028889:448	Efhd1	INSIDE	1.142	1.890	1935.79	3658.56	2.158	1768.27	3816.05
A_68_P24138290	chr5:140388742-140388786	NM_175522:4868	Elfn1	INSIDE	1.142	1.382	1371.99	1896.57	1.578	1171.16	1848.62
A_68_P24138664	chr5:140449200-140449245	NM_175522:65326	Elfn1	INSIDE	1.142	2.327	1456.27	3388.96	2.657	1164.39	3093.79
A_68_P23392749	chr4:147533784-147533828	NM_001161851:-102	Fbxo44	PROMOTER	1.142	1.388	1996.76	2771.44	1.585	1604.84	2543.39
A_68_P24325253	chr6:29166069-29166113	NM_011829:-3819	Impdh1	PROMOTER	1.142	2.299	291.55	670.30	2.625	305.52	802.08
A_68_P32141807	chr19:46119714-46119758	NM_001113408:-35	Ldb1	PROMOTER	1.142	1.702	613.53	1044.20	1.944	582.83	1132.92
A_68_P27782065	chr11:49057416-49057460	NM_001110148:-254	Mgat1	PROMOTER	1.142	1.465	1555.95	2279.67	1.673	1283.27	2146.85
A_68_P23392001	chr4:147413122-147413166	NM_010840:-41	Mthfr	DIVERGENT_PROMOTER	1.142	1.696	1563.37	2652.04	1.938	1223.33	2370.34
A_68_P32231475	chrX:5045956-5046000	NM_010850:405	Mycs	INSIDE	1.142	2.263	636.59	1440.54	2.584	348.50	900.51
A_68_P22649654	chr3:151928897-151928941	NM_199465:366	Nexn	INSIDE	1.142	1.382	1293.67	1787.47	1.578	1242.78	1961.73
A_68_P26742969	chr9:95537953-95537997	NM_029620:-72	Pcolce2	PROMOTER	1.142	1.517	554.55	841.36	1.733	513.29	889.64
A_68_P22446820	chr3:115710167-115710211	NM_023214:136	Slc30a7	INSIDE	1.142	1.587	1582.11	2511.14	1.813	1320.18	2393.82
A_68_P23308817	chr4:131429521-131429565	NM_020587:-11	Srsf4	PROMOTER	1.142	3.553	499.71	1775.50	4.058	484.82	1967.52
A_68_P25584910	chr7:147973596-147973640	NM_001143765:135	Syce1	INSIDE	1.142	3.011	2858.30	8606.63	3.438	2540.67	8734.54
A_68_P28687318	chr12:102956856-102956900	NM_001082976:-166	Tc2n	PROMOTER	1.142	2.347	4922.48	11551.08	2.679	3757.29	10065.84
A_68_P22856580	chr4:40216716-40216760	NM_134097:136	Topors	INSIDE	1.142	0.529	1290.69	682.21	0.604	1070.61	646.32
A_68_P27033509	chr10:28867346-28867390	NM_026138:3567	6330407J23Rik	INSIDE	1.141	1.889	1801.19	3401.94	2.154	1654.05	3563.34
A_68_P20026603	chr1:10222944-10222988	NM_001102430:-215	Arfgef1	PROMOTER	1.141	1.817	421.57	766.16	2.073	410.39	850.71
A_68_P32268349	chrX:13423877-13423921	NM_009806:-231	Cask	PROMOTER	1.141	2.936	1476.93	4335.55	3.349	937.02	3138.00
A_68_P20619647	chr1:134035982-134036026	NM_008795:258	Cdk18	INSIDE	1.141	2.748	897.73	2467.03	3.137	833.16	2613.40
A_68_P26238529	chr8:125736395-125736439	NM_145606:272	Chmp1a	INSIDE	1.141	1.789	1769.26	3164.82	2.041	1278.91	2610.54
A_68_P23192163	chr4:107356485-107356529	NM_019872:261	Dmrtb1	INSIDE	1.141	3.490	350.53	1223.28	3.983	299.05	1191.00
A_68_P28378464	chr12:41172641-41172685	NM_172803:23	Dock4	INSIDE	1.141	2.323	320.99	745.72	2.651	257.71	683.13
A_68_P24449831	chr6:52260423-52260467	NM_007966:-3047	Evx1	PROMOTER	1.141	4.313	3128.82	13495.28	4.920	2577.10	12680.36
A_68_P27995152	chr11:87431026-87431070	NM_001045527:383	Hsf5	INSIDE	1.141	2.267	1056.51	2395.17	2.587	918.12	2374.93
A_68_P20335537	chr1:72258509-72258553	NM_001005423:351	Mreg	INSIDE	1.141	1.377	1522.96	2097.51	1.572	1252.36	1968.69
A_68_P25581955	chr7:147234797-147234841	NM_010836:169	Msx3	INSIDE	1.141	0.549	1314.54	721.46	0.626	1005.80	629.87
A_68_P23393398	chr4:147645613-147645662	NM_001083342:16437	Ptchd2	INSIDE	1.141	2.603	450.79	1173.19	2.970	402.37	1195.09
A_68_P26816015	chr9:108564655-108564699	NM_020520:248	Slc25a20	INSIDE	1.141	3.193	1361.74	4348.06	3.644	1274.91	4646.06
A_68_P25954770	chr8:73416471-73416515	NM_053248:164	Slc5a5	INSIDE	1.141	1.687	1035.00	1745.83	1.925	923.23	1777.23
A_68_P22367896	chr3:99966241-99966285	NM_175552:64	Wdr3	INSIDE	1.141	0.401	1678.24	672.19	0.457	1461.15	667.98
A_68_P23154332	chr4:100965654-100965698	ENSMUST00000131864:28674		INSIDE	1.141	16.638	2625.93	43691.16	18.986	1836.30	34864.06
A_68_P24127046	chr5:138125901-138125945	NM_145566:-1	Agfg2	PROMOTER	1.140	2.657	14382.74	38221.34	3.029	10803.47	32723.97
A_68_P31549437	chr18:22502988-22503032	NM_001167777:-579	Asxl3	PROMOTER	1.140	1.640	1240.83	2034.48	1.869	981.96	1834.84
A_68_P26845718	chr9:114549214-114549258	NM_153585:82	Cnot10	INSIDE	1.140	0.515	1234.90	635.71	0.587	937.77	550.11
A_68_P21144122	chr2:37642341-37642385	NM_001163566:10594	Crb2	INSIDE	1.140	1.372	1424.99	1955.46	1.564	1157.99	1811.65
A_68_P26581359	chr9:64188861-64188905	NM_001177784:-302	Dis3l	PROMOTER	1.140	1.862	509.42	948.60	2.124	481.01	1021.52
A_68_P31398414	chr17:83750191-83750235	NM_001114361:-58	Eml4	PROMOTER	1.140	2.021	520.98	1052.64	2.303	540.18	1244.08
A_68_P29130720	chr13:72100566-72100611	NM_010573:583	Irx1	INSIDE	1.140	1.807	1014.61	1833.12	2.060	1215.21	2503.18
A_68_P24053344	chr5:123439364-123439408	NM_001003953:-285	Kdm2b	PROMOTER	1.140	2.657	8288.90	22026.62	3.030	5752.37	17428.50
A_68_P26082829	chr8:97876209-97876253	NM_008609:-6	Mmp15	PROMOTER	1.140	2.947	1460.00	4302.18	3.359	1203.22	4041.79
A_68_P25326013	chr7:99817798-99817842	NM_029078:602	Pcf11	INSIDE	1.140	1.806	973.23	1757.77	2.059	777.02	1600.24
A_68_P24627788	chr6:89311893-89311937	NM_008881:693	Plxna1	INSIDE	1.140	1.583	1143.52	1810.26	1.805	1090.70	1968.78
A_68_P25508221	chr7:135079319-135079363	NM_001081374:10899	Prss36	INSIDE	1.140	2.897	3483.02	10091.90	3.303	2870.21	9479.93
A_68_P31256054	chr17:56568541-56568585	NM_011218:47341	Ptprs	INSIDE	1.140	3.934	2134.59	8396.48	4.484	1636.49	7337.60
A_68_P23922674	chr5:99681727-99681771	NM_145839:198	Rasgef1b	INSIDE	1.140	1.858	1720.84	3198.16	2.118	1481.41	3138.20
A_68_P23327086	chr4:134731348-134731392	NM_019732:54811	Runx3	INSIDE	1.140	1.618	2503.94	4051.62	1.845	2053.89	3790.26
A_68_P21747605	chr2:151919256-151919300	NM_001160410:12014	Scrt2	INSIDE	1.140	1.697	1345.80	2283.95	1.935	1177.80	2279.37

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P20151303	chr1:36996367-36996411	NM_018872:-16	Tmem131	PROMOTER	1.140	2.394	2960.76	7088.56	2.729	2089.12	5700.62
A_68_P31002108	chr16:98183316-98183360	NM_001081684:448	Zfp295	INSIDE	1.140	3.915	2251.56	8814.55	4.463	1684.45	7518.43
A_68_P28053992	chr11:97884169-97884213	NM_145121:-249	Cacnb1	DIVERGENT_PROMOTER	1.139	1.455	4643.19	6755.89	1.658	3410.85	5654.04
A_68_P32383366	chrX:49966645-49966690	NM_016697:484	Gpc3	INSIDE	1.139	1.660	1330.07	2207.32	1.890	806.06	1523.15
A_68_P26550038	chr9:58671669-58671713	NM_001081192:372	Hcn4	INSIDE	1.139	0.507	1451.40	736.01	0.578	1245.16	719.43
A_68_P21321484	chr2:71625261-71625305	NM_008397:143	Itga6	INSIDE	1.139	2.643	523.77	1384.25	3.011	438.63	1320.81
A_68_P32136345	chr19:45154436-45154480	NM_178929:3830	Kazald1	DOWNSTREAM	1.139	1.859	3426.28	6369.98	2.117	2584.79	5472.58
A_68_P20348303	chr1:74438925-74438969	NR_029743:-1937	Mir26b	PROMOTER	1.139	0.527	1036.31	545.76	0.600	838.60	502.94
A_68_P24051802	chr5:123157935-123157979	NM_011026:391	P2rx4	INSIDE	1.139	2.251	1115.71	2511.71	2.563	987.41	2531.14
A_68_P24046733	chr5:122278943-122278987	NM_008507:7846	Sh2b3	INSIDE	1.139	3.173	1425.63	4522.86	3.613	1344.28	4857.28
A_68_P23608246	chr5:36873249-36873293	NM_001113364:2	Tbc1d14	INSIDE	1.139	1.530	938.48	1436.30	1.743	846.96	1476.35
A_68_P26891892	chr9:122795954-122795998	NM_001177505:-1612	Zfp167	PROMOTER	1.139	2.196	1661.44	3648.76	2.501	1448.05	3622.28
A_68_P32672910	chrX:131160541-131160585	ENSMUST00000137737:-279		PROMOTER	1.139	2.091	913.69	1910.42	2.382	512.07	1219.71
A_68_P28743345	chr12:112556826-112556880	NM_183016:59077	Cdc42bpb	INSIDE	1.138	1.685	641.65	1081.46	1.918	571.57	1096.48
A_68_P23200235	chr4:108952879-108952923	NM_007943:21	Eps15	INSIDE	1.138	1.769	2860.81	5060.18	2.013	2362.74	4755.71
A_68_P27141570	chr10:53018974-53019019	NM_001204983:80661	Gm9766	INSIDE	1.138	1.796	484.83	870.64	2.044	421.73	861.87
A_68_P28043344	chr11:96133745-96133789	NM_008270:1123	Hoxb9	INSIDE	1.138	2.292	551.78	1264.92	2.609	512.96	1338.40
A_68_P27902199	chr11:70513617-70513661	NM_213729:19	Inca1	INSIDE	1.138	1.931	1131.10	2183.78	2.197	1057.60	2324.01
A_68_P30682958	chr16:37868795-37868839	NM_177093:331	Lrrc58	INSIDE	1.138	2.125	405.07	860.73	2.418	408.08	986.86
A_68_P27011027	chr10:24589834-24589878	NM_001166416:65	Med23	INSIDE	1.138	1.418	1286.73	1825.18	1.614	1096.31	1769.01
A_68_P28269967	chr12:17355126-17355170	NM_001008421:-150	Nol10	PROMOTER	1.138	1.505	2601.68	3914.40	1.713	2127.26	3643.00
A_68_P23409032	chr4:150283998-150284042	NM_020569:10	Park7	INSIDE	1.138	1.564	1909.68	2987.47	1.780	1617.75	2879.64
A_68_P31632591	chr18:38357539-38357583	NM_029357:11856	Pcdh1	INSIDE	1.138	3.034	1272.71	3861.54	3.452	901.81	3113.24
A_68_P30423564	chr15:88991163-88991207	NM_001159521:13096	Plxnb2	INSIDE	1.138	3.484	884.01	3079.79	3.966	776.42	3078.92
A_68_P25771677	chr8:35040417-35040461	NM_001042674:-125	Rbpms	PROMOTER	1.138	1.564	624.97	977.15	1.780	778.65	1385.70
A_68_P25025186	chr7:29856672-29856716	NM_009109:53476	Ryr1	INSIDE	1.138	1.893	711.20	1346.42	2.154	526.30	1133.49
A_68_P21843418	chr2:168591344-168591388	NM_175303:1335	Sall4	INSIDE	1.138	3.052	1325.71	4045.75	3.472	1107.27	3843.90
A_68_P31709384	chr18:52928549-52928593	NM_001199154:773	Sncaip	INSIDE	1.138	1.390	2108.75	2931.07	1.581	1716.34	2713.76
A_68_P24432386	chr6:49345471-49345515	NM_029916:-110	Stk31	PROMOTER	1.138	2.814	977.94	2752.31	3.204	750.59	2404.82
A_68_P21748556	chr2:152119601-152119645	NM_024196:15	Tbc1d20	INSIDE	1.138	2.451	430.45	1054.87	2.789	382.58	1067.10
A_68_P27641463	chr11:22412449-22412493	NM_153596:185	Tmem17	INSIDE	1.138	3.343	1232.01	4118.01	3.802	1073.40	4081.58
A_68_P23185612	chr4:106311841-106311885	NM_177667:16809	Ttc22	INSIDE	1.138	2.496	1130.44	2821.23	2.841	981.37	2788.35
A_68_P20827839	chr1:173341981-173342025	NM_009480:191	Usf1	INSIDE	1.138	1.812	1426.53	2585.04	2.063	1148.99	2370.41
A_68_P30401334	chr15:85374054-85374098	NM_001163634:34424	Wnt7b	INSIDE	1.138	2.942	1235.10	3634.16	3.348	1139.66	3816.09
A_68_P33013883	chrUn_random:3232956-3233000			Unknown	1.138	2.077	846.94	1758.82	2.363	678.87	1603.83
A_68_P27340461	chr10:90644609-90644653	ENSMUST00000099357:-9871		PROMOTER	1.138	0.507	1087.58	550.98	0.576	969.83	558.94
A_68_P31939680	chr19:7491931-7491975	NM_175381:-162	2700081O15Rik	PROMOTER	1.137	1.690	1418.97	2398.14	1.922	1138.96	2189.30
A_68_P22398700	chr3:105507744-105507788	NM_001163356:-609	6530418L21Rik	PROMOTER	1.137	2.276	691.12	1573.21	2.587	624.36	1615.33
A_68_P27339935	chr10:90545393-90545437	NM_001042558:74	Apaf1	INSIDE	1.137	0.475	1087.17	516.72	0.540	1031.02	556.96
A_68_P22058858	chr3:36470838-36470882	NM_009828:58	Ccna2	INSIDE	1.137	2.578	1330.56	3430.10	2.930	1130.50	3312.56
A_68_P20139530	chr1:34636521-34636565	NM_213727:5	Fam123c	INSIDE	1.137	1.978	1105.59	2186.87	2.248	984.97	2214.32
A_68_P22450556	chr3:116365109-116365153	NM_008246:465	Hiat1	INSIDE	1.137	2.950	661.58	1951.71	3.354	600.60	2014.56
A_68_P21309973	chr2:69423496-69423540	NM_001081088:606	Lrp2	INSIDE	1.137	1.706	653.63	1115.20	1.940	655.63	1271.97
A_68_P21044978	chr2:19367856-19367900	NM_018809:589	Ptf1a	INSIDE	1.137	1.407	1024.31	1440.82	1.600	846.03	1353.62
A_68_P29622735	chr14:57021569-57021613	NM_001033043:57	Rnf17	INSIDE	1.137	3.045	2228.51	6786.90	3.464	1777.25	6156.76
A_68_P26750481	chr9:96919029-96919073	NM_145134:-276	Spsb4	PROMOTER	1.137	1.712	833.14	1426.16	1.946	713.38	1388.25
A_68_P28166384	chr11:117515968-117516012	NM_198022:388	Tnrc6c	INSIDE	1.137	1.546	1191.84	1842.42	1.757	1029.05	1808.44
A_68_P24638741	chr6:91344683-91344727	NM_009527:16659	Wnt7a	INSIDE	1.137	2.113	258.94	547.12	2.403	210.85	506.75
A_68_P29373467	chr14:4829490-4829534	ENSMUST00000165619:-301		PROMOTER	1.137	2.836	3584.78	10166.21	3.224	3373.19	10874.69
A_68_P31746201	chr18:59335430-59335474	NM_001081328:459	Chsy3	INSIDE	1.136	0.479	1428.60	683.91	0.544	1166.90	634.86
A_68_P25948480	chr8:72406164-72406208	NM_026818:5105	Cilp2	INSIDE	1.136	2.662	565.04	1504.40	3.024	564.02	1705.81

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P29334873	chr13:113254637-113254681	NM_010560:381	Il6st	INSIDE	1.136	1.546	2638.65	4079.29	1.756	2019.87	3547.22
A_68_P24804565	chr6:121423791-121423835	NM_001033354:-116	Iqsec3	PROMOTER	1.136	0.548	1171.87	641.70	0.622	977.95	608.46
A_68_P21239895	chr2:56954793-56954837	NM_013613:12635	Nr4a2	DOWNSTREAM	1.136	0.561	1099.56	616.62	0.637	1074.70	684.82
A_68_P22778509	chr4:22415123-22415167	NM_008899:134	Pou3f2	INSIDE	1.136	1.829	762.99	1395.40	2.077	650.63	1351.26
A_68_P30390277	chr15:83555041-83555085	NM_022723:389	Scube1	INSIDE	1.136	2.018	1445.64	2917.40	2.293	1238.70	2840.08
A_68_P21116239	chr2:32442606-32442650	NM_011373:-381	St6galnac4	PROMOTER	1.136	1.902	470.62	895.15	2.161	458.76	991.20
A_68_P24880088	chr6:137683751-137683795	NM_011499:170	Strap	INSIDE	1.136	2.621	467.53	1225.55	2.977	490.12	1459.09
A_68_P31254298	chr17:56301931-56301975	NM_025566:39	Tnfaip8l1	INSIDE	1.136	1.441	1132.24	1631.07	1.637	894.21	1463.53
A_68_P28787946	chr13:3358712-3358756			Unknown	1.136	2.407	840.16	2022.29	2.734	774.05	2116.13
A_68_P22039461	chr3:32608077-32608121	NM_019673:631	Actl6a	INSIDE	1.135	1.884	860.68	1621.38	2.139	815.82	1744.81
A_68_P24994776	chr7:20282146-20282190	NM_009696:2347	Apoe	INSIDE	1.135	2.429	696.47	1691.65	2.756	624.91	1722.34
A_68_P23262160	chr4:123020018-123020062	NM_007558:6	Bmp8a	INSIDE	1.135	0.545	1865.12	1016.77	0.619	1467.31	907.87
A_68_P26813082	chr9:108012831-108012875	NM_007567:79862	Bsn	INSIDE	1.135	2.328	1586.69	3694.61	2.642	1263.38	3337.69
A_68_P21580764	chr2:121239313-121239357	NM_153075:194	Catsper2	INSIDE	1.135	1.616	4136.12	6685.98	1.835	3328.44	6108.71
A_68_P25601118	chr7:150651001-150651045	NM_001161624:-4067	Cdkn1c	DIVERGENT_PROMOTER	1.135	3.697	454.16	1679.14	4.198	443.60	1862.18
A_68_P27476526	chr10:116018789-116018833	NM_001037846:-243	Cnot2	PROMOTER	1.135	3.158	1799.87	5683.88	3.585	1572.05	5636.01
A_68_P21706813	chr2:144194864-144194908	NM_181417:116	Csrp2bp	INSIDE	1.135	1.860	547.64	1018.78	2.111	480.48	1014.22
A_68_P29737940	chr14:77556610-77556654	NM_172813:10	Enox1	INSIDE	1.135	1.449	758.66	1099.67	1.646	686.66	1130.12
A_68_P28928669	chr13:32430434-32430478	NM_146041:-43	Gmds	PROMOTER	1.135	0.534	1486.36	793.48	0.606	1327.02	804.05
A_68_P21933421	chr3:8667100-8667144	NM_010423:-84	Hey1	PROMOTER	1.135	2.545	573.08	1458.68	2.888	516.10	1490.73
A_68_P25528245	chr7:138553702-138553746	NM_175115:268	Ikzf5	INSIDE	1.135	0.399	1405.83	560.46	0.453	1239.71	561.09
A_68_P27484949	chr10:117578950-117578994	NM_001162904:130	Mdm1	INSIDE	1.135	1.405	1467.01	2061.57	1.595	1226.56	1956.14
A_68_P24894481	chr6:140372708-140372752	NM_144920:111	Plekha5	INSIDE	1.135	1.474	1618.55	2385.49	1.673	1491.83	2496.12
A_68_P31953479	chr19:10969598-10969642	NM_134129:-161	Prpf19	PROMOTER	1.135	1.778	396.41	704.95	2.019	365.25	737.54
A_68_P24125229	chr5:137774819-137774863	NM_031406:-30	Slc12a9	PROMOTER	1.135	1.499	6017.14	9021.20	1.701	3977.16	6766.42
A_68_P32319890	chrX:34283973-34284017	NM_001085497:341	Slc25a43	INSIDE	1.135	1.505	1027.93	1547.46	1.709	543.60	929.16
A_68_P30360708	chr15:78370197-78370241	NM_009218:4557	Sstr3	INSIDE	1.135	1.654	888.91	1470.41	1.878	768.68	1443.43
A_68_P26470629	chr9:44773701-44773745	NM_145400:-39	Ube4a	PROMOTER	1.135	1.939	1914.96	3712.77	2.200	1453.61	3198.39
A_68_P20505871	chr1:107887105-107887149	NM_001122675:144	Zcchc2	INSIDE	1.135	2.550	1079.51	2753.24	2.894	823.13	2382.24
A_68_P32975879	A_68_P32975879			Unknown	1.135	1.732	929.03	1608.98	1.966	944.61	1857.17
A_68_P32983000	A_68_P32983000			Unknown	1.135	2.262	775.27	1753.61	2.568	794.92	2041.58
A_68_P26080209	chr8:97437362-97437406	NM_001033533:4614	Ccdc102a	INSIDE	1.134	1.537	990.63	1522.27	1.743	796.04	1387.28
A_68_P29613438	chr14:55260166-55260210	NM_199470:13	Cdh24	INSIDE	1.134	1.897	737.77	1399.69	2.151	683.00	1469.00
A_68_P24798785	chr6:120443882-120443926	NM_033567:-79	Cecr6	PROMOTER	1.134	1.745	478.57	835.24	1.978	448.44	887.20
A_68_P26505264	chr9:50536185-50536229	NM_178118:-117	Dixdc1	PROMOTER	1.134	1.567	701.53	1099.40	1.777	604.16	1073.40
A_68_P26523445	chr9:53822873-53822917	NM_177769:214	Elmod1	INSIDE	1.134	0.553	1270.53	702.32	0.627	1094.15	685.93
A_68_P28675862	chr12:100630292-100630340	NM_183186:57968	Foxn3	INSIDE	1.134	1.880	295.02	554.51	2.131	296.99	632.87
A_68_P24658382	chr6:94649670-94649714	NM_008377:447	Lrig1	INSIDE	1.134	1.895	379.50	719.02	2.149	322.08	692.01
A_68_P24009588	chr5:115890672-115890717	NM_008629:11001	Msi1	INSIDE	1.134	4.011	469.76	1884.44	4.551	374.48	1704.11
A_68_P31629193	chr18:37829497-37829541	NM_033586:-4470	Pcdhga3	PROMOTER	1.134	2.242	516.06	1156.85	2.543	426.68	1085.05
A_68_P32536213	chrX:91077623-91077667	NM_145630:-210	Pdk3	PROMOTER	1.134	1.632	1149.18	1875.44	1.850	558.78	1033.82
A_68_P24059429	chr5:124573689-124573733	NM_011256:92717	Pitpnm2	INSIDE	1.134	3.249	669.87	2176.50	3.685	567.36	2090.99
A_68_P30729957	chr16:46010656-46010700	NM_001134480:-152	Plcxd2	PROMOTER	1.134	1.632	1086.91	1773.71	1.850	987.21	1826.10
A_68_P28740620	chr12:112079116-112079160	NM_011973:11	Stk30	INSIDE	1.134	2.221	355.68	789.89	2.518	323.07	813.64
A_68_P22955049	chr4:59202246-59202290	NM_011673:-153	Ugcg	PROMOTER	1.134	2.748	474.71	1304.46	3.115	474.73	1478.80
A_68_P24427163	chr6:48388218-48388262	NM_001085415:6849	Zfp467	INSIDE	1.134	1.788	1596.39	2854.54	2.027	1261.90	2558.29
A_68_P21934023	chr3:8767607-8767651			Unknown	1.134	2.092	3179.25	6649.98	2.372	2285.15	5419.68
A_68_P32410984	chrX:56821241-56821285	ENSMUST00000119833:-14		PROMOTER	1.134	1.938	432.75	838.84	2.198	268.01	589.07
A_68_P23391463	chr4:147315197-147315241	NM_029841:215	2510039O18Rik	INSIDE	1.133	1.956	904.26	1768.69	2.216	743.95	1648.92
A_68_P21776100	chr2:157105079-157105123	NM_001039557:185	4922505G16Rik	INSIDE	1.133	1.601	932.72	1493.56	1.814	809.44	1468.62
A_68_P23447647	chr5:3928400-3928444	NM_194462:237	Akap9	INSIDE	1.133	1.419	1319.18	1871.49	1.607	1160.21	1865.01

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P21673348	chr2:138082206-138082250	NM_001025431:-91	Btbd3	PROMOTER	1.133	3.215	1850.87	5950.56	3.642	1537.36	5599.36
A_68_P25047616	chr7:35905038-35905082	NM_007678:749	Cebpa	INSIDE	1.133	0.539	4210.42	2271.41	0.611	3692.96	2256.50
A_68_P20148716	chr1:36568774-36568818	NM_001039551:76	Cnnm3	INSIDE	1.133	3.034	2912.87	8838.60	3.437	2339.06	8038.66
A_68_P25083573	chr7:50930678-50930722	NM_145582:3300	Ctu1	INSIDE	1.133	2.076	826.67	1716.12	2.352	763.67	1795.91
A_68_P31620540	chr18:36020339-36020383	NM_133687:30889	Cxxc5	INSIDE	1.133	3.049	1031.39	3144.98	3.455	827.36	2858.70
A_68_P25496227	chr7:132851431-132851475	NM_001081022:63	D430042O09Rik	INSIDE	1.133	2.950	470.41	1387.85	3.341	428.30	1431.11
A_68_P29626122	chr14:57723066-57723110	NM_008125:451	Gjb2	INSIDE	1.133	0.447	1816.05	812.43	0.507	1475.09	747.34
A_68_P21817704	chr2:164239982-164240026	NM_013592:-9890	Matn4	PROMOTER	1.133	2.320	2606.22	6046.12	2.629	1994.86	5244.03
A_68_P28246306	chr12:12948314-12948358	NM_008709:306	Mycn	INSIDE	1.133	1.839	1193.87	2195.91	2.084	1001.15	2086.53
A_68_P22355468	chr3:97462189-97462238	NM_182997:79	Prkab2	INSIDE	1.133	1.784	1722.40	3073.42	2.021	1329.38	2686.69
A_68_P24325039	chr6:29129114-29129158	NM_001101443:448	Prrt4	INSIDE	1.133	2.009	351.20	705.47	2.276	402.57	916.34
A_68_P22383501	chr3:102739596-102739640	NM_011516:405	Sycp1	INSIDE	1.133	2.771	1127.57	3124.35	3.139	952.37	2989.38
A_68_P28936502	chr13:34169897-34169941	NM_009450:-41	Tubb2a	PROMOTER	1.133	1.555	1520.94	2364.84	1.762	1313.99	2314.93
A_68_P20286081	chr1:63320021-63320065	NM_028673:200	Zdbf2	INSIDE	1.133	1.418	1173.03	1663.37	1.607	1090.62	1752.33
A_68_P28603808	A_68_P28603808			Unknown	1.133	2.003	919.76	1842.41	2.269	826.92	1876.64
A_68_P26467841	chr9:44291334-44291378	ENSMUST00000136322:4496		DOWNSTREAM	1.133	2.280	1789.97	4082.00	2.584	1453.44	3755.63
A_68_P23315558	chr4:132617847-132617891	NM_146155:50448	Ahdc1	INSIDE	1.132	2.539	2589.28	6574.24	2.874	2032.85	5841.54
A_68_P31613237	chr18:34666453-34666497	NM_146084:3	Fam13b	INSIDE	1.132	1.462	2874.26	4203.33	1.655	2339.14	3870.69
A_68_P23969766	chr5:108415737-108415781	NM_026062:338	Fam69a	INSIDE	1.132	1.456	2521.27	3670.94	1.648	2070.27	3412.25
A_68_P27289254	chr10:80841374-80841418	NM_019757:-281	Fzr1	DIVERGENT_PROMOTER	1.132	1.610	9507.21	15305.59	1.822	6175.11	11253.25
A_68_P22785943	chr4:24423379-24423423	NM_199467:-208	Mms22l	PROMOTER	1.132	2.328	1320.57	3073.64	2.635	1149.53	3028.70
A_68_P23348674	chr4:138469719-138469763	NM_028453:122	Otud3	INSIDE	1.132	4.680	283.97	1328.95	5.299	266.72	1413.40
A_68_P25435746	chr7:121558834-121558878	NM_011055:89	Pde3b	INSIDE	1.132	1.823	732.04	1334.45	2.063	693.75	1431.19
A_68_P22312796	chr3:88058579-88058623	NM_021375:6	Rhbg	INSIDE	1.132	0.517	1728.80	893.81	0.585	1309.53	766.10
A_68_P28517710	chr12:71088293-71088337	NM_022028:-325	Sav1	PROMOTER	1.132	2.472	1362.43	3367.50	2.797	1247.11	3487.91
A_68_P30370350	chr15:79963500-79963544	NM_025609:-61	Tab1	PROMOTER	1.132	2.273	1546.40	3514.63	2.573	1215.44	3127.29
A_68_P20552782	chr1:120524517-120524561	NM_023755:17	Tcfcp2l1	INSIDE	1.132	2.165	479.23	1037.66	2.452	440.91	1081.05
A_68_P27355937	chr10:93297003-93297047	NM_183199:2725	Usp44	INSIDE	1.132	1.866	1594.73	2975.74	2.112	1420.31	2999.49
A_68_P26350324	chr9:21875178-21875222	NM_177318:589	Zfp653	INSIDE	1.132	2.191	1484.34	3252.24	2.480	1254.36	3110.43
A_68_P27243854	chr10:72562038-72562082	ENSMUST00000123398:-29		PROMOTER	1.132	1.546	813.55	1257.52	1.750	691.43	1209.73
A_68_P30980681	chr16:94535120-94535164	ENSMUST00000163193:28		INSIDE	1.132	2.204	421.03	927.89	2.495	443.79	1107.48
A_68_P25956922	chr8:73987506-73987550	NM_022419:28	Abhd8	INSIDE	1.131	2.020	1162.52	2348.78	2.286	989.73	2262.10
A_68_P31792809	chr18:67770642-67770686	NM_001081073:30326	Cep76	DOWNSTREAM	1.131	2.718	912.10	2478.85	3.075	868.89	2671.83
A_68_P21144177	chr2:37648771-37648815	NM_001163566:17024	Crb2	INSIDE	1.131	1.884	942.70	1775.59	2.130	797.93	1699.64
A_68_P22478235	chr3:121426699-121426743	NM_010171:266	F3	INSIDE	1.131	3.407	867.23	2954.66	3.854	775.43	2988.73
A_68_P31769419	chr18:63546533-63546577	NM_001039485:283	Fam38b	INSIDE	1.131	1.997	581.71	1161.72	2.258	567.09	1280.64
A_68_P24084077	chr5:129107075-129107119	NM_175284:116	Fzd10	INSIDE	1.131	1.604	2129.45	3415.30	1.815	1811.96	3288.13
A_68_P25101369	chr7:54051464-54051508	NM_008186:23	Gtf2h1	INSIDE	1.131	1.661	936.05	1554.75	1.879	896.20	1683.89
A_68_P20735838	chr1:156946384-156946428	NM_010500:360	Ier5	INSIDE	1.131	2.201	1244.46	2738.95	2.490	1188.58	2959.83
A_68_P24990860	chr7:19590227-19590271	NM_178757:835	Irf2bp1	INSIDE	1.131	1.763	1837.61	3238.94	1.993	1762.95	3514.40
A_68_P25048200	chr7:35989129-35989173	NM_001024707:11214	Lrp3	INSIDE	1.131	2.902	1181.12	3427.53	3.281	1136.90	3730.09
A_68_P31950785	chr19:10531094-10531138	NM_001111140:821	Lrrc10b	INSIDE	1.131	2.153	1053.08	2267.75	2.435	839.23	2043.34
A_68_P31123769	chr17:28828900-28828944	NM_001168513:-590	Mapk14	PROMOTER	1.131	0.473	1171.18	553.93	0.535	945.80	505.85
A_68_P23912413	chr5:97821466-97821510	NM_001033191:-139	Naa11	PROMOTER	1.131	3.127	490.68	1534.16	3.537	462.38	1635.47
A_68_P27938850	chr11:77500718-77500762	NM_001024205:1100	Nufip2	INSIDE	1.131	1.901	799.40	1519.34	2.149	761.15	1635.71
A_68_P20506805	chr1:108068539-108068583	NM_133821:115	Phlpp1	INSIDE	1.131	1.759	960.77	1689.57	1.989	957.95	1905.39
A_68_P29614457	chr14:55433063-55433107	ENSMUST00000095853:-2239		PROMOTER	1.131	3.954	388.67	1536.94	4.472	346.70	1550.30
A_68_P23964211	chr5:107393205-107393249	NM_009863:-114	Cdc7	PROMOTER	1.130	0.493	1524.97	751.29	0.557	1224.76	681.98
A_68_P30978325	chr16:93919893-93919937	NM_001165925:9898	Cldn14	INSIDE	1.130	2.372	949.97	2253.51	2.680	775.30	2077.44
A_68_P23335797	chr4:136327232-136327276	NM_010142:64596	Ephb2	INSIDE	1.130	2.063	874.58	1804.27	2.330	651.95	1519.16
A_68_P20802634	chr1:168931803-168931847	NM_001160261:277	Fam78b	INSIDE	1.130	0.316	1915.80	605.47	0.357	1718.61	613.93

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28252842	chr12:14156956-14157000	NM_029007:1866	Fam84a	INSIDE	1.130	2.618	555.34	1453.73	2.959	554.02	1639.09
A_68_P24023710	chr5:118426893-118426937	NM_145564:136	Fbxo21	INSIDE	1.130	3.068	500.83	1536.34	3.465	508.89	1763.37
A_68_P20659571	chr1:140740389-140740433	NM_001025565:-1389	Lhx9	PROMOTER	1.130	1.831	1299.75	2379.48	2.069	1055.41	2183.13
A_68_P30397301	chr15:84685820-84685864	NM_001081166:717	Phf21b	INSIDE	1.130	3.178	1138.98	3619.84	3.592	842.94	3028.01
A_68_P25988741	chr8:80959478-80959522	NM_138944:1051	Pou4f2	INSIDE	1.130	3.656	4305.55	15740.83	4.132	3111.38	12857.22
A_68_P28768141	chr12:117724105-117724149	NM_011215:-66	Ptprn2	PROMOTER	1.130	1.583	1074.15	1700.39	1.789	1006.04	1800.06
A_68_P24995080	chr7:20334701-20334745	NM_008990:200	Pvrl2	INSIDE	1.130	1.346	2087.53	2810.35	1.522	1636.76	2490.75
A_68_P30602965	chr16:23431568-23431612	NM_001004151:2385	Rtp1	INSIDE	1.130	2.379	1365.49	3247.93	2.689	1055.37	2837.82
A_68_P32464062	chrX:70918709-70918753	NM_001142809:259	Slc6a8	INSIDE	1.130	2.245	1005.50	2257.49	2.538	600.47	1523.78
A_68_P24946871	chr7:3646125-3646169	NM_024168:37	Tsen34	INSIDE	1.130	1.826	930.72	1699.85	2.064	796.80	1644.50
A_68_P29052703	chr13:55097861-55097905	NM_153131:47090	Unc5a	INSIDE	1.130	1.820	850.05	1547.27	2.057	709.55	1459.72
A_68_P27287691	chr10:80607646-80607690	NM_010731:8653	Zbtb7a	INSIDE	1.130	2.238	891.42	1995.35	2.530	738.06	1866.95
A_68_P23246906	chr4:119406428-119406472	ENSMUST00000123698:5		INSIDE	1.130	1.603	645.40	1034.34	1.811	645.94	1169.68
A_68_P20140407	chr1:34807751-34807795	ENSMUST00000159021:47		INSIDE	1.130	1.687	1158.01	1953.28	1.907	1050.77	2003.67
A_68_P22831248	chr4:34498476-34498520	NM_001007589:635	Akirin2	INSIDE	1.129	1.711	696.00	1190.84	1.932	724.90	1400.82
A_68_P28118513	chr11:109287169-109287213	NM_025275:-69	Amz2	PROMOTER	1.129	3.757	13200.16	49595.05	4.243	9103.96	38625.81
A_68_P30379101	chr15:81524789-81524833	NM_001164320:2907	Chadl	INSIDE	1.129	2.269	506.69	1149.46	2.561	510.76	1308.12
A_68_P23048394	chr4:80557447-80557491	NM_026821:879	D4Bwg0951e	INSIDE	1.129	1.531	1289.37	1974.09	1.729	1187.68	2053.84
A_68_P32571131	chrX:100129101-100129145	NR_026596:440	Gm5126	INSIDE	1.129	1.972	1117.42	2203.20	2.226	614.16	1367.03
A_68_P29616399	chr14:55732726-55732770	NM_177049:3024	Jph4	INSIDE	1.129	2.261	824.86	1865.14	2.552	722.05	1842.75
A_68_P23540978	chr5:23830927-23830971	NM_013569:26474	Kcnh2	INSIDE	1.129	2.988	2107.06	6296.46	3.375	1674.04	5649.80
A_68_P27812422	chr11:54673996-54674040	NM_029327:75	Lyrm7	INSIDE	1.129	1.429	3304.07	4720.10	1.613	2508.60	4045.64
A_68_P23760677	chr5:66651381-66651425	NM_027602:39	Nsun7	INSIDE	1.129	2.403	1435.65	3449.80	2.713	1227.49	3329.77
A_68_P25046335	chr7:35697613-35697657	NM_008820:209	Pepd	INSIDE	1.129	1.376	1225.76	1686.86	1.554	1149.70	1786.12
A_68_P30421717	chr15:88692777-88692821	NM_145478:175	Pim3	INSIDE	1.129	1.394	1000.10	1393.68	1.574	916.11	1441.65
A_68_P31255958	chr17:56556525-56556570	NM_011218:59356	Ptprs	INSIDE	1.129	4.864	4355.83	21185.90	5.492	2882.79	15830.97
A_68_P26750957	chr9:97011068-97011112	NM_138756:370	Slc25a36	INSIDE	1.129	2.684	511.45	1372.60	3.031	488.22	1479.94
A_68_P31320416	chr17:69191045-69191089	NM_001206661:4591	Tmem200c	INSIDE	1.129	2.166	601.76	1303.63	2.446	534.97	1308.47
A_68_P21578172	chr2:120803100-120803144	NM_175285:325	Tmem62	INSIDE	1.129	1.454	1105.95	1608.00	1.642	921.30	1512.60
A_68_P27033726	chr10:28916932-28916976	NM_026138:53153	6330407J23Rik	INSIDE	1.128	1.859	748.58	1391.81	2.098	668.17	1401.64
A_68_P27261497	chr10:75807668-75807712	NM_001081419:317	Dip2a	INSIDE	1.128	3.131	272.03	851.86	3.531	272.92	963.72
A_68_P24114557	chr5:135540470-135540514	NM_025362:417	Dnajc30	INSIDE	1.128	2.133	1776.01	3788.39	2.406	1434.69	3452.13
A_68_P26426831	chr9:36604670-36604714	NM_007915:-39	Ei24	PROMOTER	1.128	1.592	1012.32	1611.88	1.796	922.58	1657.33
A_68_P27325079	chr10:87842398-87842442	NM_001004164:264	Gnptab	INSIDE	1.128	1.342	2931.35	3934.67	1.514	2436.78	3689.79
A_68_P30349001	chr15:76369402-76369446	NM_029643:52	Gpr172b	INSIDE	1.128	1.357	6927.26	9402.20	1.531	4481.62	6861.63
A_68_P29531951	chr14:35632882-35632926	NM_008166:-417	Grid1	PROMOTER	1.128	1.842	492.01	906.46	2.077	427.17	887.38
A_68_P30659189	chr16:33684918-33684962	NM_175256:389	Heg1	INSIDE	1.128	2.272	528.67	1201.19	2.562	558.98	1432.02
A_68_P25952861	chr8:73118130-73118174	NM_023627:-227	Isyna1	PROMOTER	1.128	2.026	3018.72	6117.16	2.286	2862.07	6543.52
A_68_P26164569	chr8:113262564-113262608	NM_198625:17203	Mtss1l	INSIDE	1.128	2.465	381.11	939.34	2.780	287.14	798.36
A_68_P31334901	chr17:71876213-71876257	NM_023294:-37	Ndc80	PROMOTER	1.128	2.978	1733.43	5161.62	3.359	1504.81	5054.96
A_68_P27095769	chr10:42311289-42311333	NM_152229:-7916	Nr2e1	PROMOTER	1.128	2.252	814.51	1833.99	2.540	721.19	1832.09
A_68_P30346946	chr15:76059550-76059594	NM_201385:355	Plec	INSIDE	1.128	1.776	652.58	1158.87	2.004	605.70	1213.76
A_68_P29507012	chr14:31439384-31439428	NM_011103:-12	Prkcd	PROMOTER	1.128	1.764	1693.98	2988.38	1.991	1341.56	2670.65
A_68_P27680407	chr11:30671725-30671769	NM_134013:-28	Psme4	PROMOTER	1.128	3.983	557.55	2220.92	4.491	488.03	2191.96
A_68_P30964118	chr16:91647937-91647981	NM_019973:-110	Son	DIVERGENT_PROMOTER	1.128	1.459	719.73	1049.93	1.646	583.50	960.53
A_68_P24136155	chr5:140020104-140020148	NM_013702:275	Uncx	INSIDE	1.128	2.398	418.23	1002.95	2.705	376.69	1019.00
A_68_P22682765	chr3:157610022-157610066	NM_001013806:-385	Ankrd13c	PROMOTER	1.127	2.003	281.45	563.66	2.258	262.83	593.44
A_68_P27383822	chr10:98377388-98377432	NM_026482:-375	Atp2b1	PROMOTER	1.127	1.958	1082.85	2120.25	2.206	1071.78	2364.26
A_68_P23262157	chr4:123019781-123019825	NM_007558:244	Bmp8a	INSIDE	1.127	1.526	2048.80	3126.73	1.721	1635.69	2814.47
A_68_P25601079	chr7:150645980-150646024	NM_001161624:953	Cdkn1c	INSIDE	1.127	2.138	1118.53	2391.11	2.410	926.98	2233.96
A_68_P25416676	chr7:118172200-118172244	NM_009431:-242	Ctr9	PROMOTER	1.127	2.911	2509.27	7304.92	3.281	1987.88	6521.38

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26702587	chr9:86916837-86916881	NM_024195:-5	Cyb5r4	PROMOTER	1.127	1.823	754.56	1375.67	2.056	720.12	1480.25
A_68_P32121690	chr19:42593224-42593268	NM_177464:-48	D19Ertd386e	PROMOTER	1.127	1.817	1137.00	2065.65	2.048	1086.35	2224.81
A_68_P25804901	chr8:41393403-41393447	NM_030110:20	Efha2	INSIDE	1.127	2.683	495.32	1329.13	3.025	443.06	1340.16
A_68_P21978661	chr3:20055140-20055184	NM_013755:-167	Gyg	PROMOTER	1.127	1.955	1641.92	3209.14	2.202	1347.68	2967.28
A_68_P24874508	chr6:136756818-136756862	NM_177688:72	H2afj	INSIDE	1.127	1.433	1278.02	1831.51	1.615	1066.15	1721.33
A_68_P32317010	chrX:33652351-33652395	NM_133990:239	Il13ra1	INSIDE	1.127	1.899	4506.61	8558.69	2.140	2304.04	4930.72
A_68_P29629465	chr14:58318680-58318724	NM_015771:46258	Lats2	INSIDE	1.127	2.930	504.95	1479.46	3.301	495.60	1636.15
A_68_P22530171	chr3:130814691-130814735	NM_010703:1324	Lef1	INSIDE	1.127	1.429	2297.82	3284.60	1.610	1885.12	3035.82
A_68_P24947963	chr7:4098615-4098659	NM_172736:9979	Leng8	INSIDE	1.127	1.830	439.99	805.26	2.063	385.96	796.09
A_68_P25962049	chr8:75072127-75072171	NM_027485:61	Med26	INSIDE	1.127	1.502	3907.00	5867.53	1.693	3200.25	5416.89
A_68_P21117012	chr2:32568363-32568407	NR_037217:24	Mir2861	INSIDE	1.127	3.167	835.73	2647.07	3.571	799.84	2856.20
A_68_P30489319	chr15:100883076-100883120	NM_011323:116397	Scn8a	DOWNSTREAM	1.127	2.092	1309.64	2740.06	2.358	1253.14	2955.06
A_68_P23330839	chr4:135411815-135411861	NM_001080387:-168	Srsf10	PROMOTER	1.127	1.682	3204.38	5389.99	1.896	2995.58	5681.04
A_68_P23012916	chr4:71861284-71861328	NM_011599:647	Tle1	INSIDE	1.127	2.671	1196.33	3194.96	3.009	952.46	2866.07
A_68_P25507829	chr7:135020578-135020622	NM_146259:-263	Zfp668	DIVERGENT_PROMOTER	1.127	2.046	823.32	1684.78	2.307	742.75	1713.48
A_68_P28724524	chr12:109155065-109155109	NM_001079883:86538	Bcl11b	INSIDE	1.126	2.863	1903.33	5449.60	3.223	1611.25	5192.94
A_68_P27170202	chr10:59165196-59165240	NM_144822:-164	Cbara1	PROMOTER	1.126	2.006	4977.36	9985.92	2.258	3719.38	8399.22
A_68_P30398340	chr15:84867516-84867560	NM_177067:47	Fam118a	INSIDE	1.126	2.443	1611.58	3937.51	2.752	1407.99	3874.08
A_68_P21903071	chr2:180069548-180069594	NM_008093:-186	Gata5	PROMOTER	1.126	1.623	1135.94	1843.92	1.827	976.85	1785.10
A_68_P26803568	chr9:106367195-106367239	NM_001159652:1055	Gpr62	INSIDE	1.126	1.666	386.43	643.71	1.875	384.51	720.93
A_68_P23609898	chr5:37221813-37221857	NM_008550:54	Man2b2	INSIDE	1.126	2.762	327.00	903.21	3.110	277.74	863.68
A_68_P23165465	chr4:102986727-102986771	NM_025909:298	Oma1	INSIDE	1.126	5.112	1188.71	6077.25	5.755	1120.92	6450.42
A_68_P27898397	chr11:69810791-69810835	NM_030064:1540	Phf23	INSIDE	1.126	2.066	7259.79	15002.29	2.327	5141.65	11964.06
A_68_P26463563	chr9:43552020-43552064	NM_021424:-616	Pvrl1	PROMOTER	1.126	2.202	1633.90	3597.46	2.479	1477.24	3661.51
A_68_P29043022	chr13:53381392-53381436	NM_013846:64	Ror2	INSIDE	1.126	3.425	617.86	2116.16	3.856	536.08	2067.12
A_68_P27138496	chr10:52410751-52410795	NM_178675:466	Slc35f1	INSIDE	1.126	1.990	1572.59	3130.09	2.241	1336.97	2995.73
A_68_P31092361	chr17:23694750-23694794	NM_001033496:6421	Zfp213	INSIDE	1.126	1.829	798.17	1460.02	2.059	675.76	1391.72
A_68_P26721513	chr9:91260697-91260741	NM_009573:-81	Zic1	DIVERGENT_PROMOTER	1.126	1.830	844.72	1545.93	2.060	792.22	1631.95
A_68_P26397765	chr9:30750581-30750625	NM_013906:455	Adamts8	INSIDE	1.125	2.011	278.48	559.91	2.263	326.96	739.84
A_68_P20415724	chr1:88995295-88995339	NM_001081082:2865	Alpi	INSIDE	1.125	2.535	1740.25	4411.02	2.851	1512.82	4312.72
A_68_P31126995	chr17:29405863-29405907	NM_030561:152	BC004004	INSIDE	1.125	4.399	837.45	3684.17	4.947	928.52	4593.58
A_68_P30577277	chr16:18066405-18066449	NM_010047:13474	Dgcr6	INSIDE	1.125	2.111	622.10	1313.52	2.375	589.46	1399.75
A_68_P26467018	chr9:44134953-44134997	NM_007875:47	Dpagt1	INSIDE	1.125	1.704	1665.61	2838.60	1.917	1318.30	2527.30
A_68_P22143243	chr3:53461165-53461209	NM_172862:91	Frem2	INSIDE	1.125	0.561	1229.20	689.04	0.631	1013.81	639.35
A_68_P29919651	chr14:115491767-115491811	NM_175500:352	Gpc5	INSIDE	1.125	1.438	1690.74	2430.92	1.618	1455.25	2354.06
A_68_P29363818	chr13:118391526-118391570	NM_010408:422	Hcn1	INSIDE	1.125	1.481	1062.38	1572.93	1.666	931.13	1551.41
A_68_P28041908	chr11:95866113-95866157	NM_009951:1124	Igf2bp1	INSIDE	1.125	1.694	717.37	1215.34	1.906	660.05	1258.22
A_68_P26348939	chr9:21599872-21599916	NM_145611:3096	Kank2	INSIDE	1.125	3.439	382.15	1314.14	3.868	340.80	1318.37
A_68_P29330802	chr13:112598180-112598224	NM_011945:989	Map3k1	INSIDE	1.125	1.958	1148.76	2249.64	2.204	1021.70	2251.52
A_68_P22171318	chr3:58810124-58810168	NM_177855:-753	Med12l	PROMOTER	1.125	4.283	1021.22	4374.12	4.820	881.59	4249.61
A_68_P29020016	chr13:48641931-48641975	NR_029725:-8311	Mirlet7a-1	PROMOTER	1.125	0.466	1396.43	651.43	0.525	1184.86	621.63
A_68_P31478451	chr18:7626517-7626561	NM_001081287:323	Mpp7	INSIDE	1.125	1.504	2215.94	3333.11	1.693	1868.73	3163.29
A_68_P30506992	chr16:3884518-3884562	NM_029090:-78	Nat15	PROMOTER	1.125	2.018	1018.83	2056.29	2.271	959.87	2180.16
A_68_P21096075	chr2:29107688-29107733	NM_133500:-4150	Ntng2	PROMOTER	1.125	1.354	3110.70	4212.44	1.523	2243.73	3417.78
A_68_P30392999	chr15:83998465-83998509	NM_054088:241	Pnpla3	INSIDE	1.125	1.500	1090.90	1636.51	1.688	843.21	1423.21
A_68_P24010226	chr5:116009731-116009775	NM_007475:277	Rplp0	INSIDE	1.125	1.643	987.19	1622.35	1.849	821.63	1518.89
A_68_P30345849	chr15:75899507-75899551	NM_134089:632	Scrib	INSIDE	1.125	1.881	480.74	904.32	2.117	420.75	890.66
A_68_P30572143	chr16:17131714-17131758	NM_022324:740	Sdf2l1	INSIDE	1.125	2.034	1252.01	2546.19	2.288	964.51	2207.23
A_68_P31253057	chr17:56110074-56110118	NM_001159523:192	Shd	INSIDE	1.125	1.748	842.82	1472.92	1.967	711.24	1398.88
A_68_P22049386	chr3:34548677-34548721	NM_011443:-228	Sox2	PROMOTER	1.125	1.999	2345.89	4690.46	2.249	1956.16	4399.36
A_68_P28137857	chr11:112646792-112646839	NM_011448:3292	Sox9	INSIDE	1.125	1.925	389.88	750.50	2.165	311.62	674.72

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P21328888	chr2:72818835-72818879	NM_001018042:-353	Sp3	PROMOTER	1.125	1.616	663.56	1072.08	1.818	670.89	1219.78
A_68_P27316753	chr10:86371829-86371873	NM_138673:98837	Stab2	INSIDE	1.125	3.402	3564.78	12127.28	3.827	2463.71	9429.19
A_68_P29619289	chr14:56300469-56300513	NM_145705:164	Tinf2	INSIDE	1.125	0.541	966.05	522.83	0.609	872.28	531.09
A_68_P23253640	chr4:120527812-120527856	ENSMUST00000106283:-6547		PROMOTER	1.125	0.498	1439.94	716.85	0.560	1221.75	684.51
A_68_P30753194	chr16:50732861-50732905	NR_028300:4	5330426P16Rik	INSIDE	1.124	1.619	1755.53	2842.94	1.821	1473.33	2682.76
A_68_P21477087	chr2:102290962-102291006	NM_010218:965	Fjx1	INSIDE	1.124	1.437	1031.17	1481.36	1.615	916.58	1480.38
A_68_P23404325	chr4:149475753-149475801	NM_177366:14165	Gpr157	INSIDE	1.124	2.965	880.82	2611.72	3.334	642.22	2140.87
A_68_P31936713	chr19:7000522-7000566	NM_008431:8461	Kcnk4	INSIDE	1.124	1.523	707.45	1077.34	1.712	615.21	1053.30
A_68_P22629212	chr3:148482607-148482651	NM_001081298:134971	Lphn2	INSIDE	1.124	2.333	916.79	2139.02	2.622	775.73	2034.33
A_68_P29360869	chr13:117813423-117813467	NM_001081009:879	Parp8	INSIDE	1.124	2.116	964.43	2041.21	2.380	921.32	2192.53
A_68_P21250383	chr2:58999148-58999192	NM_026361:264	Pkp4	INSIDE	1.124	2.186	862.41	1885.42	2.458	739.05	1816.46
A_68_P23236665	chr4:117508655-117508699	NM_008135:814	Slc6a9	INSIDE	1.124	1.965	2599.01	5107.11	2.208	1728.01	3815.76
A_68_P20002770	chr1:3661760-3661804	NM_001011874:-203	Xkr4	PROMOTER	1.124	2.102	577.43	1214.00	2.363	544.73	1286.96
A_68_P20286079	chr1:63319663-63319707	NM_028673:-158	Zdbf2	PROMOTER	1.124	0.562	1637.97	921.24	0.632	1465.82	926.32
A_68_P24155695	chr5:144016767-144016811	NM_017467:14913	Zfp316	INSIDE	1.124	2.209	2534.23	5598.63	2.483	2186.21	5428.60
A_68_P21844246	chr2:168760814-168760858	NM_009564:20251	Zfp64	INSIDE	1.124	3.814	2479.37	9455.26	4.287	2093.05	8972.35
A_68_P22360098	chr3:98232509-98232553	NM_172863:46127	Zfp697	INSIDE	1.124	2.797	707.86	1980.00	3.144	553.85	1741.06
A_68_P27835192	chr11:58977171-58977215	NM_173785:52	A230051G13Rik	INSIDE	1.123	1.786	433.89	775.06	2.005	412.37	826.87
A_68_P31016357	chr17:5342164-5342208	NM_001085355:347113	Arid1b	INSIDE	1.123	2.644	663.18	1753.23	2.969	479.02	1422.15
A_68_P23244382	chr4:118905317-118905361	NM_001012400:-9	AU022252	DIVERGENT_PROMOTER	1.123	1.442	1404.68	2026.13	1.620	1063.93	1723.14
A_68_P25952217	chr8:73018186-73018230	NM_018827:1154	Crlf1	INSIDE	1.123	1.798	5505.74	9900.80	2.020	4030.02	8140.75
A_68_P25416832	chr7:118198930-118198974	NM_009431:26488	Ctr9	INSIDE	1.123	2.798	260.89	730.04	3.142	239.10	751.26
A_68_P31329272	chr17:70865492-70865536	NM_001128180:-5935	Dlgap1	PROMOTER	1.123	2.935	1908.73	5602.06	3.295	1435.61	4730.44
A_68_P30087404	chr15:26473244-26473288	NM_176959:352053	Fbxl7	INSIDE	1.123	1.753	538.92	944.86	1.969	483.75	952.54
A_68_P30367928	chr15:79521367-79521411	NM_013818:63	Gtpbp1	INSIDE	1.123	3.069	635.17	1949.07	3.446	634.33	2185.78
A_68_P31075109	chr17:17975189-17975234	NM_001162909:7273	Ncrna00085	INSIDE	1.123	3.469	605.57	2100.56	3.894	558.81	2176.19
A_68_P30558912	chr16:13780955-13780999	NM_001039521:185	Rrn3	INSIDE	1.123	2.433	258.03	627.69	2.732	280.10	765.35
A_68_P31857887	chr18:79306987-79307031	NM_053099:-878	Setbp1	PROMOTER	1.123	0.497	1281.86	636.88	0.558	1098.54	612.95
A_68_P21911426	chr2:181316540-181316584	NM_026765:116	Uckl1	INSIDE	1.123	2.656	1267.55	3367.00	2.983	1110.50	3312.11
A_68_P32129546	chr19:44014604-44014648	ENSMUST00000122692:7821		DOWNSTREAM	1.123	1.731	2898.59	5017.33	1.943	2287.84	4445.72
A_68_P21040892	chr2:18611762-18611806	NM_001001334:-8864	BC061194	PROMOTER	1.122	0.519	1628.27	844.76	0.582	1449.80	843.79
A_68_P27278227	chr10:79144709-79144753	NM_177613:-209	Cdc34	PROMOTER	1.122	0.465	1950.56	906.64	0.522	1612.26	840.94
A_68_P31125955	chr17:29235539-29235583	NM_007669:4844	Cdkn1a	INSIDE	1.122	2.972	502.58	1493.77	3.336	409.77	1366.84
A_68_P28075715	chr11:101645928-101645972	NM_008815:674	Etv4	INSIDE	1.122	2.141	970.35	2077.23	2.402	990.51	2379.56
A_68_P31876064	chr18:82575063-82575107	NM_008082:1085	Galr1	INSIDE	1.122	1.995	1520.40	3032.62	2.238	1261.61	2824.04
A_68_P30347942	chr15:76211135-76211179	NM_001162489:-9304	Heatr7a	PROMOTER	1.122	1.474	1749.03	2578.93	1.655	1362.20	2254.57
A_68_P28044023	chr11:96214672-96214716	NM_134032:1749	Hoxb2	INSIDE	1.122	1.727	938.09	1620.24	1.938	789.67	1529.99
A_68_P26674972	chr9:81525625-81525671	NM_010482:511	Htr1b	INSIDE	1.122	1.738	911.08	1583.83	1.951	819.14	1597.96
A_68_P24479788	chr6:57652816-57652860	NM_133737:390	Lancl2	INSIDE	1.122	1.545	2724.07	4208.06	1.734	2402.54	4165.97
A_68_P24652024	chr6:93628341-93628385	NM_001083320:235322	Magi1	INSIDE	1.122	3.051	846.76	2583.12	3.423	681.07	2331.16
A_68_P31779043	chr18:65243488-65243532	NM_031881:60330	Nedd4l	INSIDE	1.122	2.066	1240.90	2563.21	2.317	1049.16	2430.79
A_68_P27709960	chr11:35821756-35821800	NM_011856:935967	Odz2	INSIDE	1.122	2.553	741.30	1892.76	2.865	568.48	1628.59
A_68_P28168391	chr11:117848501-117848545	NM_133757:352	Pgs1	INSIDE	1.122	1.519	1115.17	1694.49	1.706	956.84	1632.00
A_68_P29471618	chr14:25306180-25306224	NM_001081247:66	Polr3a	INSIDE	1.122	1.601	518.23	829.50	1.795	439.62	789.19
A_68_P31407761	chr17:85357878-85357922	NM_001159496:560	Ppm1b	INSIDE	1.122	4.425	755.98	3345.11	4.965	671.37	3333.25
A_68_P21095251	chr2:28980877-28980921	NM_198033:387	Setx	INSIDE	1.122	1.525	642.35	979.81	1.711	537.64	919.91
A_68_P29664628	chr14:64563075-64563120	NM_011446:555	Sox7	INSIDE	1.122	2.820	273.05	769.89	3.164	232.25	734.88
A_68_P30580644	chr16:18592043-18592087	NM_011532:-5002	Tbx1	PROMOTER	1.122	0.571	1145.30	653.68	0.640	948.06	606.86
A_68_P25102684	chr7:54305881-54305925	NM_026436:-107	Tmem86a	PROMOTER	1.122	2.063	564.73	1164.84	2.315	582.82	1349.42
A_68_P24425525	chr6:47997586-47997630	NM_001081382:505	Zfp777	INSIDE	1.122	1.448	766.77	1110.37	1.625	685.61	1114.02
A_68_P25600984	chr7:150631945-150631989			Unknown	1.122	1.398	1065.69	1490.18	1.569	1054.23	1654.22

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P24093843	chr5:130925785-130925831	NM_021371:1147	Caln1	INSIDE	1.121	3.360	181.75	610.69	3.767	153.56	578.45
A_68_P28331591	chr12:32183927-32183971	NM_134048:457	Cbll1	INSIDE	1.121	1.762	3052.27	5376.65	1.974	2421.00	4780.18
A_68_P23201930	chr4:109330255-109330299	NM_007671:7701	Cdkn2c	DOWNSTREAM	1.121	1.866	1386.97	2588.58	2.091	1206.84	2523.92
A_68_P24994187	chr7:20172257-20172301	NM_016680:17539	Clasrp	INSIDE	1.121	2.314	336.27	778.07	2.594	293.16	760.49
A_68_P26221731	chr8:123191547-123191591	NM_010926:444	Cox4nb	INSIDE	1.121	1.526	601.10	917.29	1.711	524.80	897.81
A_68_P23190560	chr4:107107097-107107141	NM_147221:-205	Glis1	PROMOTER	1.121	2.399	433.66	1040.29	2.688	422.84	1136.72
A_68_P30580075	chr16:18498740-18498784	NM_001081682:-98	Gnb1l	PROMOTER	1.121	4.066	4129.99	16792.92	4.560	3299.08	15042.29
A_68_P27278461	chr10:79180701-79180746	NM_008226:1345	Hcn2	INSIDE	1.121	3.153	2683.44	8461.71	3.534	1931.89	6826.56
A_68_P32094346	chr19:37282376-37282420	NM_001164337:364	Marchf5	INSIDE	1.121	2.081	1008.82	2099.36	2.333	912.38	2128.66
A_68_P30422455	chr15:88813114-88813158	NM_031260:-287	Mov10l1	DIVERGENT_PROMOTER	1.121	2.128	2273.16	4837.85	2.385	1706.98	4070.87
A_68_P20961511	chr2:3201548-3201592	NM_008708:11	Nmt2	INSIDE	1.121	2.092	330.52	691.59	2.346	364.06	854.21
A_68_P20797853	chr1:167932451-167932495	NM_011137:293	Pou2f1	INSIDE	1.121	1.428	1479.75	2112.56	1.601	1246.58	1995.60
A_68_P31929630	chr19:5602393-5602437	NM_026616:542	Rnaseh2c	INSIDE	1.121	1.413	4440.56	6275.22	1.585	3018.56	4783.04
A_68_P23896968	chr5:93371161-93371205	NM_001077596:44159	Shroom3	INSIDE	1.121	2.532	920.68	2330.91	2.838	816.76	2317.61
A_68_P20870658	chr1:181448224-181448272	NM_027188:-114	Smyd3	PROMOTER	1.121	4.340	590.33	2562.23	4.865	547.57	2663.98
A_68_P32246204	chrX:8849773-8849817	NM_023500:-115	Xk	PROMOTER	1.121	3.704	336.44	1246.18	4.152	218.63	907.79
A_68_P21565889	chr2:118571987-118572031	NR_030716:511	5430417L22Rik	INSIDE	1.120	1.486	610.76	907.70	1.664	471.16	784.02
A_68_P26744297	chr9:95758279-95758323	NM_019864:285	Atr	INSIDE	1.120	1.587	748.90	1188.77	1.778	597.84	1063.13
A_68_P28752184	chr12:113977018-113977062	NM_001024602:16656	AW555464	INSIDE	1.120	2.674	1336.86	3574.81	2.994	1027.27	3075.56
A_68_P31382676	chr17:80772525-80772569	NR_028385:336	Gm10190	INSIDE	1.120	2.192	553.15	1212.38	2.454	513.84	1260.95
A_68_P22954219	chr4:59048073-59048117	NM_025277:67	Gng10	INSIDE	1.120	4.538	1394.87	6330.21	5.085	1370.41	6968.52
A_68_P25958331	chr8:74213094-74213138	NM_013564:-34	Insl3	PROMOTER	1.120	1.626	823.07	1338.24	1.821	701.25	1276.68
A_68_P22481651	chr3:121996059-121996103	NR_030439:541	Mir760	DOWNSTREAM	1.120	2.126	448.39	953.45	2.381	459.44	1093.81
A_68_P21742435	chr2:150864820-150864864	NM_026086:273	Nanp	INSIDE	1.120	1.852	881.80	1633.27	2.074	781.06	1620.22
A_68_P21907359	chr2:180689094-180689138	NM_001141933:288	Nkain4	INSIDE	1.120	2.360	1131.09	2669.47	2.644	917.62	2426.02
A_68_P27889317	chr11:68245685-68245729	NM_177320:80	Pik3r5	INSIDE	1.120	1.729	506.43	875.69	1.936	471.89	913.70
A_68_P24059411	chr5:124571440-124571484	NM_011256:94965	Pitpnm2	INSIDE	1.120	2.346	567.72	1331.95	2.627	546.52	1435.45
A_68_P23365303	chr4:141219467-141219511	NM_001033150:542	Plekhm2	INSIDE	1.120	1.622	1466.94	2378.87	1.816	1239.60	2251.09
A_68_P32599601	chrX:108577069-108577113	NM_025949:74464	Rps6ka6	INSIDE	1.120	1.643	1972.86	3241.21	1.841	1166.85	2147.90
A_68_P25026631	chr7:30117136-30117180	NM_001081028:173321	Sipa1l3	INSIDE	1.120	3.059	2587.23	7913.82	3.427	1948.58	6678.30
A_68_P27214753	chr10:67374987-67375031	NM_178679:402	Zfp365	INSIDE	1.120	1.797	601.61	1081.00	2.012	528.76	1063.92
A_68_P26202777	chr8:119960582-119960626	NM_028941:87535	4933407C03Rik	INSIDE	1.119	2.332	584.79	1363.68	2.610	480.30	1253.47
A_68_P20977505	chr2:6051162-6051206	NM_001159657:47	5430407P10Rik	INSIDE	1.119	2.389	8410.86	20096.31	2.674	7513.35	20090.52
A_68_P20770260	chr1:163072965-163073010	NM_028664:145	Ankrd45	INSIDE	1.119	0.529	1247.57	660.19	0.592	974.04	576.73
A_68_P23915348	chr5:98364470-98364514	NM_133738:95489	Antxr2	INSIDE	1.119	2.120	1242.38	2633.50	2.372	1133.00	2687.86
A_68_P30462677	chr15:96115709-96115753	NM_175251:-2222	Arid2	PROMOTER	1.119	1.739	718.22	1249.29	1.946	719.96	1400.90
A_68_P20958788	chr1:196803083-196803130	NR_033564:47	C030002c11rik	INSIDE	1.119	2.151	717.23	1542.80	2.408	601.27	1447.62
A_68_P24420943	chr6:46994568-46994616	NM_001004357:1984533	Cntnap2	INSIDE	1.119	3.359	2278.37	7652.07	3.758	1893.91	7116.73
A_68_P26802913	chr9:106271467-106271511	NM_153459:526	Dusp7	INSIDE	1.119	0.573	1527.48	874.68	0.641	1155.71	740.71
A_68_P26200115	chr8:119516976-119517022	NM_026572:351	Gcsh	INSIDE	1.119	1.450	1471.21	2133.09	1.622	1306.36	2119.18
A_68_P26567943	chr9:61794500-61794544	NM_024245:84	Kif23	INSIDE	1.119	1.472	1282.91	1888.45	1.647	1028.16	1693.63
A_68_P29725081	chr14:75347579-75347623	NM_001033439:84	Lrch1	INSIDE	1.119	1.622	3333.98	5409.35	1.815	2695.17	4892.12
A_68_P21309974	chr2:69423570-69423614	NM_001081088:532	Lrp2	INSIDE	1.119	1.903	1382.58	2631.31	2.131	1206.67	2570.83
A_68_P21742300	chr2:150835045-150835089	NM_207204:68	Ninl	INSIDE	1.119	2.545	799.09	2033.39	2.847	712.29	2027.63
A_68_P23295438	chr4:128866763-128866807	NM_029036:-58	S100pbp	DIVERGENT_PROMOTER	1.119	1.405	2416.59	3394.19	1.571	2105.69	3308.04
A_68_P25586715	chr7:148286395-148286439	NM_023059:29	Sigirr	INSIDE	1.119	1.568	807.70	1266.29	1.754	725.84	1273.46
A_68_P25102014	chr7:54175443-54175487	NM_021884:-164	Tsg101	PROMOTER	1.119	1.970	1145.27	2256.14	2.205	988.56	2179.73
A_68_P30149950	chr15:38448838-38448882	NM_001102458:161	Azin1	INSIDE	1.118	0.528	991.93	523.53	0.590	861.13	508.13
A_68_P28752688	chr12:114047423-114047467	NM_145450:259	BC022687	INSIDE	1.118	1.656	1170.68	1939.07	1.851	933.36	1728.11
A_68_P21485631	chr2:103637120-103637164	NM_001111289:93	Caprin1	INSIDE	1.118	0.506	2067.90	1047.34	0.566	1607.56	910.60
A_68_P27934410	chr11:76660169-76660213	NM_007754:320	Cpd	INSIDE	1.118	2.471	825.48	2039.58	2.762	706.44	1951.44

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28051739	chr11:97490327-97490371	NM_175332:682	E130012A19Rik	INSIDE	1.118	2.757	390.68	1077.25	3.082	352.10	1084.99
A_68_P27278197	chr10:79138491-79138535	NM_148934:6358	Gm16517	INSIDE	1.118	3.378	1917.71	6478.74	3.776	1572.14	5935.78
A_68_P26682077	chr9:83039520-83039564	NM_026122:672	Hmgn3	INSIDE	1.118	1.602	1610.26	2579.30	1.790	1387.80	2484.26
A_68_P27865437	chr11:64248821-64248865	NM_178870:9	Hs3st3a1	INSIDE	1.118	1.960	1164.46	2282.50	2.191	988.93	2166.46
A_68_P22698900	chr4:4720461-4720505	NM_177730:-29	Impad1	PROMOTER	1.118	2.283	305.10	696.60	2.553	307.91	786.01
A_68_P21834186	chr2:167015822-167015866	NM_008420:-1545	Kcnb1	PROMOTER	1.118	1.765	846.31	1493.40	1.973	779.28	1537.66
A_68_P25034375	chr7:31758234-31758278	NM_001164184:232	Lsr	INSIDE	1.118	3.748	1408.83	5279.87	4.188	1133.35	4746.87
A_68_P29154200	chr13:76521644-76521688	NM_030174:-742	Mctp1	PROMOTER	1.118	1.674	586.81	982.13	1.871	551.60	1032.07
A_68_P29269010	chr13:101322324-101322368	NM_008756:107	Ocln	INSIDE	1.118	2.393	1313.83	3144.51	2.675	1164.18	3114.39
A_68_P28974190	chr13:40827038-40827082	NM_001122948:-1248	Tcfap2a	PROMOTER	1.118	1.546	2189.51	3385.25	1.729	1854.80	3206.15
A_68_P33007019	A_68_P33007019			Unknown	1.118	1.718	7636.02	13119.22	1.921	6500.10	12484.72
A_68_P32977626	A_68_P32977626			Unknown	1.118	2.148	250.87	538.96	2.402	196.25	471.41
A_68_P29056007	chr13:55701465-55701509	NM_146045:15	B4galt7	INSIDE	1.117	1.664	2212.00	3681.16	1.859	1699.60	3159.23
A_68_P30836894	chr16:67620955-67620999	NM_001145977:177	Cadm2	INSIDE	1.117	2.724	3542.30	9649.26	3.044	2838.72	8641.29
A_68_P20432996	chr1:91827206-91827250	NM_010262:523	Gbx2	INSIDE	1.117	1.937	4102.88	7948.25	2.163	3588.59	7763.11
A_68_P25842950	chr8:48760715-48760759	NM_023503:-223	Ing2	PROMOTER	1.117	1.899	1125.08	2136.16	2.121	1007.55	2136.62
A_68_P26228656	chr8:124277409-124277453	NM_020605:22972	Jph3	INSIDE	1.117	3.656	1070.93	3915.12	4.084	930.01	3797.91
A_68_P27285769	chr10:80298722-80298766	NM_001013758:8040	Lingo3	INSIDE	1.117	2.229	892.09	1988.62	2.489	823.80	2050.59
A_68_P24065425	chr5:125658527-125658571	NM_011424:1036	Ncor2	INSIDE	1.117	1.615	1164.70	1880.86	1.805	993.57	1793.04
A_68_P27289568	chr10:80882945-80882989	NM_008688:6952	Nfic	INSIDE	1.117	2.828	1756.96	4969.52	3.159	1329.80	4200.48
A_68_P32089884	chr19:36484605-36484649	NM_029508:31070	Pcgf5	INSIDE	1.117	3.238	263.75	853.95	3.617	289.07	1045.50
A_68_P29341546	chr13:114408820-114408864	NM_130796:-70	Snx18	PROMOTER	1.117	2.215	373.58	827.36	2.475	355.67	880.15
A_68_P28051298	chr11:97413135-97413179	NM_018873:23284	Srcin1	INSIDE	1.117	2.247	1005.72	2260.14	2.510	860.66	2160.05
A_68_P24593027	chr6:83318037-83318081	NM_183138:73614	Tet3	INSIDE	1.117	1.521	737.64	1121.77	1.699	697.04	1183.97
A_68_P29998443	chr15:8119317-8119361	NM_001162906:233	2410089E03Rik	INSIDE	1.116	1.501	1002.48	1505.21	1.675	847.70	1419.87
A_68_P26601253	chr9:67679488-67679532	NM_001163143:627	C2cd4a	INSIDE	1.116	0.579	2142.64	1240.46	0.646	1646.71	1064.16
A_68_P31103373	chr17:25522563-25522607	NM_001163691:48144	Cacna1h	INSIDE	1.116	2.200	1594.60	3508.64	2.456	1271.47	3122.18
A_68_P27101045	chr10:43298595-43298639	NM_009846:-358	Cd24a	PROMOTER	1.116	1.659	1624.72	2695.90	1.851	1304.70	2414.99
A_68_P25582339	chr7:147302298-147302342	NM_053119:2	Echs1	INSIDE	1.116	1.380	2731.68	3768.61	1.539	2205.72	3394.84
A_68_P28198383	chr12:4038752-4038796	NM_001082483:141	Efr3b	INSIDE	1.116	1.659	1178.53	1955.39	1.852	906.67	1679.13
A_68_P28577470	chr12:81858836-81858880	NM_001008423:2844	Gm1568	INSIDE	1.116	3.116	425.19	1325.03	3.477	397.47	1382.16
A_68_P24326993	chr6:29457921-29457965	NM_001029985:10	Kcp	INSIDE	1.116	1.460	1608.78	2348.02	1.630	1361.76	2219.01
A_68_P30349814	chr15:76497752-76497796	NM_010630:6704	Kifc2	INSIDE	1.116	2.587	1147.70	2968.96	2.888	958.87	2768.77
A_68_P22218636	chr3:68810008-68810052	NR_029529:-3663	Mir15b	PROMOTER	1.116	2.535	1158.84	2937.45	2.829	999.36	2827.23
A_68_P30132612	chr15:35225823-35225867	NM_054049:-22	Osr2	PROMOTER	1.116	2.510	1294.26	3248.09	2.800	1302.66	3647.52
A_68_P30346580	chr15:76007443-76007487	NM_201394:18676	Plec	INSIDE	1.116	2.179	505.18	1100.96	2.433	424.99	1033.88
A_68_P26022782	chr8:87469669-87469713	NM_144929:-1199	Rtbdn	DIVERGENT_PROMOTER	1.116	2.277	731.92	1666.68	2.541	676.60	1719.38
A_68_P31677778	chr18:46756824-46756868	NM_025698:343	Tmed7	INSIDE	1.116	2.791	628.93	1755.62	3.116	540.29	1683.46
A_68_P28166387	chr11:117516412-117516456	NM_198022:832	Tnrc6c	INSIDE	1.116	5.767	469.60	2708.04	6.435	501.11	3224.86
A_68_P25008268	chr7:25866633-25866677	NM_175477:4390	Zfp574	INSIDE	1.116	1.888	1529.88	2887.88	2.107	1202.26	2532.57
A_68_P20049945	chr1:15277016-15277060			Unknown	1.116	2.104	4269.61	8982.19	2.349	3589.69	8431.53
A_68_P28751869	chr12:113931759-113931803	AK028601:1		INSIDE	1.116	1.522	1468.97	2235.45	1.699	1275.23	2166.20
A_68_P23437422	chr4:154624331-154624375	NM_001190445:278	2610002J02Rik	INSIDE	1.115	1.638	5100.60	8357.15	1.828	3421.28	6253.01
A_68_P26548139	chr9:58335761-58335806	NM_176921:-626	6030419C18Rik	PROMOTER	1.115	1.504	2498.16	3758.16	1.677	2009.98	3371.06
A_68_P32151689	chr19:47806170-47806214	NM_026377:-53	6330577E15Rik	PROMOTER	1.115	1.534	915.79	1404.87	1.711	802.12	1372.21
A_68_P20825059	chr1:172797927-172797976	NM_001081304:-49	Atf6	PROMOTER	1.115	1.508	2595.38	3913.20	1.682	1975.76	3322.78
A_68_P29977215	chr15:3977091-3977135	NR_028266:294	BC037032	INSIDE	1.115	1.651	487.07	804.29	1.841	442.14	813.92
A_68_P28056294	chr11:98274418-98274462	NM_001003817:643	Erbb2	INSIDE	1.115	1.754	1283.51	2251.25	1.955	1241.19	2426.34
A_68_P26132791	chr8:107817394-107817438	NM_177788:2582	Exoc3l	INSIDE	1.115	2.419	1005.77	2432.82	2.696	896.78	2417.66
A_68_P23917032	chr5:98683315-98683359	NM_010203:134	Fgf5	INSIDE	1.115	1.879	1700.68	3195.80	2.095	1375.73	2881.99
A_68_P27946742	chr11:78858560-78858604	NM_013571:101274	Ksr1	INSIDE	1.115	3.805	2731.57	10394.15	4.241	1933.37	8200.24

						Sham group			TiO$_2$-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26643864	chr9:75257719-75257763	NM_027418:-574	Mapk6	PROMOTER	1.115	1.868	2591.67	4841.21	2.083	2165.48	4510.34
A_68_P22558740	chr3:136333384-136333428	NM_008913:-327	Ppp3ca	PROMOTER	1.115	1.937	1599.62	3097.88	2.159	1304.06	2815.72
A_68_P24063269	A_68_P24063269			Unknown	1.115	4.671	149.10	696.49	5.208	139.94	728.81
A_68_P27929276	chr11:75780169-75780213			Unknown	1.115	1.595	1215.60	1938.81	1.779	1111.80	1977.86
A_68_P23265703	chr4:123667997-123668041			Unknown	1.115	3.126	453.85	1418.94	3.486	376.38	1312.22
A_68_P26940976	chr10:11211956-11212000			Unknown	1.115	3.364	7792.34	26213.94	3.750	5605.59	21021.23
A_68_P31422207	chr17:87682043-87682087	NR_015506:90	4833418N02Rik	INSIDE	1.114	1.689	2165.24	3657.71	1.883	2014.50	3792.68
A_68_P24045429	chr5:122043432-122043476	NM_009656:379	Aldh2	INSIDE	1.114	1.963	787.37	1545.57	2.187	717.29	1568.84
A_68_P27854482	chr11:62352254-62352298	NM_028448:487	Cenpv	INSIDE	1.114	1.346	5253.97	7074.21	1.499	4201.58	6299.37
A_68_P22318564	chr3:89125165-89125211	NM_010108:1613	Efna3	INSIDE	1.114	2.233	276.32	616.94	2.487	261.03	649.22
A_68_P23854795	chr5:84846156-84846200	NM_007937:229	Epha5	INSIDE	1.114	2.305	1034.51	2384.41	2.568	884.68	2271.42
A_68_P25369178	chr7:107855525-107855569	NM_178764:331	Fam168a	INSIDE	1.114	3.651	10253.38	37438.04	4.068	7168.98	29160.87
A_68_P21477091	chr2:102291430-102291474	NM_010218:497	Fjx1	INSIDE	1.114	4.246	486.82	2067.13	4.729	495.88	2345.01
A_68_P24613523	chr6:86992531-86992575	NM_013528:-287	Gfpt1	PROMOTER	1.114	1.609	2066.64	3326.16	1.793	1834.27	3288.07
A_68_P25730815	chr8:27229276-27229320	NM_207659:398	Hook3	INSIDE	1.114	2.140	1155.47	2472.37	2.384	1065.43	2540.00
A_68_P28918887	chr13:30842448-30842492	NM_013674:1344	Irf4	INSIDE	1.114	1.813	1241.18	2250.41	2.021	1048.66	2118.97
A_68_P23753093	chr5:65213285-65213329	NM_008453:18545	Klf3	INSIDE	1.114	2.832	878.61	2488.43	3.154	748.01	2359.37
A_68_P29629463	chr14:58318497-58318541	NM_015771:46442	Lats2	INSIDE	1.114	4.979	903.70	4499.29	5.545	858.88	4762.66
A_68_P29233343	chr13:94943998-94944042	NM_172589:116270	Lhfpl2	INSIDE	1.114	0.567	1271.89	721.79	0.632	938.13	592.89
A_68_P31827984	chr18:73974953-73974997	NM_145494:72	Me2	INSIDE	1.114	3.584	349.24	1251.76	3.994	323.03	1290.08
A_68_P22615133	chr3:146184298-146184342	NM_027371:67	Rpf1	INSIDE	1.114	1.483	725.59	1075.86	1.652	667.49	1102.41
A_68_P20616239	chr1:133423080-133423124	NM_001081011:836	Srgap2	INSIDE	1.114	2.210	999.85	2209.17	2.461	888.08	2185.28
A_68_P27641464	chr11:22412537-22412581	NM_153596:273	Tmem17	INSIDE	1.114	2.681	566.97	1520.28	2.988	581.37	1737.13
A_68_P27287710	chr10:80610694-80610738	NM_010731:11701	Zbtb7a	INSIDE	1.114	4.580	942.47	4316.84	5.104	733.20	3742.34
A_68_P30423043	chr15:88919652-88919696	NM_027905:138	1300018J18Rik	INSIDE	1.113	3.607	327.03	1179.61	4.016	302.25	1213.94
A_68_P31939676	chr19:7491566-7491610	NM_175381:-526	2700081O15Rik	PROMOTER	1.113	1.862	501.91	934.69	2.073	520.79	1079.53
A_68_P33007147	chr9_random:49997-50041	NR_015516:-3390	4930526I15Rik	PROMOTER	1.113	2.617	1448.49	3790.79	2.912	1076.05	3133.92
A_68_P24946543	chr7:3597351-3597395	NM_146176:502	Cnot3	INSIDE	1.113	2.337	873.23	2040.34	2.601	708.26	1842.52
A_68_P33015614	chr1_random:49829-49873	NM_026866:135488	Disp1	INSIDE	1.113	2.077	392.09	814.30	2.311	386.05	892.35
A_68_P22777889	chr4:22284762-22284806	NM_172988:73	Fbxl4	INSIDE	1.113	3.532	1100.87	3887.93	3.930	966.40	3798.19
A_68_P26886027	chr9:121766646-121766690	NM_001112668:-19	Gm9790	PROMOTER	1.113	1.494	1377.26	2058.08	1.663	1255.35	2087.66
A_68_P22592457	chr3:142428332-142428376	NM_145546:144	Gtf2b	INSIDE	1.113	1.688	970.57	1638.19	1.878	920.68	1728.99
A_68_P25958255	chr8:74203600-74203644	NM_001190830:3341	Jak3	INSIDE	1.113	2.852	1118.31	3189.12	3.175	975.45	3096.71
A_68_P25022783	chr7:29383081-29383125	NM_027470:101	Pak4	INSIDE	1.113	1.474	2496.37	3680.31	1.641	1917.92	3146.56
A_68_P23891543	chr5:92392231-92392285	NM_026557:-164	Rchy1	PROMOTER	1.113	1.683	979.89	1648.88	1.873	723.63	1355.19
A_68_P31119183	chr17:28044657-28044701	NM_026836:-9	Taf11	DIVERGENT_PROMOTER	1.113	1.776	1270.30	2256.34	1.978	1129.63	2233.95
A_68_P29033261	chr13:51690524-51690568			Unknown	1.113	3.699	6892.75	25497.87	4.117	5071.89	20882.56
A_68_P29339701	chr13:114083707-114083751			Unknown	1.113	1.442	1363.39	1965.56	1.605	1129.48	1813.02
A_68_P29583268	chr14:48269057-48269101	BC075697:10		INSIDE	1.113	1.509	989.59	1493.78	1.681	941.39	1582.04
A_68_P27503018	chr10:120788390-120788434	ENSMUST00000078515:8085		DOWNSTREAM	1.113	2.683	371.36	996.39	2.986	351.03	1048.27
A_68_P23915350	chr5:98364657-98364701	NM_133738:95303	Antxr2	INSIDE	1.112	2.120	953.19	2021.14	2.359	921.02	2172.29
A_68_P24593642	chr6:83405946-83405990	NR_028382:14220	B230319C09Rik	DOWNSTREAM	1.112	1.877	751.11	1409.48	2.087	670.10	1398.28
A_68_P30404229	chr15:85809217-85809261	NM_009886:54969	Celsr1	INSIDE	1.112	3.007	1997.02	6005.57	3.346	1606.39	5374.18
A_68_P32982273	chr5:134998822-134998866	NM_001039162:29460	Clip2	INSIDE	1.112	1.982	2247.68	4454.57	2.203	1690.13	3724.02
A_68_P28056291	chr11:98274041-98274085	NM_001003817:265	Erbb2	INSIDE	1.112	2.516	612.86	1541.83	2.796	528.87	1478.90
A_68_P30468548	chr15:97154022-97154066	NM_172293:76507	Fam113b	INSIDE	1.112	1.571	831.11	1305.82	1.746	653.46	1141.25
A_68_P20091644	chr1:24107112-24107156	NM_026604:46	Fam135a	INSIDE	1.112	2.543	815.70	2074.07	2.827	776.47	2195.41
A_68_P23222369	chr4:114598689-114598733	NM_015758:-92	Foxe3	PROMOTER	1.112	2.392	2267.12	5423.63	2.659	1717.67	4568.11
A_68_P29130723	chr13:72100965-72101009	NM_010573:185	Irx1	INSIDE	1.112	0.481	2187.76	1052.03	0.535	1882.94	1006.85
A_68_P31343017	chr17:73268907-73268952	NM_029999:1285	Lbh	INSIDE	1.112	1.699	431.13	732.52	1.890	421.40	796.33
A_68_P25535616	chr7:139802586-139802630	NM_029609:283	Lhpp	INSIDE	1.112	2.313	1321.17	3055.92	2.572	1145.32	2945.89

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31256024	chr17:56564825-56564869	NM_011218:51057	Ptprs	INSIDE	1.112	1.606	936.97	1504.88	1.786	871.52	1556.46
A_68_P20785985	chr1:165859996-165860040	NM_028776:-176	Scyl3	PROMOTER	1.112	1.426	1040.08	1483.08	1.585	915.40	1450.89
A_68_P20826332	chr1:173080599-173080643	NM_025321:114	Sdhc	INSIDE	1.112	1.778	1525.95	2713.81	1.978	1417.45	2803.12
A_68_P31320372	chr17:69186496-69186540	NM_001206661:43	Tmem200c	INSIDE	1.112	2.543	813.95	2069.61	2.828	756.39	2139.13
A_68_P24838525	chr6:128306097-128306141	NM_011657:-249	Tulp3	PROMOTER	1.112	2.846	2515.29	7157.50	3.163	2156.74	6821.81
A_68_P24091287	chr5:130417556-130417600	NM_001001327:-404	Vkorc1l1	PROMOTER	1.112	2.185	13082.56	28590.68	2.430	8531.87	20730.25
A_68_P25264703	chr7:87226955-87226999	NM_175433:55863	Zfp710	INSIDE	1.112	2.269	1689.27	3833.05	2.523	1262.18	3184.37
A_68_P30639624	A_68_P30639624			Unknown	1.112	2.441	701.47	1712.38	2.715	571.63	1551.86
A_68_P27678668	chr11:30167911-30167955	ENSMUST00000006629:237		INSIDE	1.112	1.894	1065.55	2018.57	2.107	1017.12	2143.22
A_68_P21224227	chr2:53051236-53051280	NM_022989:141	Arl6ip6	INSIDE	1.111	1.879	1413.11	2655.81	2.088	1235.80	2580.52
A_68_P21040931	chr2:18616371-18616415	NM_001001334:-4256	BC061194	PROMOTER	1.111	0.540	1195.96	645.92	0.600	956.04	573.79
A_68_P24820861	chr6:125444215-125444259	NM_007657:537	Cd9	INSIDE	1.111	1.639	1070.63	1754.88	1.821	845.55	1539.34
A_68_P27263124	chr10:76077361-76077405	NM_146007:8767	Col6a2	INSIDE	1.111	2.028	1160.83	2353.72	2.253	925.57	2084.92
A_68_P22310619	chr3:87710732-87710776	NM_008231:512	Hdgf	INSIDE	1.111	1.483	1273.84	1889.26	1.648	1130.10	1862.26
A_68_P20945385	chr1:194596745-194596789	NM_144881:647	Hhat	INSIDE	1.111	1.714	2974.03	5097.13	1.905	2328.39	4434.95
A_68_P21833676	chr2:166930579-166930623	NM_008420:83699	Kcnb1	INSIDE	1.111	2.670	1288.49	3440.02	2.966	937.32	2780.49
A_68_P25088268	chr7:51844686-51844730	NM_008422:-1547	Kcnc3	PROMOTER	1.111	1.651	3342.49	5518.85	1.835	2543.23	4666.63
A_68_P29011273	chr13:47139014-47139058	NM_172262:129	Kdm1b	INSIDE	1.111	1.637	715.65	1171.28	1.818	697.83	1268.99
A_68_P22171326	chr3:58811151-58811195	NM_177855:273	Med12l	INSIDE	1.111	1.508	1081.75	1630.89	1.675	971.78	1627.37
A_68_P24027248	chr5:119010105-119010149	NM_172424:-601	Med13l	PROMOTER	1.111	4.378	748.09	3275.00	4.862	1173.50	5705.17
A_68_P20759145	chr1:161162430-161162474	NM_011931:-4	Rfwd2	PROMOTER	1.111	2.955	1143.70	3379.93	3.284	963.50	3164.05
A_68_P29047303	chr13:54167121-54167165	NM_027324:-71	Sfxn1	PROMOTER	1.111	3.541	1370.09	4851.75	3.934	1193.53	4694.97
A_68_P25034246	chr7:31740698-31740742	NM_011680:1102	Usf2	INSIDE	1.111	2.193	1123.73	2463.85	2.436	962.08	2343.40
A_68_P31257914	chr17:56856378-56856423	NM_178926:-56	Vmac	PROMOTER	1.111	4.449	2235.16	9945.32	4.945	1614.99	7986.65
A_68_P25089145	chr7:52004212-52004256	NM_133945:236	Vrk3	INSIDE	1.111	1.937	493.34	955.39	2.152	458.75	987.13
A_68_P23338967	chr4:136832827-136832871	NM_009523:-701	Wnt4	PROMOTER	1.111	1.700	2364.74	4021.18	1.890	2049.24	3872.91
A_68_P24319362	chr6:28210996-28211040	NM_001081678:583	Zfp800	INSIDE	1.111	1.471	1695.37	2494.57	1.634	1408.26	2301.25
A_68_P27258519	chr10:75226844-75226888	NM_172549:236	Cabin1	INSIDE	1.110	1.792	1206.26	2162.03	1.990	1061.42	2111.82
A_68_P31378406	chr17:80014550-80014594	NM_201361:333	Fam82a1	INSIDE	1.110	2.626	879.04	2308.04	2.914	800.64	2333.02
A_68_P25419719	chr7:118742491-118742535	NM_173739:180979	Galntl4	INSIDE	1.110	2.155	766.62	1652.06	2.392	643.39	1539.13
A_68_P22531296	chr3:130974638-130974682	NM_008212:295	Hadh	INSIDE	1.110	2.299	1623.78	3733.83	2.553	1346.68	3438.03
A_68_P29101874	chr13:65214224-65214268	NM_001083901:44	Hiatl1	INSIDE	1.110	1.621	2617.70	4243.51	1.799	2256.35	4058.67
A_68_P27704165	chr11:34935121-34935165	NM_011412:185	Slit3	INSIDE	1.110	0.571	1362.09	777.29	0.633	1173.57	743.22
A_68_P20510432	chr1:108693123-108693167	NM_009190:158	Vps4b	INSIDE	1.110	1.691	5543.94	9374.80	1.877	4039.01	7580.02
A_68_P27532857	chr10:126342966-126343010	NM_026858:-4561	Xrcc6bp1	PROMOTER	1.110	1.431	857.69	1227.16	1.588	825.60	1311.03
A_68_P28751778	chr12:113917322-113917366	NM_001100460:294	Zbtb42	INSIDE	1.110	1.609	472.21	759.56	1.785	461.88	824.44
A_68_P26152541	chr8:111238563-111238607	NM_007496:41	Zfhx3	INSIDE	1.110	2.268	1060.03	2404.62	2.518	883.51	2225.09
A_68_P21068971	chr2:24805706-24805750	NM_026021:407	Zmynd19	INSIDE	1.110	1.706	1159.62	1978.09	1.893	1062.88	2011.82
A_68_P20250390	chr1:57028403-57028447	NR_024325:112	9130024F11Rik	INSIDE	1.109	1.990	1624.83	3233.13	2.207	1255.14	2769.81
A_68_P21908931	chr2:180891580-180891624	NM_007906:118	Eef1a2	INSIDE	1.109	2.085	1456.02	3035.20	2.312	1094.41	2529.79
A_68_P27835271	chr11:58990590-58990634	NM_175452:5716	Gjc2	INSIDE	1.109	1.458	5359.93	7816.85	1.617	4170.42	6745.25
A_68_P20644876	chr1:138156784-138156828	NM_001101516:644	Gpr25	INSIDE	1.109	1.402	1287.57	1804.58	1.555	1133.29	1761.95
A_68_P28150134	chr11:114713892-114713936	NM_147217:571	Gprc5c	INSIDE	1.109	2.561	1014.17	2597.21	2.840	972.71	2762.72
A_68_P24449037	chr6:52153900-52153944	NM_010453:664	Hoxa5	INSIDE	1.109	1.494	943.76	1409.66	1.657	860.36	1425.53
A_68_P27804081	chr11:53113814-53113858	NM_008300:145	Hspa4	INSIDE	1.109	1.404	1064.35	1494.83	1.558	973.51	1516.26
A_68_P25259447	chr7:86293791-86293835	NM_001045489:134	Mfge8	INSIDE	1.109	3.213	1304.45	4190.87	3.563	1168.73	4163.92
A_68_P28161653	chr11:116715108-116715152	NM_178620:-198	Mfsd11	DIVERGENT_PROMOTER	1.109	1.625	670.74	1089.79	1.802	629.73	1134.94
A_68_P21070358	chr2:25036517-25036561	NM_025980:261	Nrarp	INSIDE	1.109	2.701	453.29	1224.50	2.995	517.98	1551.53
A_68_P31029165	chr17:8993570-8993614	NM_011866:-1017	Pde10a	PROMOTER	1.109	2.698	1862.75	5025.80	2.992	1458.19	4363.34
A_68_P24956666	chr7:6682979-6683023	NM_008817:130	Peg3	INSIDE	1.109	3.275	1574.87	5158.22	3.633	1437.93	5223.32
A_68_P25614471	chr8:3537772-3537816	NM_001122818:22411	Pnpla6	INSIDE	1.109	2.222	1529.41	3397.94	2.464	1163.71	2867.45

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P30426168	chr15:89422228-89422272	NM_026817:104	Rabl2	INSIDE	1.109	2.122	2315.54	4913.31	2.353	1862.89	4382.98
A_68_P21395216	chr2:84726819-84726863	NM_199223:9	Rtn4rl2	INSIDE	1.109	2.606	752.21	1959.94	2.889	728.75	2105.30
A_68_P31254017	chr17:56263391-56263435	NM_013662:9863	Sema6b	INSIDE	1.109	2.153	518.00	1115.45	2.388	524.22	1252.00
A_68_P22081036	chr3:40513212-40513256	NM_178386:442	Slc25a31	INSIDE	1.109	1.885	1023.93	1929.70	2.090	829.68	1734.17
A_68_P26133220	chr8:107872806-107872850	NM_001081332:671	Slc9a5	INSIDE	1.109	1.627	1288.32	2096.66	1.805	1116.65	2015.82
A_68_P27704164	chr11:34934976-34935020	NM_011412:41	Slit3	INSIDE	1.109	1.592	762.74	1214.01	1.766	751.57	1327.02
A_68_P28862224	chr13:19487507-19487551	NM_024270:93	Stard3nl	INSIDE	1.109	1.643	627.75	1031.42	1.822	530.04	965.89
A_68_P32008254	chr19:21867188-21867232	NM_001033759:14379	Tmem2	INSIDE	1.109	2.746	1146.65	3148.31	3.046	941.66	2868.34
A_68_P25772480	chr8:35217817-35217861	NM_026432:222	Tmem66	INSIDE	1.109	2.320	1364.74	3166.46	2.572	1172.19	3014.98
A_68_P21568845	chr2:119119812-119119856	NM_172269:5357	Vps18	INSIDE	1.109	2.941	487.14	1432.60	3.260	466.95	1522.27
A_68_P26494151	chr9:48644017-48644061	NM_001033324:12	Zbtb16	INSIDE	1.109	1.612	2057.02	3315.34	1.788	1692.83	3026.31
A_68_P33005900	A_68_P33005900			Unknown	1.109	1.915	696.22	1333.10	2.123	570.40	1211.18
A_68_P23692813	chr5:52504803-52504847	AK076709:-3727		PROMOTER	1.109	1.371	6727.97	9221.92	1.520	5127.52	7791.56
A_68_P31323975	chr17:69788589-69788633	NM_001145192:-55	A330050F15Rik	PROMOTER	1.108	1.828	865.81	1582.90	2.025	805.30	1630.86
A_68_P28694107	chr12:104116017-104116061	NM_172806:578	Btbd7	INSIDE	1.108	1.799	394.99	710.61	1.994	387.44	772.43
A_68_P24123515	chr5:137358798-137358842	NM_024474:157	Emid2	INSIDE	1.108	2.190	1671.07	3659.78	2.426	1545.38	3749.28
A_68_P30345427	chr15:75834015-75834059	NM_001168253:5892	Fam83h	INSIDE	1.108	1.663	484.95	806.25	1.843	533.86	983.69
A_68_P25375734	chr7:108986819-108986865	NM_010567:-102	Inppl1	PROMOTER	1.108	1.635	1188.56	1943.67	1.813	982.06	1780.17
A_68_P31937503	chr19:7131378-7131422	NM_134147:143	Macrod1	INSIDE	1.108	1.892	580.98	1099.28	2.096	535.47	1122.49
A_68_P21842270	chr2:168396257-168396301	NM_001136073:19413	Nfatc2	INSIDE	1.108	2.997	1744.82	5229.33	3.321	1309.91	4350.47
A_68_P32140286	chr19:45824101-45824145	NM_008723:-69	Npm3	PROMOTER	1.108	2.303	1914.06	4407.19	2.551	1729.97	4412.58
A_68_P31140482	chr17:31701718-31701762	NM_016670:23	Pknox1	INSIDE	1.108	2.986	1230.45	3674.08	3.308	1067.44	3530.61
A_68_P22149940	chr3:54611394-54611438	NM_133231:297	Rfxap	INSIDE	1.108	4.069	1021.37	4156.08	4.511	888.33	4006.88
A_68_P31940082	chr19:7557921-7557965	NM_001003933:-163	Rtn3	PROMOTER	1.108	1.473	2339.36	3446.39	1.632	1985.18	3240.41
A_68_P21115505	chr2:32306645-32306689	NM_001164357:324	Slc25a25	INSIDE	1.108	2.834	648.75	1838.38	3.140	581.61	1826.00
A_68_P28170836	chr11:118216495-118216539	NM_011594:209	Timp2	INSIDE	1.108	2.021	1945.18	3931.72	2.240	1600.28	3584.67
A_68_P31156941	chr17:35137890-35137934	NM_011690:61	Vars	INSIDE	1.108	2.185	750.17	1639.09	2.422	665.46	1611.67
A_68_P32246512	chrX:8905191-8905235	ENSMUST00000119858:22		INSIDE	1.108	2.126	874.93	1860.11	2.357	580.97	1369.12
A_68_P21755514	chr2:153356022-153356066	NM_001134300:-337	8430427H17Rik	PROMOTER	1.107	1.564	959.22	1500.40	1.732	866.99	1501.73
A_68_P28853784	chr13:17896191-17896235	NM_001081058:719	Cdk13	INSIDE	1.107	2.998	479.27	1436.69	3.319	441.55	1465.56
A_68_P26132792	chr8:107817484-107817528	NM_177788:2492	Exoc3l	INSIDE	1.107	1.911	1111.55	2124.45	2.116	938.78	1986.60
A_68_P30720007	chr16:44173365-44173409	NM_001029889:-123	Gm608	PROMOTER	1.107	1.694	742.62	1257.86	1.874	696.52	1305.50
A_68_P25025266	chr7:29871013-29871057	NR_035489:-2321	Mir1963	PROMOTER	1.107	2.833	743.46	2106.55	3.137	586.02	1838.43
A_68_P32565872	chrX:99045232-99045276	NM_001163610:531	Nhsl2	INSIDE	1.107	2.059	1487.49	3062.05	2.278	906.03	2064.14
A_68_P29050855	chr13:54795009-54795053	NM_001146027:-5469	Rnf44	PROMOTER	1.107	1.698	982.67	1668.84	1.879	968.95	1821.05
A_68_P32319888	chrX:34283671-34283715	NM_001085497:39	Slc25a43	INSIDE	1.107	2.735	2843.65	7776.65	3.027	1960.98	5935.99
A_68_P29421304	chr14:15535576-15535620	NM_001033270:60	Slc4a7	INSIDE	1.107	1.777	711.88	1265.01	1.966	590.96	1162.03
A_68_P27850829	chr11:61668825-61668869	NM_013881:-252	Ulk2	PROMOTER	1.107	0.562	1006.84	565.56	0.622	860.57	535.23
A_68_P30364132	chr15:78893377-78893421	NM_144849:-109	Ankrd54	PROMOTER	1.106	0.513	1153.75	591.46	0.567	1071.11	607.43
A_68_P24925473	chr6:145812067-145812111	NM_024469:1772	Bhlhe41	INSIDE	1.106	1.479	662.10	979.16	1.636	647.99	1060.21
A_68_P29487613	chr14:28321574-28321618	NM_177111:50	Ccdc66	INSIDE	1.106	1.514	2246.13	3401.48	1.674	2001.96	3351.59
A_68_P26240288	chr8:126039003-126039047	NM_001170976:331	Dbndd1	INSIDE	1.106	2.034	1752.77	3565.88	2.249	1507.31	3390.23
A_68_P27285230	chr10:80218002-80218046	NM_199322:74	Dot1l	INSIDE	1.106	3.121	897.86	2801.90	3.453	920.91	3179.56
A_68_P25505763	chr7:134622752-134622796	NM_010183:-5960	Fbrs	PROMOTER	1.106	1.964	398.67	782.89	2.172	328.57	713.71
A_68_P21768525	chr2:155768031-155768075	NM_008109:3048	Gdf5	INSIDE	1.106	1.522	934.61	1422.75	1.684	834.90	1405.67
A_68_P26805690	chr9:106788802-106788846	NM_175402:507	Rbm15b	INSIDE	1.106	0.424	1238.52	525.38	0.469	916.20	429.83
A_68_P27282554	chr10:79798280-79798324	NM_001204931:5413	Reep6	INSIDE	1.106	1.879	771.59	1449.88	2.079	716.98	1490.65
A_68_P27841610	chr11:60023907-60023951	NM_011480:10178	Srebf1	INSIDE	1.106	0.621	1827.24	1134.82	0.687	1503.79	1032.59
A_68_P24769156	chr6:115084797-115084841	NM_013681:-101	Syn2	PROMOTER	1.106	2.022	651.30	1317.15	2.238	613.98	1373.89
A_68_P25009105	chr7:26010680-26010724	NM_175436:4233	Zfp526	INSIDE	1.106	2.461	2457.13	6046.14	2.722	1969.01	5358.73
A_68_P26465230	chr9:43829019-43829063			Unknown	1.106	5.934	5061.55	30033.83	6.563	3710.44	24350.97

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25008855	chr7:25964863-25964907	X53654:547486		INSIDE	1.106	2.800	1755.03	4913.95	3.097	1511.21	4680.03
A_68_P21096084	chr2:29108807-29108851	NR_029460:-315	6530402F18Rik	PROMOTER	1.105	1.540	995.75	1533.33	1.702	875.16	1489.28
A_68_P24864545	chr6:134933738-134933782	NM_001109914:1742	Apold1	INSIDE	1.105	2.109	872.81	1840.91	2.331	797.24	1858.36
A_68_P22063090	chr3:37247843-37247887	NM_008006:290	Fgf2	INSIDE	1.105	0.582	1124.57	654.65	0.643	966.51	621.79
A_68_P20842598	chr1:176433545-176433589	NM_019445:1611	Fmn2	INSIDE	1.105	1.845	466.98	861.72	2.038	446.33	909.67
A_68_P23787823	chr5:72092225-72092269	NM_008069:992	Gabrb1	INSIDE	1.105	1.907	1544.31	2944.82	2.108	1314.96	2771.47
A_68_P21874504	chr2:174124338-174124382	NM_201617:1001	Gnas	INSIDE	1.105	1.951	1454.41	2837.99	2.157	1281.48	2763.87
A_68_P26443402	chr9:40263578-40263622	NM_172768:-251	Gramd1b	PROMOTER	1.105	1.678	961.62	1613.64	1.854	810.99	1503.22
A_68_P29228407	chr13:94073846-94073890	NM_011982:-581	Homer1	PROMOTER	1.105	0.486	1975.44	959.12	0.537	1577.57	846.52
A_68_P29284632	chr13:104123896-104123940	NM_175171:654	Mast4	INSIDE	1.105	0.548	1148.42	629.89	0.606	952.70	577.30
A_68_P27782070	chr11:49057978-49058022	NM_001110149:-2978	Mgat1	PROMOTER	1.105	1.640	1394.95	2287.59	1.812	1127.48	2043.39
A_68_P24538896	chr6:71858733-71858777	NM_027275:2	Ptcd3	INSIDE	1.105	1.680	550.76	925.12	1.855	423.21	785.21
A_68_P30012299	chr15:10644337-10644381	NM_030690:-1063	Rai14	PROMOTER	1.105	3.691	417.90	1542.63	4.078	397.96	1623.02
A_68_P23359680	chr4:140258068-140258112	NM_173867:703	Rcc2	INSIDE	1.105	1.865	1277.22	2382.41	2.061	1180.17	2432.10
A_68_P31251409	chr17:55622134-55622178	NM_172829:37142	St6gal2	INSIDE	1.105	1.806	706.85	1276.39	1.995	636.46	1269.98
A_68_P26217895	chr8:122625358-122625402	NM_133967:-8	Zdhhc7	PROMOTER	1.105	5.049	1780.50	8989.42	5.579	1358.84	7581.56
A_68_P21076584	chr2:25994375-25994419	ENSMUST00000163836:-74		PROMOTER	1.105	3.597	3267.88	11755.05	3.974	2185.98	8686.31
A_68_P26826442	chr9:110782965-110783009	NM_001146060:161	Als2cl	INSIDE	1.104	1.915	766.60	1468.20	2.113	666.98	1409.64
A_68_P24444443	chr6:51421130-51421174	NM_007624:538	Cbx3	INSIDE	1.104	3.429	744.19	2551.92	3.784	652.98	2471.20
A_68_P27294770	chr10:82448262-82448306	NM_021439:43	Chst11	INSIDE	1.104	1.350	1816.22	2452.11	1.491	1474.67	2198.48
A_68_P26864772	chr9:118059149-118059193	NM_026442:144	Cmc1	INSIDE	1.104	1.605	826.23	1326.09	1.772	748.09	1325.65
A_68_P31378939	chr17:80115332-80115376	NM_009994:-973	Cyp1b1	PROMOTER	1.104	2.163	414.69	897.11	2.388	331.30	791.21
A_68_P32054106	chr19:29722522-29722566	NM_001081213:366	Ermp1	INSIDE	1.104	1.684	908.11	1528.86	1.858	782.43	1453.68
A_68_P29671483	chr14:65695129-65695173	NM_018788:21793	Extl3	INSIDE	1.104	1.641	779.48	1279.35	1.813	745.01	1350.49
A_68_P30925475	chr16:84774232-84774276	NM_023844:-113	Jam2	PROMOTER	1.104	2.066	9365.24	19347.40	2.280	6895.73	15721.68
A_68_P31863476	chr18:80492765-80492809	NM_001190373:68207	Kcng2	INSIDE	1.104	1.948	911.09	1775.10	2.150	774.58	1665.38
A_68_P20799112	chr1:168168830-168168874	NM_175296:23	Mael	INSIDE	1.104	2.957	858.62	2538.82	3.265	785.52	2564.93
A_68_P23278937	chr4:125911565-125911609	NM_001145970:21977	Mtap7d1	INSIDE	1.104	2.305	1298.98	2994.22	2.544	973.72	2476.84
A_68_P31110189	chr17:26568886-26568930	NM_001081656:16999	Neurl1b	INSIDE	1.104	2.048	2086.40	4272.27	2.261	1670.55	3777.10
A_68_P21070359	chr2:25036616-25036660	NM_025980:361	Nrarp	INSIDE	1.104	2.327	345.04	802.90	2.570	281.12	722.45
A_68_P32114045	chr19:41338252-41338296	NM_133352:220	Tm9sf3	INSIDE	1.104	2.466	1610.59	3971.51	2.723	1259.07	3428.79
A_68_P30572940	chr16:17276845-17276889	NM_177473:474	Tmem191c	INSIDE	1.104	1.855	1979.74	3671.82	2.048	1850.86	3791.39
A_68_P24786876	chr6:118405064-118405108	NM_028335:438	Zfp248	INSIDE	1.104	1.709	3107.39	5310.41	1.886	2581.80	4868.97
A_68_P25008234	chr7:25862568-25862612	NM_175477:326	Zfp574	INSIDE	1.104	1.873	12504.21	23422.91	2.068	8698.07	17990.66
A_68_P32462526	chrX:70667546-70667590	NM_009566:11127	Zfp92	INSIDE	1.104	1.759	1280.97	2252.95	1.941	667.88	1296.26
A_68_P24058182	chr5:124357285-124357329	NM_026603:23	Denr	INSIDE	1.103	2.189	1582.48	3463.38	2.415	1266.48	3058.66
A_68_P20850632	chr1:177810893-177810937	NM_012012:6	Exo1	INSIDE	1.103	1.842	1017.41	1874.43	2.033	796.67	1619.51
A_68_P28187038	chr11:120686207-120686251	NM_007988:-367	Fasn	PROMOTER	1.103	0.548	1132.34	620.47	0.605	938.16	567.18
A_68_P24172328	chr5:148001784-148001828	NM_008178:1535	Gsx1	INSIDE	1.103	1.456	2049.90	2985.10	1.607	1790.45	2876.73
A_68_P23340287	chr4:137074439-137074483	NM_008305:49743	Hspg2	INSIDE	1.103	4.064	2019.25	8206.19	4.481	1749.57	7840.43
A_68_P21840417	chr2:168094618-168094662	NM_001081134:191	Kcng1	INSIDE	1.103	2.324	1081.48	2513.03	2.562	913.04	2339.52
A_68_P25349938	chr7:104480832-104480876	NM_001039039:22	Kctd21	INSIDE	1.103	3.201	1944.26	6224.40	3.531	1557.09	5498.11
A_68_P23756015	chr5:65770784-65770828	NM_031180:31157	Klb	INSIDE	1.103	1.735	519.81	901.72	1.913	413.66	791.47
A_68_P27284038	chr10:80031829-80031873	NM_078477:8191	Klf16	INSIDE	1.103	3.309	1243.59	4115.42	3.649	1061.80	3874.02
A_68_P31669144	chr18:44971731-44971775	NM_001085373:84	Mcc	INSIDE	1.103	2.227	1592.36	3546.67	2.456	1375.47	3378.05
A_68_P22422565	chr3:109945185-109945229	NM_001163348:1184	Ntng1	INSIDE	1.103	3.408	1935.24	6595.25	3.759	1599.62	6012.72
A_68_P31626662	chr18:37166261-37166305	NM_009960:-4229	Pcdha11	PROMOTER	1.103	1.866	459.18	856.91	2.058	466.83	960.53
A_68_P21587820	chr2:122564356-122564400	NM_019788:138	Pldn	INSIDE	1.103	2.086	722.62	1507.71	2.302	687.50	1582.35
A_68_P20770872	chr1:163180941-163180985	NM_007453:335	Prdx6	INSIDE	1.103	2.159	804.81	1737.89	2.381	686.81	1635.46
A_68_P22933503	chr4:55362594-55362638	NM_009011:-297	Rad23b	PROMOTER	1.103	2.309	1582.80	3655.15	2.547	1407.10	3583.73
A_68_P26533944	chr9:55889943-55889987	NM_011992:313	Rcn2	INSIDE	1.103	1.907	494.90	943.62	2.104	460.62	969.11

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P32957490	chr17:8138877-8138921	NM_025789:420	Rsph3a	INSIDE	1.103	2.242	852.02	1910.14	2.472	726.98	1797.16
A_68_P28535257	chr12:74145983-74146027	NM_009189:1695	Six1	INSIDE	1.103	2.991	754.03	2255.40	3.300	687.27	2267.71
A_68_P23322289	chr4:133899035-133899079	NM_001039677:72	Slc30a2	INSIDE	1.103	1.516	2312.37	3505.26	1.672	1969.05	3292.32
A_68_P28554953	chr12:77707492-77707536	NM_013675:104020	Spnb1	INSIDE	1.103	2.183	249.54	544.80	2.408	247.06	594.86
A_68_P28054165	chr11:97913498-97913542	NM_146028:1256	Stac2	INSIDE	1.103	2.089	1059.53	2213.23	2.304	949.59	2188.28
A_68_P32264675	chrX:12648851-12648895	NM_009481:249	Usp9x	INSIDE	1.103	1.647	658.30	1083.97	1.817	383.54	696.87
A_68_P30402004	chr15:85476715-85476759	AK037366:-9359		PROMOTER	1.103	1.928	1119.56	2158.66	2.126	969.47	2061.56
A_68_P22502227	chr3:126066719-126066763	NM_173451:-29	Arsj	PROMOTER	1.102	1.933	303.83	587.19	2.130	249.28	531.08
A_68_P29335931	chr13:113442236-113442280	NM_001145885:260	Ddx4	INSIDE	1.102	3.403	910.20	3097.74	3.751	786.67	2950.92
A_68_P23336931	chr4:136501821-136501865	NM_007939:10889	Epha8	INSIDE	1.102	2.063	1072.71	2213.36	2.274	887.48	2018.32
A_68_P29034745	chr13:51941936-51941980	NM_011817:-85	Gadd45g	PROMOTER	1.102	1.681	652.55	1096.73	1.852	576.13	1066.84
A_68_P28431901	chr12:52930414-52930458	NM_144788:87	Hectd1	INSIDE	1.102	1.880	886.21	1665.80	2.072	709.03	1468.91
A_68_P31927056	chr19:5118110-5118154	NM_008451:276	Klc2	INSIDE	1.102	0.614	2991.61	1836.84	0.677	2461.05	1665.73
A_68_P23547785	chr5:25003901-25003945	NM_001081383:679	Mll3	INSIDE	1.102	1.838	799.20	1468.63	2.025	717.99	1454.21
A_68_P31442548	chr17:91487890-91487934	NM_020252:4230	Nrxn1	INSIDE	1.102	1.986	552.40	1096.84	2.188	520.29	1138.44
A_68_P22031104	chr3:30868422-30868466	NM_001165954:-107	Phc3	PROMOTER	1.102	1.461	1841.08	2689.15	1.610	1606.19	2586.35
A_68_P24772420	chr6:115626105-115626149	NM_029780:527	Raf1	INSIDE	1.102	7.291	363.41	2649.50	8.034	348.64	2801.01
A_68_P23364274	chr4:141028926-141028970	NM_019763:65564	Spen	INSIDE	1.102	2.785	869.68	2421.76	3.069	680.25	2087.65
A_68_P26770338	chr9:100471400-100471444	NM_001101483:82	Tmem22	INSIDE	1.102	1.946	712.95	1387.47	2.144	671.46	1439.48
A_68_P25957477	chr8:74082522-74082566	NM_001100462:226	Tmem221	INSIDE	1.102	1.820	461.17	839.50	2.006	469.93	942.64
A_68_P25670555	chr8:13785828-13785872	NM_025924:236	Upf3a	INSIDE	1.102	2.531	970.82	2457.33	2.789	760.60	2121.07
A_68_P28611612	chr12:88030123-88030167	NM_177354:10495	Vash1	INSIDE	1.102	1.790	383.02	685.50	1.972	296.87	585.30
A_68_P21780089	chr2:157770092-157770136	NM_198627:29726	Vstm2l	INSIDE	1.102	1.909	897.85	1713.98	2.103	776.45	1632.71
A_68_P32959961	A_68_P32959961			Unknown	1.102	3.353	574.19	1925.52	3.696	463.32	1712.28
A_68_P24980670	chr7:16871649-16871693	NM_172297:-1662	Ccdc9	PROMOTER	1.101	6.756	15064.41	101777.60	7.440	9753.59	72563.67
A_68_P21425707	chr2:91805748-91805792	NM_138306:-2050	Dgkz	PROMOTER	1.101	1.803	482.99	870.86	1.986	437.06	867.93
A_68_P28158451	chr11:116144755-116144799	NM_010254:2524	Galr2	INSIDE	1.101	1.881	693.52	1304.57	2.072	601.76	1246.70
A_68_P30650845	chr16:32079162-32079206	NM_177326:175	Pak2	INSIDE	1.101	1.803	410.07	739.45	1.985	315.90	627.13
A_68_P29360872	chr13:117813736-117813780	NM_001081009:565	Parp8	INSIDE	1.101	1.705	973.67	1660.05	1.877	875.74	1643.90
A_68_P23152968	chr4:100741662-100741706	NM_183024:42	Raver2	INSIDE	1.101	2.029	550.37	1116.75	2.235	498.47	1114.08
A_68_P30960424	chr16:91011840-91011884	NM_001164483:-309	Synj1	PROMOTER	1.101	1.603	906.67	1453.61	1.766	729.98	1288.90
A_68_P27850820	chr11:61667944-61667988	NM_013881:628	Ulk2	INSIDE	1.101	2.688	914.17	2457.72	2.961	889.66	2634.44
A_68_P31323666	chr17:69732894-69732938	NM_009547:-401	Zfp161	PROMOTER	1.101	2.115	650.27	1375.15	2.328	598.19	1392.54
A_68_P30501994	chr15:102916894-102916938	AF216290:299350		INSIDE	1.101	1.419	1289.12	1829.43	1.563	1012.20	1581.61
A_68_P26080208	chr8:97437258-97437302	NM_001033533:4718	Ccdc102a	INSIDE	1.100	1.828	1651.99	3020.05	2.011	1302.23	2618.49
A_68_P23609088	chr5:37086702-37086746	NM_001081232:484	D5Ertd579e	INSIDE	1.100	2.415	917.45	2215.42	2.656	1094.76	2908.15
A_68_P28003591	chr11:88921871-88921915	NM_019505:170	Dgke	INSIDE	1.100	2.485	910.49	2262.26	2.732	793.91	2169.23
A_68_P23203770	chr4:109654911-109654955	NM_172296:4303	Dmrta2	INSIDE	1.100	1.666	1054.18	1755.89	1.832	918.82	1683.71
A_68_P21601164	chr2:125073520-125073564	NM_023595:292	Dut	INSIDE	1.100	0.462	1115.63	515.10	0.508	843.03	428.12
A_68_P23577614	chr5:31598329-31598373	NM_022424:-100	Fndc4	DIVERGENT_PROMOTER	1.100	1.478	2212.63	3271.36	1.626	2122.88	3452.10
A_68_P25098810	chr7:53651744-53651788	NM_008421:-71	Kcnc1	PROMOTER	1.100	1.496	739.26	1105.94	1.646	673.61	1108.57
A_68_P31123766	chr17:28828497-28828541	NM_001168513:-994	Mapk14	PROMOTER	1.100	2.326	351.56	817.65	2.558	328.17	839.55
A_68_P20648918	chr1:138845713-138845757	NM_001159769:4473	Nr5a2	INSIDE	1.100	3.578	750.05	2683.52	3.936	640.73	2521.92
A_68_P25089776	chr7:52119038-52119082	NM_133949:6098	Ptov1	INSIDE	1.100	2.535	3159.37	8008.01	2.788	2292.23	6390.84
A_68_P26823557	chr9:110310713-110310757	NM_001081043:-20	Ptpn23	PROMOTER	1.100	1.495	2176.48	3253.83	1.644	1839.93	3024.47
A_68_P21217116	chr2:51928627-51928671	NM_175238:292	Rif1	INSIDE	1.100	1.938	608.48	1179.52	2.132	568.79	1212.67
A_68_P21116406	chr2:32470512-32470556	NM_001025310:8054	St6galnac6	INSIDE	1.100	2.330	316.04	736.39	2.563	277.08	710.03
A_68_P31152725	chr17:34341728-34341772	NM_011530:327	Tap2	INSIDE	1.100	1.508	3651.15	5504.36	1.659	2731.87	4532.18
A_68_P20303907	chr1:66724032-66724076	NM_175510:209034	Unc80	INSIDE	1.100	1.633	876.45	1431.61	1.797	772.37	1388.03
A_68_P31092362	chr17:23694847-23694891	NM_001033496:6325	Zfp213	INSIDE	1.100	2.518	705.98	1778.01	2.770	576.10	1595.99
A_68_P24818156	chr6:124959237-124959281	NM_175557:-564	Zfp384	PROMOTER	1.100	2.394	1042.11	2495.18	2.634	951.09	2505.19

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31940131	chr19:7569296-7569340	NM_146091:391	Atl3	INSIDE	1.099	3.962	334.35	1324.64	4.353	306.89	1335.74
A_68_P25354429	chr7:105342798-105342842	NM_001081167:5165	B3gnt6	INSIDE	1.099	3.040	598.15	1818.66	3.343	619.13	2069.54
A_68_P28001993	chr11:88580214-88580258	NR_038058:280	C030037D09Rik	INSIDE	1.099	1.666	2176.43	3626.51	1.831	1482.29	2713.92
A_68_P23196907	chr4:108292428-108292472	NM_177045:-110	Cc2d1b	PROMOTER	1.099	1.563	2440.59	3813.62	1.717	2187.95	3756.16
A_68_P30368454	chr15:79604585-79604629	NM_017470:291	Dnalc4	INSIDE	1.099	1.521	3573.91	5436.54	1.671	2808.06	4692.63
A_68_P23927392	chr5:100468747-100468791	NM_001163035:-244	Enoph1	DIVERGENT_PROMOTER	1.099	0.360	2153.59	775.41	0.396	1821.03	720.89
A_68_P24795427	chr6:119797721-119797765	NM_053204:426	Erc1	INSIDE	1.099	1.919	2615.82	5019.27	2.109	2223.30	4689.08
A_68_P29671484	chr14:65695263-65695307	NM_018788:21659	Extl3	INSIDE	1.099	2.747	2218.76	6093.92	3.019	1738.86	5249.36
A_68_P22384167	chr3:102862328-102862372	NM_010937:143	Nras	INSIDE	1.099	1.740	700.71	1219.30	1.912	520.51	995.42
A_68_P24053562	chr5:123479427-123479471	NM_175423:14366	Orai1	INSIDE	1.099	2.923	1394.74	4077.28	3.213	1101.22	3538.22
A_68_P30380707	chr15:81790992-81791036	NM_013872:283	Pmm1	INSIDE	1.099	1.900	2072.56	3936.86	2.088	1585.63	3310.85
A_68_P28854348	chr13:18035877-18035921	NM_019491:153	Rala	INSIDE	1.099	2.752	261.74	720.37	3.026	245.21	741.94
A_68_P29507577	chr14:31528572-31528616	NM_001166532:-206	Sfmbt1	PROMOTER	1.099	2.466	795.22	1960.94	2.709	752.75	2039.13
A_68_P20370951	chr1:78306769-78306813	NM_001004173:-130	Sgpp2	PROMOTER	1.099	2.099	2689.27	5645.51	2.308	2342.46	5405.30
A_68_P31201839	chr17:45701335-45701379	NM_028662:256	Slc35b2	INSIDE	1.099	2.148	1556.77	3343.46	2.360	1346.47	3177.94
A_68_P25102242	chr7:54213694-54213738	NM_001040695:172	Uevld	INSIDE	1.099	1.382	3548.99	4905.88	1.519	2749.59	4175.48
A_68_P27340460	chr10:90644534-90644578	ENSMUST00000099357:-9797		PROMOTER	1.099	0.528	1456.29	768.86	0.580	1220.19	707.86
A_68_P25083583	chr7:50932042-50932086	NM_145582:4664	Ctu1	INSIDE	1.098	3.050	1089.78	3324.31	3.348	875.97	2932.86
A_68_P24122083	chr5:137041608-137041652	NM_198602:1645	Cux1	INSIDE	1.098	2.278	1845.87	4204.99	2.500	1407.34	3518.95
A_68_P22194043	chr3:63709285-63709329	NM_177856:24001	E130311K13Rik	DOWNSTREAM	1.098	2.201	745.28	1640.29	2.416	676.66	1635.08
A_68_P21393859	chr2:84499121-84499165	NM_001145100:-93	Gm13718	DIVERGENT_PROMOTER	1.098	2.504	1253.81	3139.02	2.749	1100.49	3024.84
A_68_P31055442	chr17:13108620-13108664	NM_026310:315	Mrpl18	INSIDE	1.098	1.658	793.46	1315.49	1.821	681.97	1241.58
A_68_P25377736	chr7:109371755-109371799	NM_145583:189	Pgap2	INSIDE	1.098	2.106	2797.72	5893.33	2.313	2369.32	5479.69
A_68_P25586914	chr7:148317021-148317066	NM_013782:-141	Ptdss2	PROMOTER	1.098	1.819	1844.35	3355.55	1.998	1635.86	3269.24
A_68_P23308458	chr4:131375508-131375552	NM_001083119:18663	Ptpru	INSIDE	1.098	2.372	760.89	1805.20	2.604	660.89	1720.93
A_68_P21077277	chr2:26092977-26093024	NM_153559:-60	Qsox2	PROMOTER	1.098	1.708	10144.92	17331.42	1.876	7141.09	13395.64
A_68_P24622497	chr6:88450007-88450051	NM_019685:34612	Ruvbl1	DOWNSTREAM	1.098	1.850	654.79	1211.43	2.031	730.77	1484.45
A_68_P30575812	chr16:17806955-17806999	NM_153790:9602	Scarf2	INSIDE	1.098	2.817	590.69	1663.81	3.093	535.63	1656.69
A_68_P28376736	chr12:40860722-40860766	NM_001146196:71	Scin	INSIDE	1.098	0.421	2229.60	938.53	0.462	1878.47	868.56
A_68_P22081032	chr3:40512823-40512867	NM_178386:52	Slc25a31	INSIDE	1.098	1.842	508.57	936.79	2.022	413.76	836.71
A_68_P21749134	chr2:152224754-152224798	NM_011438:-994	Sox12	PROMOTER	1.098	3.214	1100.66	3537.74	3.530	986.23	3481.83
A_68_P25016990	chr7:28157258-28157302	NM_001199235:22245	Spnb4	INSIDE	1.098	1.989	877.29	1745.03	2.185	763.84	1668.85
A_68_P22774760	chr4:21703216-21703260	NM_152825:-178	Usp45	DIVERGENT_PROMOTER	1.098	0.492	2362.77	1161.73	0.540	1998.06	1079.15
A_68_P23195052	chr4:107890429-107890473	NM_001167936:77	Zyg11a	INSIDE	1.098	1.467	1114.49	1634.49	1.611	1005.88	1620.10
A_68_P29072930	chr13:58486645-58486689	NM_027335:-80	2210016F16Rik	PROMOTER	1.097	2.187	459.36	1004.70	2.398	382.48	917.31
A_68_P25657382	chr8:11758359-11758403	NM_001113518:51	Arhgef7	INSIDE	1.097	0.424	1608.98	682.35	0.465	1259.32	586.04
A_68_P28853785	chr13:17896465-17896509	NM_001081058:445	Cdk13	INSIDE	1.097	2.067	838.02	1732.39	2.267	825.78	1872.27
A_68_P21907946	chr2:180763743-180763787	NM_015730:10118	Chrna4	INSIDE	1.097	4.949	2893.12	14319.29	5.430	1954.99	10615.68
A_68_P25565163	chr7:144500856-144500900	NM_001113414:5250	Ebf3	INSIDE	1.097	1.600	496.65	794.46	1.754	523.84	918.83
A_68_P30682953	chr16:37868211-37868255	NM_177093:-253	Lrrc58	PROMOTER	1.097	1.571	509.51	800.26	1.723	491.48	846.94
A_68_P29446633	chr14:21213077-21213121	NM_025440:-321	Mrps16	PROMOTER	1.097	1.644	1409.37	2316.45	1.803	1079.66	1947.07
A_68_P20727255	chr1:155396749-155396793	NM_028749:74	Npl	INSIDE	1.097	2.016	1154.50	2327.54	2.211	972.67	2150.41
A_68_P32089882	chr19:36484156-36484200	NM_029508:30622	Pcgf5	INSIDE	1.097	2.651	3345.17	8868.63	2.907	2595.90	7547.26
A_68_P29585964	chr14:48740853-48740897	NM_033602:331	Peli2	INSIDE	1.097	1.487	4036.71	6001.97	1.631	3043.00	4963.55
A_68_P26977747	chr10:18564707-18564751	NM_022032:-148	Perp	PROMOTER	1.097	2.292	1862.10	4267.04	2.513	1552.44	3901.69
A_68_P24983338	chr7:17396479-17396523	NM_001039878:-4737	Strn4	PROMOTER	1.097	1.683	1000.44	1683.82	1.847	929.11	1715.74
A_68_P26037060	chr8:90304857-90304901	NM_033327:178616	Zfp423	INSIDE	1.097	1.717	665.72	1143.01	1.883	532.01	1002.04
A_68_P26974631	chr10:18038563-18038607			Unknown	1.097	2.785	371.63	1034.90	3.054	372.92	1139.01
A_68_P27630019	chr11:20012621-20012665	NM_146243:312	Actr2	INSIDE	1.096	1.651	700.88	1156.98	1.810	707.93	1281.04
A_68_P27649727	chr11:24064666-24064712	NM_001159290:83994	Bcl11a	INSIDE	1.096	2.574	695.18	1789.56	2.822	572.83	1616.49
A_68_P28724520	chr12:109154600-109154644	NM_001079883:87002	Bcl11b	INSIDE	1.096	2.780	925.70	2573.37	3.048	766.16	2335.01

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28175451	chr11:118902630-118902674	NM_013926:-425	Cbx8	PROMOTER	1.096	1.609	1004.31	1615.95	1.763	885.39	1561.05
A_68_P22058857	chr3:36470723-36470767	NM_009828:174	Ccna2	INSIDE	1.096	2.081	370.59	771.15	2.280	364.34	830.64
A_68_P27543829	chr10:128347422-128347466	NM_007653:523	Cd63	INSIDE	1.096	1.574	2072.01	3262.23	1.726	1611.29	2780.36
A_68_P26078038	chr8:97056657-97056701	NM_153507:-249	Cpne2	PROMOTER	1.096	2.363	813.79	1922.83	2.589	798.90	2068.14
A_68_P28540763	chr12:75050763-75050807	NM_010431:41931	Hif1a	DOWNSTREAM	1.096	1.718	901.34	1548.12	1.882	797.19	1500.56
A_68_P23295050	chr4:128798908-128798952	NM_010471:-395	Hpca	PROMOTER	1.096	5.900	2693.09	15889.35	6.465	2172.96	14048.83
A_68_P28445676	chr12:55169720-55169764	NM_013780:820079	Npas3	INSIDE	1.096	1.652	1977.23	3265.80	1.811	1565.36	2834.71
A_68_P32508786	chrX:83437353-83437397	NM_007430:261	Nr0b1	INSIDE	1.096	1.836	787.54	1446.03	2.012	488.35	982.73
A_68_P27980113	chr11:84693476-84693520	NM_027388:199	Pigw	INSIDE	1.096	2.400	890.02	2135.74	2.630	823.70	2166.42
A_68_P25972618	chr8:77737845-77737889	NM_029182:24	Rasd2	INSIDE	1.096	3.637	1104.94	4018.87	3.986	966.16	3851.25
A_68_P30348905	chr15:76353796-76353840	NM_130893:-1259	Scrt1	PROMOTER	1.096	0.649	2464.40	1599.58	0.711	1953.71	1389.45
A_68_P22342629	chr3:94976833-94976877	NM_011351:8559	Sema6c	INSIDE	1.096	2.654	387.34	1027.96	2.909	383.05	1114.28
A_68_P25962758	chr8:75274038-75274082	NM_009188:26874	Sin3b	INSIDE	1.096	2.999	195.17	585.41	3.287	182.85	601.09
A_68_P27911315	chr11:72224926-72224970	NM_177776:267	Smtnl2	INSIDE	1.096	1.502	625.39	939.38	1.646	533.55	878.30
A_68_P22383503	chr3:102739831-102739875	NM_011516:171	Sycp1	INSIDE	1.096	1.980	389.50	771.28	2.171	393.12	853.45
A_68_P32241861	chrX:7706354-7706398	NR_029428:3597	Wdr13	INSIDE	1.096	2.726	708.04	1930.07	2.987	452.32	1351.18
A_68_P25735820	chr8:28090231-28090275	NM_001101502:2445	Zfp703	INSIDE	1.096	2.315	1698.88	3932.82	2.536	1461.03	3705.63
A_68_P22609446	chr3:145239414-145239458	NM_001081094:265	Znhit6	INSIDE	1.096	1.863	3505.74	6532.24	2.042	2613.34	5337.02
A_68_P28751871	chr12:113931919-113931963	AK028601:-159		PROMOTER	1.096	1.846	608.14	1122.38	2.023	560.09	1132.81
A_68_P26766898	chr9:99847864-99847908	ENSMUST00000104307:3759		DOWNSTREAM	1.096	2.399	459.61	1102.62	2.630	369.52	971.74
A_68_P27971501	chr11:83253964-83254008	NM_025492:2791	1700020L24Rik	INSIDE	1.095	1.590	771.86	1227.18	1.741	713.71	1242.38
A_68_P31259472	chr17:57136735-57136779	NM_025538:-5	Alkbh7	PROMOTER	1.095	2.824	2326.47	6569.20	3.093	1874.19	5796.53
A_68_P22503477	chr3:126299555-126299599	NM_001025438:-314	Camk2d	PROMOTER	1.095	0.571	1547.58	883.86	0.626	1330.01	831.96
A_68_P20716449	chr1:153602522-153602566	NM_001039644:41	Edem3	INSIDE	1.095	1.760	1489.59	2621.41	1.927	1380.28	2660.08
A_68_P28059762	chr11:98843848-98843892	NM_178596:460	Gjd3	INSIDE	1.095	3.871	483.38	1871.34	4.237	451.17	1911.80
A_68_P22141943	chr3:53267216-53267260	NM_172501:-58	Nhlrc3	DIVERGENT_PROMOTER	1.095	1.523	1173.78	1787.53	1.668	1090.97	1819.98
A_68_P20474869	chr1:99992118-99992162	NM_013626:69	Pam	INSIDE	1.095	2.214	936.07	2072.47	2.424	900.91	2183.96
A_68_P30346596	chr15:76009591-76009635	NM_201394:16528	Plec	INSIDE	1.095	3.534	655.50	2316.62	3.871	479.63	1856.44
A_68_P24171758	chr5:147889132-147889176	NM_181730:11	Polr1d	INSIDE	1.095	1.643	771.88	1268.14	1.800	718.92	1293.89
A_68_P29989756	chr15:6659356-6659404	NM_030168:1000	Rictor	INSIDE	1.095	2.369	506.49	1200.04	2.594	410.35	1064.66
A_68_P29676506	chr14:66572378-66572422	NM_172604:181	Scara3	INSIDE	1.095	1.636	551.54	902.35	1.791	478.77	857.42
A_68_P29244711	chr13:96901122-96901166	NM_029210:1388	Sv2c	INSIDE	1.095	1.659	2464.91	4089.63	1.817	1941.61	3526.98
A_68_P21890547	chr2:178142154-178142198	NM_177191:187	Sycp2	INSIDE	1.095	2.740	1751.06	4798.67	3.000	1329.81	3988.97
A_68_P25195710	chr7:74904616-74904660	NM_183312:-10	Synm	PROMOTER	1.095	1.485	948.71	1408.90	1.626	811.41	1319.28
A_68_P21817998	chr2:164286400-164286444	NM_025575:-48	Sys1	PROMOTER	1.095	0.439	1184.32	520.46	0.481	1029.52	495.43
A_68_P29880583	chr14:106505860-106505904	NM_198601:468	Trim52	INSIDE	1.095	2.842	209.31	594.90	3.112	213.04	662.96
A_68_P23865420	chr5:87233089-87233133	NM_177680:-404	Ythdc1	PROMOTER	1.095	1.800	1699.39	3058.05	1.971	1322.24	2605.80
A_68_P28396998	A_68_P28396998			Unknown	1.095	2.358	307.01	723.80	2.582	258.93	668.60
A_68_P23443314	chr5:3100163-3100207	ENSMUST00000161709:9416		DOWNSTREAM	1.095	2.099	627.81	1317.50	2.298	602.79	1385.26
A_68_P27083333	chr10:40022153-40022197	NM_009665:-180	Amd1	PROMOTER	1.094	0.552	2098.05	1158.94	0.604	1648.03	996.14
A_68_P24797812	chr6:120244301-120244345	NM_198884:255	B4galnt3	INSIDE	1.094	1.764	1475.74	2603.83	1.931	1294.51	2499.84
A_68_P32145750	chr19:46835351-46835395	NM_001102471:-726	Cnnm2	PROMOTER	1.094	2.382	953.34	2270.87	2.606	904.07	2356.42
A_68_P26584125	chr9:64659762-64659806	NM_001162917:967	Dennd4a	INSIDE	1.094	1.796	801.75	1439.91	1.965	720.56	1416.04
A_68_P32561248	chrX:97972645-97972689	NM_001177780:57	Dlg3	INSIDE	1.094	2.285	678.85	1551.46	2.500	326.80	817.04
A_68_P21221948	chr2:52717600-52717648	NM_172409:723	Fmnl2	INSIDE	1.094	1.605	686.17	1101.62	1.757	570.74	1002.80
A_68_P26512824	chr9:51856849-51856893	NR_023357:-60	Gm6981	PROMOTER	1.094	1.575	466.03	734.16	1.723	475.43	819.33
A_68_P31828825	chr18:74129885-74129929	NM_172632:94697	Mapk4	INSIDE	1.094	1.973	848.06	1673.02	2.158	728.11	1570.94
A_68_P26082830	chr8:97876281-97876325	NM_008609:66	Mmp15	INSIDE	1.094	1.684	465.56	784.15	1.843	396.54	730.78
A_68_P26789126	chr9:103905204-103905248	NM_172460:353	Nphp3	INSIDE	1.094	1.460	989.50	1444.25	1.597	820.31	1310.40
A_68_P31793419	chr18:67883751-67883795	NM_001127177:503	Ptpn2	INSIDE	1.094	0.472	1280.61	605.05	0.517	1073.88	555.17
A_68_P27359833	chr10:93977922-93977966	NM_172051:343	Tmcc3	INSIDE	1.094	1.744	755.86	1318.46	1.908	613.35	1170.34

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P24153530	chr5:143576863-143576907	NM_001122730:2182	Tnrc18	INSIDE	1.094	0.454	1851.58	840.83	0.497	1583.04	786.50
A_68_P22889130	chr4:46520205-46520249	NM_029077:28790	Trim14	INSIDE	1.094	1.548	585.74	906.90	1.693	529.81	897.02
A_68_P28693527	chr12:103996226-103996270	NM_025666:64	Ubr7	INSIDE	1.094	2.063	1864.81	3847.91	2.258	1501.32	3389.55
A_68_P20804308	chr1:169214081-169214125	NM_030724:1156	Uck2	INSIDE	1.094	2.333	233.12	543.97	2.553	191.55	488.96
A_68_P27541965	chr10:127984764-127984808	NM_134003:14	Zc3h10	INSIDE	1.094	1.926	2235.07	4304.13	2.106	1881.60	3962.33
A_68_P27613618	chr11:16851175-16851219	NR_015469:-100	2810442I21Rik	DIVERGENT_PROMOTER	1.093	1.475	1387.50	2047.09	1.612	1126.38	1816.10
A_68_P23541453	chr5:23893834-23893878	NM_001002897:4105	Atg9b	INSIDE	1.093	2.059	1197.92	2466.67	2.252	991.76	2233.05
A_68_P30365376	chr15:79092452-79092496	NM_177580:23465	Baiap2l2	INSIDE	1.093	1.453	872.48	1267.51	1.589	688.86	1094.32
A_68_P21013690	chr2:12931726-12931771	NM_153155:743	C1ql3	INSIDE	1.093	0.569	2269.11	1292.14	0.623	1999.12	1244.55
A_68_P20408506	chr1:87690361-87690405	NM_133781:361	Cab39	INSIDE	1.093	1.478	2113.71	3124.57	1.615	1995.21	3223.17
A_68_P29098741	chr13:64533952-64533996	NM_053180:114	Cdk20	INSIDE	1.093	1.674	809.96	1355.95	1.830	691.26	1265.07
A_68_P21907944	chr2:180763528-180763574	NM_015730:10332	Chrna4	INSIDE	1.093	3.030	1712.53	5188.97	3.312	1144.44	3790.51
A_68_P23417710	chr4:151656882-151656926	NM_178406:8434	Gpr153	INSIDE	1.093	2.321	1424.22	3305.77	2.536	1080.51	2740.29
A_68_P23415954	chr4:151382992-151383036	NM_001033352:15	Klhl21	INSIDE	1.093	1.545	1367.30	2112.56	1.689	1179.60	1991.84
A_68_P25193398	chr7:74517805-74517849	NM_001033713:-82	Mef2a	PROMOTER	1.093	1.375	1259.58	1732.04	1.502	1051.74	1580.16
A_68_P30506994	chr16:3884902-3884946	NM_029090:306	Nat15	INSIDE	1.093	1.522	1897.45	2888.34	1.664	1407.78	2342.56
A_68_P21006642	chr2:11457159-11457203	NM_001177758:18376	Pfkfb3	INSIDE	1.093	0.580	1354.46	785.05	0.633	1056.28	669.06
A_68_P21432203	chr2:92886316-92886360	NM_001177536:-37	Prdm11	PROMOTER	1.093	2.537	1023.81	2597.57	2.773	832.37	2308.57
A_68_P21866930	chr2:172805522-172805566	NM_001083959:202	Spo11	INSIDE	1.093	3.377	485.14	1638.48	3.690	497.32	1835.29
A_68_P32022083	chr19:24248437-24248481	NM_001198985:172	Tjp2	INSIDE	1.093	2.134	1806.97	3856.71	2.333	1673.90	3904.92
A_68_P28553607	chr12:77472331-77472375	NM_178744:1100	Zbtb1	INSIDE	1.093	1.590	2262.82	3597.87	1.738	1619.54	2814.80
A_68_P25505251	chr7:134487065-134487109	NM_146202:1742	Zfp768	INSIDE	1.093	2.159	1738.56	3753.23	2.359	1355.70	3198.30
A_68_P26559434	chr9:60369978-60370022	ENSMUST00000140824:-147		PROMOTER	1.093	2.735	343.89	940.40	2.989	326.64	976.22
A_68_P21483986	chr2:103406434-103406478	NM_178890:-10	Abtb2	PROMOTER	1.092	1.590	2469.94	3927.43	1.736	1790.45	3108.70
A_68_P23342103	chr4:137352189-137352233	NM_007431:82	Alpl	INSIDE	1.092	2.207	885.02	1953.63	2.410	865.49	2086.12
A_68_P32384237	chrX:50144177-50144221	NM_001034059:-178	Ccdc160	PROMOTER	1.092	1.926	680.66	1310.80	2.104	395.01	830.95
A_68_P26543679	chr9:57613020-57613064	NM_007713:625	Clk3	INSIDE	1.092	2.246	713.12	1601.84	2.453	624.13	1531.21
A_68_P26249217	chr8:127577984-127578028	NM_174853:-88	Disc1	PROMOTER	1.092	1.405	2176.29	3057.95	1.535	1676.53	2572.87
A_68_P27094078	chr10:41995833-41995877	NM_019740:694	Foxo3	INSIDE	1.092	1.946	1132.38	2203.31	2.125	996.06	2116.45
A_68_P24449405	chr6:52196592-52196638	NM_010450:-848	Hoxa11	PROMOTER	1.092	2.078	254.53	528.92	2.269	206.42	468.39
A_68_P24449194	chr6:52171860-52171904	NM_010455:-3310	Hoxa7	PROMOTER	1.092	2.981	816.63	2434.60	3.255	710.25	2311.83
A_68_P27160596	chr10:57206710-57206754	NM_008297:542	Hsf2	INSIDE	1.092	1.967	679.85	1336.92	2.146	676.80	1452.75
A_68_P25259449	chr7:86294014-86294058	NM_001045489:-90	Mfge8	PROMOTER	1.092	1.683	965.64	1625.51	1.838	854.34	1569.95
A_68_P26129004	chr8:107058523-107058567	NM_144931:-7	Nae1	DIVERGENT_PROMOTER	1.092	1.827	635.44	1161.02	1.996	610.90	1219.32
A_68_P32240895	chrX:7499312-7499356	NM_013892:2387	Pcsk1n	INSIDE	1.092	1.881	702.32	1321.14	2.054	388.47	797.86
A_68_P28197874	chr12:3960028-3960072	NM_008895:5100	Pomc	INSIDE	1.092	1.566	1562.96	2447.85	1.710	1350.78	2310.05
A_68_P28112588	chr11:108204767-108204813	NM_011101:412	Prkca	INSIDE	1.092	1.524	701.76	1069.68	1.664	622.72	1036.41
A_68_P21005390	chr2:11212009-11212053	NM_008859:118022	Prkcq	INSIDE	1.092	2.726	459.91	1253.81	2.977	423.30	1260.32
A_68_P25427818	chr7:120097419-120097463	NM_175279:-35	Rassf10	PROMOTER	1.092	1.871	1730.24	3236.87	2.043	1421.81	2904.66
A_68_P31985666	chr19:17468871-17468915	NM_019437:360	Rfk	INSIDE	1.092	2.565	529.91	1359.11	2.801	556.06	1557.61
A_68_P22336986	chr3:93359142-93359186	NM_009112:126	S100a10	INSIDE	1.092	1.758	1614.85	2839.13	1.920	1482.65	2846.78
A_68_P20585385	chr1:127457901-127457945	NM_028787:330	Slc35f5	INSIDE	1.092	1.638	1881.03	3081.93	1.789	1488.57	2662.31
A_68_P21875635	chr2:174298480-174298524	NM_025531:-60	Slmo2	PROMOTER	1.092	1.905	405.20	771.86	2.081	405.11	842.84
A_68_P26142249	chr8:109459792-109459836	NM_009229:165	Sntb2	INSIDE	1.092	2.236	1254.93	2806.20	2.441	1215.30	2966.75
A_68_P27332824	chr10:89208075-89208119	NM_029166:361	Uhrf1bp1l	INSIDE	1.092	2.596	597.77	1551.87	2.834	563.65	1597.36
A_68_P31208848	chr17:46910008-46910052	NM_025966:447	2310039H08Rik	INSIDE	1.091	1.438	944.27	1358.31	1.569	932.43	1463.08
A_68_P27649725	chr11:24064408-24064452	NM_001159290:83736	Bcl11a	INSIDE	1.091	2.063	1958.95	4041.01	2.251	1478.96	3329.41
A_68_P29511373	chr14:32150285-32150329	NM_009796:397	Capn7	INSIDE	1.091	3.179	1243.34	3952.01	3.468	1100.41	3816.28
A_68_P29338036	chr13:113777997-113778041	NM_001081062:9	Ccno	INSIDE	1.091	0.430	1682.61	722.85	0.469	1393.68	653.36
A_68_P32229422	chr19:61304541-61304585	NM_009970:-241	Csf2ra	PROMOTER	1.091	2.262	925.24	2092.53	2.468	849.59	2096.72
A_68_P27446113	chr10:110357232-110357276	NM_007792:23	Csrp2	INSIDE	1.091	0.558	2555.40	1425.10	0.608	1897.56	1154.62

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25462320	chr7:126327951-126327995	NM_001024138:-84	Gpr139	PROMOTER	1.091	1.512	939.92	1421.21	1.650	736.08	1214.59
A_68_P23573588	chr5:30924821-30924865	NM_010608:34300	Kcnk3	INSIDE	1.091	1.839	544.11	1000.38	2.006	558.17	1119.66
A_68_P25349937	chr7:104480730-104480774	NM_001039039:-80	Kctd21	DIVERGENT_PROMOTER	1.091	1.668	877.16	1462.83	1.819	815.43	1483.00
A_68_P25784752	chr8:37311896-37311940	NM_001081150:652	Lonrf1	INSIDE	1.091	1.739	541.73	942.17	1.898	526.66	999.42
A_68_P20023663	chr1:9690009-9690053	NM_008651:260	Mybl1	INSIDE	1.091	0.519	3635.95	1887.26	0.566	2821.43	1597.30
A_68_P24117615	chr5:136210361-136210405	NM_008898:45299	Por	INSIDE	1.091	1.734	584.65	1014.05	1.892	524.31	992.21
A_68_P26594001	chr9:66441281-66441325	NM_144937:-515	Usp3	PROMOTER	1.091	0.576	2182.33	1257.82	0.629	1688.66	1062.32
A_68_P23059230	chr4:82505564-82505608	NM_026647:-21	Zdhhc21	PROMOTER	1.091	1.889	970.77	1833.93	2.061	880.93	1815.98
A_68_P29224480	chr13:93301031-93301075	NM_173392:-287	Zfyve16	PROMOTER	1.091	0.464	1398.64	648.88	0.506	1184.82	599.58
A_68_P24908454	chr6:143048465-143048509	NM_001109688:141	5730419I09Rik	INSIDE	1.090	1.465	894.46	1309.98	1.597	742.86	1186.33
A_68_P32350054	chrX:41720980-41721024	NM_175539:512	Dcaf12l2	INSIDE	1.090	1.457	1795.18	2615.06	1.588	941.44	1495.00
A_68_P26227567	chr8:124102726-124102770	NM_133765:-42	Fbxo31	PROMOTER	1.090	2.066	2748.15	5677.93	2.252	2044.88	4604.11
A_68_P23577609	chr5:31597809-31597853	NM_022424:420	Fndc4	INSIDE	1.090	1.739	9346.16	16252.36	1.896	7226.94	13702.41
A_68_P28577468	chr12:81858602-81858646	NM_001008423:3078	Gm1568	INSIDE	1.090	1.986	1107.37	2199.70	2.164	880.52	1905.66
A_68_P28186730	chr11:120645846-120645891	NM_145370:40	Gps1	INSIDE	1.090	2.505	242.19	606.71	2.730	205.36	560.59
A_68_P27924566	chr11:74979860-74979904	NM_001098203:1772	Hic1	INSIDE	1.090	0.538	1490.23	801.41	0.586	1093.12	641.03
A_68_P23333246	chr4:135867340-135867384	NM_028871:472	Hnrnpr	INSIDE	1.090	1.697	965.19	1638.13	1.850	792.11	1465.12
A_68_P27353693	chr10:92916270-92916314	NM_008517:152	Lta4h	INSIDE	1.090	0.582	1397.76	813.35	0.634	1224.43	776.44
A_68_P32148146	chr19:47253257-47253301	NM_021360:-31	Neurl1a	PROMOTER	1.090	1.559	707.46	1102.93	1.699	612.61	1040.68
A_68_P31935410	chr19:6531540-6531584	NM_001205234:112825	Nrxn2	INSIDE	1.090	0.543	1937.03	1051.72	0.592	1523.40	901.80
A_68_P25427821	chr7:120097865-120097909	NM_175279:411	Rassf10	INSIDE	1.090	1.749	1317.82	2304.86	1.907	1209.87	2307.04
A_68_P22741779	chr4:13670817-13670861	NM_001111027:-7605	Runx1t1	PROMOTER	1.090	1.428	1342.89	1918.06	1.557	1071.37	1668.37
A_68_P25586717	chr7:148286592-148286636	NM_023059:-169	Sigirr	PROMOTER	1.090	1.757	835.30	1467.72	1.916	735.86	1409.86
A_68_P26766608	chr9:99770906-99770951	NM_011440:5661	Sox14	DOWNSTREAM	1.090	1.814	1250.11	2267.81	1.978	960.91	1900.56
A_68_P21809439	chr2:162757267-162757311	NM_026499:45	Srsf6	INSIDE	1.090	3.456	1093.28	3778.55	3.767	948.14	3571.23
A_68_P25947574	chr8:72149082-72149126	NM_001045553:-30	Zfp868	PROMOTER	1.090	0.489	1490.68	728.48	0.532	1439.65	766.58
A_68_P30413820	chr15:87375020-87375064	ENSMUST00000169110:139		INSIDE	1.090	1.546	718.08	1109.84	1.684	666.87	1123.01
A_68_P24830751	chr6:127059602-127059646	NM_177003:-54	9630033F20Rik	PROMOTER	1.089	0.585	1703.63	996.57	0.637	1313.56	836.50
A_68_P27282593	chr10:79804404-79804448	NM_001113548:6765	Adamtsl5	INSIDE	1.089	1.727	2643.31	4565.54	1.882	2176.75	4095.73
A_68_P26291034	chr9:8134431-8134475	NM_001045524:-158	AK129341	PROMOTER	1.089	2.008	727.17	1460.48	2.188	635.94	1391.47
A_68_P24758539	chr6:113233198-113233242	NM_170673:920	Cpne9	INSIDE	1.089	1.342	2195.07	2945.46	1.461	1824.69	2666.41
A_68_P30896820	chr16:78576898-78576942	NM_025967:-7	D16Ertd472e	PROMOTER	1.089	1.466	763.07	1118.89	1.596	636.63	1016.24
A_68_P25410983	chr7:117103395-117103439	NM_021494:520	Dennd5a	INSIDE	1.089	2.208	1236.91	2731.21	2.404	1097.45	2638.69
A_68_P28672826	chr12:100139771-100139815	NM_001081191:-98	Eml5	PROMOTER	1.089	2.423	1085.33	2629.26	2.637	973.42	2567.26
A_68_P29644194	chr14:60997825-60997869	NM_001164705:724	Fam123a	INSIDE	1.089	1.764	919.47	1621.70	1.921	815.23	1566.47
A_68_P32678434	chrX:132373604-132373648	NM_001163015:54	Gprasp2	INSIDE	1.089	2.036	996.22	2028.35	2.217	634.40	1406.66
A_68_P21080306	chr2:26516993-26517037	NM_010695:9788	Lcn4	DOWNSTREAM	1.089	2.024	541.27	1095.45	2.203	559.93	1233.66
A_68_P20337470	chr1:72583581-72583625	NM_001045533:-464	Marchf4	PROMOTER	1.089	4.420	1932.71	8541.63	4.815	1637.09	7882.05
A_68_P27788133	chr11:50173073-50173117	NR_030529:-1713	Mir804	PROMOTER	1.089	1.605	2614.47	4196.32	1.748	2064.20	3608.20
A_68_P27560009	chr11:4749259-4749303	NM_010898:250	Nf2	INSIDE	1.089	2.234	1172.00	2618.64	2.434	1032.93	2513.90
A_68_P27922135	chr11:74536870-74536914	NR_037610:468	Pafah1b1	INSIDE	1.089	1.440	2095.50	3017.17	1.568	1805.45	2830.26
A_68_P28594554	chr12:85113181-85113234	NM_001205343:8624	Papln	INSIDE	1.089	2.860	390.19	1115.97	3.115	341.98	1065.20
A_68_P26542154	chr9:57352236-57352280	NM_133982:350	Rpp25	INSIDE	1.089	0.584	2362.39	1379.66	0.636	1965.79	1250.12
A_68_P28036073	chr11:94871704-94871750	NM_146025:534	Samd14	INSIDE	1.089	2.107	5933.03	12498.82	2.295	3951.23	9067.87
A_68_P21075769	chr2:25876845-25876892	NM_133835:412	Ubac1	INSIDE	1.089	1.482	1130.86	1675.83	1.614	883.53	1425.81
A_68_P23254147	chr4:120624114-120624158	NM_001005788:170	Zfp69	INSIDE	1.089	2.275	2074.37	4718.46	2.476	1737.50	4302.89
A_68_P20286846	chr1:63492907-63492951	NM_001177600:451	Adam23	INSIDE	1.088	1.815	1485.81	2697.48	1.975	1305.15	2578.00
A_68_P23542163	chr5:23991120-23991164	NM_139153:33148	Agap3	INSIDE	1.088	1.597	1168.11	1864.92	1.737	1061.88	1843.97
A_68_P27103326	chr10:43724148-43724192	NM_172393:482	Aim1	INSIDE	1.088	2.573	1166.37	3000.62	2.798	972.81	2721.78
A_68_P25946258	chr8:71612629-71612673	NM_007509:16	Atp6v1b2	INSIDE	1.088	2.878	669.21	1926.00	3.130	630.15	1972.48
A_68_P20900640	chr1:187165153-187165197	NM_011794:9137	Bpnt1	INSIDE	1.088	2.192	702.20	1539.01	2.385	563.89	1345.10

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P24008368	chr5:115643546-115643590	NM_013879:-7438	Cabp1	PROMOTER	1.088	0.494	1592.32	785.95	0.537	1390.94	746.97
A_68_P29651395	chr14:62301504-62301548	NR_028264:-316	Dleu2	PROMOTER	1.088	1.774	939.19	1666.15	1.931	839.18	1620.32
A_68_P20317719	chr1:69153647-69153691	NM_010154:965	Erbb4	INSIDE	1.088	2.366	689.52	1631.39	2.575	585.82	1508.69
A_68_P23582140	chr5:32435627-32435671	NM_008037:-3196	Fosl2	PROMOTER	1.088	1.493	642.03	958.50	1.624	519.60	844.07
A_68_P24990912	chr7:19597699-19597743	NM_008260:11168	Foxa3	DOWNSTREAM	1.088	3.928	207.60	815.53	4.273	221.23	945.35
A_68_P29531946	chr14:35632404-35632448	NM_008166:-895	Grid1	PROMOTER	1.088	1.695	625.50	1059.92	1.843	535.61	987.18
A_68_P25021327	chr7:29136106-29136150	NR_028129:-430	LOC100302567	PROMOTER	1.088	2.380	5000.00	11900.01	2.590	3683.82	9542.52
A_68_P28056218	chr11:98261638-98261682	NM_001033537:144	Pgap3	INSIDE	1.088	1.799	1283.50	2309.61	1.958	1110.18	2173.68
A_68_P24170388	chr5:147656591-147656635	NM_026864:-34	Rasl11a	PROMOTER	1.088	2.313	438.53	1014.12	2.517	536.51	1350.29
A_68_P25499763	chr7:133435519-133435563	NM_145587:19408	Sbk1	INSIDE	1.088	2.004	1195.03	2395.20	2.180	992.60	2164.17
A_68_P32672217	chrX:131010986-131011030	NM_028958:21	Taf7l	INSIDE	1.088	1.990	1340.55	2667.57	2.165	535.73	1159.63
A_68_P26752041	chr9:97266267-97266311	NM_030219:4089	Trim42	INSIDE	1.088	2.208	574.16	1267.98	2.403	518.00	1244.76
A_68_P31889610	chr18:84759292-84759336	NM_001033341:-418	Zfp407	PROMOTER	1.088	2.542	1038.85	2640.85	2.765	861.68	2382.47
A_68_P25735815	chr8:28089687-28089731	NM_001101502:1901	Zfp703	INSIDE	1.088	0.611	3527.33	2156.10	0.665	2599.19	1728.05
A_68_P28677373	chr12:100883228-100883278	ENSMUST00000158736:-70		PROMOTER	1.088	2.570	228.82	588.11	2.797	197.12	551.38
A_68_P32443537	chrX:66613822-66613866	NM_008032:339	Aff2	INSIDE	1.087	1.829	895.87	1638.81	1.989	441.52	878.02
A_68_P30462686	chr15:96116941-96116985	NM_175251:-990	Arid2	PROMOTER	1.087	3.061	370.46	1134.12	3.329	336.06	1118.76
A_68_P23069979	chr4:84320697-84320741	NM_172870:272	Bnc2	INSIDE	1.087	1.825	748.75	1366.52	1.984	669.67	1328.41
A_68_P20910362	chr1:188791704-188791749	NM_033077:432	D1Pas1	INSIDE	1.087	1.845	735.33	1356.69	2.005	591.72	1186.32
A_68_P30630419	chr16:28446947-28446991	NM_183064:-1655	Fgf12	PROMOTER	1.087	2.102	459.89	966.85	2.286	384.98	879.93
A_68_P32563072	chrX:98449525-98449570	NM_018789:-319	Foxo4	PROMOTER	1.087	3.550	1639.04	5817.97	3.859	824.20	3180.59
A_68_P25348906	chr7:104230072-104230116	NM_001162477:-166	Gab2	PROMOTER	1.087	6.600	8024.21	52957.00	7.176	6424.64	46106.17
A_68_P21932362	chr3:8462856-8462900	NR_033512:220	Gm6194	INSIDE	1.087	1.934	1388.70	2686.41	2.103	980.84	2063.11
A_68_P30473864	chr15:98087423-98087467	NM_027304:294	H1fnt	INSIDE	1.087	2.348	699.76	1643.17	2.551	634.24	1618.21
A_68_P29334866	chr13:113253950-113253994	NM_010560:-305	Il6st	PROMOTER	1.087	1.445	763.05	1102.54	1.571	729.30	1145.57
A_68_P20229132	chr1:52874292-52874338	NM_008384:218	Inpp1	INSIDE	1.087	1.627	1632.95	2656.39	1.768	1277.61	2259.43
A_68_P28291801	chr12:25516771-25516815	NM_001083341:329	Mboat2	INSIDE	1.087	2.263	634.38	1435.69	2.461	555.62	1367.22
A_68_P25263202	chr7:86937639-86937683	NM_008588:816	Mesp1	INSIDE	1.087	1.465	838.96	1228.99	1.592	743.62	1184.00
A_68_P29751162	chr14:79790477-79790521	NM_025832:-23	Naa16	DIVERGENT_PROMOTER	1.087	2.084	720.03	1500.88	2.265	677.17	1534.05
A_68_P31207758	chr17:46728606-46728650	NM_175168:37825	Ptk7	INSIDE	1.087	2.213	950.09	2102.09	2.405	812.40	1954.23
A_68_P21106144	chr2:30808670-30808714	NM_133673:172	Tor1b	INSIDE	1.087	0.599	1166.94	699.08	0.651	916.87	597.27
A_68_P31372685	chr17:79024354-79024402	NM_001197028:116976	Vit	INSIDE	1.087	1.873	531.47	995.41	2.036	423.84	863.13
A_68_P32005487	chr19:21346304-21346348	NM_009551:-441	Zfand5	PROMOTER	1.087	1.405	1110.67	1560.54	1.527	935.22	1428.32
A_68_P31002112	chr16:98183669-98183713	NM_001081684:96	Zfp295	INSIDE	1.087	0.575	1056.91	607.77	0.625	866.23	541.67
A_68_P23145844	chr4:99382494-99382538	NM_001081264:196	Alg6	INSIDE	1.086	1.446	1249.49	1807.04	1.570	1044.81	1640.30
A_68_P32592613	chrX:106029430-106029474	NM_001081477:242	Brwd3	INSIDE	1.086	1.470	2860.43	4205.73	1.596	1298.59	2073.00
A_68_P22412539	chr3:108218569-108218613	NM_001004177:-178	Celsr2	PROMOTER	1.086	1.660	1216.24	2018.81	1.803	1164.73	2099.47
A_68_P27865444	chr11:64249527-64249571	NR_028445:628	F930015N05Rik	INSIDE	1.086	2.764	847.34	2342.45	3.002	908.25	2726.73
A_68_P25371472	chr7:108256614-108256658	NM_001146010:-652	Fchsd2	PROMOTER	1.086	1.650	1217.58	2008.60	1.791	1062.57	1903.24
A_68_P25770034	chr8:34764345-34764389	NM_010344:657	Gsr	INSIDE	1.086	1.433	1458.70	2090.94	1.557	1147.76	1786.55
A_68_P20193922	chr1:44608989-44609033	NM_028450:495	Gulp1	INSIDE	1.086	1.372	1587.56	2177.72	1.490	1363.86	2032.28
A_68_P22397119	chr3:105261830-105261874	NM_019931:119	Kcnd3	INSIDE	1.086	2.245	244.99	549.95	2.437	294.15	716.85
A_68_P25713199	chr8:23970569-23970613	NM_001081149:580	Myst3	INSIDE	1.086	1.479	1748.30	2585.19	1.606	1548.07	2486.77
A_68_P26022002	chr8:87323170-87323214	NM_001081982:1047	Nfix	INSIDE	1.086	1.628	834.82	1358.74	1.768	700.56	1238.27
A_68_P22878645	chr4:44716965-44717009	NM_008782:6326	Pax5	INSIDE	1.086	1.393	1322.38	1841.84	1.513	1132.00	1712.39
A_68_P31632592	chr18:38357632-38357676	NM_029357:11762	Pcdh1	INSIDE	1.086	2.484	920.03	2285.68	2.699	758.20	2046.08
A_68_P31252244	chr17:55852024-55852068	NM_028370:-120	Pot1b	PROMOTER	1.086	2.296	685.00	1572.78	2.493	624.59	1557.07
A_68_P26801800	chr9:106101470-106101514	NM_198931:-222	Ppm1m	PROMOTER	1.086	1.613	565.30	911.76	1.751	504.35	883.04
A_68_P28991175	chr13:43711506-43711550	NM_183204:363	Rnf182	INSIDE	1.086	2.249	764.36	1719.41	2.443	661.77	1616.44
A_68_P26133225	chr8:107873334-107873378	NM_001081332:1199	Slc9a5	INSIDE	1.086	0.610	1579.39	962.75	0.662	1449.88	960.12
A_68_P28159868	chr11:116395378-116395422	NM_011451:-653	Sphk1	PROMOTER	1.086	1.603	1490.45	2389.48	1.741	1146.65	1996.62

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31752326	chr18:60756117-60756161	NM_177340:27821	Synpo	INSIDE	1.086	2.221	1256.85	2791.85	2.411	1149.92	2772.93
A_68_P27356011	chr10:93308901-93308948	NM_183199:14625	Usp44	INSIDE	1.086	3.954	748.41	2959.48	4.293	558.82	2399.15
A_68_P21394210	chr2:84555540-84555584	NM_144887:-241	Zdhhc5	PROMOTER	1.086	2.374	1388.58	3297.07	2.578	1267.29	3267.24
A_68_P24783631	chr6:117791197-117791241	NM_177684:-41	Zfp637	PROMOTER	1.086	1.775	363.93	645.98	1.928	355.12	684.55
A_68_P27543827	chr10:128347191-128347235	NM_007653:291	Cd63	INSIDE	1.085	2.181	1226.97	2676.50	2.366	1107.11	2619.12
A_68_P26248668	chr8:127473510-127473554	NM_053207:-378	Egln1	PROMOTER	1.085	3.244	545.00	1767.81	3.519	514.37	1810.32
A_68_P29054917	chr13:55521884-55521928	NM_021489:6257	F12	INSIDE	1.085	4.411	3153.12	13907.92	4.784	2278.57	10899.88
A_68_P27278518	chr10:79187320-79187368	NM_008226:7966	Hcn2	INSIDE	1.085	3.426	343.67	1177.56	3.718	252.43	938.61
A_68_P26537259	chr9:56467537-56467581	NM_181074:65502	Lingo1	INSIDE	1.085	3.955	2587.53	10233.74	4.291	1897.13	8140.56
A_68_P21842273	chr2:168396596-168396647	NM_001136073:19070	Nfatc2	INSIDE	1.085	5.580	730.27	4075.04	6.053	557.44	3374.42
A_68_P31926006	chr19:4942839-4942883	NM_172835:232	Peli3	INSIDE	1.085	2.397	10563.21	25319.83	2.600	7828.38	20352.98
A_68_P27287760	chr10:80616735-80616779	NM_021501:13709	Pias4	INSIDE	1.085	2.793	1564.14	4368.36	3.029	1257.72	3809.65
A_68_P21351536	chr2:76485728-76485772	NM_011871:301	Prkra	INSIDE	1.085	1.350	1911.62	2581.54	1.465	1645.67	2410.74
A_68_P21608666	chr2:126378873-126378917	NM_011978:135	Slc27a2	INSIDE	1.085	2.275	463.89	1055.40	2.468	580.43	1432.62
A_68_P20901345	chr1:187279321-187279365	NM_001033286:616	Slc30a10	INSIDE	1.085	1.453	2158.64	3137.54	1.576	1919.78	3026.20
A_68_P30486835	chr15:100467504-100467548	NM_001033872:-230	Smagp	PROMOTER	1.085	1.373	2862.18	3929.02	1.490	2427.87	3617.65
A_68_P32557249	chrX:97016733-97016777	NM_001081283:347	Tmem28	INSIDE	1.085	2.341	759.64	1778.27	2.539	493.97	1254.15
A_68_P26253146	chr8:128193938-128193982	NM_028908:243	4933403G14Rik	INSIDE	1.084	2.367	406.41	961.89	2.566	386.04	990.76
A_68_P27320008	chr10:86956714-86956759	NM_008553:-331	Ascl1	PROMOTER	1.084	2.454	354.66	870.18	2.661	320.68	853.27
A_68_P26372312	chr9:26563608-26563652	NM_029792:4484	B3gat1	INSIDE	1.084	1.764	438.16	773.11	1.913	321.66	615.24
A_68_P24372703	chr6:37391889-37391933	NM_178661:238	Creb3l2	INSIDE	1.084	2.131	1571.80	3349.57	2.311	1302.35	3009.34
A_68_P23244385	chr4:118905637-118905681	NM_001042411:-775	Lepre1	PROMOTER	1.084	0.546	1114.00	607.96	0.591	1081.07	639.37
A_68_P32579350	chrX:102316061-102316105	NM_053201:348	Magee1	INSIDE	1.084	2.179	794.27	1730.67	2.362	509.38	1203.08
A_68_P25809394	chr8:42219374-42219418	NM_001005863:-316	Mtus1	PROMOTER	1.084	0.486	1338.27	650.56	0.527	1201.07	632.62
A_68_P22313146	chr3:88137030-88137074	NM_024246:1303	Tmem79	INSIDE	1.084	2.012	1491.70	3001.41	2.182	1211.37	2642.72
A_68_P22313144	chr3:88136817-88136861	NM_024246:1517	Tmem79	INSIDE	1.084	2.398	1419.15	3403.77	2.600	899.90	2339.69
A_68_P20352743	chr1:75216251-75216295	NM_009447:-444	Tuba4a	PROMOTER	1.084	1.351	2017.00	2723.97	1.464	1510.56	2211.38
A_68_P28220739	chr12:8214991-8215035	NM_001167767:80	1110057K04Rik	INSIDE	1.083	1.464	3392.89	4967.85	1.585	2514.03	3984.88
A_68_P20086662	chr1:23109142-23109186	NM_025746:-72	4933415F23Rik	PROMOTER	1.083	1.897	442.90	839.98	2.054	489.22	1004.88
A_68_P28889024	chr13:24894047-24894092	NM_024473:544	BC005537	INSIDE	1.083	2.116	1408.04	2979.88	2.292	1418.33	3250.86
A_68_P31485628	chr18:9449839-9449883	NM_026484:288	Ccny	INSIDE	1.083	1.420	1567.32	2225.76	1.538	1500.15	2306.85
A_68_P25637611	chr8:8660029-8660073	NM_010111:723	Efnb2	INSIDE	1.083	1.391	1911.18	2659.29	1.507	1558.59	2348.95
A_68_P23969768	chr5:108415971-108416015	NM_026062:104	Fam69a	INSIDE	1.083	1.615	3737.05	6035.04	1.749	2970.71	5195.43
A_68_P26572467	chr9:62659271-62659315	NM_010193:163	Fem1b	INSIDE	1.083	1.740	842.93	1466.63	1.884	779.02	1467.71
A_68_P25005396	chr7:25318615-25318659	NM_153134:2970	Irgq	INSIDE	1.083	2.746	2862.77	7861.91	2.975	2176.56	6474.47
A_68_P21680294	chr2:139504121-139504165	NM_001126490:229	Ism1	INSIDE	1.083	2.270	583.28	1323.92	2.457	592.64	1456.33
A_68_P32040191	chr19:27397873-27397917	NM_183179:786	Kcnv2	INSIDE	1.083	2.107	802.13	1689.80	2.281	676.91	1543.98
A_68_P29509958	chr14:31951947-31951991	NM_027289:3930	Nt5dc2	INSIDE	1.083	3.944	1570.26	6193.19	4.270	1095.93	4679.34
A_68_P27922136	chr11:74536967-74537011	NR_037610:372	Pafah1b1	INSIDE	1.083	0.512	1119.25	572.50	0.554	965.78	535.17
A_68_P32668460	chrX:130222185-130222229	NM_001105245:1326	Pcdh19	INSIDE	1.083	2.529	871.95	2205.54	2.740	550.74	1508.80
A_68_P27287762	chr10:80616963-80617007	NM_021501:13481	Pias4	INSIDE	1.083	2.001	826.10	1652.81	2.167	690.08	1495.39
A_68_P23435436	chr4:154357832-154357876	NM_001113360:27239	Plch2	INSIDE	1.083	1.624	1346.07	2185.98	1.759	1013.35	1782.85
A_68_P25025803	chr7:29965431-29965475	NM_026545:240	Psmd8	INSIDE	1.083	1.646	842.12	1386.40	1.783	665.51	1186.81
A_68_P27286999	chr10:80494095-80494139	NM_134135:2541	Slc39a3	INSIDE	1.083	2.901	805.63	2337.38	3.141	671.47	2109.37
A_68_P31093843	chr17:23956823-23956878	NM_175229:16697	Srrm2	INSIDE	1.083	3.064	209.21	640.93	3.319	205.01	680.48
A_68_P27504467	chr10:121043954-121043999	NM_001081056:19396	Xpot	INSIDE	1.083	3.310	2133.85	7062.86	3.586	1523.13	5462.33
A_68_P23588853	chr5:33777078-33777122	ENSMUST00000030994:-3256		PROMOTER	1.083	3.685	1717.52	6329.01	3.992	1460.63	5830.60
A_68_P26218687	chr8:122754031-122754075	ENSMUST00000127664:319312		INSIDE	1.083	1.449	1034.17	1498.69	1.570	934.02	1466.36
A_68_P24766863	chr6:114688424-114688468	NM_028835:95304	Atg7	INSIDE	1.082	2.256	544.41	1228.36	2.441	594.42	1450.90
A_68_P24908776	chr6:143115770-143115814	NM_029250:43	Etnk1	INSIDE	1.082	0.615	1151.54	708.24	0.665	1122.82	746.97
A_68_P25307415	chr7:96552181-96552225	NM_008055:-673	Fzd4	PROMOTER	1.082	1.848	1413.66	2611.81	2.000	1161.64	2322.89

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P24126245	chr5:137972339-137972383	NM_010312:2097	Gnb2	INSIDE	1.082	1.768	1605.49	2839.14	1.913	1433.29	2741.26
A_68_P28099139	chr11:105881776-105881820	NM_001037712:12282	Kcnh6	INSIDE	1.082	1.660	2806.09	4657.08	1.795	2058.56	3695.78
A_68_P27365816	chr10:95026259-95026303	NR_037212:-4325	Mir3058	PROMOTER	1.082	1.476	1941.81	2866.07	1.597	1704.17	2721.57
A_68_P23792521	chr5:72950400-72950444	NM_133921:462	Nfxl1	INSIDE	1.082	2.029	395.58	802.48	2.195	382.97	840.77
A_68_P31397730	chr17:83614079-83614123	NM_134117:-522	Pkdcc	PROMOTER	1.082	0.519	3450.30	1790.20	0.562	2733.35	1535.13
A_68_P30330340	chr15:73253433-73253477	NM_007982:167	Ptk2	INSIDE	1.082	1.694	1461.10	2475.21	1.833	1438.43	2636.18
A_68_P31631090	chr18:38115096-38115140	NM_153793:-94	Rell2	DIVERGENT_PROMOTER	1.082	1.446	810.48	1171.94	1.564	644.06	1007.62
A_68_P32036078	chr19:26680160-26680204	NM_011416:533	Smarca2	INSIDE	1.082	5.509	565.99	3117.79	5.958	567.26	3379.61
A_68_P27282400	chr10:79777704-79777748	NM_011789:13162	Apc2	INSIDE	1.081	4.071	1006.26	4096.37	4.403	886.28	3901.88
A_68_P29501750	chr14:30535873-30535917	NM_009785:-844	Cacna2d3	PROMOTER	1.081	1.626	1086.12	1766.39	1.758	959.50	1686.37
A_68_P24818635	chr6:125045930-125045974	NM_145979:-228	Chd4	PROMOTER	1.081	1.450	2836.15	4112.99	1.568	2092.42	3280.68
A_68_P24850799	chr6:131338430-131338474	NM_011733:16	Csda	INSIDE	1.081	2.069	1929.61	3991.90	2.236	1746.32	3904.71
A_68_P27187153	chr10:62113528-62113572	NM_053183:396	Ddx50	INSIDE	1.081	2.048	1143.95	2342.41	2.214	922.86	2043.25
A_68_P27835392	chr11:59005058-59005102	NM_001159410:-3837	Guk1	PROMOTER	1.081	0.434	1538.20	667.38	0.469	1318.39	618.25
A_68_P27482567	chr10:117147762-117147806	NM_010786:-12	Mdm2	PROMOTER	1.081	2.078	1021.72	2123.29	2.246	939.52	2110.48
A_68_P21967992	chr3:17694822-17694866	NR_029814:-817	Mir124a-2	PROMOTER	1.081	1.532	1068.35	1636.40	1.655	878.26	1453.74
A_68_P23657845	chr5:46060700-46060744	NM_019438:-441	Ncapg	PROMOTER	1.081	0.395	1322.04	522.10	0.427	1034.57	441.49
A_68_P21826979	chr2:165818066-165818110	NM_008679:-48	Ncoa3	PROMOTER	1.081	3.898	1479.50	5766.38	4.215	1277.66	5385.51
A_68_P29510249	chr14:31989749-31989793	NM_022656:30242	Nisch	INSIDE	1.081	2.747	3074.59	8445.35	2.970	2229.52	6620.63
A_68_P32114751	chr19:41450414-41450458	NM_031376:9124	Pik3ap1	INSIDE	1.081	2.173	470.08	1021.30	2.350	468.06	1099.76
A_68_P24979913	chr7:16730734-16730778	NM_148946:15108	Slc8a2	INSIDE	1.081	3.422	4275.22	14628.45	3.698	3396.45	12558.68
A_68_P23364645	chr4:141093735-141093779	NM_019763:756	Spen	INSIDE	1.081	1.702	425.82	724.88	1.841	412.57	759.45
A_68_P31093844	chr17:23956989-23957033	NM_175229:16857	Srrm2	INSIDE	1.081	2.495	1154.37	2880.62	2.698	879.58	2372.82
A_68_P25195702	chr7:74903601-74903645	NM_183312:1006	Synm	INSIDE	1.081	1.720	402.89	693.15	1.860	343.64	639.16
A_68_P25957926	chr8:74152893-74152939	NM_001029873:42740	Unc13a	INSIDE	1.081	2.049	290.24	594.71	2.216	257.69	570.92
A_68_P29604236	chr14:52626490-52626534	NM_027248:13896	Zfp219	INSIDE	1.081	3.110	922.81	2870.24	3.361	889.59	2989.75
A_68_P30708314	chr16:42190481-42190525	ENSMUST00000099761:657353		DOWNSTREAM	1.081	1.478	761.15	1125.35	1.598	672.20	1074.34
A_68_P24944594	chr6:149302348-149302392	ENSMUST00000121073:-22		DIVERGENT_PROMOTER	1.081	2.873	1197.78	3441.02	3.105	1060.99	3294.70
A_68_P30575977	chr16:17834072-17834116	NR_027959:883	B830017H08Rik	INSIDE	1.080	2.123	423.75	899.43	2.293	375.44	860.84
A_68_P23201926	chr4:109329790-109329834	NM_007671:8165	Cdkn2c	DOWNSTREAM	1.080	1.387	1720.82	2386.25	1.498	1604.44	2403.75
A_68_P28158071	chr11:116083426-116083470	NM_025276:15957	Evpl	INSIDE	1.080	1.744	649.04	1131.68	1.883	565.73	1065.47
A_68_P29631462	chr14:58689892-58689936	NM_013518:-1608	Fgf9	PROMOTER	1.080	3.630	1037.56	3765.94	3.921	926.49	3632.53
A_68_P25348904	chr7:104229911-104229955	NM_001162477:-328	Gab2	PROMOTER	1.080	2.251	784.80	1766.58	2.430	662.88	1610.91
A_68_P25885333	chr8:58773316-58773360	NM_008278:-10	Hpgd	PROMOTER	1.080	2.028	1609.36	3264.26	2.191	1324.83	2902.42
A_68_P31113973	chr17:27194296-27194340	NM_080553:70	Itpr3	INSIDE	1.080	1.466	1219.41	1787.40	1.583	1010.75	1599.96
A_68_P31304302	chr17:66450798-66450842	NM_028388:11	Ndufv2	INSIDE	1.080	2.986	664.31	1983.83	3.226	630.97	2035.74
A_68_P22101773	chr3:45184916-45184960	NM_011043:2619	Pcdh10	INSIDE	1.080	1.638	1512.32	2477.22	1.769	1373.93	2430.73
A_68_P22593188	chr3:142544925-142544969	NM_178654:22	Pkn2	INSIDE	1.080	2.339	460.27	1076.56	2.525	454.22	1146.90
A_68_P32479509	chrX:75041437-75041481	NM_016979:-159	Prkx	PROMOTER	1.080	2.647	639.09	1691.40	2.857	431.93	1234.13
A_68_P29262747	chr13:100114515-100114559	NM_026873:97	Ptcd2	INSIDE	1.080	1.599	667.57	1067.12	1.727	623.50	1076.51
A_68_P22378031	chr3:101728081-101728125	NM_001039371:274	Slc22a15	INSIDE	1.080	2.650	958.43	2539.64	2.863	722.35	2068.17
A_68_P21901051	chr2:179777462-179777506	NM_178750:297	Ss18l1	INSIDE	1.080	1.566	2947.62	4615.63	1.691	2650.81	4483.44
A_68_P31826836	chr18:73782887-73782931	ENSMUST00000103753:-1673		PROMOTER	1.080	1.586	581.03	921.63	1.713	522.88	895.68
A_68_P31422206	chr17:87681968-87682012	NR_015506:164	4833418N02Rik	INSIDE	1.079	1.609	915.83	1473.86	1.737	770.39	1338.11
A_68_P21774855	chr2:156866013-156866057	NM_001164663:38967	9830001H06Rik	INSIDE	1.079	3.132	487.81	1527.71	3.380	415.22	1403.27
A_68_P31599408	chr18:31920327-31920372	NM_153515:816	Ammecr1l	INSIDE	1.079	1.533	1633.84	2504.64	1.654	1132.02	1872.67
A_68_P26459688	chr9:42913910-42913954	NM_027144:-131	Arhgef12	PROMOTER	1.079	2.318	406.31	941.75	2.502	531.04	1328.68
A_68_P31564332	chr18:25327565-25327609	NM_001033532:66	AW554918	INSIDE	1.079	1.955	595.66	1164.41	2.109	551.44	1163.19
A_68_P25948481	chr8:72406321-72406365	NM_026818:4949	Cilp2	INSIDE	1.079	2.303	966.50	2225.58	2.484	875.81	2175.71
A_68_P24122107	chr5:137044683-137044727	NM_009986:-1403	Cux1	PROMOTER	1.079	1.641	442.58	726.35	1.771	436.97	773.82
A_68_P30010734	chr15:10399494-10399539	NM_030046:755	Dnajc21	INSIDE	1.079	2.893	470.80	1361.79	3.121	503.18	1570.42

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25565208	chr7:144505952-144505996	NM_001113414:154	Ebf3	INSIDE	1.079	2.957	598.24	1769.23	3.192	563.20	1797.99
A_68_P20562756	chr1:122499449-122499493	NM_010133:407	En1	INSIDE	1.079	1.480	1523.21	2254.00	1.597	1317.12	2103.82
A_68_P31214871	chr17:48041296-48041340	NM_001110824:20263	Foxp4	INSIDE	1.079	1.418	1234.48	1750.63	1.531	971.42	1486.99
A_68_P30580077	chr16:18498909-18498953	NM_023120:-33	Gnb1l	PROMOTER	1.079	1.525	921.52	1405.22	1.645	843.32	1387.48
A_68_P30482739	chr15:99705810-99705854	NM_001113545:55	Lima1	INSIDE	1.079	1.401	2145.87	3006.05	1.511	1822.19	2753.12
A_68_P29425004	chr14:16271153-16271197	NM_146052:327	Lrrc3b	INSIDE	1.079	1.974	1095.17	2161.49	2.129	925.23	1970.21
A_68_P27287759	chr10:80616606-80616650	NM_021501:13837	Pias4	DOWNSTREAM	1.079	2.959	692.09	2048.17	3.193	636.26	2031.37
A_68_P30390280	chr15:83555410-83555454	NM_022723:19	Scube1	INSIDE	1.079	2.419	753.21	1821.69	2.608	764.83	1995.01
A_68_P26591325	chr9:65972739-65972783	NM_019727:-67	Snx1	DIVERGENT_PROMOTER	1.079	1.924	2572.37	4949.01	2.076	2215.56	4599.79
A_68_P20322000	chr1:69873617-69873661	NM_029160:77	Spag16	INSIDE	1.079	0.538	1306.32	703.40	0.581	1074.64	624.13
A_68_P24593030	chr6:83318306-83318350	NM_183138:73344	Tet3	INSIDE	1.079	2.358	790.16	1863.46	2.545	541.70	1378.72
A_68_P27848242	chr11:61221514-61221558	ENSMUST00000121719:8781		DOWNSTREAM	1.079	1.971	588.37	1159.59	2.126	543.62	1155.95
A_68_P26347944	chr9:21397144-21397188	NM_178619:1	1810026J23Rik	INSIDE	1.078	1.400	1296.34	1814.42	1.509	1053.54	1589.38
A_68_P26242727	chr8:126506886-126506930	NM_019552:114	Abcb10	INSIDE	1.078	1.899	585.73	1112.47	2.047	555.28	1136.82
A_68_P25597930	chr7:150154345-150154389	NM_008554:803	Ascl2	INSIDE	1.078	1.679	552.15	927.15	1.809	510.03	922.81
A_68_P29369780	chr13:119503164-119503208	NM_008002:-319	Fgf10	PROMOTER	1.078	1.516	1114.00	1688.30	1.634	928.25	1516.71
A_68_P29071667	chr13:58229346-58229390	NM_029872:549	Hnrnpa0	INSIDE	1.078	1.940	1563.14	3032.76	2.092	1369.68	2865.29
A_68_P30433466	chr15:90879641-90879685	NM_001109040:717	Kif21a	INSIDE	1.078	2.587	1505.35	3893.82	2.788	1061.34	2958.71
A_68_P24385097	chr6:39761053-39761097	NM_001010930:-139	Mrps33	PROMOTER	1.078	1.674	1580.80	2646.78	1.804	1307.30	2358.52
A_68_P20418213	chr1:89406454-89406498	NM_019867:461	Ngef	INSIDE	1.078	0.554	1066.15	590.96	0.598	894.26	534.44
A_68_P27483042	chr10:117229727-117229771	NM_134010:13	Nup107	INSIDE	1.078	1.711	723.11	1237.56	1.846	720.16	1329.08
A_68_P28946211	chr13:36060705-36060749	NM_029628:952	Ppp1r3g	INSIDE	1.078	2.598	870.26	2261.21	2.800	730.42	2045.41
A_68_P25427828	chr7:120098728-120098772	NM_175279:1275	Rassf10	INSIDE	1.078	1.446	734.25	1062.04	1.560	649.71	1013.32
A_68_P26872698	chr9:119394966-119395010	NM_021544:93146	Scn5a	INSIDE	1.078	1.925	817.81	1573.94	2.075	645.15	1338.74
A_68_P27630973	chr11:20232357-20232401	NM_018861:338	Slc1a4	INSIDE	1.078	0.540	1228.82	663.41	0.582	1068.08	621.84
A_68_P28357645	chr12:37043657-37043701	NM_025312:2923	Sostdc1	INSIDE	1.078	1.680	667.21	1121.04	1.811	597.50	1082.35
A_68_P31802712	chr18:69505723-69505767	NM_001083967:370	Tcf4	INSIDE	1.078	0.628	1732.31	1088.73	0.678	1465.99	993.56
A_68_P31201713	chr17:45683888-45683932	NM_001013749:2716	Tmem151b	INSIDE	1.078	1.767	562.80	994.66	1.905	442.37	842.69
A_68_P28159935	chr11:116403194-116403238	NM_173755:39545	Ube2o	INSIDE	1.078	2.007	1088.81	2185.09	2.164	951.58	2058.87
A_68_P25349897	chr7:104474502-104474546	NM_001177412:-50	Usp35	DIVERGENT_PROMOTER	1.078	2.459	1831.48	4503.34	2.651	1575.47	4175.82
A_68_P22964623	chr4:62131950-62131994	NM_023597:-66	Wdr31	DIVERGENT_PROMOTER	1.078	2.056	574.20	1180.53	2.217	512.48	1135.98
A_68_P29703312	chr14:71166447-71166491	NM_023045:-33	Xpo7	DIVERGENT_PROMOTER	1.078	2.789	409.11	1140.91	3.006	359.01	1079.07
A_68_P31092440	chr17:23713162-23713206	NM_011747:23270	Zfp13	INSIDE	1.078	2.504	1189.02	2977.49	2.701	965.76	2608.10
A_68_P28336342	chr12:33064298-33064342	NM_001162903:667	2010109K11Rik	INSIDE	1.077	2.382	546.52	1302.02	2.566	493.92	1267.26
A_68_P22142066	chr3:53282945-53282989	NM_173382:15228	2810046L04Rik	INSIDE	1.077	2.661	2085.95	5549.77	2.865	1645.65	4715.00
A_68_P24008812	chr5:115729714-115729758	NM_026504:26	Coq5	INSIDE	1.077	1.747	671.62	1173.45	1.882	655.67	1233.76
A_68_P28446510	chr12:55304616-55304660	NM_028133:223	Egln3	INSIDE	1.077	2.054	522.12	1072.55	2.212	508.72	1125.28
A_68_P21874503	chr2:174124272-174124316	NM_201617:935	Gnas	INSIDE	1.077	1.529	684.87	1046.89	1.646	615.93	1013.59
A_68_P25090529	chr7:52253176-52253220	NM_016849:169	Irf3	INSIDE	1.077	3.535	1325.06	4684.13	3.806	1166.81	4441.09
A_68_P21840390	chr2:168088577-168088621	NM_001081134:6233	Kcng1	INSIDE	1.077	3.037	4213.25	12796.91	3.271	3132.88	10248.27
A_68_P26321969	chr9:15083907-15083951	NM_144933:383	Med17	INSIDE	1.077	2.562	373.86	957.76	2.758	307.90	849.21
A_68_P32266426	chrX:13063861-13063905	NM_173415:19085	Nyx	INSIDE	1.077	2.471	535.52	1323.03	2.660	274.70	730.75
A_68_P20614487	chr1:133142076-133142120	NM_018750:-343	Rassf5	PROMOTER	1.077	0.578	1301.26	751.59	0.622	1038.32	646.09
A_68_P25414288	chr7:117758585-117758629	NM_177324:-172	Sbf2	PROMOTER	1.077	2.206	783.19	1727.71	2.377	731.47	1738.51
A_68_P21266438	chr2:61649821-61649865	NM_009322:7333	Tbr1	INSIDE	1.077	2.900	603.50	1750.02	3.123	553.44	1728.40
A_68_P28538087	chr12:74646709-74646753	NM_178715:652	Tmem30b	INSIDE	1.077	2.743	759.87	2084.56	2.955	637.27	1883.10
A_68_P26154295	chr8:111474184-111474229	NM_007496:235663	Zfhx3	INSIDE	1.077	3.115	1123.79	3500.89	3.356	883.92	2966.63
A_68_P31092622	chr17:23747282-23747326	NM_001033425:9482	Zscan10	INSIDE	1.077	1.982	747.96	1482.47	2.135	606.33	1294.51
A_68_P32554231	chrX:96412395-96412439			Unknown	1.077	2.034	2212.71	4501.10	2.192	1277.74	2800.61
A_68_P29102523	chr13:65361108-65361152	ENSMUST00000099425:284		INSIDE	1.077	1.912	464.78	888.47	2.058	410.84	845.70
A_68_P23801180	chr5:74488973-74489017	NR_015531:-113	2700023E23Rik	PROMOTER	1.076	2.452	1241.04	3042.83	2.639	1069.01	2821.04

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31499176	chr18:12327130-12327174	NM_029623:-86	3110002H16Rik	PROMOTER	1.076	1.704	536.63	914.34	1.834	497.05	911.51
A_68_P32143650	chr19:46469545-46469589	NM_016860:659	Actr1a	INSIDE	1.076	4.088	3386.97	13844.71	4.397	2397.83	10544.04
A_68_P30645474	chr16:31081440-31081484	NM_198626:56	AI480653	INSIDE	1.076	3.419	762.59	2607.41	3.680	634.02	2333.29
A_68_P24735709	chr6:108733062-108733106	NM_026011:32	Arl8b	INSIDE	1.076	0.643	1563.37	1004.57	0.692	1296.01	896.31
A_68_P24800930	chr6:120866663-120866707	NM_007544:154	Bid	INSIDE	1.076	1.426	2162.82	3085.01	1.535	1746.23	2681.08
A_68_P24631554	chr6:90259619-90259663	NM_027928:15539	Chst13	INSIDE	1.076	2.274	555.12	1262.56	2.447	549.58	1344.71
A_68_P25371478	chr7:108257374-108257418	NM_001146010:108	Fchsd2	INSIDE	1.076	1.650	2019.03	3330.68	1.775	1526.09	2708.13
A_68_P30631086	chr16:28564499-28564543	NM_010199:188768	Fgf12	INSIDE	1.076	2.233	764.97	1708.10	2.402	672.14	1614.74
A_68_P28293548	chr12:25785727-25785771	NM_010496:-4791	Id2	PROMOTER	1.076	2.409	2706.49	6519.67	2.592	2173.80	5634.35
A_68_P25095112	chr7:53050502-53050546	NM_001005511:11208	Lmtk3	INSIDE	1.076	2.825	935.66	2643.11	3.039	808.11	2455.56
A_68_P23428418	chr4:153386065-153386109	NM_201226:175	Lrrc47	INSIDE	1.076	4.769	644.55	3073.55	5.130	530.64	2722.12
A_68_P25424701	chr7:119571229-119571273	NM_020606:31	Parva	INSIDE	1.076	1.728	716.98	1238.97	1.860	583.11	1084.57
A_68_P27230712	chr10:70062823-70062867	NM_178621:-805	Phyhipl	PROMOTER	1.076	1.509	1085.49	1637.65	1.624	951.35	1544.51
A_68_P27901222	chr11:70353684-70353728	NM_008876:41	Pld2	INSIDE	1.076	0.586	1130.51	662.51	0.630	929.07	585.65
A_68_P31107656	chr17:26122124-26122168	NM_153140:36659	Rab11fip3	DOWNSTREAM	1.076	1.519	1016.75	1544.33	1.635	871.14	1424.14
A_68_P26579233	chr9:63801395-63801439	NM_008542:68450	Smad6	INSIDE	1.076	1.661	828.55	1376.32	1.787	785.52	1403.60
A_68_P27992700	chr11:86940726-86940770	NM_197987:170	Trim37	INSIDE	1.076	6.146	231.32	1421.65	6.615	258.04	1707.03
A_68_P24428347	chr6:48569751-48569795	NM_173429:6594	Zfp775	INSIDE	1.076	1.977	783.47	1549.15	2.128	604.91	1287.51
A_68_P20038596	A_68_P20038596			Unknown	1.076	1.638	817.49	1339.39	1.762	747.56	1317.46
A_68_P24059259	chr5:124540142-124540186	NM_019875:5643	Abcb9	INSIDE	1.075	2.290	1497.55	3429.39	2.462	1143.95	2816.15
A_68_P22321216	chr3:89519299-89519343	NM_001038587:377	Adar	INSIDE	1.075	2.404	904.82	2175.30	2.585	816.35	2110.58
A_68_P28751741	chr12:113912366-113912410	NM_001165894:99	Akt1	INSIDE	1.075	1.850	565.86	1046.91	1.989	554.20	1102.27
A_68_P30542889	chr16:10545693-10545737	NM_001204229:283	Clec16a	INSIDE	1.075	0.565	1526.95	862.85	0.607	1143.88	694.64
A_68_P23279249	chr4:125963943-125963987	NM_199473:-73	Col8a2	PROMOTER	1.075	3.385	2655.88	8990.38	3.638	2397.93	8724.28
A_68_P26543014	chr9:57493074-57493118	NM_007783:-109	Csk	PROMOTER	1.075	0.482	1192.25	575.02	0.518	985.15	510.72
A_68_P31161105	chr17:35960212-35960256	NM_008027:-67	Flot1	PROMOTER	1.075	1.463	899.60	1315.98	1.573	860.01	1353.00
A_68_P29257128	chr13:99125244-99125288	NM_008242:1067	Foxd1	INSIDE	1.075	1.950	1163.48	2269.12	2.096	1029.83	2159.02
A_68_P25951930	chr8:72975613-72975657	NM_001122830:25208	Klhl26	INSIDE	1.075	1.620	904.54	1465.51	1.742	855.74	1490.99
A_68_P24378360	chr6:38586324-38586368	NM_001033171:893	Klrg2	INSIDE	1.075	0.557	1057.67	589.12	0.599	965.04	577.67
A_68_P28582490	chr12:82833202-82833246	NM_001174107:48933	Map3k9	INSIDE	1.075	2.320	342.41	794.50	2.493	331.86	827.41
A_68_P27854128	chr11:62271118-62271162	NM_011308:-306	Ncor1	DIVERGENT_PROMOTER	1.075	2.116	518.80	1097.80	2.275	474.78	1080.12
A_68_P24477532	chr6:56873994-56874038	NM_026004:-90	Nt5c3	PROMOTER	1.075	2.384	315.92	753.10	2.563	321.98	825.27
A_68_P30346595	chr15:76009519-76009563	NM_201394:16600	Plec	INSIDE	1.075	3.383	964.85	3263.94	3.637	848.06	3084.08
A_68_P30651713	chr16:32277691-32277735	NM_027355:166	Rnf168	INSIDE	1.075	1.398	1089.18	1522.73	1.503	1021.13	1534.57
A_68_P23491409	chr5:14025282-14025326	NM_011348:29	Sema3e	INSIDE	1.075	1.411	2172.41	3065.14	1.517	1906.94	2892.16
A_68_P25584911	chr7:147973663-147973707	NM_001143765:69	Syce1	INSIDE	1.075	2.629	765.88	2013.22	2.826	675.00	1907.22
A_68_P24374363	chr6:37821300-37821344	NM_145076:512	Trim24	INSIDE	1.075	2.037	2161.44	4403.23	2.191	1896.05	4153.95
A_68_P30363494	chr15:78798409-78798453	NM_001039155:20277	Triobp	INSIDE	1.075	2.911	4576.66	13321.16	3.128	3181.12	9950.05
A_68_P31323665	chr17:69732730-69732774	NM_009547:-565	Zfp161	PROMOTER	1.075	0.626	3053.22	1909.84	0.672	2725.38	1832.44
A_68_P27033722	chr10:28916520-28916567	NM_026138:52742	6330407J23Rik	INSIDE	1.074	1.710	1249.87	2137.50	1.837	1023.13	1879.42
A_68_P25614033	chr8:3452130-3452174	NM_133962:59145	Arhgef18	INSIDE	1.074	1.960	997.98	1956.00	2.106	795.20	1674.63
A_68_P31038473	chr17:10512600-10512644	NR_037588:-161	B930003M22Rik	DIVERGENT_PROMOTER	1.074	1.612	470.29	758.22	1.732	458.84	794.52
A_68_P28724519	chr12:109154477-109154521	NM_001079883:87126	Bcl11b	INSIDE	1.074	2.790	2650.28	7393.52	2.996	2141.19	6414.49
A_68_P23397278	chr4:148274906-148274950	NM_027195:96428	Casz1	INSIDE	1.074	3.590	4243.14	15231.23	3.855	3263.12	12578.86
A_68_P25637616	chr8:8660606-8660650	NM_010111:145	Efnb2	INSIDE	1.074	1.495	1235.25	1846.59	1.606	1131.29	1816.36
A_68_P23227298	chr4:115690557-115690601	NM_010173:-71	Faah	PROMOTER	1.074	2.041	563.15	1149.64	2.192	547.15	1199.43
A_68_P28577489	chr12:81861416-81861460	NM_001008423:264	Gm1568	INSIDE	1.074	2.530	1439.51	3642.27	2.717	1197.06	3252.59
A_68_P24637119	chr6:91106721-91106765	NM_144919:-66	Hdac11	PROMOTER	1.074	2.520	1255.28	3162.76	2.707	1083.44	2933.12
A_68_P24483218	chr6:58781700-58781744	NM_028705:-1971	Herc3	PROMOTER	1.074	2.150	795.93	1711.36	2.310	686.71	1586.40
A_68_P26400214	chr9:31193743-31193787	NM_172766:-12	Nfrkb	PROMOTER	1.074	2.276	1066.76	2427.81	2.445	924.86	2261.53
A_68_P23435438	chr4:154358119-154358163	NM_001113360:26953	Plch2	INSIDE	1.074	2.426	638.97	1550.26	2.605	558.84	1455.73

						Sham group			TiO$_2$-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25499768	chr7:133436020-133436064	NM_145587:19910	Sbk1	INSIDE	1.074	2.866	705.12	2020.95	3.079	598.49	1842.91
A_68_P25090605	chr7:52263349-52263393	NM_001008422:8249	Scaf1	INSIDE	1.074	2.232	558.85	1247.24	2.396	494.64	1185.27
A_68_P31202055	chr17:45732191-45732235	NM_001199113:-1623	Slc29a1	PROMOTER	1.074	1.837	1381.82	2537.95	1.973	1142.71	2254.56
A_68_P29286847	chr13:104563945-104563989	NM_172592:-9304	Srek1	PROMOTER	1.074	1.489	2351.32	3500.96	1.599	1665.93	2663.25
A_68_P31175226	chr17:39982856-39982900	ENSMUST00000157647:-1192		PROMOTER	1.074	2.067	51240.87	105902.50	2.220	40303.34	89483.25
A_68_P23438433	chr4:154783299-154783343	NM_001166029:22	2010015L04Rik	INSIDE	1.073	0.571	1323.91	755.64	0.613	1052.35	644.56
A_68_P30728224	chr16:45742850-45742894	NM_172511:147	Abhd10	INSIDE	1.073	1.996	1583.16	3160.57	2.142	1394.50	2986.70
A_68_P28071366	chr11:100870700-100870746	NM_016920:-46	Atp6v0a1	PROMOTER	1.073	6.364	1580.45	10058.17	6.830	1232.12	8415.00
A_68_P32289635	chrX:20265624-20265668	NM_011049:28	Cdk16	INSIDE	1.073	2.414	723.96	1747.80	2.590	412.28	1067.70
A_68_P30486146	chr15:100325931-100325975	NM_153407:-282	Csrnp2	PROMOTER	1.073	0.584	1409.79	822.86	0.626	1104.17	691.70
A_68_P29241522	chr13:96374151-96374199	NM_010169:14214	F2r	INSIDE	1.073	3.436	1403.80	4823.40	3.685	1042.39	3841.51
A_68_P32028427	chr19:25311713-25311757	NM_181404:43	Kank1	INSIDE	1.073	1.592	1172.85	1867.71	1.708	1084.53	1852.50
A_68_P24776189	chr6:116288297-116288341	NM_027920:178	Marchf8	INSIDE	1.073	1.683	1662.62	2798.91	1.807	1480.71	2675.06
A_68_P24333874	chr6:30688204-30688248	NR_029900:-3072	Mir335	PROMOTER	1.073	2.065	405.20	836.80	2.217	366.46	812.31
A_68_P31127485	chr17:29484900-29484944	NM_019880:-73	Mtch1	PROMOTER	1.073	1.846	1536.11	2836.39	1.982	1213.50	2405.24
A_68_P25846164	chr8:49313858-49313902	NM_001145937:446164	Odz3	INSIDE	1.073	1.720	1092.17	1878.99	1.846	823.93	1521.27
A_68_P26573399	chr9:62828500-62828544	NM_019663:164	Pias1	INSIDE	1.073	1.763	2345.69	4134.86	1.892	2086.12	3946.98
A_68_P22522616	chr3:129582033-129582077	NM_183423:-2047	Pla2g12a	PROMOTER	1.073	7.093	13889.41	98523.11	7.608	8851.94	67343.55
A_68_P28186391	chr11:120582930-120582974	NM_133223:171	Rac3	INSIDE	1.073	2.156	1843.94	3976.11	2.313	1501.64	3473.02
A_68_P32790793	chrX:159198362-159198406	NM_009031:81	Rbbp7	INSIDE	1.073	2.663	296.30	789.04	2.856	199.67	570.28
A_68_P29871953	chr14:104921479-104921523	NM_026047:383	Rnf219	INSIDE	1.073	1.629	465.37	758.21	1.748	428.73	749.31
A_68_P21095250	chr2:28980805-28980849	NM_198033:315	Setx	INSIDE	1.073	2.593	1350.45	3501.48	2.782	1105.95	3077.07
A_68_P20038599	chr1:12982807-12982851	NM_172841:-1612	Slco5a1	PROMOTER	1.073	3.350	6202.21	20776.82	3.594	4614.42	16586.42
A_68_P32464772	chrX:71032781-71032825	NM_009279:321	Ssr4	INSIDE	1.073	1.494	1004.81	1501.53	1.603	588.72	943.93
A_68_P32341134	chrX:39503420-39503464	NM_021465:-435	Stag2	PROMOTER	1.073	2.332	627.42	1463.19	2.502	425.17	1063.94
A_68_P24636064	chr6:90937651-90937695			Unknown	1.073	1.900	1116.61	2121.45	2.038	973.01	1982.95
A_68_P21836345	chr2:167422781-167422825	ENSMUST00000127006:43989		INSIDE	1.073	3.956	1989.37	7869.04	4.246	1491.25	6331.42
A_68_P26807592	chr9:107199260-107199304	NM_009895:263	Cish	INSIDE	1.072	1.520	3516.66	5345.27	1.629	2706.95	4410.47
A_68_P30495773	chr15:101904768-101904812	NM_145625:587	Eif4b	INSIDE	1.072	0.291	1925.63	560.02	0.312	1710.09	533.01
A_68_P24112562	chr5:134789379-134789423	NM_001080746:1216	Gtf2i	INSIDE	1.072	2.096	790.98	1658.23	2.248	707.85	1591.16
A_68_P24634435	chr6:90687050-90687094	NM_001134384:73045	Iqsec1	INSIDE	1.072	2.378	505.07	1200.99	2.549	519.28	1323.41
A_68_P32016045	chr19:23210547-23210591	NM_010638:-5147	Klf9	PROMOTER	1.072	2.519	610.54	1538.06	2.700	608.50	1643.02
A_68_P27971661	chr11:83276581-83276625	NM_080453:-139	Mmp28	PROMOTER	1.072	1.355	1879.87	2547.96	1.454	1684.99	2449.36
A_68_P29368026	chr13:119175523-119175567	NM_021556:515	Mrps30	INSIDE	1.072	2.987	863.92	2580.19	3.202	800.26	2562.16
A_68_P32266425	chrX:13063695-13063739	NM_173415:18919	Nyx	INSIDE	1.072	2.416	982.29	2372.88	2.589	562.57	1456.42
A_68_P29056696	chr13:55828862-55828906	NM_028281:156	Pcbd2	INSIDE	1.072	2.246	597.22	1341.65	2.408	601.40	1448.34
A_68_P31106582	chr17:25969835-25969879	NM_019719:450	Stub1	INSIDE	1.072	2.136	1107.61	2366.10	2.289	952.01	2179.23
A_68_P26037062	chr8:90305072-90305116	NM_033327:178400	Zfp423	INSIDE	1.072	2.129	646.97	1377.45	2.282	570.51	1302.04
A_68_P27534005	chr10:126528987-126529031	NM_001033263:13046	Agap2	INSIDE	1.071	1.944	12855.71	24996.72	2.083	9244.10	19256.38
A_68_P27298385	chr10:83111453-83111497	NM_145220:-65	Appl2	PROMOTER	1.071	1.942	435.80	846.21	2.079	326.23	678.12
A_68_P28450019	chr12:56086318-56086362	NM_013815:983	Baz1a	INSIDE	1.071	1.656	544.69	901.83	1.774	512.86	909.78
A_68_P30480361	chr15:99300972-99301016	NM_029236:4167	Bcdin3d	INSIDE	1.071	2.525	648.39	1637.22	2.704	575.58	1556.42
A_68_P27674147	chr11:29273422-29273466	NM_176841:-330	Ccdc88a	PROMOTER	1.071	2.303	923.17	2126.28	2.466	864.44	2131.50
A_68_P28853776	chr13:17895335-17895379	NM_001081058:1575	Cdk13	INSIDE	1.071	2.216	564.66	1251.35	2.374	463.42	1100.04
A_68_P31227869	chr17:50432800-50432844	NM_010021:102	Dazl	INSIDE	1.071	2.893	591.71	1711.96	3.098	486.05	1505.99
A_68_P30483524	chr15:99869292-99869336	NM_001159361:220	Dip2b	INSIDE	1.071	3.295	1462.67	4819.15	3.528	1311.32	4626.49
A_68_P23317858	chr4:133042766-133042810	NM_175307:6741	Fam46b	INSIDE	1.071	1.791	473.57	848.26	1.919	427.24	819.90
A_68_P26550035	chr9:58671367-58671411	NM_001081192:70	Hcn4	INSIDE	1.071	1.689	1976.89	3338.64	1.809	1485.12	2686.89
A_68_P25005393	chr7:25318304-25318348	NM_153134:2660	Irgq	INSIDE	1.071	1.927	555.56	1070.73	2.063	482.73	996.05
A_68_P29725072	chr14:75346702-75346746	NM_001033439:960	Lrch1	INSIDE	1.071	1.657	818.49	1356.26	1.774	803.53	1425.41
A_68_P21421185	chr2:91022943-91022987	NM_001177720:-3486	Madd	PROMOTER	1.071	3.002	1125.65	3379.66	3.216	975.03	3135.34

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25956626	chr8:73904570-73904614	NM_010150:1259	Nr2f6	INSIDE	1.071	1.990	658.39	1310.35	2.131	581.25	1238.39
A_68_P21095669	chr2:29050154-29050198	NM_133500:53384	Ntng2	DOWNSTREAM	1.071	1.693	1465.30	2481.14	1.814	1219.03	2211.03
A_68_P26504100	chr9:50336652-50336696	NM_011220:72	Pts	INSIDE	1.071	2.247	513.32	1153.34	2.406	472.49	1136.98
A_68_P26165185	chr8:113370432-113370477	NR_028559:-7956	Snord111	PROMOTER	1.071	0.562	1168.45	656.78	0.602	1106.26	665.91
A_68_P30253390	chr15:59146277-59146321	NM_009270:-348	Sqle	PROMOTER	1.071	1.662	851.93	1415.64	1.780	723.87	1288.32
A_68_P31612301	chr18:34490799-34490843	NM_025527:22	Srp19	INSIDE	1.071	2.056	1161.83	2389.23	2.201	975.79	2148.17
A_68_P30250405	chr15:58655411-58655455	NM_175212:-450	Tmem65	PROMOTER	1.071	1.806	830.32	1499.75	1.935	683.58	1322.54
A_68_P24428346	chr6:48569573-48569617	NM_173429:6416	Zfp775	INSIDE	1.071	1.804	411.54	742.26	1.931	314.33	607.02
A_68_P32462527	chrX:70667702-70667746	NM_009566:11283	Zfp92	INSIDE	1.071	1.685	1026.63	1729.37	1.804	494.28	891.53
A_68_P32783799	chrX:157736143-157736189	ENSMUST00000141946:10779		INSIDE	1.071	3.167	1363.28	4317.58	3.391	568.23	1926.81
A_68_P32319554	chrX:34185327-34185371	NM_001081956:61	Akap17b	INSIDE	1.070	1.844	825.37	1521.95	1.973	477.44	941.88
A_68_P24046043	chr5:122162421-122162465	NM_009125:825	Atxn2	INSIDE	1.070	2.130	1666.70	3549.36	2.279	1404.11	3200.24
A_68_P24946541	chr7:3597064-3597108	NM_146176:216	Cnot3	INSIDE	1.070	1.908	461.46	880.33	2.041	361.20	737.32
A_68_P23417815	chr4:151671322-151671366	NM_133788:22	Icmt	INSIDE	1.070	2.202	809.29	1782.35	2.357	727.75	1715.59
A_68_P21908760	chr2:180869636-180869680	NM_001003824:272	Kcnq2	INSIDE	1.070	2.253	545.18	1228.40	2.412	503.17	1213.43
A_68_P25954900	chr8:73438460-73438504	NM_173013:8610	Mtap1s	INSIDE	1.070	2.439	1248.31	3044.72	2.609	1034.02	2697.92
A_68_P26133402	chr8:107898609-107898653	NM_001081333:-650	Plekhg4	PROMOTER	1.070	1.966	2703.44	5315.59	2.104	2276.92	4791.54
A_68_P26453529	chr9:41932012-41932056	NM_011436:338	Sorl1	INSIDE	1.070	2.168	652.09	1413.91	2.319	624.90	1449.43
A_68_P25508613	chr7:135153669-135153713	NM_001079932:5799	Trim72	INSIDE	1.070	2.699	4632.02	12500.85	2.887	3522.92	10169.13
A_68_P24124221	chr5:137507075-137507119	NM_001039385:932	Vgf	INSIDE	1.070	1.416	899.29	1273.07	1.514	896.06	1356.98
A_68_P31925604	chr19:4878831-4878875	NM_001168517:163	Zdhhc24	INSIDE	1.070	1.825	2497.29	4557.02	1.952	2035.55	3973.72
A_68_P26077485	chr8:96958377-96958421	NR_015514:605	9330175E14Rik	INSIDE	1.069	2.252	3191.46	7186.08	2.407	2541.57	6118.28
A_68_P29523396	chr14:34133331-34133375	NM_153800:103344	Arhgap22	INSIDE	1.069	0.613	1444.11	885.39	0.655	1243.71	814.90
A_68_P31369867	chr17:78599714-78599759	NM_015800:149	Crim1	INSIDE	1.069	1.578	1214.56	1916.59	1.688	1156.97	1952.47
A_68_P29335935	chr13:113442657-113442701	NM_001145885:-160	Ddx4	DIVERGENT_PROMOTER	1.069	2.259	452.55	1022.28	2.415	435.72	1052.33
A_68_P25547706	chr7:141862876-141862920	NM_001033420:529	Dock1	INSIDE	1.069	1.753	929.22	1629.38	1.874	864.22	1619.67
A_68_P27997243	chr11:87800391-87800435	NM_001168472:-325	Dynll2	PROMOTER	1.069	0.479	2199.34	1054.57	0.513	1883.23	965.68
A_68_P26986428	chr10:20067570-20067614	NM_027930:-32	Fam54a	PROMOTER	1.069	1.670	836.41	1396.86	1.785	790.88	1411.88
A_68_P26761435	chr9:98856857-98856901	NM_012020:853	Foxl2	INSIDE	1.069	0.518	1493.26	773.99	0.554	1279.99	709.43
A_68_P28748130	chr12:113382569-113382613	NM_001097621:-1828	Kif26a	PROMOTER	1.069	2.404	349.89	841.26	2.571	297.08	763.77
A_68_P23809993	chr5:75971506-75971550	NM_021099:513	Kit	INSIDE	1.069	1.780	420.38	748.18	1.903	412.88	785.80
A_68_P27262524	chr10:75994246-75994290	NM_146006:-103	Lss	PROMOTER	1.069	1.923	491.53	945.06	2.056	441.10	906.99
A_68_P28178600	chr11:119411075-119411119	NM_008730:-1962	Nptx1	PROMOTER	1.069	1.757	638.48	1122.01	1.878	636.03	1194.77
A_68_P27280129	chr10:79440293-79440337	NM_001003949:6761	ORF61	INSIDE	1.069	3.303	2255.16	7447.80	3.530	1815.09	6407.46
A_68_P31846729	chr18:77493099-77493143	NM_013666:68535	St8sia5	INSIDE	1.069	2.766	1461.26	4042.37	2.958	1155.86	3419.28
A_68_P26023336	chr8:87561629-87561686	NM_001122843:591	Tnpo2	INSIDE	1.069	3.364	268.81	904.32	3.596	224.13	805.87
A_68_P27234635	chr10:70747809-70747853	NM_145420:180	Ube2d1	INSIDE	1.069	0.596	1429.21	852.29	0.637	1296.95	826.80
A_68_P22417418	chr3:109143649-109143693	NM_020505:70	Vav3	INSIDE	1.069	2.461	389.83	959.42	2.631	408.05	1073.51
A_68_P23416419	chr4:151460529-151460574	ENSMUST00000118648:-415		PROMOTER	1.069	3.478	984.81	3424.77	3.718	797.52	2965.00
A_68_P24686643	chr6:99471350-99471394	ENSMUST00000155466:145419		INSIDE	1.069	0.613	2466.91	1512.10	0.655	2035.70	1333.82
A_68_P24006302	chr5:115263981-115264025	NR_027817:-17	1500011B03Rik	PROMOTER	1.068	1.838	1942.54	3571.14	1.964	1463.30	2873.76
A_68_P27812108	chr11:54600567-54600611	NM_178626:617	Cdc42se2	INSIDE	1.068	0.594	1334.22	792.35	0.634	1091.79	692.69
A_68_P24138647	chr5:140447479-140447523	NM_175522:63604	Elfn1	INSIDE	1.068	2.193	901.68	1977.41	2.343	824.47	1931.59
A_68_P30361918	chr15:78549192-78549236	NM_183141:-671	Elfn2	PROMOTER	1.068	1.752	2668.57	4674.10	1.871	1948.84	3646.39
A_68_P29287630	chr13:104711739-104711783	NM_001005868:-1166	Erbb2ip	PROMOTER	1.068	5.682	3000.78	17049.53	6.068	2284.84	13864.31
A_68_P23969235	chr5:108298266-108298310	NM_007964:5838	Evi5	INSIDE	1.068	1.708	1535.23	2622.70	1.824	1358.86	2478.50
A_68_P24620355	chr6:88148400-88148444	NM_008090:-235	Gata2	PROMOTER	1.068	2.105	1239.12	2608.22	2.248	1173.52	2637.73
A_68_P29097469	chr13:64263530-64263574	NM_019986:379	Habp4	INSIDE	1.068	2.541	414.14	1052.23	2.714	445.10	1207.80
A_68_P27812443	chr11:54679796-54679846	NM_008248:-119	Hint1	DIVERGENT_PROMOTER	1.068	2.105	261.60	550.65	2.249	216.90	487.70
A_68_P28043747	chr11:96181632-96181676	NM_010459:2074	Hoxb4	INSIDE	1.068	1.769	556.46	984.65	1.890	535.78	1012.81
A_68_P21137728	chr2:35946930-35946974	NM_001083126:12628	Lhx6	INSIDE	1.068	1.733	654.95	1135.16	1.852	542.36	1004.23

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P23189553	chr4:106926047-106926091	NM_029985:70	Lrrc42	INSIDE	1.068	1.518	1928.94	2927.35	1.621	1541.12	2497.59
A_68_P31503253	chr18:13020852-13020896	NM_207530:79355	Osbpl1a	INSIDE	1.068	2.496	918.50	2292.39	2.665	824.15	2196.29
A_68_P21818280	chr2:164332796-164332840	NM_133779:9794	Pigt	INSIDE	1.068	3.026	1989.20	6018.73	3.232	1197.74	3870.93
A_68_P29681987	chr14:67530058-67530102	NM_175498:36	Pnma2	INSIDE	1.068	0.635	2489.00	1581.34	0.679	2020.23	1370.76
A_68_P25574426	chr7:146038756-146038800	NM_026391:710	Ppp2r2d	INSIDE	1.068	2.181	1217.08	2654.37	2.328	966.88	2251.22
A_68_P27807840	chr11:53841165-53841209	NM_019687:406	Slc22a4	INSIDE	1.068	1.794	1193.11	2140.03	1.916	1017.07	1948.55
A_68_P24983341	chr7:17396988-17397032	NM_001039878:-4227	Strn4	PROMOTER	1.068	1.901	2335.08	4438.41	2.029	1975.72	4009.50
A_68_P22383505	chr3:102740035-102740079	NM_011516:-33	Sycp1	PROMOTER	1.068	1.583	1047.06	1657.13	1.690	899.22	1519.52
A_68_P30574322	chr16:17530755-17530799	NM_026909:369	Thap7	INSIDE	1.068	0.578	2458.96	1420.16	0.617	1782.36	1099.53
A_68_P30991291	chr16:96366989-96367033	NM_207301:-15	Wrb	PROMOTER	1.068	1.414	1096.66	1551.14	1.511	874.97	1322.03
A_68_P31342569	chr17:73186874-73186918	NM_027166:853	Ypel5	INSIDE	1.068	1.492	1088.88	1624.08	1.592	943.62	1502.60
A_68_P28950039	chr13:36670467-36670511	AK135154:190947		INSIDE	1.068	1.815	599.71	1088.65	1.939	579.69	1124.26
A_68_P24619475	chr6:87994860-87994904	ENSMUST00000113598:129		INSIDE	1.068	1.506	781.69	1177.05	1.608	776.84	1249.39
A_68_P28182344	chr11:119959816-119959860	NM_183137:207	2410002I01Rik	INSIDE	1.067	0.635	2000.66	1269.49	0.677	1506.96	1020.30
A_68_P20354314	chr1:75472567-75472611	NM_001001565:3458	Chpf	INSIDE	1.067	2.115	855.37	1809.19	2.256	586.08	1322.21
A_68_P32567803	chrX:99446637-99446681	NM_007709:450	Cited1	INSIDE	1.067	1.578	1156.58	1824.62	1.683	574.61	966.80
A_68_P27897959	chr11:69734325-69734369	NM_001166590:-214	Eif5a	PROMOTER	1.067	0.532	1355.27	721.46	0.568	1116.84	634.31
A_68_P21202298	chr2:49306701-49306745	NM_172663:-283	Epc2	PROMOTER	1.067	2.469	688.54	1699.97	2.635	602.74	1588.28
A_68_P27594240	chr11:11925551-11925597	NM_001177629:2400	Grb10	INSIDE	1.067	1.888	872.01	1645.98	2.014	699.64	1409.01
A_68_P24798117	chr6:120314589-120314634	NM_145997:495	Kdm5a	INSIDE	1.067	2.106	450.76	949.53	2.248	385.06	865.43
A_68_P23658795	chr5:46248998-46249042	NM_178142:-241	Lcorl	PROMOTER	1.067	1.616	1180.70	1908.36	1.724	993.44	1712.92
A_68_P26980659	chr10:19076945-19076989	NM_053008:622	Olig3	INSIDE	1.067	1.491	3743.93	5581.89	1.591	2784.14	4430.55
A_68_P26815241	chr9:108420024-108420068	NM_001114119:629	Qrich1	INSIDE	1.067	1.618	489.89	792.64	1.727	464.16	801.48
A_68_P32599600	chrX:108576921-108576965	NM_025949:74612	Rps6ka6	INSIDE	1.067	2.037	1127.39	2295.95	2.172	737.79	1602.60
A_68_P23338973	chr4:136833633-136833677	NM_009523:105	Wnt4	INSIDE	1.067	2.461	590.60	1453.17	2.626	506.47	1330.03
A_68_P26023270	chr8:87551092-87551137	NM_026760:383	2310036O22Rik	INSIDE	1.066	1.773	1876.67	3326.65	1.890	1547.29	2924.30
A_68_P28167621	chr11:117722126-117722170	NM_001085535:83	Cldn27	INSIDE	1.066	2.088	290.76	607.19	2.226	278.10	619.04
A_68_P24906446	chr6:142705458-142705502	NM_009908:275	Cmas	INSIDE	1.066	0.522	1282.60	669.67	0.557	1036.94	577.15
A_68_P27263162	chr10:76086244-76086288	NM_146007:-117	Col6a2	PROMOTER	1.066	1.768	1103.03	1950.02	1.884	880.30	1658.62
A_68_P27272484	chr10:77632233-77632277	NM_138601:259	D10Jhu81e	INSIDE	1.066	0.591	1279.44	756.61	0.630	1051.98	662.99
A_68_P29446598	chr14:21208189-21208233	NM_134081:-78	Dnajc9	PROMOTER	1.066	2.422	1119.97	2712.50	2.582	978.53	2526.78
A_68_P25827947	chr8:46108650-46108696	NM_001081286:73111	Fat1	INSIDE	1.066	2.500	368.52	921.47	2.665	345.10	919.73
A_68_P32139834	chr19:45734660-45734704	NM_013907:1	Fbxw4	INSIDE	1.066	1.489	2500.73	3723.63	1.587	1882.33	2987.01
A_68_P20510204	chr1:108656008-108656052	NM_027534:289	Kdsr	INSIDE	1.066	1.579	1322.12	2087.69	1.683	1187.20	1997.81
A_68_P25016729	chr7:28116317-28116361	NM_001113549:2329	Ltbp4	INSIDE	1.066	1.541	854.92	1317.85	1.642	708.89	1164.33
A_68_P25953978	chr8:73300295-73300339	NM_008841:295	Pik3r2	INSIDE	1.066	1.444	1291.32	1864.47	1.539	1033.67	1590.69
A_68_P24117614	chr5:136210246-136210290	NM_008898:45185	Por	INSIDE	1.066	2.178	1217.63	2651.88	2.321	1026.64	2382.86
A_68_P21091624	chr2:28389115-28389159	NM_001145835:153	Ralgds	INSIDE	1.066	1.744	712.69	1243.09	1.859	642.17	1193.73
A_68_P25094160	chr7:52888072-52888116	NM_028544:5188	Rasip1	INSIDE	1.066	2.168	737.80	1599.44	2.311	691.74	1598.91
A_68_P31256957	chr17:56706054-56706098	NM_001029979:17930	Safb2	INSIDE	1.066	2.415	366.58	885.23	2.574	357.62	920.35
A_68_P27167593	chr10:58684415-58684459	NM_001024910:159	Septin10	INSIDE	1.066	2.713	435.09	1180.55	2.893	430.32	1244.77
A_68_P23590297	chr5:33995249-33995293	NM_009193:-315	Slbp	PROMOTER	1.066	0.513	1039.37	533.38	0.547	929.15	508.24
A_68_P23353414	chr4:139225201-139225245	NM_031873:15770	Tas1r2	INSIDE	1.066	1.735	630.17	1093.56	1.851	531.26	983.19
A_68_P23998980	chr5:114037914-114037958	NM_177292:118470	Wscd2	INSIDE	1.066	2.233	1300.40	2903.15	2.380	998.19	2375.29
A_68_P31669245	chr18:44988148-44988192	NM_001163013:-148	Ythdc2	PROMOTER	1.066	1.960	568.50	1114.09	2.090	490.84	1025.65
A_68_P22630568	chr3:148652007-148652051	ENSMUST00000098518:252		INSIDE	1.066	1.830	765.09	1400.31	1.951	741.71	1447.07
A_68_P23978457	chr5:110660379-110660423	NM_027922:341	Ankle2	INSIDE	1.065	1.420	1244.39	1767.16	1.512	1051.58	1589.95
A_68_P31926489	chr19:5039460-5039504	NM_175383:657	B3gnt1	INSIDE	1.065	1.696	2170.05	3679.70	1.806	1716.78	3101.32
A_68_P25093322	chr7:52721892-52721936	NM_007527:354	Bax	INSIDE	1.065	1.464	1172.94	1717.28	1.559	999.87	1558.81
A_68_P20137272	chr1:34234902-34234946	NM_133833:166255	Dst	INSIDE	1.065	3.338	574.40	1917.21	3.555	529.93	1884.15
A_68_P29712956	chr14:72931825-72931869	NM_207636:177964	Fndc3a	DOWNSTREAM	1.065	1.912	1643.13	3140.92	2.036	1410.63	2871.85

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P23250423	chr4:119955345-119955389	NM_194060:4500	Foxo6	INSIDE	1.065	1.435	2217.29	3182.43	1.529	1976.76	3021.94
A_68_P28558329	chr12:78339501-78339545	NM_016893:-485	Fut8	PROMOTER	1.065	1.640	679.96	1115.02	1.746	554.76	968.50
A_68_P28577467	chr12:81858507-81858551	NM_001008423:3174	Gm1568	INSIDE	1.065	2.221	793.23	1761.72	2.365	672.98	1591.65
A_68_P26891191	chr9:122656494-122656538	NM_001199736:53	Gm9524	INSIDE	1.065	2.823	1069.85	3019.78	3.007	871.87	2621.91
A_68_P21874515	chr2:174125570-174125614	NM_201617:2233	Gnas	INSIDE	1.065	1.514	633.41	959.05	1.613	589.31	950.39
A_68_P25011764	chr7:26539484-26539528	NM_178089:214	Hnrnpul1	INSIDE	1.065	0.533	1101.26	587.23	0.568	928.86	527.38
A_68_P26026700	chr8:88364563-88364607	NM_028007:264	Itfg1	INSIDE	1.065	1.915	835.48	1599.64	2.038	745.02	1518.50
A_68_P29616394	chr14:55732300-55732344	NM_177049:3450	Jph4	INSIDE	1.065	2.290	349.86	801.22	2.438	357.50	871.64
A_68_P24816534	chr6:124662607-124662651	NM_007531:322	Phb2	INSIDE	1.065	0.507	2195.04	1112.58	0.540	1679.32	906.21
A_68_P27034633	chr10:29081479-29081523	NM_001110196:748	Rnf146	INSIDE	1.065	0.588	1387.27	816.22	0.627	1299.81	814.71
A_68_P29675225	chr14:66349795-66349839	NM_001168318:64577	Scara5	INSIDE	1.065	1.946	850.29	1654.80	2.073	748.60	1551.83
A_68_P22523675	chr3:129763103-129763147	NM_207209:701	Sec24b	INSIDE	1.065	2.126	1415.44	3008.78	2.264	1355.15	3067.49
A_68_P28730170	chr12:110065141-110065185	NM_181328:8924	Slc25a29	INSIDE	1.065	2.184	557.17	1216.63	2.324	500.81	1164.10
A_68_P31099197	chr17:24856900-24856944	NR_027900:-12	Snhg9	DIVERGENT_PROMOTER	1.065	0.622	2445.04	1519.80	0.662	1921.63	1272.48
A_68_P21813370	chr2:163428210-163428254	NM_029512:183	Ttpal	INSIDE	1.065	1.433	2253.30	3229.02	1.525	1857.85	2834.10
A_68_P27446662	chr10:110447016-110447060	NM_172554:84	Zdhhc17	INSIDE	1.065	1.596	821.53	1310.95	1.699	822.01	1396.54
A_68_P26736547	chr9:94438241-94438285	NM_001033145:238	1190002N15Rik	INSIDE	1.064	1.403	1025.81	1438.88	1.492	993.80	1482.93
A_68_P21084956	chr2:27331496-27331540	NM_001113573:-325	Brd3	PROMOTER	1.064	1.825	398.45	727.09	1.942	348.84	677.42
A_68_P25520724	chr7:137409910-137409954	NM_010207:390	Fgfr2	INSIDE	1.064	2.159	742.01	1601.66	2.296	666.96	1531.48
A_68_P25174403	chr7:71083373-71083417	NM_021366:407	Klf13	INSIDE	1.064	0.462	1384.41	639.74	0.492	1243.27	611.15
A_68_P27560004	chr11:4748803-4748847	NM_010898:706	Nf2	INSIDE	1.064	0.586	1353.85	793.15	0.623	1150.75	717.31
A_68_P28457435	chr12:57634322-57634366	NM_001146198:1749	Nkx2-1	INSIDE	1.064	1.621	531.31	861.22	1.724	569.79	982.34
A_68_P27287757	chr10:80616441-80616485	NM_021501:14003	Pias4	DOWNSTREAM	1.064	3.121	6991.11	21817.94	3.320	4931.95	16373.16
A_68_P21568534	chr2:119063096-119063140	NM_016907:23	Spint1	INSIDE	1.064	2.479	675.39	1674.53	2.639	588.94	1554.16
A_68_P26626134	chr9:71959499-71959543	NM_011544:106	Tcf12	INSIDE	1.064	3.050	214.12	652.99	3.245	195.47	634.31
A_68_P25393403	chr7:112781845-112781889	NM_018880:147	Trim3	INSIDE	1.064	1.435	13126.83	18842.37	1.528	9134.82	13955.10
A_68_P30094472	chr15:27703695-27703739	NM_001081302:251887	Trio	INSIDE	1.064	2.354	1311.68	3088.05	2.505	1110.35	2781.30
A_68_P20737715	chr1:157264567-157264611	NM_011273:-14	Xpr1	PROMOTER	1.064	1.456	1651.21	2404.07	1.549	1360.31	2107.17
A_68_P26885416	chr9:121672100-121672144	NM_001166644:2972	Zfp651	INSIDE	1.064	2.065	496.15	1024.62	2.197	480.38	1055.22
A_68_P27977895	chr11:84326684-84326729	NM_019816:297	Aatf	INSIDE	1.063	0.543	1178.74	640.54	0.578	1054.55	609.34
A_68_P20633262	chr1:136311950-136311994	NM_028320:-71	Adipor1	PROMOTER	1.063	0.393	1840.01	723.62	0.418	1581.37	660.79
A_68_P28153228	chr11:115255096-115255140	NM_001080929:11889	Cdr2l	INSIDE	1.063	1.533	647.86	992.88	1.629	574.04	935.20
A_68_P21633705	chr2:131005466-131005510	NM_007682:260	Cenpb	INSIDE	1.063	2.135	1286.26	2746.41	2.270	1141.88	2591.50
A_68_P27303129	chr10:83996944-83996988	NM_175451:-333	Ckap4	PROMOTER	1.063	1.501	1001.56	1503.09	1.595	874.68	1395.05
A_68_P32364770	chrX:45807712-45807756	NM_019680:8575	Elf4	INSIDE	1.063	1.586	2361.48	3744.24	1.685	1202.67	2027.07
A_68_P32743829	chrX:147451959-147452003	NM_198110:-115	Gnl3l	PROMOTER	1.063	1.734	1767.66	3065.15	1.844	921.10	1698.05
A_68_P32152399	chr19:47940223-47940267	NM_026619:-39	Gsto2	PROMOTER	1.063	2.550	815.09	2078.66	2.711	740.63	2007.90
A_68_P24623143	chr6:88577556-88577600	NM_001142724:-139	Kbtbd12	PROMOTER	1.063	1.804	2698.05	4866.07	1.917	2325.06	4456.69
A_68_P22406473	chr3:107262834-107262878	NM_145922:-1040	Kcnc4	PROMOTER	1.063	3.764	355.56	1338.39	4.003	321.77	1288.04
A_68_P20939667	chr1:193542758-193542803	NM_001134829:507	Lpgat1	INSIDE	1.063	2.502	803.87	2011.04	2.660	639.01	1700.02
A_68_P31442545	chr17:91487617-91487661	NM_020252:4504	Nrxn1	INSIDE	1.063	2.714	1118.21	3034.47	2.883	968.72	2793.29
A_68_P27648122	chr11:23794713-23794757	NM_172555:536	Papolg	INSIDE	1.063	1.539	3514.20	5409.15	1.636	2725.59	4458.97
A_68_P22774297	chr4:21605606-21605652	NM_001080771:7482	Prdm13	INSIDE	1.063	0.526	991.35	521.58	0.559	823.33	460.63
A_68_P25100826	chr7:53965778-53965822	NM_030233:221	Saal1	INSIDE	1.063	1.377	3165.68	4358.13	1.463	2524.93	3693.33
A_68_P20457300	chr1:95651043-95651087	NM_025920:351	Thap4	INSIDE	1.063	1.678	1225.61	2056.95	1.784	1090.13	1944.65
A_68_P22360091	chr3:98231564-98231608	NM_172863:45183	Zfp697	INSIDE	1.063	2.487	9225.38	22946.94	2.643	6303.91	16664.00
A_68_P27268023	chr10:76880611-76880655	NM_001024837:386	Adarb1	INSIDE	1.062	2.130	274.09	583.67	2.261	257.87	583.08
A_68_P28776185	chr12:119082606-119082650	NM_146040:295	Cdca7l	INSIDE	1.062	2.321	618.93	1436.62	2.465	588.78	1451.09
A_68_P30431386	chr15:90509992-90510036	NM_025815:-195	Cpne8	PROMOTER	1.062	1.646	1667.61	2744.88	1.747	1316.08	2299.69
A_68_P23362416	chr4:140703968-140704012	NM_172518:154	Fbxo42	INSIDE	1.062	2.346	1727.15	4051.36	2.492	1524.92	3800.28
A_68_P21811851	chr2:163164903-163164947	NM_021566:58785	Jph2	INSIDE	1.062	4.607	12198.30	56200.61	4.892	8024.74	39258.66

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31125154	chr17:29089463-29089507	NM_025888:-676	Kctd20	PROMOTER	1.062	2.042	1483.60	3029.40	2.169	1363.23	2956.52
A_68_P22006133	chr3:26230419-26230463	NM_138666:391	Nlgn1	INSIDE	1.062	1.470	2019.90	2969.89	1.561	1737.47	2712.86
A_68_P21628850	chr2:130099716-130099773	NM_024193:-403	Nop56	PROMOTER	1.062	2.046	1007.80	2062.32	2.174	799.96	1739.26
A_68_P30397307	chr15:84686477-84686521	NM_001081166:61	Phf21b	INSIDE	1.062	2.626	366.48	962.46	2.790	366.20	1021.60
A_68_P31934550	chr19:6413237-6413281	NM_011242:12676	Rasgrp2	INSIDE	1.062	2.376	4064.02	9656.89	2.523	3087.76	7789.77
A_68_P21867216	chr2:172847313-172847357	NM_019547:-68	Rbm38	PROMOTER	1.062	1.909	1387.85	2650.05	2.027	1160.68	2352.58
A_68_P27286998	chr10:80494022-80494066	NM_134135:2613	Slc39a3	INSIDE	1.062	2.534	1329.83	3370.15	2.691	1130.74	3042.74
A_68_P26750365	chr9:96896276-96896320	NM_145134:22476	Spsb4	INSIDE	1.062	2.697	275.25	742.40	2.865	327.43	938.18
A_68_P20736178	chr1:157006310-157006354	NM_021433:500	Stx6	INSIDE	1.062	1.602	1110.11	1778.35	1.702	952.30	1620.80
A_68_P30015972	chr15:11313703-11313747	NM_033074:15689	Tars	INSIDE	1.062	1.777	1080.26	1919.16	1.887	851.29	1606.72
A_68_P21658149	chr2:135485033-135485077	ENSMUST00000139480:-235		PROMOTER	1.062	3.161	598.57	1891.91	3.358	559.15	1877.62
A_68_P28939817	chr13:34744234-34744278	NM_025831:294	1300014I06Rik	INSIDE	1.061	2.666	808.78	2156.33	2.829	733.80	2075.72
A_68_P24006039	chr5:115224465-115224516	NR_027872:502	4930515G01Rik	INSIDE	1.061	2.045	565.94	1157.19	2.170	532.57	1155.79
A_68_P20395057	chr1:82835935-82835979	NM_010472:-101	Agfg1	PROMOTER	1.061	1.362	1745.30	2376.30	1.445	1464.82	2116.42
A_68_P28175391	chr11:118895720-118895764	NM_007623:11400	Cbx2	DOWNSTREAM	1.061	0.593	1506.85	893.24	0.629	1058.78	666.16
A_68_P22412513	chr3:108215712-108215756	NM_001004177:2678	Celsr2	INSIDE	1.061	2.553	789.99	2016.61	2.709	618.72	1676.15
A_68_P25603237	chr7:151015959-151016003	NM_007856:6909	Dhcr7	INSIDE	1.061	1.650	1159.42	1912.59	1.750	1010.83	1768.51
A_68_P22858439	chr4:40670130-40670174	NM_001164672:190	Dnaja1	INSIDE	1.061	1.820	950.46	1729.82	1.931	905.48	1748.68
A_68_P29287625	chr13:104710556-104710600	NM_001005868:16	Erbb2ip	INSIDE	1.061	1.864	599.15	1116.96	1.978	499.04	986.94
A_68_P21909701	chr2:181022187-181022231	NM_198169:463	Gmeb2	INSIDE	1.061	1.359	2571.75	3495.74	1.442	1885.13	2718.02
A_68_P30142979	chr15:37162921-37162965	NM_026496:152	Grhl2	INSIDE	1.061	1.924	2064.37	3972.78	2.043	1671.31	3413.99
A_68_P29469007	chr14:24822857-24822901	NM_010610:549	Kcnma1	INSIDE	1.061	1.588	7468.40	11856.67	1.685	5299.67	8928.22
A_68_P25187996	chr7:73532827-73532871	NM_146191:379	Lrrk1	INSIDE	1.061	2.385	930.46	2218.78	2.531	863.50	2185.34
A_68_P27845570	chr11:60745579-60745623	NM_008928:42	Map2k3	INSIDE	1.061	0.589	1373.01	808.14	0.624	1114.73	696.08
A_68_P30083232	chr15:25710801-25710845	NM_019472:158518	Myo10	INSIDE	1.061	3.772	279.12	1052.73	4.000	252.46	1009.88
A_68_P20184670	chr1:42754004-42754048	NM_008900:36	Pou3f3	INSIDE	1.061	1.445	1123.59	1623.28	1.532	1003.27	1537.18
A_68_P26805183	chr9:106691283-106691327	NM_030730:240	Rad54l2	INSIDE	1.061	1.653	570.21	942.66	1.754	543.20	952.57
A_68_P24992476	chr7:19872340-19872384	NM_001025364:-4085	Rtn2	PROMOTER	1.061	1.809	631.69	1142.92	1.920	563.16	1081.39
A_68_P20870656	chr1:181448020-181448064	NM_027188:92	Smyd3	INSIDE	1.061	1.370	3062.67	4196.61	1.454	2340.54	3404.07
A_68_P20005797	chr1:4482373-4482417	NM_011441:4100	Sox17	INSIDE	1.061	1.589	1431.99	2275.11	1.685	1269.05	2138.80
A_68_P31953435	chr19:10956222-10956266	NM_134142:-11	Tmem109	PROMOTER	1.061	1.493	664.98	992.99	1.585	558.09	884.31
A_68_P32709177	chrX:139116370-139116414	NM_001199360:124	Tmem164	INSIDE	1.061	2.766	3568.80	9870.08	2.933	1703.12	4996.04
A_68_P25056444	chr7:37481116-37481160	NM_172298:-1998	Tshz3	PROMOTER	1.061	1.823	774.46	1411.53	1.933	782.37	1512.34
A_68_P21779875	chr2:157741034-157741081	NM_198627:669	Vstm2l	INSIDE	1.061	2.846	1593.58	4535.74	3.020	1121.35	3386.19
A_68_P31479223	chr18:7868850-7868894	NM_001146298:-322	Wac	PROMOTER	1.061	1.841	1009.63	1858.37	1.953	961.15	1876.87
A_68_P25272791	chr7:88716304-88716348	NM_001004185:149	Whamm	INSIDE	1.061	2.277	502.90	1145.19	2.416	441.36	1066.21
A_68_P22970352	chr4:63077484-63077528	NM_001008797:16850	Whrn	INSIDE	1.061	3.007	1577.22	4743.33	3.191	1120.71	3576.58
A_68_P28751779	chr12:113917392-113917436	NM_001100460:364	Zbtb42	INSIDE	1.061	2.635	1111.42	2928.60	2.795	968.56	2707.36
A_68_P29656177	chr14:63174859-63174903	ENSMUST00000160745:269		INSIDE	1.061	1.420	3267.38	4640.35	1.507	2526.30	3807.42
A_68_P21833421	chr2:166888085-166888129	NM_001081005:-327	1500012F01Rik	PROMOTER	1.060	1.588	1268.52	2014.59	1.683	1043.61	1756.61
A_68_P21528938	chr2:112295037-112295081	NM_133749:-123	2900064A13Rik	PROMOTER	1.060	1.852	740.97	1372.23	1.963	722.01	1417.44
A_68_P30743457	chr16:48994281-48994325	NM_172616:2	C330027C09Rik	INSIDE	1.060	2.351	491.36	1155.44	2.492	454.13	1131.90
A_68_P31208114	chr17:46787782-46787826	NM_025611:518	Cul7	INSIDE	1.060	1.970	4081.36	8039.80	2.089	2929.86	6120.46
A_68_P28525542	chr12:72419588-72419632	NM_001190466:8740	Dact1	INSIDE	1.060	3.038	767.91	2332.87	3.221	664.44	2140.12
A_68_P27924584	chr11:74982007-74982051	NM_001098203:-374	Hic1	PROMOTER	1.060	1.368	1812.80	2479.49	1.451	1430.02	2074.25
A_68_P23333242	chr4:135866928-135866972	NM_028871:60	Hnrnpr	INSIDE	1.060	1.841	577.01	1062.14	1.952	501.30	978.34
A_68_P23949339	chr5:104339900-104339944	NM_178741:326	Klhl8	INSIDE	1.060	1.633	1033.11	1686.87	1.730	907.33	1570.10
A_68_P29725073	chr14:75346827-75346871	NM_001033439:836	Lrch1	INSIDE	1.060	0.569	1359.68	773.58	0.603	1192.40	719.43
A_68_P23334046	chr4:136018440-136018484	NM_024452:-7213	Luzp1	PROMOTER	1.060	2.968	516.83	1533.93	3.145	457.54	1439.03
A_68_P28744816	chr12:112812796-112812840	NM_021516:98	Mark3	INSIDE	1.060	1.445	2876.14	4157.17	1.532	2477.93	3796.47
A_68_P27154487	chr10:55835680-55835724	NM_001163833:8980	Msl3l2	INSIDE	1.060	0.517	1013.81	524.34	0.548	885.39	485.56

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P32395552	chrX:53627636-53627680	NR_028086:-104	Ncrna00086	PROMOTER	1.060	1.889	3488.88	6590.57	2.003	1753.31	3512.07
A_68_P23310229	chr4:131669398-131669442	NM_013622:30981	Oprd1	INSIDE	1.060	1.686	860.07	1450.16	1.787	757.83	1354.48
A_68_P24956667	chr7:6683071-6683115	NM_008817:38	Peg3	INSIDE	1.060	1.978	1601.52	3167.82	2.096	1446.95	3032.79
A_68_P31207976	chr17:46766512-46766556	NM_175168:-81	Ptk7	PROMOTER	1.060	3.291	776.86	2556.42	3.487	550.58	1920.14
A_68_P27478506	chr10:116387438-116387482	NM_001003950:-24	Rab3ip	DIVERGENT_PROMOTER	1.060	2.100	451.75	948.55	2.225	407.29	906.15
A_68_P21875633	chr2:174298255-174298299	NM_025531:166	Slmo2	INSIDE	1.060	1.722	905.44	1558.74	1.825	723.15	1319.59
A_68_P25507646	chr7:134985207-134985251	NM_009294:-93	Stx4a	PROMOTER	1.060	2.442	814.24	1988.54	2.588	724.96	1876.17
A_68_P23429326	chr4:153514732-153514776	NM_011642:-437	Trp73	DIVERGENT_PROMOTER	1.060	0.492	1158.68	570.25	0.522	761.71	397.32
A_68_P30476460	chr15:98620564-98620608	NM_021279:299	Wnt1	INSIDE	1.060	1.439	1148.78	1652.99	1.525	955.89	1457.45
A_68_P25008265	chr7:25866336-25866380	NM_175477:4094	Zfp574	INSIDE	1.060	3.211	2802.17	8997.55	3.403	2116.24	7200.92
A_68_P30593947	chr16:21694402-21694446	NM_001001881:314	2510009E07Rik	INSIDE	1.059	1.999	885.99	1770.92	2.117	742.17	1571.17
A_68_P31053603	chr17:12934351-12934395	NR_002853:196	Airn	INSIDE	1.059	1.529	692.12	1058.04	1.618	532.10	861.14
A_68_P27540826	chr10:127774827-127774871	NM_026444:-39	Cs	PROMOTER	1.059	1.523	1535.64	2339.05	1.614	1391.23	2244.95
A_68_P29098528	chr13:64471285-64471329	NM_009984:308	Ctsl	INSIDE	1.059	0.500	1138.75	568.84	0.529	1060.20	561.09
A_68_P25587954	chr7:148479800-148479844	NM_007878:1918	Drd4	INSIDE	1.059	1.829	1443.30	2639.20	1.937	1062.54	2058.48
A_68_P22019967	chr3:28981485-28981529	NM_001167748:8	Egfem1	INSIDE	1.059	2.634	290.88	766.04	2.790	316.41	882.72
A_68_P20741944	chr1:158134876-158134920	NM_177838:258	Fam163a	INSIDE	1.059	1.727	968.26	1671.80	1.829	885.33	1619.25
A_68_P25827954	chr8:46109471-46109515	NM_001081286:73931	Fat1	INSIDE	1.059	2.821	481.61	1358.76	2.987	389.89	1164.46
A_68_P26614159	chr9:69860258-69860302	NM_001039519:-76	Gtf2a2	PROMOTER	1.059	1.626	2138.39	3476.20	1.721	1760.89	3031.25
A_68_P29952571	chr14:121309972-121310016	NM_023579:-421	Ipo5	PROMOTER	1.059	2.136	1579.28	3373.73	2.263	1389.96	3145.78
A_68_P26022956	chr8:87501679-87501723	NM_008416:947	Junb	INSIDE	1.059	1.397	1255.84	1753.94	1.479	1081.04	1598.85
A_68_P26159963	chr8:112486245-112486304	NM_212447:-169	Marveld3	PROMOTER	1.059	3.847	195.21	751.04	4.074	144.33	588.01
A_68_P22569091	chr3:138151998-138152042	NM_175224:326	Metap1	INSIDE	1.059	1.496	1236.11	1849.05	1.584	1295.42	2051.42
A_68_P24140928	chr5:140807887-140807931	NM_008637:33	Nudt1	INSIDE	1.059	1.682	3017.50	5075.70	1.782	2160.48	3850.28
A_68_P26261059	chr8:129588231-129588275	NM_001122850:297	Pard3	INSIDE	1.059	2.957	1688.89	4993.65	3.131	1505.81	4715.29
A_68_P31629192	chr18:37829317-37829361	NM_033586:-4650	Pcdhga3	PROMOTER	1.059	1.846	603.99	1114.93	1.956	533.65	1043.59
A_68_P26240712	chr8:126177554-126177598	NM_133955:-252	Rhou	PROMOTER	1.059	1.534	2986.59	4580.97	1.624	2510.70	4077.90
A_68_P26996376	chr10:21713866-21713910	NM_011361:-583	Sgk1	PROMOTER	1.059	1.983	1151.96	2283.92	2.100	1056.35	2218.78
A_68_P32148715	chr19:47341968-47342012	NM_001164717:196911	Sh3pxd2a	INSIDE	1.059	1.547	774.55	1198.18	1.639	701.42	1149.35
A_68_P31056398	chr17:13898109-13898153	NM_022311:271	Tcte2	INSIDE	1.059	1.539	1718.22	2644.64	1.629	1469.46	2394.26
A_68_P20742450	chr1:158233703-158233747	NM_001134741:-245	Tdrd5	DIVERGENT_PROMOTER	1.059	2.025	1011.27	2047.58	2.143	886.64	1900.28
A_68_P27709779	chr11:35793475-35793519	NM_170779:95	Wwc1	INSIDE	1.059	0.536	1425.82	764.12	0.567	1318.86	748.40
A_68_P31092364	chr17:23695056-23695100	NM_001033496:6115	Zfp213	INSIDE	1.059	1.918	698.09	1339.16	2.031	565.09	1147.84
A_68_P22411476	chr3:108042892-108042936	ENSMUST00000119163:-85		PROMOTER	1.059	2.014	896.15	1804.52	2.133	703.63	1500.63
A_68_P22169028	chr3:58380988-58381032	NM_001040396:431	2810407C02Rik	INSIDE	1.058	4.492	626.81	2815.45	4.751	546.52	2596.71
A_68_P22888785	chr4:46463681-46463725	NM_130889:-286	Anp32b	PROMOTER	1.058	1.571	1536.02	2413.20	1.663	1314.47	2185.39
A_68_P28091583	chr11:104411776-104411820	NM_145436:136	Cdc27	INSIDE	1.058	1.646	659.82	1086.32	1.742	586.91	1022.41
A_68_P23342965	chr4:137513918-137513962	NM_199307:95789	Ece1	INSIDE	1.058	2.303	255.87	589.17	2.437	195.40	476.10
A_68_P31493063	chr18:11054641-11054685	NM_010258:2155	Gata6	INSIDE	1.058	2.204	806.82	1778.10	2.332	668.66	1559.61
A_68_P25951136	chr8:72854054-72854098	NM_008107:413	Gdf1	INSIDE	1.058	1.735	818.33	1419.97	1.835	633.07	1161.78
A_68_P23274586	chr4:125167342-125167386	NM_001081097:-710	Grik3	PROMOTER	1.058	1.939	942.42	1827.71	2.051	774.82	1589.31
A_68_P25512006	chr7:135831552-135831596	NM_178641:76696	Inpp5f	INSIDE	1.058	1.995	1990.64	3971.85	2.111	1415.63	2988.14
A_68_P21571260	chr2:119570038-119570082	NM_146125:1988	Itpka	INSIDE	1.058	1.756	1020.41	1791.98	1.857	737.20	1369.33
A_68_P31847801	chr18:77680289-77680333	NM_172834:159614	Loxhd1	INSIDE	1.058	2.145	751.68	1612.64	2.271	589.52	1338.68
A_68_P26133403	chr8:107898777-107898821	NM_001081333:-482	Plekhg4	PROMOTER	1.058	2.482	697.04	1729.99	2.626	547.69	1438.39
A_68_P20779537	chr1:164670744-164670788	NM_001081290:-79	Prrc2c	PROMOTER	1.058	2.054	463.32	951.72	2.173	524.43	1139.81
A_68_P24085128	chr5:129287634-129287678	NM_001081388:171581	Rimbp2	INSIDE	1.058	3.773	684.36	2581.84	3.992	544.94	2175.21
A_68_P28958207	chr13:38129003-38129047	NM_024242:167	Riok1	INSIDE	1.058	1.391	10890.04	15142.99	1.471	7834.30	11522.48
A_68_P29517812	chr14:33278202-33278246	NM_021712:-188	Slc18a3	PROMOTER	1.058	2.412	641.13	1546.44	2.551	537.59	1371.62
A_68_P24981575	chr7:17038564-17038608	NM_026938:459	Tmem160	INSIDE	1.058	1.627	2953.81	4807.15	1.722	2303.19	3966.17
A_68_P25506497	chr7:134754654-134754698	NM_177226:3271	Zfp629	INSIDE	1.058	2.535	994.16	2520.31	2.683	840.85	2255.58

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27581769	chr11:9050712-9050764	ENSMUST00000121861:-138		PROMOTER	1.058	3.527	343.26	1210.85	3.731	231.03	862.01
A_68_P27932459	chr11:76308651-76308695	NM_198018:14249	Abr	INSIDE	1.057	0.652	2263.69	1474.90	0.689	1685.87	1161.15
A_68_P20430407	chr1:91477732-91477776	NM_001037136:126369	Agap1	INSIDE	1.057	2.516	228.92	575.93	2.660	225.27	599.13
A_68_P27089722	chr10:41239137-41239181	NM_016898:-147	Cd164	PROMOTER	1.057	0.442	1605.16	708.75	0.467	1296.73	605.32
A_68_P23327246	chr4:134762197-134762241	NM_013885:66457	Clic4	DOWNSTREAM	1.057	0.528	1258.89	664.21	0.558	817.20	455.72
A_68_P26754210	chr9:97601436-97601480	NM_022319:332128	Clstn2	INSIDE	1.057	2.034	3961.10	8057.47	2.150	3618.28	7780.61
A_68_P32007551	chr19:21727608-21727652	NM_146096:-168	Fam108b	DIVERGENT_PROMOTER	1.057	2.358	1529.81	3607.88	2.492	1308.71	3260.86
A_68_P20832290	chr1:174242716-174242760	NM_080419:201	Igsf8	INSIDE	1.057	1.361	2664.04	3624.75	1.438	2007.34	2886.58
A_68_P25953856	chr8:73285042-73285086	NM_183170:-244	Mpv17l2	PROMOTER	1.057	1.367	2760.76	3774.32	1.445	2194.05	3171.31
A_68_P31108289	chr17:26232390-26232434	NM_019731:3	Nme4	INSIDE	1.057	3.019	629.76	1901.12	3.190	655.49	2090.71
A_68_P20823479	chr1:172519702-172519746	NM_001109985:256	Nos1ap	INSIDE	1.057	1.571	561.61	882.04	1.659	578.11	959.34
A_68_P27553494	chr11:3605439-3605483	NM_152818:158446	Osbp2	INSIDE	1.057	1.867	1416.13	2643.41	1.974	1031.88	2036.59
A_68_P22741774	chr4:13670169-13670215	NM_001111026:-256	Runx1t1	PROMOTER	1.057	1.369	1717.95	2352.57	1.448	1428.54	2068.48
A_68_P23999962	chr5:114221210-114221254	NM_016926:426	Sart3	INSIDE	1.057	1.502	930.30	1397.20	1.588	821.62	1304.54
A_68_P27807841	chr11:53841272-53841316	NM_019687:298	Slc22a4	INSIDE	1.057	1.500	1050.08	1575.54	1.587	882.39	1400.04
A_68_P28730243	chr12:110074111-110074155	NM_181328:-46	Slc25a29	DIVERGENT_PROMOTER	1.057	1.662	478.86	795.81	1.756	448.89	788.30
A_68_P20723681	chr1:154749520-154749564	NM_001005507:234	Smg7	INSIDE	1.057	1.688	2507.49	4232.90	1.785	2284.79	4077.93
A_68_P26447521	chr9:40965188-40965232	NM_176860:367	Ubash3b	INSIDE	1.057	0.477	1290.92	615.80	0.504	1015.36	511.84
A_68_P30351141	chr15:76741990-76742034	NM_001168276:13866	Zfp647	INSIDE	1.057	2.842	320.76	911.60	3.003	313.80	942.27
A_68_P28523846	chr12:72117418-72117462	NM_001081195:487	Arid4a	INSIDE	1.056	1.416	2031.79	2876.65	1.494	1627.43	2432.05
A_68_P28453876	chr12:56937237-56937281	NM_001037756:-94	Brms1l	PROMOTER	1.056	0.462	1942.78	897.35	0.488	1488.85	726.42
A_68_P20887293	chr1:184447465-184447509	NM_009794:128	Capn2	INSIDE	1.056	0.590	1254.56	740.30	0.623	981.52	611.84
A_68_P24326228	chr6:29352876-29352920	NM_001201378:3973	Ccdc136	INSIDE	1.056	2.108	529.94	1117.19	2.227	529.06	1178.27
A_68_P25601117	chr7:150650897-150650941	NM_001161624:-3963	Cdkn1c	DIVERGENT_PROMOTER	1.056	2.187	539.69	1180.27	2.309	488.56	1128.06
A_68_P26504859	chr9:50467279-50467323	NM_145614:585	Dlat	INSIDE	1.056	0.387	1993.49	771.49	0.409	1668.74	681.68
A_68_P30175461	chr15:43113914-43113958	NM_008388:346	Eif3e	INSIDE	1.056	1.371	7102.04	9737.71	1.448	5870.64	8499.43
A_68_P27849837	chr11:61498300-61498344	NM_178618:411	Fam83g	INSIDE	1.056	1.530	2112.87	3232.09	1.615	1749.23	2825.58
A_68_P23979337	chr5:110807040-110807084	NM_028596:9084	Fbrsl1	INSIDE	1.056	2.950	3275.52	9661.68	3.116	2391.06	7451.09
A_68_P20457531	chr1:95700822-95700866	NM_025454:303	Ing5	INSIDE	1.056	2.268	1986.89	4506.64	2.394	1654.74	3961.71
A_68_P27927253	chr11:75444214-75444258	NM_008916:-285	Inpp5k	PROMOTER	1.056	1.434	1820.73	2610.98	1.515	1628.18	2466.08
A_68_P24009511	chr5:115880792-115880836	NM_008629:1121	Msi1	INSIDE	1.056	2.141	2233.33	4781.69	2.260	1746.57	3947.79
A_68_P30083239	chr15:25711450-25711494	NM_019472:159168	Myo10	INSIDE	1.056	2.264	375.50	850.17	2.390	318.95	762.46
A_68_P23134167	chr4:97418430-97418474	NM_001122952:169819	Nfia	INSIDE	1.056	1.607	573.29	921.14	1.696	592.97	1005.80
A_68_P27922137	chr11:74537095-74537139	NR_037610:244	Pafah1b1	INSIDE	1.056	0.573	1423.04	815.03	0.605	1159.20	700.99
A_68_P22696143	chr4:4065948-4065992	NM_001002927:-378	Penk	PROMOTER	1.056	2.076	603.07	1252.11	2.192	548.77	1202.84
A_68_P30558910	chr16:13780799-13780843	NM_001039521:29	Rrn3	INSIDE	1.056	2.008	525.43	1055.06	2.120	481.71	1021.39
A_68_P28635987	chr12:92885819-92885865	NM_175367:139034	Ston2	INSIDE	1.056	1.874	351.83	659.28	1.978	282.14	558.15
A_68_P27340406	chr10:90633535-90633579	NM_001080129:771	Tmpo	INSIDE	1.056	0.566	1391.68	788.31	0.598	1222.33	731.42
A_68_P23394412	chr4:147818678-147818722	NM_027873:160	Ubiad1	INSIDE	1.056	1.902	1383.96	2632.85	2.010	1072.93	2156.11
A_68_P31554072	chr18:23469485-23469529	X95227:781		INSIDE	1.056	2.309	2242.99	5179.88	2.438	1865.05	4547.67
A_68_P25906688	chr8:63369041-63369085	NM_028299:-185	2700029M09Rik	PROMOTER	1.055	1.602	1276.12	2044.51	1.690	1232.98	2084.30
A_68_P28269862	chr12:17331276-17331320	NM_001159632:238	Atp6v1c2	INSIDE	1.055	1.599	1138.87	1821.02	1.687	927.34	1564.40
A_68_P32268348	chrX:13423751-13423795	NM_009806:-105	Cask	PROMOTER	1.055	2.579	462.92	1193.84	2.721	297.99	810.83
A_68_P31125934	chr17:29232562-29232606	NM_007669:1868	Cdkn1a	INSIDE	1.055	1.586	1440.75	2285.51	1.673	1257.85	2104.35
A_68_P21836888	chr2:167514985-167515029	NM_009883:592	Cebpb	INSIDE	1.055	3.231	264.49	854.57	3.408	241.91	824.38
A_68_P21746889	chr2:151796098-151796142	NM_028666:3590	Fam110a	INSIDE	1.055	3.222	3512.24	11317.41	3.399	2684.79	9124.54
A_68_P31740999	chr18:58369270-58369314	NM_010181:288	Fbn2	INSIDE	1.055	0.649	1970.59	1278.49	0.685	1453.34	995.20
A_68_P32143277	chr19:46403804-46403848	NM_133694:1153	Fbxl15	INSIDE	1.055	2.039	1473.79	3004.47	2.151	1315.25	2829.17
A_68_P30630415	chr16:28446508-28446552	NM_183064:-1217	Fgf12	PROMOTER	1.055	1.827	1937.39	3539.41	1.927	1790.36	3449.45
A_68_P32401468	chrX:54756573-54756617	NM_001033360:340	Gpr101	INSIDE	1.055	2.029	1236.25	2507.86	2.140	643.32	1376.75
A_68_P31117112	chr17:27693865-27693909	NM_001166476:289	Hmga1-rs1	INSIDE	1.055	15.964	895.81	14301.03	16.843	740.24	12468.17

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P24990865	chr7:19590861-19590905	NM_178757:1469	Irf2bp1	INSIDE	1.055	2.267	1171.62	2656.17	2.392	1123.33	2686.48
A_68_P30660049	chr16:33829724-33829768	NM_001145884:-4	Itgb5	PROMOTER	1.055	1.430	886.09	1266.92	1.508	801.75	1208.98
A_68_P20451521	chr1:94745114-94745158	NR_029559:-1818	Mir149	PROMOTER	1.055	2.266	13460.81	30504.50	2.391	9543.91	22820.53
A_68_P24009623	chr5:115897106-115897158	NM_008629:17439	Msi1	INSIDE	1.055	2.116	312.79	661.78	2.232	260.78	581.96
A_68_P31110247	chr17:26576151-26576195	NM_001081656:24263	Neurl1b	INSIDE	1.055	2.392	794.24	1899.89	2.523	771.29	1945.87
A_68_P27638931	chr11:21903874-21903918	NM_011023:-2242	Otx1	PROMOTER	1.055	1.400	1731.64	2424.22	1.477	1488.25	2197.65
A_68_P22567229	chr3:137806950-137806994	NM_175389:471	Rg9mtd2	INSIDE	1.055	2.151	521.04	1120.51	2.270	467.62	1061.40
A_68_P27290119	chr10:80961961-80962005	NM_010102:900	S1pr4	INSIDE	1.055	1.517	951.89	1444.04	1.600	822.44	1315.83
A_68_P26022400	chr8:87396607-87396651	NM_001168244:472	Syce2	INSIDE	1.055	2.054	743.06	1526.57	2.167	689.01	1493.41
A_68_P31020006	chr17:5941362-5941406	NM_001113352:105	Synj2	INSIDE	1.055	2.227	728.88	1623.51	2.351	685.94	1612.60
A_68_P21571904	chr2:119698870-119698914	ENSMUST00000120952:5247		DOWNSTREAM	1.055	4.291	779.40	3344.27	4.526	596.63	2700.21
A_68_P27680364	chr11:30655100-30655144	ENSMUST00000121590:-161		PROMOTER	1.055	3.041	761.54	2315.47	3.209	711.79	2284.05
A_68_P26202775	chr8:119960432-119960476	NM_028941:87385	4933407C03Rik	INSIDE	1.054	3.269	2328.27	7610.33	3.445	1725.53	5943.98
A_68_P23069985	chr4:84321596-84321640	NM_172870:-628	Bnc2	PROMOTER	1.054	1.518	1443.33	2191.06	1.600	1132.77	1812.62
A_68_P26020781	chr8:87141111-87141156	NM_007578:201871	Cacna1a	INSIDE	1.054	1.955	1845.60	3608.54	2.061	1385.11	2854.61
A_68_P24063260	chr5:125342106-125342150	NM_144819:463	Ccdc92	INSIDE	1.054	1.558	1062.96	1655.96	1.642	875.82	1438.27
A_68_P26875427	chr9:119883344-119883388	NM_153287:10410	Csrnp1	INSIDE	1.054	4.579	401.52	1838.77	4.825	340.88	1644.75
A_68_P22569292	chr3:138190910-138190954	NM_007917:1778	Eif4e	INSIDE	1.054	1.403	1694.19	2377.79	1.479	1461.31	2161.80
A_68_P24084081	chr5:129107610-129107654	NM_175284:652	Fzd10	INSIDE	1.054	1.559	2088.20	3254.69	1.643	1626.70	2673.19
A_68_P22565471	chr3:137528339-137528383	NM_016750:798	H2afz	INSIDE	1.054	1.339	3314.99	4440.02	1.411	2522.63	3559.91
A_68_P25186205	chr7:73224603-73224647	NM_024439:90	H47	INSIDE	1.054	1.539	954.93	1469.86	1.622	799.43	1296.53
A_68_P20600072	chr1:130256315-130256359	NM_008567:-103	Mcm6	PROMOTER	1.054	0.409	1603.33	656.47	0.432	1304.49	563.18
A_68_P21150010	chr2:38566321-38566365	NM_139051:3720	Nr5a1	INSIDE	1.054	0.476	1375.42	654.74	0.502	1174.48	589.04
A_68_P27896908	chr11:69571787-69571831	NM_009089:-83	Polr2a	PROMOTER	1.054	1.652	780.39	1288.81	1.741	709.33	1234.91
A_68_P23814584	chr5:76613501-76613545	NM_011626:618	Tmem165	INSIDE	1.054	5.120	893.40	4574.28	5.397	871.61	4704.38
A_68_P24630039	chr6:89785616-89785660	NM_053221:9893	Vmn1r42	DOWNSTREAM	1.054	2.230	1167.94	2603.99	2.351	1040.78	2446.92
A_68_P30509169	chr16:4268211-4268255			Unknown	1.054	2.676	320.66	858.12	2.821	314.92	888.35
A_68_P21041599	chr2:18722024-18722068	AK018938:-386		PROMOTER	1.054	2.464	1024.88	2525.63	2.597	863.48	2242.86
A_68_P26253145	chr8:128193794-128193838	NM_028908:99	4933403G14Rik	INSIDE	1.053	2.251	1672.01	3764.39	2.370	1482.81	3513.91
A_68_P26617807	chr9:70527537-70527581	NM_007399:751	Adam10	INSIDE	1.053	1.490	1177.32	1753.86	1.568	890.70	1396.93
A_68_P27566543	chr11:5965060-5965104	NM_001174053:669	Camk2b	INSIDE	1.053	2.056	1793.20	3686.79	2.165	1521.95	3295.16
A_68_P21836882	chr2:167514407-167514451	NM_009883:14	Cebpb	INSIDE	1.053	1.895	1684.07	3191.26	1.995	1550.56	3093.73
A_68_P20442010	chr1:93263130-93263174	NM_173395:146	Fam132b	INSIDE	1.053	0.591	1211.65	715.90	0.622	950.85	591.53
A_68_P20025037	chr1:9957276-9957320	NM_145692:41903	Lrrc67	DOWNSTREAM	1.053	1.443	1283.38	1851.83	1.519	1099.49	1669.96
A_68_P22705748	chr4:6380821-6380865	NM_010945:576	Nsmaf	INSIDE	1.053	1.963	953.82	1872.73	2.067	863.77	1785.63
A_68_P30346556	chr15:76004532-76004576	NM_201394:21586	Plec	INSIDE	1.053	2.876	325.47	936.00	3.028	257.29	779.00
A_68_P29950625	chr14:120877439-120877483	NM_029519:-222	Rap2a	PROMOTER	1.053	1.376	1520.92	2092.20	1.448	1218.89	1764.88
A_68_P25265265	chr7:87343187-87343231	NM_013659:11482	Sema4b	INSIDE	1.053	1.391	1203.42	1674.53	1.465	939.80	1377.09
A_68_P21999683	chr3:25043045-25043089	AK054291:117		INSIDE	1.053	2.391	1303.05	3115.62	2.517	1121.31	2822.76
A_68_P27212538	chr10:67011354-67011398	NM_001005419:327	Ado	INSIDE	1.052	2.588	613.18	1587.05	2.722	568.66	1547.97
A_68_P24797811	chr6:120244232-120244276	NM_198884:323	B4galnt3	INSIDE	1.052	3.257	1237.02	4029.08	3.428	1061.68	3639.20
A_68_P27183503	chr10:61441267-61441311	NM_007731:568	Col13a1	INSIDE	1.052	1.653	1199.32	1982.09	1.738	1046.49	1818.82
A_68_P25587956	chr7:148480038-148480082	NM_007878:2156	Drd4	INSIDE	1.052	1.413	1485.78	2099.20	1.486	1150.20	1709.28
A_68_P27561403	chr11:4998729-4998773	NM_007968:330	Ewsr1	INSIDE	1.052	0.612	1267.66	776.17	0.644	1084.66	698.96
A_68_P24290982	chr6:22306343-22306387	NM_138587:-283	Fam3c	PROMOTER	1.052	0.643	1268.33	815.93	0.677	1112.26	752.57
A_68_P26248333	chr8:127422026-127422070	NM_001111141:263	Gm505	INSIDE	1.052	1.953	2039.54	3984.00	2.055	1734.51	3563.75
A_68_P20391719	chr1:82287804-82287848	NM_010570:188	Irs1	INSIDE	1.052	1.899	821.78	1560.92	1.999	696.01	1391.34
A_68_P25034849	chr7:31852601-31852645	NM_144556:7669	Lgi4	INSIDE	1.052	2.127	1036.33	2204.40	2.238	956.97	2141.61
A_68_P28155818	chr11:115719846-115719890	NM_145438:34497	Llgl2	DOWNSTREAM	1.052	1.669	1419.85	2369.94	1.757	1131.73	1987.96
A_68_P31112804	chr17:26988009-26988053	NM_008700:-9520	Nkx2-5	PROMOTER	1.052	0.586	1144.98	671.45	0.617	835.57	515.69
A_68_P28068129	chr11:100302265-100302309	NM_026561:117	Nt5c3l	INSIDE	1.052	0.487	1655.61	805.64	0.512	1315.62	673.52

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P21095897	chr2:29083296-29083340	NM_133500:20242	Ntng2	INSIDE	1.052	1.704	513.89	875.65	1.793	421.70	755.91
A_68_P31757527	chr18:61558226-61558270	NM_133249:1837	Ppargc1b	INSIDE	1.052	1.715	1483.80	2544.46	1.803	1200.70	2165.31
A_68_P25502256	chr7:133936075-133936119	NM_019674:-111	Ppp4c	PROMOTER	1.052	1.828	872.59	1594.69	1.923	761.80	1465.02
A_68_P31375071	chr17:79419979-79420023	NM_001171004:156	Prkd3	INSIDE	1.052	1.482	1005.33	1490.25	1.559	937.40	1461.61
A_68_P29716897	chr14:73725909-73725953	NM_009029:-332	Rb1	PROMOTER	1.052	2.514	1631.85	4102.83	2.645	1447.63	3828.78
A_68_P21750310	chr2:152460214-152460258	NM_009047:7493	Rem1	INSIDE	1.052	1.755	525.16	921.46	1.845	396.97	732.43
A_68_P27284267	chr10:80069318-80069362	NM_019575:3714	Scamp4	INSIDE	1.052	2.011	822.67	1654.62	2.115	638.23	1349.88
A_68_P20946921	chr1:194861981-194862025	NM_181546:-110	Syt14	PROMOTER	1.052	1.607	2183.09	3508.01	1.691	1720.17	2908.36
A_68_P32340726	chrX:39421609-39421653	NM_009688:618	Xiap	INSIDE	1.052	1.914	570.87	1092.78	2.014	324.52	653.44
A_68_P20141345	chr1:34986894-34986938			Unknown	1.052	2.407	845.36	2034.56	2.531	767.32	1942.04
A_68_P32975994	chr12:18394285-18394329	ENSMUST00000080502:-254		PROMOTER	1.052	1.915	940.51	1800.94	2.015	983.34	1981.19
A_68_P21587204	chr2:122456531-122456575	NM_001004174:-7070	AA467197	PROMOTER	1.051	1.751	540.62	946.38	1.839	454.27	835.39
A_68_P21317589	chr2:70956028-70956072	NM_028593:-60	Cybrd1	PROMOTER	1.051	1.795	2991.99	5371.34	1.887	2390.59	4510.55
A_68_P32553702	chrX:96332024-96332068	NM_010110:578	Efnb1	INSIDE	1.051	2.353	702.59	1653.05	2.473	475.70	1176.47
A_68_P22045622	chr3:33919516-33919560	NM_001113188:538	Fxr1	INSIDE	1.051	1.621	2612.45	4233.95	1.703	2544.75	4334.78
A_68_P23600191	chr5:35731800-35731844	NM_010445:57	Hmx1	INSIDE	1.051	2.439	829.20	2022.42	2.564	790.07	2026.07
A_68_P27902205	chr11:70514397-70514441	NM_153103:369	Kif1c	INSIDE	1.051	0.629	1261.57	794.05	0.662	1082.59	716.25
A_68_P28049242	chr11:97048472-97048516	NM_008379:712	Kpnb1	INSIDE	1.051	1.380	1851.96	2556.02	1.450	1415.02	2051.84
A_68_P29629466	chr14:58318760-58318804	NM_015771:46178	Lats2	INSIDE	1.051	2.590	486.01	1258.84	2.723	490.72	1336.23
A_68_P25094514	chr7:52949352-52949396	NM_001033356:9591	Ntn5	INSIDE	1.051	3.158	680.85	2150.12	3.318	570.34	1892.21
A_68_P26609887	chr9:69138471-69138515	NM_013646:636884	Rora	INSIDE	1.051	2.963	682.70	2023.12	3.113	648.29	2018.35
A_68_P23768851	chr5:67999755-67999799	NM_001033415:655	Shisa3	INSIDE	1.051	0.329	1560.48	514.04	0.346	1366.36	473.21
A_68_P27765282	chr11:45793719-45793763	NM_173384:-71	Sox30	PROMOTER	1.051	1.575	1214.37	1912.48	1.654	973.82	1611.11
A_68_P21833061	chr2:166821891-166821935	NM_001109905:-134	Stau1	PROMOTER	1.051	0.519	1805.84	937.10	0.545	1488.97	812.04
A_68_P29052711	chr13:55098855-55098899	NM_153131:48084	Unc5a	INSIDE	1.051	2.447	2647.86	6479.58	2.572	2006.29	5160.56
A_68_P27564655	chr11:5616910-5616954	NM_178623:24247	Urgcp	INSIDE	1.051	2.198	475.93	1046.27	2.310	430.77	994.96
A_68_P27926119	chr11:75258911-75258955	NM_138950:9287	Wdr81	INSIDE	1.051	2.013	1915.73	3855.87	2.115	1500.98	3174.13
A_68_P22148835	chr3:54437544-54437588	ENSMUST00000172420:2206		INSIDE	1.051	2.079	592.78	1232.16	2.184	496.45	1084.27
A_68_P32070028	chr19:32463753-32463797	NR_033198:69	2700046G09Rik	INSIDE	1.050	0.424	1428.36	605.23	0.445	1170.14	520.77
A_68_P26202778	chr8:119960709-119960753	NM_028941:87661	4933407C03Rik	INSIDE	1.050	1.915	383.68	734.86	2.011	334.99	673.69
A_68_P30512949	chr16:4964346-4964390	NM_028301:-38	Anks3	PROMOTER	1.050	2.010	2053.66	4127.84	2.111	1559.87	3292.99
A_68_P25957040	chr8:74005621-74005665	NM_001164679:4324	Ano8	INSIDE	1.050	3.611	1476.63	5332.22	3.793	1238.30	4696.38
A_68_P21013692	chr2:12931915-12931959	NM_153155:555	C1ql3	INSIDE	1.050	1.576	1567.65	2470.71	1.654	1278.29	2114.85
A_68_P26235087	chr8:125202646-125202690	NM_001109873:-593	Cbfa2t3	PROMOTER	1.050	1.683	682.28	1148.03	1.767	573.00	1012.51
A_68_P28727030	chr12:109512594-109512638	NM_001159910:1011	Ccdc85c	INSIDE	1.050	0.453	1493.68	676.58	0.476	1113.60	529.76
A_68_P30540341	chr16:9992483-9992527	NM_008170:122	Grin2a	INSIDE	1.050	1.990	1252.76	2493.26	2.090	1058.42	2212.56
A_68_P20587179	chr1:127808497-127808541	NM_145100:273	Lypd1	INSIDE	1.050	2.114	790.24	1670.53	2.219	786.51	1745.39
A_68_P27282701	chr10:79819469-79819513	NM_183152:287	Plk5	INSIDE	1.050	1.401	1074.47	1505.53	1.471	923.17	1357.77
A_68_P24117611	chr5:136209975-136210019	NM_008898:44913	Por	INSIDE	1.050	2.162	762.60	1648.69	2.269	697.84	1583.39
A_68_P23012915	chr4:71861101-71861145	NM_011599:831	Tle1	INSIDE	1.050	1.865	1133.65	2114.25	1.958	1008.58	1975.09
A_68_P32143438	chr19:46431466-46431510	NM_029186:119	Tmem180	INSIDE	1.050	1.925	722.99	1391.54	2.021	591.88	1196.06
A_68_P32144311	chr19:46577241-46577285	NM_053100:1125	Trim8	INSIDE	1.050	1.599	754.38	1206.13	1.678	670.76	1125.53
A_68_P30351138	chr15:76741648-76741692	NM_001168276:14208	Zfp647	INSIDE	1.050	1.826	512.82	936.61	1.917	428.50	821.38
A_68_P27288888	chr10:80788031-80788075	NM_027381:4205	2510012J08Rik	INSIDE	1.049	2.327	867.89	2019.48	2.441	819.38	2000.17
A_68_P22128531	chr3:51028825-51028869	NM_009834:478	Ccrn4l	INSIDE	1.049	2.349	1254.26	2945.68	2.463	1059.50	2610.00
A_68_P28992095	chr13:43880702-43880746	NM_009856:249	Cd83	INSIDE	1.049	1.769	1338.22	2367.69	1.855	1251.62	2322.16
A_68_P20741943	chr1:158134761-158134805	NM_177838:374	Fam163a	INSIDE	1.049	0.681	2702.78	1839.89	0.714	2009.85	1435.20
A_68_P29571201	chr14:46149666-46149710	NM_146054:52	Fermt2	INSIDE	1.049	1.977	456.96	903.43	2.074	472.78	980.78
A_68_P27812595	chr11:54716247-54716291	NM_001083929:-86	Gpx3	PROMOTER	1.049	1.768	979.29	1731.09	1.854	844.59	1566.24
A_68_P31255288	chr17:56465651-56465695	NM_172132:200	Kdm4b	INSIDE	1.049	3.446	1077.34	3712.56	3.616	972.87	3517.87
A_68_P21111931	chr2:31742789-31742833	NM_011836:10	Lamc3	INSIDE	1.049	4.163	2263.15	9421.92	4.369	1664.87	7274.08

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P23839618	chr5:81758787-81758831	NM_198702:308191	Lphn3	INSIDE	1.049	1.859	1201.07	2233.14	1.950	1092.70	2130.77
A_68_P23324341	chr4:134259355-134259399	NM_207237:829	Man1c1	INSIDE	1.049	2.118	1675.38	3548.46	2.222	1487.47	3305.27
A_68_P27971660	chr11:83276484-83276528	NM_080453:-43	Mmp28	PROMOTER	1.049	1.399	1238.65	1732.52	1.468	1036.90	1521.65
A_68_P23617869	chr5:38550496-38550540	NM_010942:188	Nsg1	INSIDE	1.049	0.548	1884.92	1033.36	0.575	1339.06	770.13
A_68_P25089828	chr7:52125095-52125139	NM_133949:42	Ptov1	INSIDE	1.049	1.362	1562.37	2128.62	1.430	1255.48	1795.11
A_68_P28774234	chr12:118772641-118772685	NM_175930:17711	Rapgef5	INSIDE	1.049	2.364	335.52	793.07	2.481	270.92	672.04
A_68_P25349895	chr7:104474236-104474280	NM_001177412:216	Usp35	INSIDE	1.049	2.001	604.08	1208.82	2.099	669.02	1404.04
A_68_P30401628	chr15:85412235-85412279	NM_009528:-5	Wnt7b	PROMOTER	1.049	3.132	351.23	1100.02	3.286	387.70	1274.05
A_68_P23321770	chr4:133801322-133801366	NM_024215:162	Zfp593	INSIDE	1.049	1.984	1228.98	2437.74	2.080	1050.59	2185.13
A_68_P26465225	chr9:43828528-43828572			Unknown	1.049	4.163	480.45	2000.05	4.367	447.19	1952.97
A_68_P28089255	chr11:103995098-103995142	NM_007762:925	Crhr1	INSIDE	1.048	2.180	1742.31	3797.37	2.284	1525.84	3485.54
A_68_P30367146	chr15:79376680-79376724	NM_199079:287	Ddx17	INSIDE	1.048	1.518	1520.01	2306.90	1.591	1297.53	2064.19
A_68_P32463901	chrX:70885738-70885782	NM_029352:981	Dusp9	INSIDE	1.048	2.255	1021.84	2304.06	2.364	782.32	1849.10
A_68_P25565214	chr7:144506892-144506936	NM_001113414:-786	Ebf3	PROMOTER	1.048	1.828	481.15	879.64	1.917	463.32	888.02
A_68_P23200234	chr4:108952731-108952775	NM_007943:-127	Eps15	PROMOTER	1.048	1.629	2198.26	3581.63	1.707	1811.87	3093.69
A_68_P25828113	chr8:46129756-46129800	NM_001081286:94217	Fat1	INSIDE	1.048	3.776	2422.66	9146.86	3.955	1772.67	7010.95
A_68_P26141795	chr8:109394997-109395041	NM_008217:877	Has3	INSIDE	1.048	2.766	1222.06	3379.71	2.899	903.80	2619.99
A_68_P20156459	chr1:37947346-37947390	NM_027098:-29	Mrpl30	DIVERGENT_PROMOTER	1.048	0.644	2410.00	1552.09	0.675	1960.83	1323.03
A_68_P24993781	chr7:20109373-20109417	NM_027116:5315	Nkpd1	INSIDE	1.048	2.383	1383.75	3297.38	2.496	1230.05	3070.42
A_68_P24754175	chr6:112439230-112439274	NM_001081147:550	Oxtr	INSIDE	1.048	1.991	636.99	1268.46	2.087	605.87	1264.22
A_68_P24618287	chr6:87761915-87761959	NM_001039394:-163	Rab43	PROMOTER	1.048	3.263	6897.71	22505.88	3.419	4611.99	15767.68
A_68_P31925086	chr19:4787882-4787926	NM_009032:5973	Rbm4	INSIDE	1.048	3.117	2028.35	6322.46	3.267	1572.73	5137.99
A_68_P27641466	chr11:22412783-22412827	NM_153596:519	Tmem17	INSIDE	1.048	0.584	1407.57	821.64	0.612	1229.51	752.42
A_68_P26644961	chr9:75458869-75458913	NM_016711:242	Tmod2	INSIDE	1.048	2.402	631.49	1517.09	2.519	584.43	1471.94
A_68_P29097418	chr13:64254293-64254337	NM_175494:193	Zfp367	INSIDE	1.048	1.750	908.79	1590.78	1.835	743.70	1364.40
A_68_P24862403	A_68_P24862403			Unknown	1.048	20.204	320.02	6465.77	21.166	244.54	5176.12
A_68_P26584120	chr9:64659199-64659243	NM_001162917:403	Dennd4a	INSIDE	1.047	0.596	1289.86	768.18	0.624	1185.43	739.14
A_68_P23981795	chr5:111199426-111199470	NM_029337:288	Ep400	INSIDE	1.047	4.730	11570.70	54734.01	4.952	8287.44	41043.16
A_68_P23270839	chr4:124558845-124558889	NM_177671:-162	Epha10	PROMOTER	1.047	0.668	1790.53	1196.25	0.699	1538.33	1075.72
A_68_P28492940	chr12:66018887-66018931	NM_001025605:11	Gm527	INSIDE	1.047	2.490	1105.72	2753.14	2.607	999.15	2604.59
A_68_P24904451	chr6:142363030-142363089	NM_145572:58570	Gys2	DOWNSTREAM	1.047	2.695	1234.14	3325.79	2.822	795.13	2243.52
A_68_P31208331	chr17:46818042-46818086	NM_010787:-21	Mea1	DIVERGENT_PROMOTER	1.047	2.264	4024.30	9112.49	2.370	2451.76	5811.57
A_68_P28057821	chr11:98544135-98544179	NM_009439:289	Psmd3	INSIDE	1.047	1.824	2282.55	4163.46	1.909	1794.48	3426.56
A_68_P23018374	chr4:73436830-73436874	NM_001017427:-346	Rasef	PROMOTER	1.047	2.450	436.09	1068.61	2.565	439.75	1128.06
A_68_P21000493	chr2:10294275-10294319	NM_001198809:234	Sfmbt2	INSIDE	1.047	1.768	1264.93	2236.73	1.852	1200.31	2222.74
A_68_P32005495	chr19:21347202-21347246	NM_009551:457	Zfand5	INSIDE	1.047	1.709	350.84	599.41	1.789	366.47	655.58
A_68_P24951677	chr7:4982359-4982403	NM_001033383:10403	Zfp865	INSIDE	1.047	2.175	704.58	1532.78	2.278	649.15	1478.81
A_68_P26948855	chr10:12780660-12780705	FJ425893:373		INSIDE	1.047	1.874	860.53	1613.05	1.962	740.60	1453.24
A_68_P23327635	chr4:134828183-134828227	NM_013885:471	Clic4	INSIDE	1.046	2.012	680.57	1369.61	2.105	665.49	1401.01
A_68_P27289088	chr10:80820220-80820264	NM_028657:-72	F630110N24Rik	DIVERGENT_PROMOTER	1.046	1.901	475.19	903.48	1.988	471.41	937.16
A_68_P31159262	chr17:35607004-35607048	NM_010391:-7	H2-Q10	PROMOTER	1.046	2.079	1028.06	2137.54	2.175	924.66	2010.83
A_68_P20799111	chr1:168168733-168168779	NM_175296:119	Mael	INSIDE	1.046	2.369	332.64	788.10	2.478	283.30	702.14
A_68_P30346618	chr15:76012196-76012240	NM_201394:13922	Plec	INSIDE	1.046	1.801	369.10	664.84	1.883	368.36	693.77
A_68_P22825897	chr4:33334510-33334554	NM_001033225:1230	Pnrc1	INSIDE	1.046	0.642	1333.43	856.62	0.672	1142.52	767.72
A_68_P26167600	chr8:113824005-113824049	NM_146218:96	Rfwd3	INSIDE	1.046	0.555	3761.29	2086.67	0.580	3013.35	1747.97
A_68_P32562269	chrX:98255087-98255141	NM_031384:-136	Tex11	PROMOTER	1.046	2.096	1224.91	2567.23	2.193	466.72	1023.46
A_68_P24428350	chr6:48570111-48570155	NM_173429:6954	Zfp775	INSIDE	1.046	2.360	1162.00	2742.71	2.468	971.23	2397.32
A_68_P28183976	chr11:120211624-120211668	NR_038126:1655	0610009L18Rik	INSIDE	1.045	2.195	665.37	1460.41	2.295	601.76	1380.79
A_68_P21068909	chr2:24790606-24790650	NM_001162485:173	Arrdc1	INSIDE	1.045	0.467	1546.09	722.38	0.488	1310.47	639.65
A_68_P29613381	chr14:55251101-55251145	NM_199470:9079	Cdh24	INSIDE	1.045	2.153	1071.20	2306.36	2.249	952.55	2142.57
A_68_P27954535	chr11:80290099-80290143	NM_009871:-427	Cdk5r1	PROMOTER	1.045	1.772	957.36	1696.41	1.852	825.51	1529.14

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26504860	chr9:50467402-50467446	NM_145614:461	Dlat	INSIDE	1.045	0.604	1224.75	740.09	0.632	1142.35	721.57
A_68_P30512416	chr16:4879609-4879653	NM_145359:221	Fam100a	INSIDE	1.045	0.613	1038.60	636.17	0.640	901.87	577.51
A_68_P24112572	chr5:134790667-134790711	NM_001080746:-72	Gtf2i	PROMOTER	1.045	2.524	1564.41	3949.03	2.638	1374.38	3625.59
A_68_P26021243	chr8:87225571-87225617	NM_008535:239	Lyl1	INSIDE	1.045	1.688	1632.11	2755.34	1.764	1303.98	2300.28
A_68_P31556967	chr18:23962508-23962552	NM_153058:60	Mapre2	INSIDE	1.045	1.384	2864.47	3964.89	1.447	2179.63	3153.12
A_68_P27855154	chr11:62478652-62478704	NM_175002:16513	Mmgt2	INSIDE	1.045	1.836	365.93	671.76	1.919	332.43	637.78
A_68_P29314989	chr13:109906595-109906639	NM_011056:462246	Pde4d	INSIDE	1.045	0.634	1460.52	925.84	0.662	1194.99	791.55
A_68_P26350663	chr9:21961255-21961299	NM_001082532:-13	Pigyl	PROMOTER	1.045	3.047	1304.98	3976.91	3.184	1021.61	3252.37
A_68_P21749132	chr2:152224537-152224581	NM_011438:-776	Sox12	PROMOTER	1.045	2.310	611.12	1411.45	2.413	577.78	1393.90
A_68_P25030459	chr7:31016969-31017013	NM_025548:58	Tbcb	INSIDE	1.045	0.482	1388.93	669.17	0.504	1198.39	603.56
A_68_P27644762	chr11:23155768-23155812	NM_001035226:-250	Xpo1	PROMOTER	1.045	0.679	2353.67	1597.27	0.709	1775.56	1258.75
A_68_P28751777	chr12:113917151-113917195	NM_001100460:122	Zbtb42	INSIDE	1.045	2.009	869.55	1746.68	2.099	848.73	1781.51
A_68_P24596107	chr6:83864866-83864910	NM_001166371:542	Zfml	INSIDE	1.045	1.530	722.16	1104.90	1.598	583.64	932.73
A_68_P26038359	chr8:90483614-90483658	NM_033327:-142	Zfp423	PROMOTER	1.045	1.373	1466.81	2014.03	1.435	1255.04	1801.28
A_68_P26235083	A_68_P26235083			Unknown	1.045	2.431	553.02	1344.46	2.541	473.46	1202.92
A_68_P23334942	chr4:136193562-136193606	ENSMUST00000146123:15078		INSIDE	1.045	0.585	1122.30	656.00	0.611	1046.54	639.31
A_68_P21969036	chr3:17955303-17955347	NM_021560:1000	Bhlhe22	INSIDE	1.044	1.685	837.92	1412.20	1.760	807.05	1420.08
A_68_P26135495	chr8:108228498-108228542	NM_198299:3548	E130303B06Rik	INSIDE	1.044	3.241	897.85	2910.09	3.385	658.64	2229.34
A_68_P24993062	chr7:19979665-19979709	NM_007949:12299	Ercc2	INSIDE	1.044	2.893	276.61	800.13	3.019	227.67	687.30
A_68_P23416734	chr4:151506423-151506467	NM_019585:-3410	Espn	PROMOTER	1.044	1.554	1907.23	2964.13	1.622	1427.44	2315.43
A_68_P24046863	chr5:122299245-122299289	NM_175474:230	Fam109a	INSIDE	1.044	1.865	1301.20	2427.36	1.948	1093.39	2129.73
A_68_P25531564	chr7:139158932-139158976	NM_173410:812	Gpr26	INSIDE	1.044	0.575	1305.07	749.95	0.600	1046.30	627.96
A_68_P28605005	chr12:86939999-86940043	NM_001205052:-34	Jdp2	PROMOTER	1.044	1.828	1103.33	2017.21	1.909	1020.13	1947.39
A_68_P26022553	chr8:87426545-87426589	NM_010635:740	Klf1	INSIDE	1.044	1.392	1297.55	1806.29	1.454	1080.75	1571.32
A_68_P30148787	chr15:38229176-38229220	NM_013692:1264	Klf10	INSIDE	1.044	2.644	386.74	1022.47	2.761	400.73	1106.49
A_68_P25951938	chr8:72976513-72976557	NM_001122830:24308	Klhl26	INSIDE	1.044	2.053	551.03	1131.07	2.142	496.89	1064.42
A_68_P29269304	chr13:101386895-101386939	NM_178410:-17	Marveld2	PROMOTER	1.044	1.795	1108.65	1990.45	1.874	1096.50	2054.39
A_68_P30083234	chr15:25710990-25711034	NM_019472:158708	Myo10	INSIDE	1.044	3.394	281.59	955.84	3.545	230.09	815.76
A_68_P30480087	chr15:99256378-99256422	NM_001001884:31779	Nckap5l	INSIDE	1.044	2.160	708.07	1529.56	2.255	586.30	1322.29
A_68_P23544555	chr5:24414575-24414619	NM_001170555:-269	Prkag2	PROMOTER	1.044	2.782	288.31	802.23	2.906	255.47	742.26
A_68_P25094157	chr7:52887692-52887738	NM_028544:4808	Rasip1	INSIDE	1.044	1.716	1975.86	3390.32	1.792	1625.60	2913.17
A_68_P27833618	chr11:58752100-58752144	NM_022423:286	Rnf187	INSIDE	1.044	1.443	944.71	1363.65	1.507	868.54	1309.22
A_68_P27798413	chr11:52096958-52097002	NM_009331:-1228	Tcf7	PROMOTER	1.044	0.571	928.18	529.67	0.596	864.90	515.51
A_68_P26845368	chr9:114471438-114471482	NM_001042503:2027	Trim71	INSIDE	1.044	2.685	604.08	1621.88	2.804	480.27	1346.57
A_68_P22970877	chr4:63156474-63156518	NM_001008791:489	Whrn	INSIDE	1.044	1.760	3493.85	6149.62	1.837	2795.05	5134.03
A_68_P20859687	chr1:179372004-179372048	NM_001012330:-2765	Zfp238	PROMOTER	1.044	0.546	1085.20	592.60	0.570	902.20	514.48
A_68_P32634536	chrX:120217471-120217515	NM_028426:325	3110007F17Rik	INSIDE	1.043	1.383	4445.64	6147.00	1.442	2163.02	3119.10
A_68_P24800466	chr6:120772672-120772716	NM_007510:9	Atp6v1e1	INSIDE	1.043	1.400	1144.93	1602.54	1.460	1022.63	1493.49
A_68_P24863574	chr6:134742286-134742330	NM_001048054:338	Dusp16	INSIDE	1.043	1.876	587.19	1101.66	1.958	575.64	1126.84
A_68_P25564250	chr7:144390350-144390394	NM_001113414:115756	Ebf3	INSIDE	1.043	4.902	2181.37	10692.79	5.111	1666.03	8514.54
A_68_P22569283	chr3:138189837-138189881	NM_007917:704	Eif4e	INSIDE	1.043	2.081	415.97	865.56	2.170	383.89	832.98
A_68_P24466826	chr6:54988021-54988065	NM_180678:48	Gars	INSIDE	1.043	2.327	1113.92	2592.41	2.426	1037.95	2518.29
A_68_P24448669	chr6:52108855-52108899	NM_010449:-560	Hoxa1	PROMOTER	1.043	0.342	1799.12	614.87	0.357	1544.28	550.61
A_68_P23756016	chr5:65770881-65770930	NM_031180:31256	Klb	INSIDE	1.043	2.516	232.44	584.88	2.624	208.75	547.83
A_68_P26537261	chr9:56467792-56467836	NM_181074:65246	Lingo1	INSIDE	1.043	1.712	2456.36	4205.16	1.786	1592.78	2844.00
A_68_P27542074	chr10:128002848-128002892	NM_011119:120	Pa2g4	INSIDE	1.043	0.572	1497.55	856.73	0.597	1231.77	735.32
A_68_P31629586	chr18:37881660-37881706	NM_033591:-3677	Pcdhga8	PROMOTER	1.043	1.839	491.62	903.97	1.917	419.24	803.83
A_68_P26293554	chr9:8901675-8901719	NM_008829:1864	Pgr	INSIDE	1.043	2.294	779.59	1788.72	2.392	749.73	1793.51
A_68_P25972608	chr8:77736812-77736856	NM_029182:-1008	Rasd2	PROMOTER	1.043	0.641	3512.42	2251.36	0.668	2725.01	1821.52
A_68_P33007022	A_68_P33007022			Unknown	1.043	2.062	31059.58	64030.31	2.150	25863.33	55609.81
A_68_P24127513	chr5:138220985-138221029	NM_027242:861	2010007H12Rik	INSIDE	1.042	1.733	1168.45	2025.09	1.807	928.40	1677.37

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P30778637	chr16:55974341-55974385	NR_027965:368	2310061J03Rik	INSIDE	1.042	1.663	1118.02	1859.62	1.733	996.69	1727.51
A_68_P22142064	chr3:53282739-53282783	NM_173382:15022	2810046L04Rik	INSIDE	1.042	3.519	5006.99	17618.96	3.666	3465.81	12705.92
A_68_P32233088	chrX:5660010-5660054	NM_001033211:506	AU022751	INSIDE	1.042	1.522	3159.39	4809.60	1.586	1454.19	2305.82
A_68_P21067991	chr2:24618118-24618162	NM_001042528:427	Cacna1b	INSIDE	1.042	1.615	2750.23	4441.73	1.683	2350.54	3955.88
A_68_P31921836	chr19:4214356-4214400	NM_019952:-13	Clcf1	PROMOTER	1.042	1.836	1029.34	1890.17	1.913	958.78	1834.13
A_68_P33015620	chr1_random:50449-50497	NM_026866:134866	Disp1	INSIDE	1.042	2.771	442.48	1226.17	2.889	347.14	1002.75
A_68_P23392782	chr4:147538404-147538448	NM_176848:3650	Fbxo2	INSIDE	1.042	1.866	871.05	1625.16	1.944	765.16	1487.79
A_68_P22448209	chr3:115954867-115954911	NM_022427:1514	Gpr88	INSIDE	1.042	2.531	539.14	1364.84	2.639	501.70	1323.88
A_68_P22210129	chr3:67267888-67267932	NM_016753:-81	Lxn	PROMOTER	1.042	1.515	927.53	1404.92	1.578	734.14	1158.50
A_68_P30000056	chr15:8395496-8395540	NM_027707:-1055	Nipbl	PROMOTER	1.042	1.520	857.10	1303.04	1.584	834.71	1321.84
A_68_P25092986	chr7:52670982-52671026	NM_198190:1940	Ntf5	INSIDE	1.042	2.173	407.44	885.24	2.265	367.05	831.33
A_68_P25499770	chr7:133436200-133436244	NM_145587:20090	Sbk1	INSIDE	1.042	2.112	1006.85	2126.92	2.201	796.38	1753.09
A_68_P26142247	chr8:109459545-109459589	NM_009229:-83	Sntb2	PROMOTER	1.042	2.493	736.32	1835.98	2.599	644.29	1674.54
A_68_P24163027	chr5:145612055-145612099	NM_001081362:82416	Trrap	INSIDE	1.042	1.919	830.14	1592.73	1.998	577.01	1153.12
A_68_P29097416	chr13:64254085-64254129	NM_175494:401	Zfp367	INSIDE	1.042	3.502	925.04	3239.57	3.648	847.03	3089.96
A_68_P23299680	chr4:129684126-129684170	NM_001199696:21827	Bai2	INSIDE	1.041	2.939	565.69	1662.69	3.059	499.91	1529.35
A_68_P21646221	chr2:133378682-133378726	NM_007553:-230	Bmp2	PROMOTER	1.041	2.647	1696.40	4490.61	2.755	1388.78	3825.80
A_68_P23351275	chr4:138908526-138908570	NM_001039200:41	C230096C10Rik	INSIDE	1.041	1.718	2977.06	5115.51	1.789	2277.70	4075.38
A_68_P24631550	chr6:90259089-90259133	NM_027928:16069	Chst13	INSIDE	1.041	1.923	930.71	1790.20	2.002	772.41	1546.42
A_68_P22305775	chr3:86723959-86724003	NM_001195496:826	Dclk2	INSIDE	1.041	1.575	1090.96	1718.79	1.640	975.17	1599.18
A_68_P23280649	chr4:126210358-126210402	NM_153177:322	Eif2c4	INSIDE	1.041	2.923	1288.88	3767.39	3.042	1349.21	4104.17
A_68_P28563526	chr12:79327709-79327753	NM_145965:89	Gphn	INSIDE	1.041	1.667	692.64	1154.90	1.736	666.40	1156.92
A_68_P21834173	chr2:167013977-167014021	NM_008420:301	Kcnb1	INSIDE	1.041	2.569	1455.04	3738.70	2.676	1336.33	3575.85
A_68_P25951931	chr8:72975757-72975801	NM_001122830:25064	Klhl26	INSIDE	1.041	2.492	367.21	915.26	2.596	336.42	873.19
A_68_P31130476	chr17:30026783-30026828	NM_001081160:-1978	Mdga1	PROMOTER	1.041	1.819	668.52	1215.82	1.893	543.92	1029.49
A_68_P26017636	chr8:86536527-86536571	NR_035431:-1016	Mir1199	DIVERGENT_PROMOTER	1.041	0.572	1480.52	846.54	0.595	1269.41	755.29
A_68_P26164570	chr8:113262638-113262682	NM_198625:17277	Mtss1l	INSIDE	1.041	1.891	354.50	670.49	1.968	342.76	674.59
A_68_P20474868	chr1:99991929-99991973	NM_013626:259	Pam	INSIDE	1.041	0.520	2382.96	1240.10	0.542	2136.84	1157.41
A_68_P26504618	chr9:50425465-50425510	NM_028300:62	Pih1d2	INSIDE	1.041	1.732	855.79	1482.45	1.804	815.32	1470.88
A_68_P26823384	chr9:110283423-110283467	NM_001001144:47648	Scap	INSIDE	1.041	2.276	508.24	1156.95	2.369	440.12	1042.78
A_68_P22218623	chr3:68808767-68808811	NM_133786:-105	Smc4	DIVERGENT_PROMOTER	1.041	1.704	932.28	1588.71	1.774	863.15	1531.25
A_68_P22336393	chr3:93247754-93247798	NM_001163098:1525	Tchh	INSIDE	1.041	1.830	872.91	1597.72	1.905	701.58	1336.32
A_68_P25011333	chr7:26472908-26472952	NM_011577:910	Tgfb1	INSIDE	1.041	1.606	653.23	1049.15	1.671	561.79	938.88
A_68_P29880578	chr14:106505252-106505296	NM_198601:-140	Trim52	PROMOTER	1.041	2.026	319.67	647.56	2.108	265.76	560.32
A_68_P24124211	chr5:137505950-137505994	NM_001039385:-192	Vgf	PROMOTER	1.041	1.723	843.90	1454.12	1.794	762.20	1367.58
A_68_P31092444	chr17:23713564-23713608	NM_011747:22868	Zfp13	INSIDE	1.041	2.787	934.23	2603.98	2.903	790.19	2293.70
A_68_P24065807	chr5:125726086-125726130			Unknown	1.041	0.418	1395.60	583.26	0.435	1041.88	453.23
A_68_P31149281	chr17:33661172-33661216	NM_172619:54	Adamts10	INSIDE	1.040	0.619	1420.75	880.04	0.644	1104.84	711.93
A_68_P26023161	chr8:87535204-87535248	NM_001130193:3004	Best2	INSIDE	1.040	1.483	1355.93	2011.05	1.542	1274.61	1965.91
A_68_P32268345	chrX:13423285-13423329	NM_009806:361	Cask	INSIDE	1.040	2.319	513.28	1190.17	2.412	330.41	796.96
A_68_P23336932	chr4:136501941-136501985	NM_007939:10769	Epha8	INSIDE	1.040	2.435	1675.12	4078.45	2.532	1277.19	3233.46
A_68_P30720006	chr16:44173216-44173260	NM_001029889:-271	Gm608	PROMOTER	1.040	1.359	2434.22	3307.92	1.414	1899.95	2685.64
A_68_P28748382	chr12:113412288-113412332	NM_001097621:27892	Kif26a	INSIDE	1.040	2.659	685.56	1822.57	2.766	590.06	1632.09
A_68_P24378364	chr6:38586770-38586814	NM_001033171:447	Klrg2	INSIDE	1.040	2.189	1205.08	2637.46	2.276	1086.49	2472.73
A_68_P22210124	chr3:67267480-67267524	NM_016753:327	Lxn	INSIDE	1.040	0.625	1803.38	1127.06	0.650	1374.83	893.78
A_68_P27279099	chr10:79281830-79281874	NM_001161747:25536	Palm	INSIDE	1.040	2.752	274.85	756.34	2.862	195.87	560.53
A_68_P30346634	chr15:76014247-76014291	NM_201394:11872	Plec	INSIDE	1.040	2.761	1003.49	2770.64	2.873	761.57	2187.78
A_68_P21417953	chr2:90419832-90419876	NM_008982:950	Ptprj	INSIDE	1.040	1.979	1396.89	2764.15	2.057	1241.18	2553.45
A_68_P29675226	chr14:66349915-66349959	NM_001168318:64697	Scara5	INSIDE	1.040	1.882	563.51	1060.26	1.956	485.53	949.92
A_68_P32168795	chr19:50753385-50753429	NM_021377:-304	Sorcs1	PROMOTER	1.040	1.427	1397.99	1994.69	1.484	1288.34	1912.38
A_68_P31513732	chr18:14840635-14840679	NM_001161369:767	Ss18	INSIDE	1.040	1.438	1617.10	2325.69	1.496	1518.86	2272.81

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P21612437	chr2:127095568-127095612	NM_139308:-374	Stard7	PROMOTER	1.040	1.435	1214.92	1742.80	1.492	1099.80	1640.49
A_68_P25614230	chr8:3496425-3496469	NM_080461:3309	Zfp358	INSIDE	1.040	2.652	2418.50	6414.67	2.757	1936.61	5340.06
A_68_P22630570	chr3:148652214-148652258	ENSMUST00000098518:44		INSIDE	1.040	1.400	2742.44	3840.44	1.456	2214.13	3223.95
A_68_P20936908	chr1:193048383-193048427	ENSMUST00000139056:52		INSIDE	1.040	1.412	996.51	1406.78	1.469	864.50	1269.72
A_68_P20456909	chr1:95582007-95582051	NM_016778:-242	Bok	PROMOTER	1.039	1.853	1276.27	2365.49	1.926	1214.63	2339.16
A_68_P23818508	chr5:77287446-77287490	NM_001163793:17845	C530008M17Rik	INSIDE	1.039	1.758	869.28	1528.10	1.826	659.57	1204.48
A_68_P23440734	chr4:155186580-155186624	NM_207678:5	Ccnl2	INSIDE	1.039	0.435	2062.61	896.78	0.452	1736.83	784.33
A_68_P26843397	chr9:113935916-113935960	NM_178624:-69	Fbxl2	PROMOTER	1.039	0.578	1245.84	720.25	0.601	1178.26	707.58
A_68_P20553868	chr1:120734527-120734571	NM_001081125:215648	Gli2	INSIDE	1.039	2.093	1221.98	2557.06	2.173	847.19	1841.31
A_68_P23438947	chr4:154866365-154866409	NM_001160016:917	Gnb1	INSIDE	1.039	0.439	2353.45	1032.60	0.456	1960.08	893.17
A_68_P26867068	chr9:118468753-118468797	NM_018748:53339	Golga4	INSIDE	1.039	2.785	1156.63	3221.46	2.893	928.84	2687.11
A_68_P25525510	chr7:138079636-138079680	NM_019564:-58	Htra1	PROMOTER	1.039	1.463	1067.31	1561.54	1.520	886.73	1348.05
A_68_P32029536	chr19:25484468-25484512	NM_181404:172799	Kank1	INSIDE	1.039	2.607	1038.04	2706.33	2.709	826.18	2238.26
A_68_P25018409	chr7:28443259-28443303	NM_001081292:16337	Map3k10	INSIDE	1.039	1.733	2167.04	3754.61	1.800	1817.53	3271.69
A_68_P25954142	chr8:73321226-73321270	NM_199308:-4916	Mast3	PROMOTER	1.039	2.706	4368.49	11819.08	2.811	2760.84	7760.00
A_68_P22039667	chr3:32635840-32635884	NM_025316:-122	Ndufb5	DIVERGENT_PROMOTER	1.039	1.470	1598.16	2348.95	1.527	1266.94	1934.85
A_68_P27261658	chr10:75837803-75837847	NM_008787:67833	Pcnt	INSIDE	1.039	5.183	127.46	660.66	5.388	126.38	680.94
A_68_P27362365	chr10:94407441-94407485	NM_018797:-250	Plxnc1	PROMOTER	1.039	1.774	567.67	1007.33	1.844	450.72	831.11
A_68_P20598630	chr1:130000293-130000337	NM_181750:432	R3hdm1	INSIDE	1.039	3.943	390.35	1538.97	4.098	433.83	1777.67
A_68_P21747682	chr2:151931567-151931611	NM_029688:123	Srxn1	INSIDE	1.039	0.441	2156.03	950.82	0.458	1629.59	746.88
A_68_P29734164	chr14:76904319-76904363	NM_009366:24	Tsc22d1	INSIDE	1.039	1.787	470.76	841.10	1.857	446.09	828.18
A_68_P23185482	chr4:106295106-106295150	NM_177667:75	Ttc22	INSIDE	1.039	3.272	1376.86	4504.94	3.399	1162.89	3953.08
A_68_P28160202	chr11:116442703-116442747	NM_173755:37	Ube2o	INSIDE	1.039	2.036	1996.47	4063.88	2.114	1789.66	3784.15
A_68_P30571779	chr16:17070377-17070421	NM_023249:-5	Ypel1	PROMOTER	1.039	3.962	934.43	3702.52	4.115	866.05	3564.00
A_68_P28939815	chr13:34744074-34744118	NM_025831:454	1300014I06Rik	INSIDE	1.038	0.626	1166.07	730.49	0.650	995.92	647.60
A_68_P28420020	chr12:50492378-50492422	NR_026733:1762	3110039M20Rik	INSIDE	1.038	1.364	1668.80	2275.82	1.415	1462.19	2068.92
A_68_P28198915	chr12:4133424-4133468	NM_138305:-706	Adcy3	PROMOTER	1.038	1.655	1073.26	1776.42	1.719	945.52	1625.09
A_68_P25415075	chr7:117912319-117912363	NM_009667:-3777	Ampd3	PROMOTER	1.038	3.083	473.86	1460.75	3.201	423.67	1356.15
A_68_P25537314	chr7:140051211-140051255	NM_198017:325	Fam175b	INSIDE	1.038	1.511	726.58	1097.76	1.569	590.46	926.24
A_68_P27284855	chr10:80154115-80154159	NM_172457:10429	Mobkl2a	INSIDE	1.038	1.781	498.65	888.18	1.848	439.66	812.52
A_68_P20377655	chr1:79772877-79772921	NM_001081210:306	Mrpl44	INSIDE	1.038	2.123	914.60	1941.32	2.204	839.76	1850.73
A_68_P23260198	chr4:122673656-122673700	NM_008506:337	Mycl1	INSIDE	1.038	2.448	1007.83	2466.73	2.540	904.36	2296.66
A_68_P28178596	chr11:119410661-119410705	NM_008730:-1548	Nptx1	PROMOTER	1.038	1.426	839.25	1196.76	1.481	745.33	1103.61
A_68_P26742500	chr9:95460884-95460928	NM_198414:671	Paqr9	INSIDE	1.038	2.436	1252.77	3052.29	2.529	1258.48	3182.23
A_68_P27278598	chr10:79198902-79198960	NM_172551:10396	Polrmt	INSIDE	1.038	3.322	984.85	3272.10	3.450	777.88	2683.31
A_68_P23649335	chr5:44492359-44492403	NM_001163584:-6373	Prom1	PROMOTER	1.038	1.951	3737.68	7292.88	2.025	2978.63	6031.96
A_68_P27287274	chr10:80542595-80542639	NM_022653:9789	Thop1	INSIDE	1.038	4.436	1488.23	6602.37	4.604	1068.13	4917.69
A_68_P23340750	chr4:137150373-137150417	NM_130879:291	Usp48	INSIDE	1.038	0.464	2020.14	938.28	0.482	1501.88	724.18
A_68_P31120933	chr17:28314032-28314076	NM_172617:-308	Zfp523	PROMOTER	1.038	2.786	696.21	1939.46	2.893	639.86	1850.80
A_68_P25769255	chr8:34627820-34627864	ENSMUST00000124496:47		INSIDE	1.038	3.548	786.16	2788.97	3.682	751.30	2766.48
A_68_P32097048	chr19:37767375-37767419	NM_001105201:7227	Cyp26c1	INSIDE	1.037	0.617	1787.14	1103.34	0.640	1365.30	874.17
A_68_P28558336	chr12:78340320-78340364	NM_016893:335	Fut8	INSIDE	1.037	2.225	639.18	1422.50	2.308	614.72	1418.76
A_68_P29612959	chr14:55172748-55172792	NM_145462:428	Haus4	INSIDE	1.037	1.658	982.69	1629.49	1.719	936.91	1610.96
A_68_P28067971	chr11:100275626-100275670	NM_176830:485	Leprel4	INSIDE	1.037	1.591	1039.17	1653.26	1.650	1005.57	1659.17
A_68_P23837517	chr5:81448669-81448713	NM_198702:-1927	Lphn3	PROMOTER	1.037	2.101	632.54	1328.75	2.179	663.81	1446.45
A_68_P30447287	chr15:93333954-93333998	NM_001033217:92346	Prickle1	INSIDE	1.037	3.695	766.22	2830.95	3.832	677.95	2597.98
A_68_P24983629	chr7:17441116-17441160	NM_178900:12725	Prkd2	INSIDE	1.037	3.555	992.75	3529.03	3.685	790.63	2913.61
A_68_P26349530	chr9:21722254-21722298	NM_031874:289	Rab3d	INSIDE	1.037	1.541	639.79	985.72	1.598	696.64	1113.24
A_68_P26816016	chr9:108564748-108564792	NM_020520:342	Slc25a20	INSIDE	1.037	3.447	447.33	1541.75	3.574	449.75	1607.19
A_68_P26042147	chr8:91151173-91151217	NM_027840:8833	Snx20	INSIDE	1.037	2.059	367.65	756.90	2.135	339.76	725.27
A_68_P21266382	chr2:61643297-61643341	NM_009322:809	Tbr1	INSIDE	1.037	0.446	1421.80	634.29	0.463	1192.75	551.66

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25701520	chr8:18950897-18950941	NM_001113350:55	Xkr5	INSIDE	1.037	1.822	1512.55	2756.17	1.889	1278.15	2414.99
A_68_P24951573	chr7:4966992-4967036	NM_025324:-95	Zfp524	DIVERGENT_PROMOTER	1.037	1.743	1867.69	3256.12	1.809	1541.37	2787.69
A_68_P27590827	chr11:11362280-11362324	NM_001185153:120	Zpbp	INSIDE	1.037	1.561	685.69	1070.22	1.618	651.09	1053.62
A_68_P31116860	chr17:27650768-27650812	ENSMUST00000088073:-504		DIVERGENT_PROMOTER	1.037	1.512	879.05	1329.36	1.568	733.42	1149.87
A_68_P31791923	chr18:67608414-67608458	NM_027130:354	Afg3l2	INSIDE	1.036	1.438	1375.24	1977.83	1.490	1222.52	1821.31
A_68_P32710890	chrX:139401516-139401560	NM_019496:-267	Ammecr1	PROMOTER	1.036	4.018	347.15	1394.69	4.162	215.96	898.81
A_68_P27278226	chr10:79144635-79144681	NM_177613:-281	Cdc34	PROMOTER	1.036	1.428	1182.18	1688.34	1.479	1022.12	1511.95
A_68_P23448649	chr5:4104754-4104798	NM_020010:-79	Cyp51	PROMOTER	1.036	0.596	1307.18	778.61	0.617	1031.83	636.76
A_68_P31258212	chr17:56901669-56901713	NM_144858:-2483	Dus3l	DIVERGENT_PROMOTER	1.036	1.343	2116.79	2841.86	1.391	1599.41	2224.80
A_68_P28187033	chr11:120685676-120685720	NM_007988:163	Fasn	INSIDE	1.036	1.650	2813.18	4640.61	1.710	2482.17	4243.68
A_68_P24115931	chr5:135825936-135825980	NM_033571:-97	Fkbp6	DIVERGENT_PROMOTER	1.036	2.488	621.20	1545.26	2.578	519.02	1338.02
A_68_P21874405	chr2:174111730-174111779	NM_019690:1934	Gnas	INSIDE	1.036	1.839	537.74	988.94	1.905	404.64	770.93
A_68_P28997685	chr13:44829480-44829524	NM_001205043:2863	Jarid2	INSIDE	1.036	0.548	1286.57	705.20	0.568	1014.16	576.16
A_68_P26643862	chr9:75257222-75257266	NM_027418:-78	Mapk6	PROMOTER	1.036	2.289	799.88	1830.75	2.371	724.01	1716.95
A_68_P23345718	chr4:137990544-137990588	NM_026689:-20	Mul1	PROMOTER	1.036	1.630	2063.11	3362.57	1.689	1589.54	2684.37
A_68_P31866222	chr18:80894933-80894977	NM_001164111:9958	Nfatc1	INSIDE	1.036	2.134	555.22	1185.09	2.212	487.50	1078.39
A_68_P30346558	chr15:76004732-76004776	NM_201394:21386	Plec	INSIDE	1.036	3.094	237.53	734.95	3.206	181.82	582.85
A_68_P26240715	chr8:126178067-126178111	NM_133955:260	Rhou	INSIDE	1.036	0.536	1978.12	1059.92	0.555	1563.45	868.16
A_68_P23234754	chr4:117166920-117166964	NM_025739:2578	Rnf220	INSIDE	1.036	1.395	1066.48	1488.12	1.446	905.07	1308.34
A_68_P29041945	chr13:53206732-53206776	NM_013846:174724	Ror2	INSIDE	1.036	2.572	1137.57	2926.33	2.665	813.07	2166.50
A_68_P20634554	chr1:136543381-136543425	NM_009307:145	Syt2	INSIDE	1.036	1.661	576.40	957.34	1.721	519.74	894.59
A_68_P25615129	chr8:3679115-3679159	NM_025701:2660	Trappc5	INSIDE	1.036	3.334	647.76	2159.57	3.454	608.65	2102.57
A_68_P32753664	chrX:149932965-149933009	NM_018798:212	Ubqln2	INSIDE	1.036	2.845	611.01	1738.17	2.948	373.69	1101.56
A_68_P27645074	chr11:23207052-23207096	NM_001190401:180	Usp34	INSIDE	1.036	1.397	2055.29	2871.92	1.448	1681.68	2435.10
A_68_P20350471	chr1:74830842-74830886	NM_009526:12399	Wnt6	INSIDE	1.036	2.541	844.23	2144.90	2.633	769.42	2026.00
A_68_P32403976	chrX:55291949-55291993	NM_009575:8166	Zic3	DOWNSTREAM	1.036	1.984	1757.44	3486.15	2.055	950.45	1952.99
A_68_P31022096	chr17:6257118-6257162	ENSMUST00000121576:3238		DOWNSTREAM	1.036	0.620	2682.79	1664.52	0.643	2215.00	1424.37
A_68_P28050435	chr11:97277300-97277344	ENSMUST00000121799:476		INSIDE	1.036	1.627	1294.40	2106.35	1.685	1108.73	1868.33
A_68_P27813411	chr11:54846956-54847000	NM_001110211:-5	Anxa6	PROMOTER	1.035	0.698	2470.01	1722.97	0.722	1877.85	1355.44
A_68_P24761384	chr6:113709003-113709047	NM_001036684:132346	Atp2b2	INSIDE	1.035	2.056	579.35	1190.93	2.127	442.24	940.81
A_68_P28752037	chr12:113960819-113960863	NM_001024602:456	AW555464	INSIDE	1.035	1.627	566.01	921.04	1.684	538.58	906.72
A_68_P26844380	chr9:114294100-114294144	NM_019922:5708	Crtap	INSIDE	1.035	2.128	491.74	1046.51	2.203	392.87	865.70
A_68_P22288618	chr3:83843229-83843273	NM_172681:833	D930015E06Rik	INSIDE	1.035	0.591	1843.04	1088.83	0.611	1386.08	847.12
A_68_P28525539	chr12:72419195-72419245	NM_001190466:8350	Dact1	INSIDE	1.035	3.546	626.62	2222.31	3.671	501.31	1840.30
A_68_P26674979	chr9:81526399-81526443	NM_010482:-261	Htr1b	PROMOTER	1.035	1.798	869.89	1563.66	1.860	717.48	1334.53
A_68_P27282840	chr10:79845290-79845334	NM_198615:5084	Mex3d	INSIDE	1.035	2.294	1765.78	4050.84	2.374	1251.80	2971.21
A_68_P23585506	chr5:33128194-33128238	NM_177298:59	Pisd	INSIDE	1.035	1.408	4637.86	6529.07	1.456	3578.25	5211.23
A_68_P26804663	chr9:106587992-106588036	NM_011573:-16	Tex264	PROMOTER	1.035	2.154	942.34	2030.14	2.230	738.81	1647.26
A_68_P27564657	chr11:5617071-5617115	NM_178623:24087	Urgcp	INSIDE	1.035	3.082	624.35	1924.52	3.190	544.05	1735.43
A_68_P28611535	chr12:88019970-88020014	NM_177354:343	Vash1	INSIDE	1.035	1.527	597.85	913.12	1.581	572.44	905.30
A_68_P32455383	chrX:69062125-69062169	NM_001081356:29	Vma21	INSIDE	1.035	1.730	832.67	1440.21	1.790	468.95	839.62
A_68_P21779867	chr2:157739997-157740041	NM_198627:-370	Vstm2l	PROMOTER	1.035	1.567	7678.84	12031.63	1.622	5888.38	9553.04
A_68_P24097667	chr5:131782979-131783023	NM_145218:392	Wbscr17	INSIDE	1.035	1.617	584.26	944.73	1.674	430.13	719.94
A_68_P23396095	chr4:148098538-148098582	ENSMUST00000139895:10749		DOWNSTREAM	1.035	1.650	1767.98	2917.94	1.708	1445.35	2469.34
A_68_P26430868	chr9:37296656-37296700	NM_146222:-227	BC024479	PROMOTER	1.034	2.113	814.37	1720.44	2.185	716.10	1565.02
A_68_P32680074	chrX:132749644-132749688	NM_009052:386	Bex1	INSIDE	1.034	1.702	1050.85	1788.73	1.760	644.26	1133.76
A_68_P31111039	chr17:26698374-26698418	NM_026170:-60	Ergic1	PROMOTER	1.034	0.698	2460.87	1716.89	0.721	1979.24	1427.78
A_68_P24046890	chr5:122302790-122302834	NM_175474:3776	Fam109a	INSIDE	1.034	2.385	1289.17	3074.46	2.467	1194.99	2948.05
A_68_P28266915	chr12:16807626-16807670	NM_015764:44	Greb1	INSIDE	1.034	1.747	1038.38	1814.19	1.806	1010.22	1824.18
A_68_P25285298	chr7:91032485-91032529	NM_030705:345	Mesdc1	INSIDE	1.034	1.865	338.08	630.54	1.928	308.74	595.31
A_68_P21840229	chr2:168056835-168056879	NM_001160330:735	Mocs3	INSIDE	1.034	3.492	763.98	2667.45	3.609	780.08	2815.64

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P20936019	chr1:192887145-192887189	NM_198654:267	Nsl1	INSIDE	1.034	1.556	689.60	1072.86	1.608	623.14	1002.03
A_68_P28941007	chr13:34967553-34967597	NM_013830:212	Prpf4b	INSIDE	1.034	0.472	1266.44	597.40	0.488	1056.25	515.21
A_68_P25499769	chr7:133436111-133436155	NM_145587:20000	Sbk1	INSIDE	1.034	2.798	709.88	1986.10	2.892	637.95	1845.02
A_68_P26823380	chr9:110283014-110283058	NM_001001144:47240	Scap	INSIDE	1.034	2.914	1065.15	3104.32	3.013	827.75	2493.91
A_68_P24764863	chr6:114232692-114232736	NM_178703:86	Slc6a1	INSIDE	1.034	1.392	3900.18	5428.39	1.440	2471.85	3558.28
A_68_P28048175	chr11:96880255-96880299	NM_031183:5394	Sp6	INSIDE	1.034	2.620	533.59	1398.23	2.711	486.20	1317.99
A_68_P25283749	chr7:90780539-90780583	NM_023377:34	Stard5	INSIDE	1.034	0.561	1071.33	601.53	0.581	928.65	539.09
A_68_P22949805	chr4:58219063-58219107	NM_022814:384	Svep1	INSIDE	1.034	4.156	1248.61	5189.78	4.299	1134.26	4876.02
A_68_P25409834	chr7:116895598-116895642	NM_020050:157	Tmem9b	INSIDE	1.034	2.971	944.98	2807.67	3.073	830.74	2552.76
A_68_P23400514	chr4:148800490-148800534	NM_022022:228	Ube4b	INSIDE	1.034	1.679	4742.69	7961.41	1.735	4031.17	6995.60
A_68_P29650713	chr14:62175501-62175545	NM_025697:201	6330409N04Rik	INSIDE	1.033	3.506	910.36	3191.78	3.623	774.37	2805.39
A_68_P25960290	chr8:74764202-74764246	NM_007456:194	Ap1m1	INSIDE	1.033	1.751	901.83	1578.83	1.809	790.96	1430.45
A_68_P27180607	chr10:60915001-60915045	NM_010124:395	Eif4ebp2	INSIDE	1.033	1.604	895.74	1437.11	1.657	817.39	1354.26
A_68_P25979792	chr8:79423193-79423237	NR_028579:858	Gm10649	INSIDE	1.033	1.714	524.68	899.44	1.772	434.27	769.35
A_68_P31116317	chr17:27571773-27571817	NM_001013385:68455	Grm4	INSIDE	1.033	2.342	1021.64	2392.55	2.419	829.42	2006.29
A_68_P24637120	chr6:91106803-91106847	NM_144919:16	Hdac11	INSIDE	1.033	1.558	1397.49	2177.90	1.610	1268.38	2041.58
A_68_P30991214	chr16:96349614-96349659	NM_008251:-304	Hmgn1	PROMOTER	1.033	0.585	1727.85	1009.99	0.604	1372.90	828.79
A_68_P24132969	chr5:139470681-139470725	NM_008808:205	Pdgfa	INSIDE	1.033	4.776	2010.46	9602.70	4.932	1705.12	8409.32
A_68_P30423621	chr15:88997899-88997943	NM_001159521:6360	Plxnb2	INSIDE	1.033	1.589	1142.49	1815.02	1.642	1039.96	1707.18
A_68_P31257077	chr17:56723655-56723699	NM_001029979:330	Safb2	INSIDE	1.033	0.625	2293.84	1434.48	0.646	1865.71	1204.66
A_68_P24153011	chr5:143194631-143194675	NM_146257:16598	Slc29a4	INSIDE	1.033	3.144	6262.46	19691.47	3.248	4624.55	15019.87
A_68_P25425958	chr7:119823278-119823322	NM_001166584:467	Tead1	INSIDE	1.033	0.500	1122.70	560.84	0.516	1034.62	533.95
A_68_P24761358	chr6:113705242-113705289	NM_001036684:136105	Atp2b2	INSIDE	1.032	2.418	240.07	580.50	2.496	224.38	560.05
A_68_P29977063	chr15:3945932-3945978	NM_145930:-202	AW549877	PROMOTER	1.032	1.823	1176.72	2145.28	1.881	862.16	1622.06
A_68_P24791288	chr6:119058455-119058499	NM_001159533:-269	Cacna1c	PROMOTER	1.032	2.194	601.87	1320.49	2.264	535.79	1213.15
A_68_P25601084	chr7:150646850-150646894	NM_001161624:83	Cdkn1c	INSIDE	1.032	1.796	1092.50	1961.75	1.853	1020.12	1890.63
A_68_P24597420	chr6:84085413-84085457	NM_021469:116052	Dysf	INSIDE	1.032	2.164	995.28	2154.09	2.233	803.20	1793.80
A_68_P28940414	chr13:34838852-34838896	NM_138746:7364	Fam50b	INSIDE	1.032	2.562	747.74	1915.36	2.643	659.01	1741.99
A_68_P22291214	chr3:84284017-84284061	NM_001205355:-625	Fhdc1	PROMOTER	1.032	0.660	2215.56	1461.68	0.681	1695.82	1154.59
A_68_P26587423	chr9:65239016-65239060	NM_028974:421	Kbtbd13	INSIDE	1.032	1.553	733.37	1139.15	1.603	665.63	1067.01
A_68_P25954428	chr8:73366677-73366723	NM_032397:14207	Kcnn1	INSIDE	1.032	2.860	277.02	792.18	2.952	224.19	661.88
A_68_P31777748	chr18:65047791-65047835	NM_001114386:403	Nedd4l	INSIDE	1.032	2.290	1227.91	2811.75	2.364	1109.68	2623.49
A_68_P27280127	chr10:79440093-79440137	NM_001003949:6961	ORF61	INSIDE	1.032	2.253	781.01	1759.84	2.326	697.31	1622.13
A_68_P27993896	chr11:87171950-87171994	NM_177167:524	Ppm1e	INSIDE	1.032	0.546	1676.43	915.18	0.563	1398.89	787.82
A_68_P31938928	chr19:7343225-7343269	NM_054048:-1007	Rcor2	PROMOTER	1.032	1.538	1092.18	1679.46	1.588	1006.77	1598.35
A_68_P28755238	chr12:114425814-114425858	NM_153776:1723	Tmem121	INSIDE	1.032	0.606	1071.35	648.71	0.625	848.34	529.96
A_68_P31092443	chr17:23713479-23713523	NM_011747:22954	Zfp13	INSIDE	1.032	1.768	1244.52	2200.40	1.825	980.74	1790.06
A_68_P25005236	chr7:25292275-25292319	NM_146183:191	Zfp428	INSIDE	1.032	0.421	1788.70	752.68	0.434	1410.15	612.15
A_68_P28175550	chr11:118914821-118914865			Unknown	1.032	0.416	2274.58	947.24	0.430	1714.19	736.82
A_68_P31929125	chr19:5503714-5503758	NM_023781:51	1700020D05Rik	INSIDE	1.031	1.782	751.37	1338.60	1.838	584.78	1074.55
A_68_P25656693	chr8:11636046-11636090	NM_133971:-314	Ankrd10	PROMOTER	1.031	1.475	4424.38	6526.53	1.520	3366.26	5117.39
A_68_P25614032	chr8:3451969-3452013	NM_133962:58983	Arhgef18	INSIDE	1.031	2.770	694.50	1923.90	2.857	611.76	1747.75
A_68_P30026214	chr15:13103007-13103051	NM_007666:366	Cdh6	INSIDE	1.031	3.209	3263.97	10475.47	3.308	2614.19	8647.59
A_68_P29578607	chr14:47452213-47452258	NM_026832:317	Cgrrf1	INSIDE	1.031	2.074	2204.15	4571.36	2.139	1837.85	3930.78
A_68_P23327636	chr4:134828309-134828353	NM_013885:345	Clic4	INSIDE	1.031	0.466	1285.36	599.31	0.481	1328.66	638.97
A_68_P29487107	chr14:28241923-28241967	NM_001114879:-88	D14Abb1e	PROMOTER	1.031	1.647	607.28	1000.34	1.699	551.34	936.48
A_68_P30414446	chr15:87454576-87454620	NM_134096:-1061	Fam19a5	PROMOTER	1.031	1.865	1069.29	1994.25	1.923	974.99	1874.71
A_68_P23438375	chr4:154771703-154771749	NM_008072:452	Gabrd	INSIDE	1.031	1.985	466.35	925.85	2.047	386.00	790.26
A_68_P28041930	chr11:95868489-95868534	NM_009951:-1253	Igf2bp1	PROMOTER	1.031	2.012	490.71	987.56	2.074	458.50	950.99
A_68_P28605006	chr12:86940162-86940206	NM_030887:-181	Jdp2	PROMOTER	1.031	1.751	1925.30	3371.83	1.805	1656.70	2990.08
A_68_P31779041	chr18:65243342-65243386	NM_031881:60184	Nedd4l	INSIDE	1.031	2.770	1161.82	3217.72	2.856	880.80	2515.17

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26551405	chr9:58884860-58884904	NM_001042752:-634	Neo1	PROMOTER	1.031	1.443	882.00	1273.04	1.489	889.29	1323.91
A_68_P25088122	chr7:51807387-51807431	NM_009473:1885	Nr1h2	INSIDE	1.031	1.923	1669.20	3209.82	1.982	1448.21	2870.47
A_68_P31626610	chr18:37159323-37159367	NM_009961:-5629	Pcdha10	PROMOTER	1.031	1.794	857.81	1539.11	1.849	649.94	1202.03
A_68_P27230709	chr10:70062556-70062600	NM_178621:-539	Phyhipl	PROMOTER	1.031	2.478	392.58	972.95	2.555	363.29	928.34
A_68_P28085165	chr11:103273873-103273917	NM_183034:84	Plekhm1	INSIDE	1.031	0.540	1694.59	914.47	0.556	1399.44	778.57
A_68_P21870537	chr2:173411492-173411536	NR_027957:73526	Ppp4r1l-ps	INSIDE	1.031	1.561	4188.44	6538.08	1.609	3094.03	4979.29
A_68_P25457393	chr7:125387260-125387304	NM_001031814:-131	Smg1	DIVERGENT_PROMOTER	1.031	1.808	2888.02	5220.40	1.864	1957.15	3648.09
A_68_P22049387	chr3:34548813-34548857	NM_011443:-92	Sox2	PROMOTER	1.031	2.841	1505.07	4275.21	2.929	1248.18	3655.46
A_68_P25261546	chr7:86660511-86660555	ENSMUST00000150985:415		INSIDE	1.031	1.979	1308.76	2590.42	2.041	1185.14	2418.82
A_68_P24686651	chr6:99472059-99472103	ENSMUST00000155466:144711		INSIDE	1.031	1.535	1974.88	3031.03	1.582	1741.99	2755.71
A_68_P30413823	chr15:87375395-87375439	ENSMUST00000169110:513		INSIDE	1.031	2.093	961.66	2012.79	2.157	899.73	1940.63
A_68_P32290254	chrX:20425761-20425805	NM_001159645:114	Araf	INSIDE	1.030	2.332	2458.89	5733.16	2.401	1085.01	2604.74
A_68_P26132519	chr8:107778394-107778438	NM_178879:635	B3gnt9-ps	INSIDE	1.030	1.638	1660.69	2720.64	1.688	1382.40	2333.64
A_68_P28731502	chr12:110271962-110272006	NM_001163175:34443	Begain	INSIDE	1.030	2.963	1096.64	3249.30	3.052	976.94	2981.76
A_68_P20969749	chr2:4639031-4639075	NM_001190400:176	Bend7	INSIDE	1.030	2.808	866.13	2432.12	2.894	794.12	2297.88
A_68_P24397197	chr6:42214753-42214798	NM_007610:-262	Casp2	PROMOTER	1.030	2.111	410.37	866.29	2.173	344.71	749.19
A_68_P30382334	chr15:82074972-82075016	NM_001080158:-228	Cenpm	PROMOTER	1.030	1.446	876.38	1267.41	1.490	759.77	1131.79
A_68_P27212449	chr10:67001247-67001291	NM_010118:652	Egr2	INSIDE	1.030	1.820	2986.82	5436.32	1.875	2064.55	3870.68
A_68_P20091641	chr1:24106778-24106822	NM_026604:380	Fam135a	INSIDE	1.030	2.049	898.59	1841.41	2.111	786.19	1659.41
A_68_P27813684	chr11:54911411-54911457	NM_010299:-52	Gm2a	PROMOTER	1.030	1.568	1881.73	2950.07	1.615	1496.02	2416.33
A_68_P27572312	chr11:7113377-7113421	NM_008343:528	Igfbp3	INSIDE	1.030	1.451	1149.90	1668.58	1.494	1051.19	1570.37
A_68_P30366726	chr15:79315953-79315997	NM_008427:19697	Kcnj4	INSIDE	1.030	3.981	698.63	2781.50	4.102	558.33	2290.29
A_68_P31491264	chr18:10726495-10726539	NM_144860:894	Mib1	INSIDE	1.030	1.556	1000.29	1556.00	1.602	881.42	1412.41
A_68_P24627746	chr6:89306761-89306805	NM_008881:5825	Plxna1	INSIDE	1.030	3.123	1312.80	4100.27	3.218	1051.69	3384.75
A_68_P28599774	chr12:86039811-86039855	NM_001033334:-75	Tmem90a	PROMOTER	1.030	2.358	2319.90	5470.56	2.430	1980.16	4810.80
A_68_P26721504	chr9:91259471-91259515	NM_009573:1145	Zic1	INSIDE	1.030	1.441	996.30	1435.20	1.484	894.71	1327.57
A_68_P30501997	chr15:102917300-102917348	AF216290:299758		INSIDE	1.030	1.945	657.00	1277.56	2.004	611.37	1224.95
A_68_P28153581	chr11:115309405-115309449	NM_001033775:7568	4933422H20Rik	INSIDE	1.029	5.051	1178.85	5954.61	5.198	1109.58	5767.92
A_68_P26756438	chr9:97933240-97933284	NM_022319:324	Clstn2	INSIDE	1.029	2.744	1649.89	4526.86	2.822	1299.56	3667.51
A_68_P29644189	chr14:60997251-60997301	NM_001164705:154	Fam123a	INSIDE	1.029	1.827	441.69	806.97	1.881	406.27	764.14
A_68_P25671124	chr8:13907951-13907995	NM_025785:167	Fbxo25	INSIDE	1.029	1.811	1804.36	3267.53	1.864	1521.83	2835.98
A_68_P28707017	chr12:106270861-106270905	NM_028419:-16	Glrx5	DIVERGENT_PROMOTER	1.029	1.782	845.17	1505.92	1.833	596.79	1094.13
A_68_P24932466	chr6:147039958-147040002	NM_001081237:384	Klhdc5	INSIDE	1.029	1.895	1143.85	2168.01	1.950	1026.11	2000.51
A_68_P24333872	chr6:30688012-30688056	NM_008590:-28	Mest	PROMOTER	1.029	2.211	2738.46	6053.36	2.274	2072.98	4714.91
A_68_P30369637	chr15:79832097-79832141	NM_011057:13120	Pdgfb	INSIDE	1.029	2.780	1506.62	4189.03	2.860	1458.62	4171.71
A_68_P32065918	chr19:31738447-31738491	NM_011160:392	Prkg1	INSIDE	1.029	0.667	1407.21	938.85	0.687	1170.65	803.78
A_68_P20930617	chr1:191994889-191994933	NM_008937:-351	Prox1	PROMOTER	1.029	1.873	704.80	1320.18	1.927	573.73	1105.50
A_68_P31067739	chr17:15963621-15963665	NM_178615:-92	Rgmb	PROMOTER	1.029	1.495	2763.43	4131.25	1.538	2182.18	3356.38
A_68_P30955585	chr16:90220935-90220979	NM_011434:-30	Sod1	PROMOTER	1.029	1.353	4048.46	5476.61	1.392	2993.45	4168.26
A_68_P30721026	chr16:44347402-44347446	NM_144550:-89	Spice1	PROMOTER	1.029	1.435	2417.05	3467.50	1.477	1935.51	2858.10
A_68_P23416137	chr4:151406428-151406472	NM_031867:6149	Tas1r1	INSIDE	1.029	2.737	646.19	1768.58	2.817	533.31	1502.54
A_68_P28755248	chr12:114426981-114427025	NM_153776:2889	Tmem121	INSIDE	1.029	2.173	1000.10	2173.21	2.236	691.94	1546.86
A_68_P23984845	chr5:111706231-111706275	NM_024477:397431	Ttc28	INSIDE	1.029	2.617	807.63	2113.17	2.693	666.53	1794.99
A_68_P24424708	chr6:47827424-47827468	NM_146175:-107	Zfp282	PROMOTER	1.029	2.437	522.35	1272.86	2.507	523.32	1311.98
A_68_P22630578	chr3:148653042-148653086	ENSMUST00000098518:-784		PROMOTER	1.029	0.613	1707.96	1046.38	0.630	1327.81	836.92
A_68_P31292456	chr17:64213464-64213508	ENSMUST00000112829:123		INSIDE	1.029	1.843	910.38	1678.06	1.896	954.33	1809.76
A_68_P23361671	chr4:140581070-140581114	NM_172122:28484	Crocc	INSIDE	1.028	2.620	842.33	2207.10	2.694	726.82	1957.86
A_68_P31827569	chr18:73913791-73913835	NM_053255:321	Elac1	INSIDE	1.028	1.683	749.08	1260.90	1.731	697.67	1207.77
A_68_P29050429	chr13:54723129-54723173	NM_178397:6	Faf2	INSIDE	1.028	2.981	599.81	1787.77	3.065	558.94	1713.31
A_68_P25727490	chr8:26629802-26629846	NM_001079908:581	Fgfr1	INSIDE	1.028	2.094	893.57	1870.77	2.152	775.80	1669.74
A_68_P26348935	chr9:21599484-21599528	NM_145611:3484	Kank2	INSIDE	1.028	2.743	331.55	909.31	2.821	275.87	778.14

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25926103	chr8:67373325-67373369	NM_178633:370	Klhl2	INSIDE	1.028	0.540	1851.67	999.81	0.555	1586.97	881.25
A_68_P27289569	chr10:80883025-80883071	NM_008688:6870	Nfic	INSIDE	1.028	1.833	3172.79	5816.68	1.884	2464.77	4644.44
A_68_P26345851	chr9:20988585-20988629	NM_183408:18449	Pde4a	INSIDE	1.028	1.967	2097.02	4125.40	2.022	1792.47	3623.98
A_68_P24117821	chr5:136253656-136253701	NM_029659:577	Styxl1	INSIDE	1.028	2.078	537.56	1117.04	2.136	435.59	930.37
A_68_P31542078	chr18:21054518-21054562	NM_177038:39	Trappc8	INSIDE	1.028	1.560	747.21	1166.00	1.605	800.51	1284.73
A_68_P23246907	chr4:119406501-119406545	ENSMUST00000123698:77		INSIDE	1.028	2.880	473.12	1362.40	2.959	494.46	1463.14
A_68_P28078743	chr11:102157246-102157290	NM_001098836:675	Atxn7l3	INSIDE	1.027	0.526	1465.70	771.14	0.540	1137.92	614.75
A_68_P25784088	chr8:37210172-37210216	NM_172911:52313	D8Ertd82e	INSIDE	1.027	1.990	424.02	843.70	2.043	376.04	768.22
A_68_P25301154	chr7:95279055-95279099	NM_001081414:546399	Grm5	INSIDE	1.027	1.437	1700.77	2444.06	1.476	1368.65	2019.52
A_68_P29510250	chr14:31989817-31989861	NM_022656:30174	Nisch	INSIDE	1.027	2.494	2451.47	6113.60	2.561	1754.26	4493.47
A_68_P30636603	chr16:29579592-29579636	NM_001199177:195	Opa1	INSIDE	1.027	1.518	1031.24	1565.35	1.558	833.61	1299.02
A_68_P30346604	chr15:76010482-76010526	NM_201394:15636	Plec	INSIDE	1.027	4.748	1550.08	7360.37	4.877	1184.22	5774.88
A_68_P26815238	chr9:108419578-108419622	NM_001114119:183	Qrich1	INSIDE	1.027	1.938	7807.01	15130.27	1.990	6392.04	12718.33
A_68_P27277981	chr10:79100167-79100211	NM_001024539:475	Shc2	INSIDE	1.027	0.527	1308.34	689.71	0.541	1099.81	595.21
A_68_P27287001	chr10:80494270-80494314	NM_134135:2365	Slc39a3	INSIDE	1.027	2.104	748.31	1574.15	2.160	627.41	1354.92
A_68_P21303492	chr2:68308957-68309001	NM_016866:1060	Stk39	INSIDE	1.027	1.759	969.76	1705.49	1.805	902.91	1630.02
A_68_P25747456	chr8:30329801-30329845	NM_153135:286	Unc5d	INSIDE	1.027	0.640	1231.07	787.39	0.657	995.09	653.57
A_68_P27913323	chr11:72609942-72609986	NM_001045536:237	Zzef1	INSIDE	1.027	1.574	719.01	1132.08	1.616	650.65	1051.67
A_68_P24319038	chr6:28165391-28165435	ENSMUST00000143099:-142		PROMOTER	1.027	2.278	470.05	1070.56	2.339	462.41	1081.67
A_68_P32233086	chrX:5659825-5659869	NM_001033211:692	AU022751	INSIDE	1.026	2.302	794.90	1830.10	2.362	377.97	892.88
A_68_P26478981	chr9:46091218-46091262	NM_146000:146	Bud13	INSIDE	1.026	1.535	2546.08	3907.83	1.575	2083.47	3282.14
A_68_P32289636	chrX:20265804-20265848	NM_011049:208	Cdk16	INSIDE	1.026	2.864	421.62	1207.52	2.940	302.01	887.85
A_68_P30478218	chr15:98927458-98927502	NM_176835:-2434	Dnajc22	DIVERGENT_PROMOTER	1.026	1.578	1156.73	1825.76	1.620	955.25	1547.19
A_68_P27352992	chr10:92773316-92773360	NM_013508:566	Elk3	INSIDE	1.026	2.203	3554.40	7828.68	2.260	2902.43	6558.71
A_68_P23314728	chr4:132478506-132478550	NM_001163792:-62	Fam76a	PROMOTER	1.026	0.523	1280.54	670.25	0.537	1036.71	556.84
A_68_P27190083	chr10:62707080-62707124	NM_026101:558	Herc4	INSIDE	1.026	1.765	677.61	1195.73	1.810	589.06	1066.27
A_68_P25951932	chr8:72975857-72975901	NM_001122830:24964	Klhl26	INSIDE	1.026	2.361	764.72	1805.58	2.422	631.47	1529.65
A_68_P31211857	chr17:47506227-47506271	NM_183086:103	Mrps10	INSIDE	1.026	2.186	1619.25	3539.48	2.244	1374.76	3084.54
A_68_P30346581	chr15:76007523-76007567	NM_201394:18596	Plec	INSIDE	1.026	2.287	801.30	1832.20	2.347	674.74	1583.46
A_68_P25471035	chr7:128061434-128061478	NM_001164096:199	Polr3e	INSIDE	1.026	1.602	527.68	845.45	1.644	576.54	948.10
A_68_P21820739	chr2:164786459-164786503	NM_020333:-7007	Slc12a5	PROMOTER	1.026	2.368	619.14	1465.91	2.430	599.66	1457.04
A_68_P26876104	chr9:120020031-120020078	NM_144793:538	Slc25a38	INSIDE	1.026	2.314	1098.90	2542.73	2.373	861.23	2043.90
A_68_P27942761	chr11:78156911-78156955	NM_011676:-91	Unc119	PROMOTER	1.026	2.187	402.10	879.19	2.243	358.93	805.03
A_68_P31879481	chr18:83126670-83126714	NM_001177464:42669	Zfp516	INSIDE	1.026	2.442	969.19	2366.47	2.504	806.05	2018.55
A_68_P26749717	chr9:96789706-96789750	NM_153420:113	Acpl2	INSIDE	1.025	0.604	3115.70	1882.41	0.619	2338.69	1447.60
A_68_P32769556	chrX:154481512-154481556	NM_177751:-492	Cnksr2	PROMOTER	1.025	3.574	639.33	2284.70	3.664	381.93	1399.59
A_68_P20870811	chr1:181476719-181476763	NM_146105:81	Cnst	INSIDE	1.025	2.397	742.11	1778.92	2.456	670.12	1646.15
A_68_P29257121	chr13:99124384-99124428	NM_008242:207	Foxd1	INSIDE	1.025	1.950	1538.04	2999.29	1.999	1137.47	2273.92
A_68_P24451816	chr6:52590190-52590234	NM_145567:82	Hibadh	INSIDE	1.025	0.427	1427.75	609.72	0.438	1318.86	577.21
A_68_P21717108	chr2:146049089-146049133	NM_016889:1378	Insm1	INSIDE	1.025	0.527	2024.34	1066.68	0.540	1592.62	860.26
A_68_P32281774	chrX:17738988-17739032	NM_009483:-782	Kdm6a	PROMOTER	1.025	0.463	1210.69	560.30	0.474	635.66	301.50
A_68_P21080307	chr2:26517162-26517206	NM_010695:9618	Lcn4	DOWNSTREAM	1.025	2.560	1240.57	3175.65	2.623	1124.59	2949.77
A_68_P24045146	chr5:121995041-121995098	NM_010765:832	Mapkapk5	INSIDE	1.025	2.178	464.60	1012.04	2.233	450.66	1006.30
A_68_P26313303	chr9:13553960-13554004	NM_023858:358	Mtmr2	INSIDE	1.025	0.532	1192.30	634.45	0.546	986.86	538.38
A_68_P21842271	chr2:168396389-168396433	NM_001136073:19281	Nfatc2	INSIDE	1.025	3.087	2554.74	7885.31	3.164	2163.59	6845.88
A_68_P26400213	chr9:31193594-31193638	NM_172766:-160	Nfrkb	PROMOTER	1.025	0.444	1532.71	681.01	0.455	1276.68	581.26
A_68_P28185532	chr11:120459254-120459298	NM_011568:403	Thoc4	INSIDE	1.025	1.576	822.59	1296.05	1.614	755.28	1219.32
A_68_P30484946	chr15:100111437-100111481	NM_183109:191	Tmprss12	INSIDE	1.025	2.275	1109.55	2523.83	2.332	902.42	2104.41
A_68_P28013351	chr11:90548942-90548986	NM_028011:-49	Tom1l1	PROMOTER	1.025	1.749	1225.06	2142.89	1.794	1077.29	1932.23
A_68_P21476822	chr2:102240840-102240884	NM_020267:195	Trim44	INSIDE	1.025	2.329	538.38	1253.89	2.386	533.37	1272.82
A_68_P26699327	chr9:86358534-86358578	NM_027394:-33	Ube2cbp	DIVERGENT_PROMOTER	1.025	1.970	1186.50	2337.17	2.020	1008.33	2036.52

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P30568844	chr16:16303089-16303133	NM_198246:53	Yars2	INSIDE	1.025	2.030	597.55	1213.15	2.081	551.38	1147.44
A_68_P26335718	chr9:17902323-17902375			Unknown	1.025	2.554	670.70	1712.81	2.617	610.72	1598.02
A_68_P25032016	chr7:31319911-31319955	NM_178252:96	Arhgap33	INSIDE	1.024	0.503	4569.67	2299.00	0.515	3116.57	1605.22
A_68_P24758532	chr6:113232291-113232335	NM_170673:12	Cpne9	INSIDE	1.024	3.063	1063.33	3257.38	3.138	931.86	2924.51
A_68_P25952211	chr8:73017252-73017296	NM_018827:220	Crlf1	INSIDE	1.024	1.760	958.09	1686.29	1.802	809.04	1457.87
A_68_P30964443	chr16:91688927-91688971	NM_021720:25	Donson	INSIDE	1.024	1.674	976.54	1634.92	1.714	838.75	1437.66
A_68_P24295389	chr6:23198493-23198537	NM_028462:-250	Fezf1	PROMOTER	1.024	1.744	1782.75	3108.58	1.786	1553.11	2774.09
A_68_P23190570	chr4:107108505-107108549	NM_147221:1203	Glis1	INSIDE	1.024	1.676	717.73	1202.66	1.715	719.66	1234.45
A_68_P27289052	chr10:80813045-80813089	NM_001163165:105	Hmg20b	INSIDE	1.024	0.441	1373.11	606.19	0.452	1150.76	520.41
A_68_P27288649	chr10:80755618-80755662	NM_001146687:-76	Pip5k1c	DIVERGENT_PROMOTER	1.024	3.049	918.73	2801.60	3.123	855.35	2671.26
A_68_P21784244	chr2:158493590-158493634	NM_001159662:742	Ppp1r16b	INSIDE	1.024	1.652	786.31	1299.15	1.692	677.23	1146.21
A_68_P32066440	chr19:31838752-31838796	NM_001013833:749	Prkg1	INSIDE	1.024	1.417	1912.14	2709.03	1.450	1645.24	2385.95
A_68_P27950228	chr11:79474495-79474539	NM_175543:69803	Rab11fip4	INSIDE	1.024	2.273	633.82	1440.51	2.328	563.80	1312.67
A_68_P28325481	chr12:31058300-31058344	NM_172951:-82	Sntg2	PROMOTER	1.024	1.787	11660.29	20842.30	1.830	8641.24	15812.10
A_68_P24444652	chr6:51473918-51473962	NM_001127349:39	Snx10	INSIDE	1.024	1.786	1187.00	2120.55	1.829	997.31	1823.87
A_68_P20946919	chr1:194861703-194861747	NM_181546:168	Syt14	INSIDE	1.024	1.506	2431.84	3661.40	1.541	2025.70	3121.60
A_68_P32147459	chr19:47142283-47142327	NM_177342:67	Taf5	INSIDE	1.024	2.082	628.45	1308.67	2.133	529.81	1130.04
A_68_P32114047	chr19:41338628-41338672	NM_133352:-156	Tm9sf3	PROMOTER	1.024	1.671	514.03	858.99	1.712	485.70	831.46
A_68_P23409802	chr4:150431872-150431916	NM_009498:168	Vamp3	INSIDE	1.024	3.257	538.28	1753.27	3.334	532.25	1774.42
A_68_P30446389	chr15:93167185-93167229	NM_024189:160	Yaf2	INSIDE	1.024	2.908	664.21	1931.51	2.979	706.23	2103.81
A_68_P23591264	chr5:34162817-34162861	ENSMUST00000075812:-535		PROMOTER	1.024	2.351	611.03	1436.53	2.407	634.60	1527.66
A_68_P24197924	chr6:3151637-3151681	ENSMUST00000158475:442		DOWNSTREAM	1.024	3.131	1179.43	3692.58	3.206	902.62	2893.64
A_68_P32362519	chrX:45387638-45387682	NM_013912:369	Apln	INSIDE	1.023	2.283	2640.04	6026.68	2.336	1375.86	3214.14
A_68_P23295632	chr4:128901619-128901663	NM_001033189:24047	C77080	INSIDE	1.023	1.562	1033.23	1613.46	1.598	826.12	1320.32
A_68_P27172912	chr10:59648749-59648793	NM_016803:33238	Chst3	INSIDE	1.023	2.004	2010.02	4028.20	2.050	1746.71	3580.00
A_68_P27995153	chr11:87431204-87431248	NM_001045527:561	Hsf5	INSIDE	1.023	2.076	1308.97	2716.89	2.124	921.70	1957.46
A_68_P31156853	chr17:35115138-35115182	NM_013558:5513	Hspa1l	INSIDE	1.023	2.745	593.03	1628.04	2.809	522.76	1468.56
A_68_P30350209	chr15:76552567-76552611	NM_198119:15	Lrrc24	INSIDE	1.023	0.520	1141.47	593.08	0.532	895.77	476.12
A_68_P30339720	chr15:74630372-74630416	NM_029627:4	Ly6k	INSIDE	1.023	3.400	904.03	3073.26	3.479	750.71	2612.02
A_68_P24135186	chr5:139848163-139848207	NR_029768:-2485	Mir339	DIVERGENT_PROMOTER	1.023	0.628	1396.32	876.46	0.642	1192.55	765.78
A_68_P29263992	chr13:100286417-100286461	NM_008634:119	Mtap1b	INSIDE	1.023	2.087	1145.37	2390.55	2.135	985.53	2103.78
A_68_P32218818	chr19:59419895-59419939	NM_001033222:354	Pdzd8	INSIDE	1.023	2.667	901.00	2402.85	2.729	836.30	2281.91
A_68_P21765151	chr2:155183097-155183141	NM_001004721:42	Pigu	INSIDE	1.023	2.182	1897.17	4139.78	2.232	1561.28	3484.34
A_68_P28314232	chr12:29320359-29320403	NM_011300:438	Rps7	INSIDE	1.023	1.618	766.41	1239.93	1.656	698.92	1157.19
A_68_P26346144	chr9:21048991-21049035	NM_053190:3875	S1pr5	INSIDE	1.023	0.377	2938.41	1107.13	0.385	2326.68	896.81
A_68_P22523678	chr3:129763488-129763532	NM_207209:315	Sec24b	INSIDE	1.023	3.911	228.74	894.54	4.000	298.89	1195.53
A_68_P23364646	chr4:141093876-141093920	NM_019763:614	Spen	INSIDE	1.023	2.693	357.16	961.65	2.754	375.58	1034.38
A_68_P30230210	chr15:54903527-54903571	NM_001081288:159	Taf2	INSIDE	1.023	1.421	1168.33	1660.71	1.454	907.72	1320.09
A_68_P24874567	chr6:136765429-136765473	NM_021714:11287	Wbp11	INSIDE	1.023	1.744	1602.22	2794.05	1.785	1361.23	2429.36
A_68_P20305039	chr1:66909588-66909632	NM_007381:231	Acadl	INSIDE	1.022	2.083	775.59	1615.21	2.128	729.79	1553.21
A_68_P30338800	chr15:74502963-74503007	NM_018790:16	Arc	INSIDE	1.022	0.564	2107.27	1189.10	0.577	1601.99	924.05
A_68_P24011285	chr5:116182026-116182070	NM_001080808:-480	Ccdc64	PROMOTER	1.022	1.838	744.45	1368.58	1.878	694.82	1305.21
A_68_P20829087	chr1:173609897-173609941	NM_007649:-2267	Cd48	PROMOTER	1.022	2.030	951.66	1931.77	2.076	754.70	1566.40
A_68_P28672821	chr12:100139294-100139338	NM_001081191:378	Eml5	INSIDE	1.022	1.885	1262.34	2379.11	1.926	1135.88	2187.85
A_68_P27534775	chr10:126676335-126676379	NM_001039000:24063	Kif5a	INSIDE	1.022	1.997	980.39	1957.75	2.041	769.83	1570.90
A_68_P32148598	chr19:47327938-47327982	NM_001163480:24628	Neurl1a	INSIDE	1.022	3.550	330.76	1174.16	3.626	273.57	992.00
A_68_P22878716	chr4:44725913-44725957	NM_008782:-2622	Pax5	PROMOTER	1.022	0.413	1857.96	766.86	0.422	1444.18	609.07
A_68_P26815232	chr9:108418960-108419004	NM_001114119:-435	Qrich1	PROMOTER	1.022	2.148	2467.90	5301.53	2.195	1856.56	4074.34
A_68_P25669975	chr8:13677504-13677548	NM_009025:61	Rasa3	INSIDE	1.022	0.549	1636.73	898.26	0.561	1411.62	791.60
A_68_P25989168	chr8:81033011-81033055	NM_029736:-201	Slc10a7	DIVERGENT_PROMOTER	1.022	0.617	1545.93	954.29	0.631	1180.52	744.77
A_68_P27682721	chr11:31270001-31270045	NM_011491:39	Stc2	INSIDE	1.022	1.666	1754.05	2922.98	1.704	1305.15	2223.57

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26710363	chr9:88377377-88377421	NM_019796:-163	Syncrip	PROMOTER	1.022	1.617	1014.18	1640.33	1.653	849.59	1404.27
A_68_P31023472	chr17:7165401-7165445	NM_147155:83	Tagap1	INSIDE	1.022	0.631	1034.27	652.39	0.645	938.77	605.23
A_68_P22894263	chr4:47366193-47366237	NM_009370:38	Tgfbr1	INSIDE	1.022	0.436	1812.93	790.28	0.445	1688.42	752.15
A_68_P20620973	chr1:134257439-134257483	NM_178874:30398	Tmcc2	INSIDE	1.022	5.315	2714.33	14425.84	5.429	1737.92	9435.27
A_68_P25615130	chr8:3679220-3679265	NM_025701:2766	Trappc5	INSIDE	1.022	4.629	1951.75	9033.75	4.730	1661.71	7859.64
A_68_P27850825	chr11:61668376-61668420	NM_013881:196	Ulk2	INSIDE	1.022	2.009	466.65	937.38	2.052	487.87	1001.29
A_68_P25505249	chr7:134486849-134486893	NM_146202:1958	Zfp768	INSIDE	1.022	1.800	1009.04	1816.27	1.839	713.76	1312.88
A_68_P31219172	chr17:48925673-48925717			Unknown	1.022	3.770	1278.87	4820.77	3.853	939.74	3621.19
A_68_P25354924	chr7:105457494-105457538	NM_025408:521	Acer3	INSIDE	1.021	1.431	1908.32	2730.38	1.461	1415.53	2068.19
A_68_P31152214	chr17:34256524-34256568	NR_037970:299	Brd2	INSIDE	1.021	1.500	1232.66	1849.54	1.532	994.53	1523.14
A_68_P31676223	chr18:46471587-46471631	NM_001160399:-26	Ccdc112	PROMOTER	1.021	2.183	2824.92	6165.53	2.229	2178.65	4855.79
A_68_P25578900	chr7:146768561-146768605	NR_027857:114	Nkx6-2	INSIDE	1.021	2.125	841.90	1789.21	2.169	681.78	1478.80
A_68_P29237596	chr13:95653350-95653394	NM_011021:7791	Otp	INSIDE	1.021	2.595	1338.12	3471.96	2.649	1169.82	3098.28
A_68_P30422817	chr15:88890519-88890563	NM_001002005:385	Panx2	INSIDE	1.021	2.000	586.15	1172.43	2.041	638.26	1302.89
A_68_P29518733	chr14:33411046-33411090	NM_001001796:-2044	Prrxl1	PROMOTER	1.021	1.564	1602.67	2505.86	1.597	1446.97	2310.76
A_68_P24618288	chr6:87762030-87762074	NM_001039394:-279	Rab43	PROMOTER	1.021	2.506	16931.45	42428.15	2.559	10823.86	27701.08
A_68_P25370036	chr7:108011436-108011480	NM_177073:469	Relt	INSIDE	1.021	0.423	1289.14	545.59	0.432	1047.76	452.94
A_68_P24155044	chr5:143874288-143874332	NM_080561:389	Rnf216	INSIDE	1.021	2.000	707.15	1414.39	2.043	652.90	1333.75
A_68_P27340133	chr10:90586197-90586241	NM_133668:490	Slc25a3	INSIDE	1.021	1.459	820.30	1196.64	1.489	757.39	1127.91
A_68_P23570613	chr5:30400253-30400312	NM_021288:-117	Tyms	PROMOTER	1.021	4.723	264.46	1249.07	4.821	294.08	1417.62
A_68_P28178429	chr11:119385860-119385904			Unknown	1.021	2.305	928.70	2140.93	2.353	928.24	2184.23
A_68_P29509887	chr14:31944357-31944401	NR_024069:-2262	2010107H07Rik	DIVERGENT_PROMOTER	1.020	0.477	1480.76	706.82	0.487	1415.77	689.47
A_68_P20977349	chr2:6021517-6021561	NM_001159657:29693	5430407P10Rik	INSIDE	1.020	2.215	739.59	1638.06	2.258	685.79	1548.66
A_68_P26362426	chr9:24307746-24307790	NM_172920:-184	Dpy19l1	PROMOTER	1.020	3.375	194.09	655.01	3.441	187.45	645.09
A_68_P28728198	chr12:109701817-109701861	NM_001043335:40813	Eml1	INSIDE	1.020	2.002	616.84	1234.94	2.042	469.66	958.84
A_68_P23235082	chr4:117222946-117222990	NM_080469:-130	Eri3	PROMOTER	1.020	2.103	1053.77	2216.36	2.145	981.45	2104.96
A_68_P27503063	chr10:120802153-120802197	NM_029364:29	Gns	INSIDE	1.020	0.450	2215.37	997.29	0.459	1951.91	896.60
A_68_P31730289	chr18:56591860-56591904	NM_026240:97	Gramd3	INSIDE	1.020	2.011	1369.11	2753.57	2.051	1277.02	2619.72
A_68_P27568544	chr11:6344567-6344611	NM_029938:-142	H2afv	PROMOTER	1.020	0.607	1227.61	745.36	0.619	945.58	585.77
A_68_P28103517	chr11:106649497-106649541	NR_037224:-5445	Mir3064	PROMOTER	1.020	0.545	1238.11	674.83	0.556	953.12	529.81
A_68_P30456842	chr15:95059493-95059537	NM_016743:299623	Nell2	INSIDE	1.020	2.582	638.71	1649.12	2.633	579.90	1526.61
A_68_P26345840	chr9:20986196-20986240	NM_183408:16061	Pde4a	INSIDE	1.020	0.475	1150.47	546.32	0.484	948.82	459.62
A_68_P26138375	chr8:108734930-108734974	NM_145404:-1	Prmt7	DIVERGENT_PROMOTER	1.020	1.695	2048.09	3470.53	1.728	1800.77	3112.18
A_68_P31121838	chr17:28466106-28466150	NM_011287:713	Rpl10a	INSIDE	1.020	2.448	890.67	2180.77	2.496	829.73	2071.29
A_68_P31052340	chr17:12700162-12700206	NM_011395:386	Slc22a3	INSIDE	1.020	0.594	1901.85	1129.57	0.606	1524.43	923.15
A_68_P22477034	chr3:121235139-121235183	NM_145394:102	Slc44a3	INSIDE	1.020	1.802	889.15	1602.51	1.839	788.96	1451.00
A_68_P22314617	chr3:88383670-88383714	NM_025448:100	Ssr2	INSIDE	1.020	1.438	1292.82	1859.69	1.467	1187.67	1742.19
A_68_P31846341	chr18:77424704-77424748	NM_013666:141	St8sia5	INSIDE	1.020	1.891	1384.89	2619.23	1.930	1245.02	2402.77
A_68_P25102013	chr7:54175369-54175413	NM_021884:-90	Tsg101	PROMOTER	1.020	1.822	757.12	1379.50	1.858	780.55	1450.46
A_68_P28344355	chr12:34642855-34642899	NM_011658:341	Twist1	INSIDE	1.020	2.068	623.88	1290.22	2.108	634.56	1337.93
A_68_P23576666	chr5:31440580-31440624	NM_021290:666	Ucn	INSIDE	1.020	1.614	535.03	863.51	1.646	540.28	889.50
A_68_P31926824	chr19:5088863-5088907	NM_026553:347	Yif1a	INSIDE	1.020	1.689	1402.00	2367.45	1.723	1228.88	2117.32
A_68_P24057005	chr5:124134134-124134178	NM_019765:144	Clip1	INSIDE	1.019	1.432	958.82	1373.43	1.460	789.24	1152.39
A_68_P25564251	chr7:144390467-144390511	NM_001113414:115640	Ebf3	INSIDE	1.019	3.218	2651.42	8531.69	3.278	1957.18	6416.54
A_68_P23270865	chr4:124562969-124563014	NM_177671:3963	Epha10	INSIDE	1.019	2.145	554.25	1188.79	2.186	504.52	1103.07
A_68_P26134296	chr8:108042857-108042901	NM_008289:233	Hsd11b2	INSIDE	1.019	2.457	648.37	1593.00	2.503	574.47	1437.86
A_68_P22397063	chr3:105255456-105255500	NM_019931:-6255	Kcnd3	PROMOTER	1.019	0.387	1741.27	674.03	0.394	1388.21	547.61
A_68_P25991119	chr8:81344708-81344752	NM_001191004:321	Lsm6	INSIDE	1.019	1.745	1208.81	2108.85	1.777	1009.64	1794.12
A_68_P27787504	chr11:50050408-50050452	NM_008521:1543	Ltc4s	INSIDE	1.019	1.655	1603.64	2653.39	1.686	1361.70	2295.41
A_68_P31934086	chr19:6341582-6341626	NM_009006:355	Map4k2	INSIDE	1.019	1.587	936.29	1486.19	1.617	812.32	1313.93
A_68_P27796190	chr11:51671242-51671287	NM_199299:-281	Phf15	PROMOTER	1.019	3.109	446.27	1387.51	3.168	359.05	1137.33

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25988753	chr8:80961280-80961324	NM_138944:-751	Pou4f2	PROMOTER	1.019	4.509	2900.66	13080.03	4.593	2072.27	9518.50
A_68_P21834481	chr2:167065786-167065830	NM_008968:229	Ptgis	INSIDE	1.019	0.384	1726.09	662.74	0.391	1416.61	554.37
A_68_P29050814	chr13:54788639-54788683	NM_001146025:509	Rnf44	INSIDE	1.019	2.736	1084.01	2965.45	2.789	783.01	2183.69
A_68_P31256955	chr17:56705842-56705886	NM_001029979:18142	Safb2	INSIDE	1.019	1.925	1834.39	3531.08	1.961	1461.14	2865.45
A_68_P27280661	chr10:79520418-79520462	NM_183426:45007	Sbno2	INSIDE	1.019	1.509	1079.23	1628.19	1.537	847.31	1302.73
A_68_P32136769	chr19:45224972-45225016	NM_021901:-210	Tlx1	PROMOTER	1.019	0.630	1171.63	738.08	0.642	1055.56	677.73
A_68_P25272788	chr7:88716073-88716117	NM_001004185:-83	Whamm	DIVERGENT_PROMOTER	1.019	3.711	761.27	2825.20	3.780	706.19	2669.66
A_68_P28104776	chr11:106889479-106889523	NM_001163473:-36	1810010H24Rik	PROMOTER	1.018	2.485	350.78	871.55	2.529	343.57	868.95
A_68_P28050940	chr11:97361543-97361587	NM_021493:50091	Arhgap23	INSIDE	1.018	2.543	1212.72	3084.07	2.588	1056.17	2733.61
A_68_P31616439	chr18:35278605-35278649	NM_009818:61	Ctnna1	INSIDE	1.018	0.554	1713.40	948.65	0.563	1351.12	761.35
A_68_P25083585	chr7:50932262-50932306	NM_145582:4884	Ctu1	INSIDE	1.018	2.581	787.80	2033.08	2.627	739.20	1941.94
A_68_P31933640	chr19:6277337-6277381	NM_010119:463	Ehd1	INSIDE	1.018	0.512	1828.20	935.72	0.521	1528.88	796.26
A_68_P22737304	chr4:12834151-12834195	NM_001171801:189	Gm11818	INSIDE	1.018	2.482	519.50	1289.49	2.527	498.95	1260.72
A_68_P32571133	chrX:100129283-100129327	NR_026596:258	Gm5126	INSIDE	1.018	1.708	811.88	1386.57	1.739	476.40	828.52
A_68_P23355140	chr4:139521655-139521700	NM_173427:2264	Klhdc7a	INSIDE	1.018	3.061	1402.90	4294.47	3.115	1090.17	3396.27
A_68_P25087546	chr7:51717127-51717171	NM_198250:19292	Lrrc4b	INSIDE	1.018	1.630	1109.24	1808.35	1.659	978.40	1623.26
A_68_P21842275	chr2:168396762-168396807	NM_001136073:18907	Nfatc2	INSIDE	1.018	2.770	762.29	2111.55	2.819	649.90	1832.23
A_68_P22309971	chr3:87587854-87587898	NM_001033124:11208	Ntrk1	INSIDE	1.018	2.081	936.35	1948.86	2.118	789.74	1672.89
A_68_P24636899	chr6:91066454-91066498	NM_018815:344	Nup210	INSIDE	1.018	1.547	926.76	1433.54	1.575	746.26	1175.41
A_68_P31229018	chr17:50648295-50648339	NM_013880:-555	Plcl2	PROMOTER	1.018	2.163	537.99	1163.90	2.203	566.54	1248.21
A_68_P24117608	chr5:136209662-136209706	NM_008898:44601	Por	INSIDE	1.018	3.740	3233.32	12093.06	3.808	2181.72	8308.72
A_68_P23298637	chr4:129497229-129497273	NM_008974:-472	Ptp4a2	PROMOTER	1.018	2.011	1478.98	2974.61	2.048	1235.54	2530.55
A_68_P27926514	chr11:75323805-75323849	NM_001029938:231	Rilp	INSIDE	1.018	3.142	647.09	2032.91	3.197	585.68	1872.45
A_68_P23339118	chr4:136852527-136852571	NM_009523:18999	Wnt4	INSIDE	1.018	1.855	472.09	875.67	1.888	419.03	790.93
A_68_P29235876	chr13:95365929-95365973			Unknown	1.018	2.202	920.47	2026.61	2.242	830.88	1862.54
A_68_P30711910	chr16:42875216-42875260	ENSMUST00000142270:462		INSIDE	1.018	1.734	1375.71	2386.15	1.765	1192.57	2105.32
A_68_P25352335	chr7:104937048-104937092	ENSMUST00000172423:20		INSIDE	1.018	0.657	1925.05	1264.30	0.669	1705.34	1140.52
A_68_P25608516	chr7:151864802-151864846	NM_178642:59559	Ano1	INSIDE	1.017	2.007	322.54	647.47	2.042	299.49	611.62
A_68_P25429184	chr7:120351143-120351187	NM_007489:186	Arntl	INSIDE	1.017	1.853	377.53	699.52	1.884	392.14	738.73
A_68_P24172963	chr5:148116041-148116085	NM_007673:2763	Cdx2	INSIDE	1.017	1.417	1109.13	1571.40	1.442	930.91	1341.94
A_68_P24056166	chr5:123974219-123974263	NM_023232:-67	Diablo	PROMOTER	1.017	0.339	1819.62	616.63	0.345	1453.42	501.13
A_68_P24138646	chr5:140447394-140447438	NM_175522:63520	Elfn1	INSIDE	1.017	2.221	2382.98	5291.46	2.259	1880.37	4247.98
A_68_P31161106	chr17:35960328-35960372	NM_008027:49	Flot1	INSIDE	1.017	1.451	1122.42	1629.13	1.476	989.82	1460.69
A_68_P29228414	chr13:94074555-94074599	NM_152134:-3412	Homer1	PROMOTER	1.017	1.551	1198.09	1858.08	1.578	1033.15	1629.84
A_68_P28290825	chr12:25336262-25336306	NM_178357:49	Klf11	INSIDE	1.017	2.733	830.83	2270.37	2.778	740.79	2057.97
A_68_P21818285	chr2:164333404-164333448	NM_133779:10402	Pigt	INSIDE	1.017	2.149	956.00	2054.27	2.185	851.94	1861.28
A_68_P24120143	chr5:136720679-136720723	NM_018825:73	Sh2b2	INSIDE	1.017	2.003	1292.96	2589.23	2.036	1186.73	2416.36
A_68_P31850941	chr18:78243939-78243983	NM_001101038:10047	Siglec15	INSIDE	1.017	1.549	657.87	1018.73	1.575	623.08	981.63
A_68_P23364273	chr4:141028839-141028883	NM_019763:65652	Spen	INSIDE	1.017	2.210	2740.52	6057.52	2.247	1916.89	4307.02
A_68_P25195708	chr7:74904333-74904377	NM_183312:274	Synm	INSIDE	1.017	1.519	1274.06	1935.50	1.546	1125.34	1739.29
A_68_P20141348	chr1:34987329-34987373			Unknown	1.017	1.967	1236.31	2431.97	2.001	1052.53	2106.05
A_68_P26128335	chr8:106919047-106919091	NM_153582:528	Cmtm4	INSIDE	1.016	1.850	894.07	1654.47	1.880	844.66	1587.76
A_68_P28525538	chr12:72419084-72419128	NM_001190466:8236	Dact1	INSIDE	1.016	1.753	794.77	1393.56	1.782	639.90	1140.24
A_68_P31286859	chr17:63232405-63232449	NM_010109:-1760	Efna5	PROMOTER	1.016	1.874	331.66	621.60	1.903	330.00	628.16
A_68_P25369179	chr7:107855638-107855683	NM_178764:445	Fam168a	INSIDE	1.016	8.960	2670.60	23928.05	9.103	1674.27	15240.13
A_68_P25048201	chr7:35989266-35989310	NM_001024707:11076	Lrp3	INSIDE	1.016	2.233	829.96	1853.41	2.268	689.75	1564.32
A_68_P26575781	chr9:63225502-63225546	NM_011840:135	Map2k5	INSIDE	1.016	1.555	984.16	1530.81	1.580	901.52	1424.54
A_68_P25354128	chr7:105293642-105293686	NM_011010:293	Omp	INSIDE	1.016	2.863	1432.66	4101.71	2.909	1168.14	3397.84
A_68_P29041946	chr13:53206812-53206856	NM_013846:174644	Ror2	INSIDE	1.016	2.057	2601.12	5351.79	2.091	1847.13	3862.63
A_68_P31254141	chr17:56279185-56279230	NM_013662:-5932	Sema6b	PROMOTER	1.016	3.127	259.03	810.09	3.178	280.49	891.52
A_68_P31850954	chr18:78245651-78245695	NM_001101038:8335	Siglec15	INSIDE	1.016	1.909	1558.53	2975.74	1.940	1387.78	2692.01

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P23339119	chr4:136852669-136852713	NM_009523:19141	Wnt4	INSIDE	1.016	3.092	498.27	1540.41	3.140	516.62	1622.32
A_68_P21839557	chr2:167942759-167942803			Unknown	1.016	3.053	581.51	1775.15	3.101	529.29	1641.09
A_68_P21037845	chr2:17953722-17953766	NR_028376:5624	A930004D18Rik	INSIDE	1.015	2.053	566.94	1164.05	2.083	451.20	939.92
A_68_P21441217	chr2:94278208-94278252	NM_007466:74	Api5	INSIDE	1.015	0.568	1743.55	989.72	0.576	1415.17	815.23
A_68_P27383821	chr10:98377167-98377211	NM_026482:-597	Atp2b1	PROMOTER	1.015	1.770	607.96	1076.19	1.797	605.89	1088.74
A_68_P26807071	chr9:107096201-107096245	NM_153413:38018	Dock3	INSIDE	1.015	1.745	792.40	1382.94	1.771	736.95	1305.00
A_68_P20146386	chr1:36160613-36160657	NM_015818:35390	Hs6st1	INSIDE	1.015	2.158	869.63	1876.25	2.190	750.58	1644.13
A_68_P28748144	chr12:113384449-113384493	NM_001097621:52	Kif26a	INSIDE	1.015	2.190	831.65	1821.24	2.222	717.14	1593.27
A_68_P23753092	chr5:65213185-65213229	NM_008453:18445	Klf3	INSIDE	1.015	2.258	573.82	1295.52	2.292	440.10	1008.89
A_68_P26017699	chr8:86550056-86550100	NM_028877:4706	Palm3	INSIDE	1.015	1.803	1404.78	2532.57	1.830	1228.64	2248.92
A_68_P25094417	chr7:52934632-52934676	NM_019934:274	Sec1	INSIDE	1.015	2.394	867.21	2075.92	2.429	757.04	1839.20
A_68_P27927812	chr11:75546197-75546241	NM_009536:-170	Ywhae	PROMOTER	1.015	1.773	1414.14	2507.42	1.800	1256.66	2261.99
A_68_P21067989	chr2:24617842-24617886	NM_001042528:703	Cacna1b	INSIDE	1.014	1.377	4255.00	5859.70	1.397	3168.92	4426.03
A_68_P23316406	chr4:132776655-132776700	NM_027152:-46	Cd164l2	DIVERGENT_PROMOTER	1.014	3.110	397.54	1236.39	3.154	313.71	989.46
A_68_P26844287	chr9:114277292-114277336	NM_019922:22516	Crtap	DOWNSTREAM	1.014	1.733	1719.52	2979.48	1.757	1524.39	2678.85
A_68_P32982442	chr5:135115011-135115055	NM_033561:166	Eif4h	INSIDE	1.014	0.546	1207.47	659.26	0.554	916.99	507.75
A_68_P28940413	chr13:34838757-34838801	NM_138746:7268	Fam50b	INSIDE	1.014	2.543	368.97	938.27	2.579	336.41	867.71
A_68_P25666781	chr8:13200390-13200434	NM_025768:212	Grtp1	INSIDE	1.014	1.465	1125.60	1649.24	1.485	1047.05	1555.01
A_68_P29616396	chr14:55732459-55732503	NM_177049:3292	Jph4	INSIDE	1.014	2.253	1169.56	2635.17	2.285	1041.20	2379.30
A_68_P27947419	chr11:78959894-78959938	NM_013571:-60	Ksr1	PROMOTER	1.014	1.502	3094.52	4648.20	1.523	2556.05	3892.26
A_68_P25368691	chr7:107757091-107757135	NR_003559:-602	Mrpl48	PROMOTER	1.014	0.603	1410.81	851.24	0.612	1116.13	683.04
A_68_P22342235	chr3:94910203-94910247	NM_008847:556	Pip5k1a	INSIDE	1.014	0.569	1403.59	798.30	0.576	1035.68	597.02
A_68_P24054126	chr5:123588945-123588989	NM_175092:-6328	Rhof	PROMOTER	1.014	1.924	660.05	1269.78	1.952	657.46	1283.12
A_68_P26476666	chr9:45714950-45714994	NM_178709:-12	Rnf214	PROMOTER	1.014	1.892	728.81	1378.68	1.918	644.17	1235.64
A_68_P31093842	chr17:23956720-23956764	NM_175229:16589	Srrm2	INSIDE	1.014	3.328	834.28	2776.45	3.373	591.45	1994.92
A_68_P30363681	chr15:78823328-78823373	NM_001024716:9865	Triobp	INSIDE	1.014	2.259	1654.09	3736.50	2.290	1179.71	2701.38
A_68_P21365117	chr2:78709405-78709449	NM_009454:223	Ube2e3	INSIDE	1.014	2.795	780.54	2181.78	2.834	746.57	2115.65
A_68_P26217007	chr8:122480845-122480889	NM_009462:46115	Usp10	INSIDE	1.014	3.210	1206.90	3874.09	3.254	1113.49	3623.31
A_68_P30633251	chr16:28929310-28929354	NM_177718:452	1600021P15Rik	INSIDE	1.013	1.395	1324.84	1847.92	1.413	1015.53	1434.97
A_68_P28183252	chr11:120098764-120098808	NM_198423:4526	Bahcc1	INSIDE	1.013	1.649	671.53	1107.56	1.672	654.90	1094.68
A_68_P28724522	chr12:109154828-109154872	NM_001079883:86774	Bcl11b	INSIDE	1.013	1.999	461.41	922.13	2.024	421.72	853.50
A_68_P24318693	chr6:28084879-28084923	NM_008174:-531	Grm8	PROMOTER	1.013	0.574	1194.61	685.64	0.581	921.40	535.66
A_68_P23435246	chr4:154334733-154334777	NM_010419:-277	Hes5	PROMOTER	1.013	2.014	989.10	1992.23	2.041	922.83	1883.36
A_68_P22344946	chr3:95462398-95462442	NM_008562:-222	Mcl1	PROMOTER	1.013	1.635	484.53	792.15	1.656	511.46	846.92
A_68_P31621832	chr18:36227944-36227988	NM_001167891:128848	Nrg2	INSIDE	1.013	2.233	1152.09	2572.24	2.261	1044.89	2362.36
A_68_P21782730	chr2:158236015-158236059	NM_177658:448	Ralgapb	INSIDE	1.013	1.807	537.36	970.97	1.831	504.21	923.07
A_68_P23896972	chr5:93371791-93371835	NM_001077596:44789	Shroom3	INSIDE	1.013	3.740	570.92	2135.49	3.790	622.83	2360.71
A_68_P21973812	chr3:19062717-19062761	NM_028840:327	Armc1	INSIDE	1.012	1.519	1032.29	1568.44	1.538	849.62	1306.98
A_68_P32233090	chrX:5660210-5660254	NM_001033211:306	AU022751	INSIDE	1.012	2.497	646.75	1615.14	2.527	366.40	925.79
A_68_P26349690	chr9:21752178-21752222	NM_144935:9483	BC018242	INSIDE	1.012	2.016	1399.69	2821.67	2.040	1070.25	2182.84
A_68_P20499743	chr1:106665396-106665440	NM_011800:23	Cdh20	INSIDE	1.012	0.615	1911.54	1175.65	0.622	1635.89	1017.94
A_68_P23976362	chr5:109987925-109987969	NM_001164735:66	Crlf2	INSIDE	1.012	0.465	1240.84	576.63	0.470	1004.97	472.64
A_68_P31614615	chr18:34937144-34937188	NM_001081256:505	Kdm3b	INSIDE	1.012	1.790	473.38	847.35	1.812	473.69	858.42
A_68_P25950174	chr8:72682451-72682495	NM_001045484:5796	Mef2b	INSIDE	1.012	1.931	2110.83	4075.30	1.954	1855.97	3626.75
A_68_P23278933	chr4:125911136-125911183	NM_001145970:22404	Mtap7d1	INSIDE	1.012	2.787	630.04	1755.81	2.821	546.32	1541.15
A_68_P24950724	chr7:4781725-4781769	NM_172737:14552	Shisa7	INSIDE	1.012	2.196	3129.99	6872.76	2.222	2439.66	5421.08
A_68_P30486832	chr15:100467219-100467263	NM_174992:46	Smagp	INSIDE	1.012	3.127	692.71	2166.03	3.164	701.87	2220.55
A_68_P31923332	chr19:4477049-4477093	NM_134164:73	Syt12	INSIDE	1.012	1.926	639.69	1231.78	1.948	604.18	1177.16
A_68_P25009655	chr7:26100173-26100217	NM_183311:9068	Tmem145	INSIDE	1.012	2.226	6421.23	14294.07	2.253	4633.53	10440.78
A_68_P21836349	chr2:167423229-167423273	NM_023230:34255	Ube2v1	DOWNSTREAM	1.012	1.669	2968.08	4953.87	1.689	2335.93	3945.19
A_68_P26342783	A_68_P26342783			Unknown	1.012	1.466	1444.83	2118.13	1.484	1277.74	1895.80

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26580034	chr9:63932732-63932776	AK011166:4187		INSIDE	1.012	1.539	1307.95	2012.57	1.557	1070.35	1666.64
A_68_P24067081	chr5:125956133-125956177	NM_030210:-88	Aacs	PROMOTER	1.011	1.365	4018.89	5484.01	1.380	2988.95	4124.90
A_68_P23005030	chr4:69910440-69910484	NM_145990:160939	Cdk5rap2	INSIDE	1.011	2.938	699.38	2054.96	2.971	679.00	2017.47
A_68_P24568082	chr6:77929708-77929753	NM_001109764:-69	Ctnna2	PROMOTER	1.011	1.909	690.35	1317.99	1.930	598.55	1155.48
A_68_P21612765	chr2:127162244-127162288	NM_010090:372	Dusp2	INSIDE	1.011	1.642	535.98	880.06	1.659	490.61	814.12
A_68_P27093482	chr10:41917067-41917111	NM_019740:79460	Foxo3	INSIDE	1.011	2.142	1238.06	2652.45	2.166	934.39	2024.22
A_68_P26745534	chr9:96020049-96020093	NM_177352:223	Gk5	INSIDE	1.011	0.543	1819.24	987.26	0.548	1628.24	892.95
A_68_P23226010	chr4:115500724-115500768	NM_175308:50	Mobkl2c	INSIDE	1.011	0.535	1002.96	536.94	0.541	801.46	433.77
A_68_P20347699	chr1:74331738-74331785	NM_025580:154	Pnkd	INSIDE	1.011	1.691	758.95	1283.02	1.709	559.87	956.66
A_68_P24951460	chr7:4945585-4945629	NM_026741:2097	Zfp579	INSIDE	1.011	2.230	1910.44	4259.86	2.254	1348.44	3038.83
A_68_P26017563	chr8:86525640-86525684	NM_183097:58	1700067K01Rik	INSIDE	1.010	2.204	752.06	1657.50	2.227	753.10	1677.15
A_68_P32362518	chrX:45387551-45387595	NM_013912:457	Apln	INSIDE	1.010	2.013	1801.68	3626.97	2.033	884.07	1796.93
A_68_P23440845	chr4:155205317-155205361	NM_025338:-416	Aurkaip1	PROMOTER	1.010	0.508	1126.88	572.90	0.514	957.57	491.81
A_68_P29530306	chr14:35315823-35315867	NM_009758:-112	Bmpr1a	PROMOTER	1.010	3.763	505.08	1900.53	3.799	552.53	2098.93
A_68_P29696921	chr14:70132430-70132474	NM_134078:-75	Chmp7	PROMOTER	1.010	1.422	2147.44	3053.09	1.436	1764.10	2533.06
A_68_P21144178	chr2:37648888-37648932	NM_001163566:17142	Crb2	INSIDE	1.010	2.973	1359.61	4041.92	3.003	1095.21	3289.18
A_68_P31630972	chr18:38094826-38094871	NM_007858:217	Diap1	INSIDE	1.010	3.595	557.32	2003.72	3.632	562.94	2044.53
A_68_P23284224	chr4:126913454-126913498	NM_198618:66962	Dlgap3	INSIDE	1.010	1.495	1391.98	2080.57	1.510	1181.16	1783.87
A_68_P32027007	chr19:25073867-25073911	NM_028785:-130	Dock8	PROMOTER	1.010	4.875	260.05	1267.68	4.923	279.03	1373.52
A_68_P25286998	chr7:91300735-91300779	NM_133722:-353	Fam108c	PROMOTER	1.010	1.437	1560.32	2242.21	1.452	1184.32	1719.21
A_68_P24046893	chr5:122303149-122303193	NM_175474:4134	Fam109a	INSIDE	1.010	2.419	593.54	1435.60	2.443	537.66	1313.34
A_68_P27497672	chr10:119912710-119912754	NM_010441:1259	Hmga2	INSIDE	1.010	1.607	890.13	1430.01	1.623	900.92	1462.32
A_68_P27788208	chr11:50191636-50191680	NM_021510:438	Hnrnph1	INSIDE	1.010	0.473	1172.77	555.28	0.478	972.22	464.97
A_68_P28293530	chr12:25783788-25783832	NM_010496:-2853	Id2	PROMOTER	1.010	2.008	269.06	540.19	2.028	285.86	579.62
A_68_P31614612	chr18:34936814-34936858	NM_001081256:175	Kdm3b	INSIDE	1.010	0.550	1664.94	916.45	0.556	1670.41	928.88
A_68_P27285759	chr10:80297631-80297675	NM_001013758:9132	Lingo3	INSIDE	1.010	1.710	684.92	1171.13	1.728	563.57	973.59
A_68_P29661996	chr14:64162753-64162797	NM_177594:16	Mtmr9	INSIDE	1.010	1.836	2333.69	4285.60	1.855	1564.53	2902.65
A_68_P24983630	chr7:17441193-17441237	NM_178900:12801	Prkd2	INSIDE	1.010	2.522	1875.45	4729.09	2.547	1467.04	3736.58
A_68_P24459349	chr6:53770114-53770158	NM_025817:683	Tril	INSIDE	1.010	1.998	2589.86	5174.29	2.018	2293.26	4628.66
A_68_P32144292	chr19:46574510-46574557	NM_053100:-1604	Trim8	PROMOTER	1.010	0.525	1206.72	633.26	0.530	1104.49	585.53
A_68_P27234637	chr10:70747983-70748027	NM_145420:6	Ube2d1	INSIDE	1.010	1.772	519.76	921.14	1.791	465.17	832.92
A_68_P27564654	chr11:5616764-5616808	NM_178623:24393	Urgcp	INSIDE	1.010	2.461	312.41	768.82	2.486	349.49	868.85
A_68_P29601197	chr14:51978178-51978222	ENSMUST00000162079:3332		DOWNSTREAM	1.010	1.722	1202.64	2070.65	1.738	1030.84	1791.81
A_68_P31103776	chr17:25569955-25569999	NM_001163691:752	Cacna1h	INSIDE	1.009	1.427	1370.68	1955.87	1.440	1124.35	1618.75
A_68_P30330813	chr15:73342857-73342901	NM_001081066:-111	Dennd3	PROMOTER	1.009	1.664	2966.96	4937.93	1.679	2315.90	3888.75
A_68_P31932438	chr19:6058043-6058087	NM_001190436:98	Fau	INSIDE	1.009	1.496	3182.57	4760.79	1.509	2526.55	3812.69
A_68_P23193164	chr4:107518873-107518917	NM_001080926:44031	Lrp8	INSIDE	1.009	1.953	1565.41	3057.58	1.971	1287.31	2537.44
A_68_P25954896	chr8:73437919-73437963	NM_173013:8068	Mtap1s	INSIDE	1.009	1.754	700.91	1229.73	1.771	486.55	861.71
A_68_P29162262	chr13:78334257-78334301	NM_010151:3965	Nr2f1	INSIDE	1.009	0.548	996.14	545.77	0.553	902.03	498.63
A_68_P30422879	chr15:88898490-88898534	NM_001002005:8357	Panx2	INSIDE	1.009	1.660	824.96	1369.59	1.675	671.27	1124.22
A_68_P29059921	chr13:56322911-56322955	ENSMUST00000127754:22369		DOWNSTREAM	1.009	1.948	1010.11	1967.44	1.966	849.57	1670.45
A_68_P21615625	chr2:127618048-127618092	NR_015476:154	1500011K16Rik	INSIDE	1.008	1.715	1826.80	3132.61	1.729	1407.15	2433.34
A_68_P33007150	chr9_random:50340-50384	NR_015516:-3046	4930526I15Rik	PROMOTER	1.008	3.159	4502.30	14222.42	3.184	2977.33	9479.68
A_68_P24138255	chr5:140384458-140384502	NM_175522:584	Elfn1	INSIDE	1.008	2.956	360.77	1066.50	2.981	288.15	859.02
A_68_P27284174	chr10:80049350-80049394	NM_145421:3714	Fam108a	INSIDE	1.008	2.250	444.84	1001.10	2.270	412.50	936.18
A_68_P28603297	chr12:86629542-86629586	NM_172414:24	Fam164c	INSIDE	1.008	1.465	1028.09	1505.74	1.477	837.25	1236.28
A_68_P23253012	chr4:120419677-120419721	NM_001081142:83	Kcnq4	INSIDE	1.008	2.915	864.16	2518.82	2.937	827.59	2430.77
A_68_P25368689	chr7:107756875-107756919	NR_003559:-386	Mrpl48	PROMOTER	1.008	1.444	2725.65	3935.18	1.456	1948.57	2836.21
A_68_P21821257	chr2:164860379-164860423	NM_144892:-121	Ncoa5	PROMOTER	1.008	0.651	1672.78	1088.72	0.656	1413.82	927.64
A_68_P29448699	chr14:21553663-21553707	NM_010811:100	Ndst2	INSIDE	1.008	1.733	609.99	1057.13	1.747	594.94	1039.31
A_68_P31633051	chr18:38428772-38428818	NM_017378:15261	Pcdh12	INSIDE	1.008	2.192	395.43	866.62	2.208	324.50	716.63

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P29637348	chr14:59820302-59820347	NM_027764:260	Rcbtb1	INSIDE	1.008	1.812	415.53	752.95	1.827	419.01	765.41
A_68_P29041999	chr13:53214193-53214237	NM_013846:167264	Ror2	INSIDE	1.008	2.409	2226.22	5362.56	2.429	1769.41	4297.48
A_68_P23236667	chr4:117508851-117508895	NM_008135:1010	Slc6a9	INSIDE	1.008	1.790	2295.98	4109.55	1.805	1805.86	3259.59
A_68_P32672206	chrX:131009632-131009676	NM_028958:1375	Taf7l	INSIDE	1.008	1.980	655.92	1298.44	1.995	289.32	577.28
A_68_P31155254	chr17:34817160-34817204	NM_031176:9703	Tnxb	INSIDE	1.008	2.338	1740.76	4069.74	2.356	1394.26	3285.44
A_68_P30588066	chr16:20535808-20535852	NM_009679:254	Ap2m1	INSIDE	1.007	1.478	1137.84	1681.89	1.488	1032.94	1537.22
A_68_P31118685	chr17:27957394-27957438	NM_001033279:71	D17Wsu92e	INSIDE	1.007	1.898	964.71	1831.38	1.912	926.36	1771.00
A_68_P27093484	chr10:41917285-41917329	NM_019740:79242	Foxo3	INSIDE	1.007	2.237	990.21	2215.21	2.252	784.37	1766.72
A_68_P31936820	chr19:7016078-7016122	NM_001177362:-103	Gpr137	DIVERGENT_PROMOTER	1.007	1.876	486.50	912.75	1.890	440.05	831.78
A_68_P23417748	chr4:151661232-151661276	NM_008237:4517	Hes3	INSIDE	1.007	1.432	1667.53	2387.37	1.441	1274.33	1836.72
A_68_P27279590	chr10:79362078-79362122	NM_001163276:9583	Med16	INSIDE	1.007	1.578	761.35	1201.04	1.588	527.52	837.75
A_68_P22038556	chr3:32428603-32428647	NM_024200:221	Mfn1	INSIDE	1.007	0.557	1335.70	744.06	0.561	1182.42	663.26
A_68_P23615665	chr5:38208583-38208627	NM_010835:7220	Msx1	DOWNSTREAM	1.007	1.433	2007.23	2877.15	1.443	1648.83	2380.03
A_68_P27909148	chr11:71864535-71864579	NM_001024927:84835	Pitpnm3	INSIDE	1.007	1.668	4574.97	7632.05	1.680	4016.57	6749.75
A_68_P31023591	chr17:7182888-7182932	NM_026611:-298	Rnaset2b	PROMOTER	1.007	4.818	4524.14	21797.33	4.850	3298.44	15998.23
A_68_P31351304	chr17:74794846-74794890	NM_144798:-103	Slc30a6	PROMOTER	1.007	0.606	1054.37	638.52	0.610	871.46	531.30
A_68_P29699983	chr14:70605493-70605537	NM_011366:1930	Sorbs3	INSIDE	1.007	0.670	1342.98	899.67	0.675	1134.47	765.68
A_68_P25009106	chr7:26010791-26010835	NM_175436:4343	Zfp526	INSIDE	1.007	2.151	1569.87	3377.11	2.167	1196.81	2593.15
A_68_P25504741	chr7:134388254-134388298	NM_177362:237	Zfp771	INSIDE	1.007	0.505	1146.43	579.16	0.509	1017.06	517.56
A_68_P30665796	chr16:34745100-34745144	ENSMUST00000155268:-173		PROMOTER	1.007	2.874	274.14	787.92	2.894	278.81	806.94
A_68_P23155321	chr4:101169179-101169223	NM_198412:-52	Dnajc6	PROMOTER	1.006	2.036	954.91	1944.31	2.049	846.14	1733.69
A_68_P27550688	chr11:3102520-3102564	NM_023743:-43	Eif4enif1	PROMOTER	1.006	1.707	616.43	1052.56	1.719	621.81	1068.60
A_68_P31490817	chr18:10609887-10609931	NM_001081222:442	Esco1	INSIDE	1.006	1.449	909.60	1318.25	1.459	858.72	1252.47
A_68_P21278821	chr2:63936348-63936392	NM_021716:-301	Fign	PROMOTER	1.006	1.576	1081.45	1704.32	1.585	1018.56	1614.78
A_68_P23451693	chr5:4758175-4758219	NM_021457:20	Fzd1	INSIDE	1.006	1.814	1211.79	2198.78	1.825	993.84	1814.15
A_68_P30143280	chr15:37209165-37209209	NM_026496:46396	Grhl2	INSIDE	1.006	2.350	234.00	549.91	2.365	201.84	477.27
A_68_P23340289	chr4:137074647-137074691	NM_008305:49951	Hspg2	INSIDE	1.006	3.265	739.05	2413.32	3.284	579.80	1903.98
A_68_P29620045	chr14:56442427-56442471	NM_001168346:-1183	Nfatc4	PROMOTER	1.006	2.332	454.75	1060.33	2.347	383.31	899.49
A_68_P25370888	chr7:108147418-108147462	NM_008773:13065	P2ry2	INSIDE	1.006	8.220	2586.95	21264.25	8.265	1766.71	14602.70
A_68_P27215088	chr10:67442788-67442832	NM_001081346:465	Rtkn2	INSIDE	1.006	0.540	1011.31	546.00	0.543	835.68	453.98
A_68_P26137064	chr8:108489850-108489894	NM_009195:67	Slc12a4	INSIDE	1.006	0.456	2060.77	939.01	0.458	1391.72	637.74
A_68_P26814194	chr9:108208208-108208252	NM_133986:52	Tcta	INSIDE	1.006	1.690	894.57	1511.87	1.700	735.98	1251.44
A_68_P31190361	chr17:43766788-43766832	NM_001161366:438	Tdrd6	INSIDE	1.006	3.590	951.40	3415.20	3.611	912.93	3296.31
A_68_P26596757	chr9:66897011-66897055	NM_001164249:-12	Tpm1	PROMOTER	1.006	1.442	3824.26	5514.37	1.451	2927.24	4247.17
A_68_P22037675	chr3:32264764-32264808	NM_009517:-199	Zmat3	PROMOTER	1.006	1.633	996.45	1627.40	1.643	880.81	1446.98
A_68_P20722811	chr1:154613676-154613720	NM_026369:27	Arpc5	INSIDE	1.005	1.558	713.77	1112.18	1.566	616.26	964.87
A_68_P29020671	chr13:48758693-48758737	NM_007526:310	Barx1	INSIDE	1.005	1.639	999.27	1637.75	1.647	923.83	1521.97
A_68_P23295624	chr4:128900663-128900707	NM_001033189:25003	C77080	INSIDE	1.005	1.626	781.47	1270.36	1.634	673.90	1100.85
A_68_P21073094	chr2:25433567-25433611	NM_001005424:2031	Gm996	INSIDE	1.005	1.888	904.89	1708.26	1.898	938.00	1780.18
A_68_P20146387	chr1:36160737-36160781	NM_015818:35514	Hs6st1	INSIDE	1.005	2.040	583.09	1189.37	2.051	506.11	1037.92
A_68_P31096079	chr17:24346336-24346380	NM_010947:-26	Ntn3	PROMOTER	1.005	1.464	1130.61	1655.35	1.472	1167.37	1718.29
A_68_P23543338	chr5:24191818-24191862	NM_016736:208	Nub1	INSIDE	1.005	1.918	911.88	1749.16	1.928	782.21	1508.27
A_68_P20971762	chr2:4985136-4985180	NM_181848:-174	Optn	PROMOTER	1.005	2.105	5285.74	11125.04	2.114	4344.30	9185.21
A_68_P22590676	chr3:142058482-142058526	NM_001190857:-3690	Pdlim5	PROMOTER	1.005	0.719	2330.56	1674.66	0.722	1825.16	1317.80
A_68_P26630945	chr9:72887670-72887714	NM_018889:-186	Pigb	DIVERGENT_PROMOTER	1.005	3.054	642.40	1961.74	3.068	708.79	2174.67
A_68_P28314292	chr12:29334596-29334640	NM_011275:152	Rnaseh1	INSIDE	1.005	0.588	1334.25	785.20	0.591	1063.12	628.47
A_68_P23668846	chr5:48374552-48374596	NM_178804:181	Slit2	INSIDE	1.005	0.554	924.62	512.65	0.557	731.04	407.43
A_68_P25670557	chr8:13786121-13786165	NM_025924:528	Upf3a	INSIDE	1.005	0.547	1048.31	573.12	0.549	827.64	454.76
A_68_P25614226	chr8:3495954-3495998	NM_080461:2839	Zfp358	INSIDE	1.005	3.586	411.15	1474.50	3.606	414.49	1494.65
A_68_P25714452	chr8:24168992-24169036	NM_031158:268	Ank1	INSIDE	1.004	1.617	1589.37	2570.48	1.624	1204.46	1956.55
A_68_P21067471	chr2:24534614-24534658	NM_001042528:83931	Cacna1b	INSIDE	1.004	2.402	766.26	1840.88	2.412	629.44	1518.37

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25392337	chr7:112583863-112583907	NM_007627:9551	Cckbr	INSIDE	1.004	3.326	1134.41	3772.78	3.338	903.46	3015.59
A_68_P31755198	chr18:61195223-61195267	NM_009880:609	Cdx1	INSIDE	1.004	1.758	498.10	875.64	1.764	444.91	785.00
A_68_P27286398	chr10:80392047-80392091	NM_008655:-767	Gadd45b	PROMOTER	1.004	0.557	1109.90	618.49	0.560	881.38	493.28
A_68_P22344501	chr3:95363489-95363533	NM_026489:-88	Hormad1	PROMOTER	1.004	1.968	538.50	1059.68	1.976	506.20	1000.35
A_68_P30672049	chr16:35770608-35770652	NM_175111:159	Hspbap1	INSIDE	1.004	1.495	1440.81	2154.42	1.501	1329.84	1995.72
A_68_P26162181	chr8:112889462-112889508	NM_172916:98608	Hydin	INSIDE	1.004	2.920	1290.45	3767.60	2.931	965.91	2831.17
A_68_P26586059	chr9:64989179-64989223	NM_008988:205	Igdcc3	INSIDE	1.004	2.150	1190.39	2559.14	2.158	1077.88	2326.10
A_68_P23229577	chr4:116180041-116180085	NM_008389:-91	Ipp	PROMOTER	1.004	0.605	1228.39	742.84	0.607	1041.42	632.32
A_68_P22201289	chr3:65469993-65470037	NM_001166659:-135	Lekr1	PROMOTER	1.004	3.210	3808.32	12225.65	3.225	2718.05	8764.56
A_68_P23297038	chr4:129191512-129191557	NM_010807:710	Marcksl1	INSIDE	1.004	1.516	2234.44	3387.35	1.522	1760.81	2679.96
A_68_P25210675	chr7:77491224-77491268	NM_009697:14233	Nr2f2	DOWNSTREAM	1.004	1.966	1162.56	2285.15	1.973	932.26	1838.90
A_68_P24984114	chr7:17532348-17532392	NM_001099636:2340	Pnmal2	INSIDE	1.004	0.346	1548.55	536.49	0.348	1202.49	418.06
A_68_P24117613	chr5:136210132-136210176	NM_008898:45071	Por	INSIDE	1.004	2.407	583.53	1404.36	2.416	544.81	1316.22
A_68_P20855860	chr1:178744266-178744310	NM_029756:-654	Sdccag8	DIVERGENT_PROMOTER	1.004	1.776	2194.73	3897.06	1.783	1890.77	3371.18
A_68_P24009124	chr5:115791228-115791272	NM_026933:-5	Triap1	DIVERGENT_PROMOTER	1.004	0.522	1318.21	688.47	0.524	1140.89	598.14
A_68_P22766407	chr4:19635843-19635887	NM_177327:276	Wwp1	INSIDE	1.004	0.469	1326.52	622.78	0.471	1278.87	602.88
A_68_P23577042	chr5:31502796-31502840	NM_001177901:1597	Zfp513	INSIDE	1.004	3.891	4411.39	17165.75	3.905	3484.29	13606.99
A_68_P29339700	chr13:114083617-114083661			Unknown	1.004	1.401	1770.64	2479.85	1.406	1500.91	2110.57
A_68_P25065735	chr7:38968873-38968917	NM_028166:89	1600014C10Rik	INSIDE	1.003	0.637	1185.99	754.94	0.639	909.21	580.67
A_68_P27033723	chr10:28916701-28916745	NM_026138:52921	6330407J23Rik	INSIDE	1.003	1.906	1741.22	3318.11	1.911	1379.64	2636.34
A_68_P22322689	chr3:89767337-89767382	NM_001081182:71	Atp8b2	INSIDE	1.003	1.651	2632.80	4347.19	1.657	2094.98	3471.03
A_68_P24157328	chr5:144383397-144383441	NM_011182:103	Cyth3	INSIDE	1.003	1.920	768.05	1474.66	1.926	649.74	1251.70
A_68_P23103729	chr4:91037950-91037994	NM_010486:774	Elavl2	INSIDE	1.003	0.666	2011.99	1339.58	0.668	1748.82	1168.08
A_68_P25954892	chr8:73437474-73437518	NM_173013:7624	Mtap1s	INSIDE	1.003	3.008	679.04	2042.53	3.018	517.91	1563.17
A_68_P30346611	chr15:76011370-76011414	NM_201394:14748	Plec	INSIDE	1.003	3.411	558.28	1904.44	3.420	481.25	1646.09
A_68_P28035919	chr11:94852484-94852528	NM_172261:-19	Ppp1r9b	PROMOTER	1.003	4.171	547.41	2283.01	4.185	542.52	2270.32
A_68_P27674870	chr11:29415061-29415105	NM_001163454:-49	Prorsd1	PROMOTER	1.003	0.668	1582.33	1056.42	0.670	1375.76	921.61
A_68_P26471637	chr9:44946814-44946858	NM_001013390:-288	Scn4b	DIVERGENT_PROMOTER	1.003	0.507	1123.27	569.87	0.509	1003.86	510.81
A_68_P20616238	chr1:133422989-133423033	NM_001081011:928	Srgap2	INSIDE	1.003	0.711	4267.27	3034.24	0.713	3794.25	2706.89
A_68_P24755317	chr6:112677286-112677330	NM_080448:219952	Srgap3	INSIDE	1.003	3.678	1760.66	6475.38	3.687	1153.35	4252.87
A_68_P32008255	chr19:21867281-21867325	NM_001033759:14471	Tmem2	INSIDE	1.003	3.014	1349.89	4068.02	3.024	1140.00	3447.19
A_68_P28280591	chr12:21423034-21423078	NM_011739:241	Ywhaq	INSIDE	1.003	0.599	1853.43	1110.18	0.601	1525.07	915.92
A_68_P29072927	chr13:58486285-58486329	NM_027335:280	2210016F16Rik	INSIDE	1.002	1.425	1227.37	1748.57	1.427	1112.04	1586.72
A_68_P21311081	chr2:69627424-69627468	NM_001077684:97	4930578N16Rik	INSIDE	1.002	1.952	637.55	1244.40	1.956	569.84	1114.80
A_68_P27234934	chr10:70807560-70807604	NM_134007:15	Cisd1	INSIDE	1.002	2.009	1802.07	3620.55	2.013	1646.42	3314.53
A_68_P23999130	chr5:114064140-114064194	NM_008153:36233	Cmklr1	INSIDE	1.002	7.755	1360.90	10553.40	7.770	1067.04	8290.79
A_68_P31458150	chr18:3337100-3337144	NM_001110850:465	Crem	INSIDE	1.002	1.481	868.72	1286.63	1.484	802.48	1191.11
A_68_P20613816	chr1:133034598-133034642	NM_145508:191	Dyrk3	INSIDE	1.002	1.349	2436.63	3286.10	1.351	2270.32	3067.97
A_68_P24388787	chr6:40386026-40386070	NM_175528:84	E330009J07Rik	INSIDE	1.002	2.277	486.02	1106.42	2.281	506.50	1155.30
A_68_P23445681	chr5:3543833-3543877	NM_001042501:22	Fam133b	INSIDE	1.002	0.641	2179.93	1396.43	0.642	1670.71	1071.98
A_68_P21565622	chr2:118529841-118529885	NM_001081971:-163	Gm1337	PROMOTER	1.002	2.729	419.05	1143.54	2.733	349.67	955.76
A_68_P24828004	chr6:126593418-126593462	NM_010595:2379	Kcna1	INSIDE	1.002	1.765	859.28	1516.22	1.768	709.71	1255.05
A_68_P29106491	chr13:67034356-67034400	NM_025547:-370	Mterfd1	PROMOTER	1.002	3.182	413.13	1314.68	3.187	459.25	1463.80
A_68_P26350702	chr9:21969587-21969631	NM_001082532:8319	Pigyl	DOWNSTREAM	1.002	2.022	1436.01	2902.98	2.026	1195.41	2421.70
A_68_P21349792	chr2:76208467-76208511	NM_153405:448	Rbm45	INSIDE	1.002	1.506	2977.07	4484.37	1.509	2362.36	3564.91
A_68_P29637346	chr14:59820048-59820093	NM_027764:6	Rcbtb1	INSIDE	1.002	1.954	323.30	631.79	1.958	313.85	614.51
A_68_P30363606	chr15:78813601-78813645	NM_001024716:137	Triobp	INSIDE	1.002	2.081	942.81	1961.67	2.085	878.42	1831.90
A_68_P20820924	chr1:172105271-172105315	NM_133806:-215	Uap1	PROMOTER	1.002	0.575	1316.76	756.52	0.575	1083.12	623.33
A_68_P21149699	chr2:38527835-38527879	ENSMUST00000152645:-200		PROMOTER	1.002	2.125	837.78	1780.58	2.130	683.64	1456.02
A_68_P32683271	chrX:133462182-133462226	NM_027067:341	1700014N06Rik	INSIDE	1.001	4.503	1528.00	6879.82	4.505	686.58	3092.99
A_68_P24760449	chr6:113554951-113554995	NM_133937:207	6720456B07Rik	INSIDE	1.001	0.578	1938.36	1120.30	0.579	1620.54	937.64

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25708739	chr8:23123882-23123926	NM_007511:46642	Atp7b	INSIDE	1.001	1.710	977.14	1670.45	1.712	846.17	1448.32
A_68_P31933858	chr19:6306849-6306893	NM_001033342:414	Cdc42bpg	INSIDE	1.001	1.793	1243.97	2230.48	1.795	1069.75	1920.01
A_68_P22355190	chr3:97413997-97414041	NM_026539:95	Chd1l	INSIDE	1.001	2.590	611.24	1582.88	2.592	610.65	1582.68
A_68_P27281410	chr10:79627471-79627515	NM_007705:-3093	Cirbp	PROMOTER	1.001	1.936	1128.46	2184.35	1.938	903.92	1751.96
A_68_P30507167	chr16:3908948-3908992	NM_029738:-38	Cluap1	DIVERGENT_PROMOTER	1.001	0.583	1104.12	644.07	0.584	908.10	530.47
A_68_P27952486	chr11:79894373-79894417	NM_018776:63	Crlf3	INSIDE	1.001	1.979	1368.96	2708.73	1.980	1208.10	2392.53
A_68_P22954048	chr4:59016217-59016261	NM_001033165:174	Dnajc25	INSIDE	1.001	1.826	408.85	746.45	1.828	358.06	654.36
A_68_P25564248	chr7:144390170-144390214	NM_001113414:115936	Ebf3	INSIDE	1.001	4.113	3266.90	13437.90	4.119	2477.94	10206.66
A_68_P26617704	chr9:70504900-70504944	NM_172772:59	Fam63b	INSIDE	1.001	2.570	697.55	1792.65	2.573	769.23	1979.39
A_68_P29928896	chr14:117324667-117324711	NM_001079844:152	Gpc6	INSIDE	1.001	1.768	1998.31	3532.86	1.769	1657.61	2932.72
A_68_P27568543	chr11:6344478-6344522	NM_029938:-54	H2afv	PROMOTER	1.001	0.412	1695.25	698.80	0.413	1425.40	588.36
A_68_P29942852	chr14:119537211-119537255	NM_015820:-254	Hs6st3	PROMOTER	1.001	2.083	685.49	1428.16	2.084	615.86	1283.75
A_68_P32746465	chrX:148238176-148238221	NM_021523:374	Huwe1	INSIDE	1.001	2.184	3499.70	7644.24	2.186	1699.28	3714.16
A_68_P20739568	chr1:157584694-157584738	NM_010712:4441	Lhx4	INSIDE	1.001	0.634	1644.18	1041.84	0.634	1262.79	801.23
A_68_P26537376	chr9:56482845-56482889	NM_181074:50194	Lingo1	INSIDE	1.001	0.537	1729.64	929.27	0.538	1418.17	762.47
A_68_P20348301	chr1:74438711-74438755	NR_029743:-2151	Mir26b	PROMOTER	1.001	5.814	793.29	4612.24	5.821	763.86	4446.28
A_68_P24191791	chr5:151397312-151397356	NM_133898:-234	N4bp2l1	PROMOTER	1.001	1.664	588.10	978.45	1.666	568.62	947.41
A_68_P31866221	chr18:80894853-80894897	NM_001164111:10038	Nfatc1	INSIDE	1.001	1.650	1020.30	1683.16	1.652	770.54	1272.96
A_68_P29054897	chr13:55516522-55516566	NM_029303:49	Pfn3	INSIDE	1.001	0.520	1325.73	689.16	0.520	1006.69	523.58
A_68_P27568687	chr11:6375581-6375625	NM_011221:318	Purb	INSIDE	1.001	1.893	476.34	901.68	1.895	503.04	953.43
A_68_P21782731	chr2:158236154-158236198	NM_177658:588	Ralgapb	INSIDE	1.001	2.788	2187.42	6099.31	2.790	1832.50	5112.94
A_68_P31138857	chr17:31433598-31433642	NM_153062:1193	Slc37a1	INSIDE	1.001	1.916	1401.63	2684.97	1.918	1134.51	2176.18
A_68_P22543384	chr3:133208009-133208053	NM_001040400:-676	Tet2	PROMOTER	1.001	2.501	932.77	2333.05	2.505	819.82	2053.37
A_68_P22820140	chr4:32326028-32326072	ENSMUST00000149201:-1		PROMOTER	1.001	1.440	1105.42	1592.01	1.441	1016.43	1464.60
A_68_P20562758	chr1:122499691-122499735	NM_010133:649	En1	INSIDE	1.000	2.775	1810.25	5024.30	2.774	1534.25	4256.35
A_68_P26804353	chr9:106550228-106550272	NM_001160353:8190	Grm2	INSIDE	1.000	1.849	396.78	733.67	1.849	337.51	624.06
A_68_P31053794	chr17:12962250-12962294	NM_010515:300	Igf2r	INSIDE	1.000	2.114	812.96	1718.60	2.115	748.12	1581.99
A_68_P27340038	chr10:90564802-90564859	NM_027078:19047	Ikbip	INSIDE	1.000	4.183	770.88	3224.39	4.185	644.40	2696.50
A_68_P29334869	chr13:113254155-113254199	NM_010560:-101	Il6st	PROMOTER	1.000	2.473	720.39	1781.77	2.473	643.17	1590.61
A_68_P32147196	chr19:47089352-47089396	NM_146100:187	Ina	INSIDE	1.000	1.629	591.63	964.03	1.630	530.30	864.16
A_68_P25111232	chr7:56502025-56502069	NM_175272:488	Nav2	INSIDE	1.000	1.904	1561.73	2973.72	1.905	1228.89	2340.61
A_68_P30165311	chr15:41279202-41279246	NM_001130166:197	Oxr1	INSIDE	1.000	1.483	1196.71	1774.96	1.483	1051.71	1559.45
A_68_P20641451	chr1:137662928-137662972	NM_013750:289	Phlda3	INSIDE	1.000	1.648	653.33	1076.81	1.648	647.38	1066.93
A_68_P24984543	chr7:17612915-17612959	NM_011155:327	Ppp5c	INSIDE	1.000	2.526	813.45	2055.03	2.526	786.34	1986.38
A_68_P25090467	chr7:52241632-52241676	NM_019830:48	Prmt1	INSIDE	1.000	0.563	2673.91	1505.32	0.563	2064.17	1161.69
A_68_P31255961	chr17:56556971-56557015	NM_011218:58911	Ptprs	INSIDE	1.000	2.726	2495.12	6800.53	2.726	1799.25	4905.24
A_68_P26822090	chr9:110034578-110034622	NM_009211:73	Smarcc1	INSIDE	1.000	0.587	1716.41	1007.15	0.587	1489.01	873.48
A_68_P26752043	chr9:97266499-97266543	NM_030219:3857	Trim42	INSIDE	1.000	3.580	2124.53	7605.45	3.580	1367.72	4896.73
A_68_P21911428	chr2:181316733-181316777	NM_026765:-76	Uckl1	PROMOTER	1.000	0.550	2365.67	1300.63	0.550	1911.27	1051.32
A_68_P24638867	chr6:91361318-91361362	NM_009527:23	Wnt7a	INSIDE	1.000	0.534	1200.04	640.63	0.534	943.05	503.65
A_68_P21622216	chr2:128769433-128769477	NM_020594:302	Zc3h8	INSIDE	1.000	0.661	3469.05	2291.63	0.661	2788.06	1841.73
A_68_P31159051	chr17:35495987-35496031	M19687:92193		INSIDE	1.000	1.623	852.55	1383.39	1.622	692.14	1122.72
A_68_P31632850	chr18:38398968-38399012	NR_015475:10862	1700086O06Rik	INSIDE	0.999	2.657	1930.10	5128.40	2.653	1700.15	4510.89
A_68_P22888515	chr4:46402231-46402275	NM_029086:43	5830415F09Rik	INSIDE	0.999	0.586	3453.67	2025.56	0.586	2807.81	1645.52
A_68_P25509658	chr7:135381901-135381945	NM_177001:-377	9130023H24Rik	PROMOTER	0.999	1.842	1505.89	2773.86	1.840	1308.44	2406.96
A_68_P26397637	chr9:30728994-30729041	NM_001024139:1020	Adamts15	INSIDE	0.999	2.179	523.50	1140.66	2.176	427.05	929.30
A_68_P25589622	chr7:148748160-148748204	NM_007459:104	Ap2a2	INSIDE	0.999	2.413	690.05	1665.06	2.411	645.41	1556.04
A_68_P28517159	chr12:70993954-70993998	NM_178628:-115	Atl1	PROMOTER	0.999	2.421	257.97	624.52	2.419	228.35	552.45
A_68_P28183246	chr11:120098017-120098061	NM_198423:3778	Bahcc1	INSIDE	0.999	0.671	2111.42	1416.75	0.670	1828.52	1225.29
A_68_P21751444	chr2:152656729-152656773	NM_009743:668	Bcl2l1	INSIDE	0.999	0.483	1434.21	692.88	0.483	1306.97	630.63
A_68_P25951052	chr8:72839724-72839768	NM_001163282:73	Gdf1	INSIDE	0.999	0.549	1349.95	741.73	0.549	1069.18	586.87

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27278193	chr10:79138046-79138092	NM_148934:5914	Gm16517	INSIDE	0.999	2.462	415.58	1023.07	2.459	315.78	776.61
A_68_P27279643	chr10:79371605-79371649	NM_001163276:57	Med16	INSIDE	0.999	3.411	4547.19	15510.39	3.409	4065.17	13858.61
A_68_P23260200	chr4:122673850-122673894	NM_008506:531	Mycl1	INSIDE	0.999	2.358	2423.27	5714.37	2.357	2125.77	5009.77
A_68_P30497261	chr15:102156542-102156586	NM_027044:18	Pfdn5	INSIDE	0.999	0.647	2071.67	1340.46	0.646	1745.19	1127.84
A_68_P26750484	chr9:96919484-96919528	NM_145134:-732	Spsb4	PROMOTER	0.999	2.141	1284.14	2749.85	2.139	1093.79	2340.05
A_68_P27845269	chr11:60692535-60692579	NM_001168507:-16	Tmem11	PROMOTER	0.999	0.550	1323.77	727.90	0.549	969.23	532.31
A_68_P23240958	chr4:118214708-118214752	NM_172383:1601	Tmem125	INSIDE	0.999	2.109	1245.79	2627.70	2.107	992.87	2092.00
A_68_P24067083	chr5:125956377-125956421	NM_030210:156	Aacs	INSIDE	0.998	0.603	1336.15	805.51	0.602	1025.60	616.95
A_68_P30762452	chr16:52452809-52452853	NM_009655:280	Alcam	INSIDE	0.998	0.339	1713.94	580.70	0.338	1668.29	564.12
A_68_P23576264	chr5:31371183-31371228	NM_023525:14022	Cad	INSIDE	0.998	3.213	598.79	1923.96	3.207	454.70	1458.27
A_68_P27924577	chr11:74981143-74981187	NM_001098203:490	Hic1	INSIDE	0.998	2.270	565.78	1284.39	2.267	434.21	984.21
A_68_P23333956	chr4:135998848-135998894	NM_008309:19432	Htr1d	INSIDE	0.998	2.131	351.60	749.42	2.127	252.44	536.90
A_68_P31829406	chr18:74223918-74223962	NM_172632:663	Mapk4	INSIDE	0.998	1.442	2017.22	2908.79	1.439	1555.75	2239.24
A_68_P30368654	chr15:79634541-79634585	NM_030689:577	Nptxr	INSIDE	0.998	1.960	489.40	959.03	1.956	468.66	916.49
A_68_P29116252	chr13:69672648-69672692	NM_001169131:72	Papd7	INSIDE	0.998	3.351	553.07	1853.12	3.345	451.07	1509.02
A_68_P23576466	chr5:31397923-31397967	NM_011773:-2044	Slc30a3	PROMOTER	0.998	1.857	619.34	1150.15	1.854	570.84	1058.10
A_68_P29238030	chr13:95746505-95746549	NM_172590:224	Wdr41	INSIDE	0.998	1.934	361.03	698.29	1.929	334.92	646.20
A_68_P29614458	chr14:55433137-55433182	ENSMUST00000095853:-2164		PROMOTER	0.998	2.005	1026.89	2058.78	2.001	872.72	1745.93
A_68_P24973686	chr7:13514022-13514066	NM_029809:1280	2310014L17Rik	INSIDE	0.997	1.983	2957.50	5863.54	1.978	2257.46	4464.18
A_68_P28098902	chr11:105849980-105850024	NM_009598:13481	Ace	INSIDE	0.997	3.371	2790.42	9406.29	3.361	1956.84	6576.26
A_68_P28751739	chr12:113912106-113912150	NM_001165894:359	Akt1	INSIDE	0.997	1.867	988.87	1845.84	1.862	865.73	1611.66
A_68_P31500013	chr18:12464044-12464088	NM_001190371:163	Ankrd29	INSIDE	0.997	0.530	1194.05	633.15	0.529	906.64	479.31
A_68_P20722814	chr1:154614048-154614092	NM_026369:399	Arpc5	INSIDE	0.997	0.508	1445.23	733.62	0.506	1186.65	600.79
A_68_P23332635	chr4:135762482-135762526	NM_001008232:225	Asap3	INSIDE	0.997	1.446	2295.55	3318.93	1.441	1657.39	2388.62
A_68_P20294242	chr1:64781496-64781540	NM_001042659:2806	Fzd5	INSIDE	0.997	2.794	629.47	1758.50	2.784	552.56	1538.30
A_68_P28553888	chr12:77518476-77518520	NM_001163103:-87	Gm70	PROMOTER	0.997	1.733	679.79	1178.21	1.727	697.08	1204.08
A_68_P31259627	chr17:57162083-57162127	NM_010613:8826	Khsrp	INSIDE	0.997	2.439	1125.22	2744.81	2.431	860.59	2092.42
A_68_P30365873	chr15:79178383-79178427	NM_010755:297	Maff	INSIDE	0.997	1.377	3938.23	5423.92	1.374	2859.41	3928.10
A_68_P30370811	chr15:80042269-80042313	NM_010795:38140	Mgat3	INSIDE	0.997	2.631	865.28	2276.38	2.622	728.36	1909.78
A_68_P29116249	chr13:69672357-69672401	NM_001169131:364	Papd7	INSIDE	0.997	2.373	430.14	1020.63	2.366	473.01	1119.05
A_68_P24980577	chr7:16858327-16858371	NM_001136270:693	Prr24	INSIDE	0.997	1.584	735.36	1165.10	1.580	698.37	1103.34
A_68_P32071925	chr19:32832040-32832084	NM_008960:-4	Pten	PROMOTER	0.997	0.393	2158.87	847.85	0.392	1626.33	636.79
A_68_P26872699	chr9:119395083-119395128	NM_021544:93029	Scn5a	INSIDE	0.997	6.691	1675.87	11213.76	6.669	1240.89	8275.00
A_68_P28054174	chr11:97914443-97914487	NM_146028:312	Stac2	INSIDE	0.997	1.516	1351.03	2048.05	1.511	1116.39	1687.37
A_68_P21910189	chr2:181100664-181100708	NM_001048148:559	Zgpat	INSIDE	0.997	1.533	1047.54	1605.55	1.528	912.86	1394.56
A_68_P21967925	chr3:17686263-17686307	NR_033490:-3636	2610100L16Rik	PROMOTER	0.996	1.832	700.79	1283.61	1.824	671.51	1224.61
A_68_P26809314	chr9:107429770-107429814	NM_001174047:127582	Cacna2d2	INSIDE	0.996	2.280	4757.54	10847.27	2.270	3392.77	7701.93
A_68_P23193626	chr4:107596160-107596204	NM_009949:12	Cpt2	INSIDE	0.996	0.568	1778.95	1010.03	0.566	1435.54	812.00
A_68_P27386041	chr10:98726685-98726729	NM_026268:842	Dusp6	INSIDE	0.996	1.374	1779.75	2445.20	1.369	1581.44	2164.98
A_68_P27479722	chr10:116585133-116585177	NM_177798:376	Frs2	INSIDE	0.996	1.876	4085.68	7664.93	1.868	3157.32	5897.78
A_68_P27790976	chr11:50673440-50673484	NM_173372:9276	Grm6	INSIDE	0.996	3.290	1696.71	5582.56	3.277	1165.85	3820.51
A_68_P28727296	chr12:109556884-109556928	NM_001044380:12427	Hhipl1	INSIDE	0.996	1.574	2623.55	4129.92	1.567	2017.20	3161.77
A_68_P21261715	chr2:60800332-60800376	NM_020296:907	Rbms1	INSIDE	0.996	0.371	3510.84	1303.82	0.370	1038.29	384.24
A_68_P21297863	chr2:67403728-67403772			Unknown	0.996	2.896	374.84	1085.70	2.886	345.96	998.55
A_68_P32565208	chrX:98893525-98893573	ENSMUST00000073812:-6359		PROMOTER	0.996	4.092	858.36	3512.21	4.077	365.29	1489.31
A_68_P23562832	chr5:28785049-28785093	NR_015562:-8453	9530036O11Rik	PROMOTER	0.995	1.861	900.53	1675.67	1.852	815.55	1510.14
A_68_P23315555	chr4:132617504-132617548	NM_146155:50106	Ahdc1	INSIDE	0.995	2.198	2866.16	6300.82	2.187	2036.49	4454.39
A_68_P31304169	chr17:66426588-66426632	NM_001025572:-224	Ankrd12	PROMOTER	0.995	1.367	2946.48	4027.20	1.360	2267.77	3083.51
A_68_P31015191	chr17:5189996-5190040	NM_001085355:194945	Arid1b	INSIDE	0.995	1.921	867.83	1667.48	1.911	812.52	1552.65
A_68_P26505535	chr9:50576596-50576640	NM_198675:276	Fdxacb1	INSIDE	0.995	1.526	1064.15	1623.66	1.518	972.54	1475.91
A_68_P30673113	chr16:35983288-35983332	NM_008465:-138	Kpna1	PROMOTER	0.995	2.069	641.80	1328.17	2.060	610.60	1257.66

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27528047	chr10:125403454-125403498	NM_177152:202	Lrig3	INSIDE	0.995	1.897	1111.46	2108.73	1.888	1074.76	2028.77
A_68_P22569094	chr3:138152230-138152274	NM_175224:94	Metap1	INSIDE	0.995	0.558	1421.82	793.85	0.556	1294.07	719.08
A_68_P23230187	chr4:116299629-116299673	NM_001081475:452	Nasp	INSIDE	0.995	2.444	818.05	1998.97	2.431	775.57	1885.28
A_68_P21322071	chr2:71711579-71711623	NM_172665:272	Pdk1	INSIDE	0.995	1.869	408.41	763.22	1.860	451.21	839.30
A_68_P29701214	chr14:70828882-70828926	NM_021308:-3	Piwil2	PROMOTER	0.995	2.654	1207.94	3206.23	2.641	914.92	2416.33
A_68_P20412582	chr1:88421547-88421591	NM_008972:-1742	Ptma	PROMOTER	0.995	0.620	1245.87	771.94	0.616	971.73	598.81
A_68_P25957632	chr8:74108446-74108490	NM_011977:15643	Slc27a1	INSIDE	0.995	1.632	1076.80	1757.14	1.623	876.30	1422.62
A_68_P24983334	chr7:17396097-17396141	NM_001039878:-5119	Strn4	PROMOTER	0.995	1.522	1647.32	2507.44	1.515	1366.68	2070.67
A_68_P24757154	chr6:112996444-112996488	NM_008188:146	Thumpd3	INSIDE	0.995	1.737	4296.78	7462.07	1.729	3293.29	5693.23
A_68_P27017611	chr10:25798724-25798768	NM_029881:112	Tmem200a	INSIDE	0.995	2.407	411.15	989.66	2.395	378.57	906.74
A_68_P28272753	chr12:17888729-17888773	ENSMUST00000169996:-252		PROMOTER	0.995	3.529	636.40	2245.90	3.512	605.21	2125.64
A_68_P23319352	chr4:133309797-133309841	NM_001080819:-292	Arid1a	PROMOTER	0.994	2.271	259.06	588.20	2.257	268.11	605.25
A_68_P26020866	chr8:87163478-87163522	NM_007578:224238	Cacna1a	INSIDE	0.994	3.412	181.89	620.63	3.391	273.43	927.22
A_68_P25392336	chr7:112583704-112583750	NM_007627:9393	Cckbr	INSIDE	0.994	1.993	772.15	1538.80	1.982	691.06	1369.49
A_68_P21080069	chr2:26483908-26483952	NM_019833:-46	Fam69b	PROMOTER	0.994	2.648	1676.41	4438.84	2.632	1413.20	3719.47
A_68_P23980412	chr5:110973428-110973472	NM_198306:87	Galnt9	INSIDE	0.994	2.402	1560.80	3749.46	2.389	1323.60	3162.07
A_68_P22448207	chr3:115954695-115954739	NM_022427:1686	Gpr88	INSIDE	0.994	3.688	1626.77	5999.23	3.666	1173.73	4302.61
A_68_P30473862	chr15:98087209-98087253	NM_027304:508	H1fnt	INSIDE	0.994	2.372	828.18	1964.16	2.357	742.30	1749.38
A_68_P20146151	chr1:36125666-36125710	NM_015818:444	Hs6st1	INSIDE	0.994	1.782	1059.26	1887.91	1.771	864.25	1530.45
A_68_P20058117	chr1:17081719-17081763	NM_020604:6230	Jph1	INSIDE	0.994	2.415	432.87	1045.23	2.400	437.87	1050.67
A_68_P30365872	chr15:79178280-79178324	NM_010755:195	Maff	INSIDE	0.994	1.455	860.84	1252.58	1.447	853.34	1234.36
A_68_P27279642	chr10:79371508-79371552	NM_001163276:153	Med16	INSIDE	0.994	1.480	5316.32	7868.73	1.472	4037.00	5940.95
A_68_P31918144	chr19:3575377-3575421	NM_001164159:351	Ppp6r3	INSIDE	0.994	2.928	226.67	663.80	2.910	224.20	652.39
A_68_P30577449	chr16:18088865-18088909	NM_011172:397	Prodh	INSIDE	0.994	0.663	3212.32	2130.88	0.660	2666.40	1758.78
A_68_P26145652	chr8:110111876-110111920	NM_010817:484	Psmd7	INSIDE	0.994	1.754	1356.42	2379.29	1.744	984.47	1716.67
A_68_P29094190	chr13:63669109-63669153	NM_008957:-2302	Ptch1	PROMOTER	0.994	0.643	1264.45	812.72	0.639	1079.27	689.55
A_68_P20826099	chr1:173032693-173032737			Unknown	0.994	1.419	4354.08	6179.40	1.410	3366.74	4747.43
A_68_P23236238	chr4:117402055-117402099	ENSMUST00000119463:-172		PROMOTER	0.994	3.803	377.85	1436.81	3.780	332.07	1255.28
A_68_P23358590	chr4:140071282-140071326	NM_001112723:133367	Arhgef10l	INSIDE	0.993	2.016	607.45	1224.71	2.003	460.13	921.44
A_68_P23069061	chr4:84191429-84191473	NM_172870:129540	Bnc2	INSIDE	0.993	2.050	730.17	1496.77	2.035	684.91	1393.86
A_68_P20162792	chr1:38954736-38954780	NM_145142:247	Chst10	INSIDE	0.993	1.434	1466.35	2103.29	1.425	1325.92	1889.34
A_68_P21566331	chr2:118640254-118640305	NM_026412:541	D2Ertd750e	INSIDE	0.993	3.780	189.64	716.82	3.754	202.56	760.45
A_68_P20884849	chr1:183950484-183950528	NM_001083120:-395	Enah	PROMOTER	0.993	2.101	3415.11	7174.11	2.087	2834.83	5915.61
A_68_P25095110	chr7:53050321-53050365	NM_001005511:11026	Lmtk3	INSIDE	0.993	1.941	685.01	1329.93	1.928	599.14	1155.30
A_68_P26164574	chr8:113263014-113263058	NM_198625:17653	Mtss1l	INSIDE	0.993	2.608	774.49	2019.64	2.591	637.24	1650.87
A_68_P32065927	chr19:31739233-31739277	NM_011160:-394	Prkg1	PROMOTER	0.993	2.083	7892.51	16437.63	2.067	5044.98	10428.48
A_68_P27949797	chr11:79405082-79405126	NM_175543:391	Rab11fip4	INSIDE	0.993	3.847	243.01	934.92	3.821	240.95	920.65
A_68_P27804897	chr11:53277337-53277381	NM_027917:6652	Shroom1	INSIDE	0.993	3.196	478.62	1529.53	3.173	432.98	1373.82
A_68_P30425030	chr15:89240388-89240432	NM_001162882:284	1700007E06Rik	INSIDE	0.992	4.670	1754.18	8192.88	4.632	1273.24	5897.68
A_68_P28990875	chr13:43655667-43655711	NM_001081059:-128	Ccdc90a	PROMOTER	0.992	1.488	2361.83	3513.87	1.476	1911.69	2822.43
A_68_P26055365	chr8:93352513-93352557	NM_177224:-199	Chd9	PROMOTER	0.992	2.663	568.34	1513.73	2.642	535.13	1413.73
A_68_P32982272	chr5:134998625-134998669	NM_001039162:29658	Clip2	INSIDE	0.992	2.331	2254.36	5255.17	2.312	1835.41	4244.26
A_68_P27284503	chr10:80101463-80101507	NM_001159591:9084	Csnk1g2	INSIDE	0.992	2.078	1387.24	2882.12	2.061	995.37	2051.67
A_68_P22019081	chr3:28680448-28680492	NM_177586:238	Eif5a2	INSIDE	0.992	0.645	1422.03	917.80	0.640	1312.04	839.68
A_68_P29237510	chr13:95643777-95643821	NM_011021:-1783	Otp	PROMOTER	0.992	1.508	1105.73	1667.74	1.497	944.99	1414.31
A_68_P29437783	chr14:19103060-19103104	NM_025586:418	Rpl15	INSIDE	0.992	0.499	1339.28	668.87	0.495	1211.93	600.36
A_68_P21293424	chr2:66472811-66472855	NM_018852:177	Scn9a	INSIDE	0.992	0.633	1601.71	1014.38	0.628	1282.15	805.12
A_68_P25100396	chr7:53895073-53895117	NM_013789:83	Sergef	INSIDE	0.992	1.898	771.68	1464.98	1.882	671.26	1263.58
A_68_P31958012	chr19:11893471-11893515	NM_011502:-109	Stx3	PROMOTER	0.992	2.210	922.69	2038.75	2.191	894.54	1959.78
A_68_P32021816	chr19:24205473-24205517	NM_001198985:43136	Tjp2	INSIDE	0.992	3.244	1594.51	5172.06	3.218	1164.87	3748.69
A_68_P28747158	chr12:113205217-113205261	NM_027360:-50	2010107E04Rik	DIVERGENT_PROMOTER	0.991	1.582	1091.43	1727.06	1.569	962.54	1510.08

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P30362447	chr15:78629670-78629714	NM_130859:3780	Card10	INSIDE	0.991	2.938	2744.23	8062.68	2.913	2408.44	7015.37
A_68_P27172914	chr10:59648890-59648934	NM_016803:33096	Chst3	INSIDE	0.991	2.824	436.94	1233.82	2.799	379.51	1062.24
A_68_P26841766	chr9:113650462-113650506	NM_001114347:-106	Clasp2	PROMOTER	0.991	1.484	956.75	1419.92	1.471	794.79	1168.91
A_68_P32145200	chr19:46728723-46728767	NM_001177813:30854	D19Wsu162e	INSIDE	0.991	2.603	856.94	2230.90	2.579	754.84	1947.05
A_68_P30590964	chr16:21204925-21204969	NM_010143:79	Ephb3	INSIDE	0.991	0.692	1919.35	1329.08	0.686	1639.78	1125.32
A_68_P24951532	chr7:4959919-4959963	NM_001110330:4904	Fiz1	INSIDE	0.991	1.724	2321.68	4002.67	1.708	2045.57	3494.79
A_68_P30083238	chr15:25711367-25711411	NM_019472:159084	Myo10	INSIDE	0.991	1.799	980.50	1763.81	1.783	779.10	1389.16
A_68_P25353646	chr7:105227755-105227799	NM_008663:40227	Myo7a	INSIDE	0.991	1.580	894.89	1413.47	1.565	796.39	1246.73
A_68_P23134314	chr4:97438807-97438855	NM_001122953:-5486	Nfia	PROMOTER	0.991	1.589	561.28	892.12	1.575	521.62	821.32
A_68_P21580770	chr2:121240019-121240063	NM_007952:403	Pdia3	INSIDE	0.991	0.715	1728.78	1235.54	0.709	1475.76	1045.67
A_68_P25090608	chr7:52263818-52263862	NM_001008422:7779	Scaf1	INSIDE	0.991	1.607	1196.28	1922.74	1.592	956.34	1522.78
A_68_P22342628	chr3:94976704-94976748	NM_011351:8431	Sema6c	INSIDE	0.991	1.756	720.73	1265.74	1.741	642.58	1118.69
A_68_P28755250	chr12:114427183-114427227	NM_153776:3091	Tmem121	INSIDE	0.991	3.686	1213.87	4474.68	3.655	1068.91	3906.50
A_68_P30566189	chr16:15594510-15594554	NM_001159351:79	Ube2v2	INSIDE	0.991	1.415	2170.14	3071.20	1.403	1695.05	2378.10
A_68_P24118487	chr5:136386793-136386840	NM_018871:23695	Ywhag	INSIDE	0.991	2.762	310.23	856.83	2.736	245.32	671.20
A_68_P32603679	chrX:109714349-109714393	NM_177747:236	Zfp711	INSIDE	0.991	2.455	464.94	1141.53	2.434	289.87	705.61
A_68_P26232729	chr8:124860750-124860794	NM_009569:54732	Zfpm1	INSIDE	0.991	1.687	666.89	1125.17	1.672	568.14	949.98
A_68_P26276224	chr9:4260268-4260312			Unknown	0.991	1.504	1229.05	1848.69	1.490	927.93	1382.64
A_68_P21774735	chr2:156846821-156846865	NM_001164663:58159	9830001H06Rik	INSIDE	0.990	1.965	425.28	835.52	1.946	418.09	813.42
A_68_P27383819	chr10:98376903-98376947	NM_026482:-861	Atp2b1	PROMOTER	0.990	1.436	1235.63	1774.96	1.422	1076.44	1530.53
A_68_P25586497	chr7:148254408-148254452	NM_177897:7258	B4galnt4	INSIDE	0.990	2.607	495.52	1291.70	2.580	446.78	1152.81
A_68_P28175482	chr11:118906328-118906372	NM_013926:-4123	Cbx8	PROMOTER	0.990	1.958	739.25	1447.66	1.939	674.22	1307.55
A_68_P23418119	chr4:151713113-151713157	NM_001081376:375	Chd5	INSIDE	0.990	2.392	2509.82	6002.41	2.367	2237.51	5297.09
A_68_P20553863	chr1:120734057-120734104	NM_001081125:216116	Gli2	INSIDE	0.990	2.316	1210.84	2804.00	2.293	959.38	2199.99
A_68_P23977824	chr5:110537149-110537193	NM_145147:46	Gtpbp6	INSIDE	0.990	1.441	3217.96	4637.99	1.427	2416.16	3448.39
A_68_P26346744	chr9:21172242-21172286	NM_001042708:-182	Ilf3	PROMOTER	0.990	0.575	1430.63	822.38	0.569	1082.06	615.89
A_68_P21117014	chr2:32568718-32568762	NR_037217:-332	Mir2861	DIVERGENT_PROMOTER	0.990	1.400	1642.46	2298.77	1.385	1568.19	2172.01
A_68_P24810881	chr6:122824922-122824967	NM_026267:370	Necap1	INSIDE	0.990	0.631	3086.28	1948.66	0.625	2397.67	1499.10
A_68_P30368806	chr15:79659338-79659382	NM_001013360:5403	Npcd	INSIDE	0.990	2.081	1115.25	2321.14	2.060	916.46	1887.95
A_68_P29697194	chr14:70196895-70196939	NM_153514:8436	Rhobtb2	INSIDE	0.990	2.714	2553.13	6929.77	2.687	1854.22	4981.90
A_68_P30602963	chr16:23431338-23431382	NM_001004151:2155	Rtp1	INSIDE	0.990	2.822	258.41	729.15	2.793	243.89	681.29
A_68_P27877796	chr11:66340159-66340203	NM_001034874:-552	Shisa6	PROMOTER	0.990	2.622	1594.17	4180.25	2.597	1209.43	3140.43
A_68_P28100604	chr11:106133705-106133749	NM_031878:-4780	Smarcd2	PROMOTER	0.990	1.482	2228.00	3301.56	1.468	1870.66	2745.54
A_68_P26453530	chr9:41932147-41932191	NM_011436:204	Sorl1	INSIDE	0.990	1.637	761.75	1246.69	1.620	667.80	1082.07
A_68_P29493964	chr14:29331522-29331566	NM_009524:12886	Wnt5a	INSIDE	0.990	1.819	1162.20	2113.59	1.800	998.13	1796.91
A_68_P26020864	A_68_P26020864			Unknown	0.990	1.619	578.31	936.50	1.604	527.62	846.20
A_68_P29309086	chr13:108834463-108834507	NM_001048250:-183	2810008M24Rik	PROMOTER	0.989	1.482	2401.68	3558.36	1.465	2094.99	3070.03
A_68_P22415393	chr3:108743147-108743191	NM_001078646:-306	4921515J06Rik	PROMOTER	0.989	3.883	830.22	3223.45	3.839	712.46	2735.20
A_68_P30339173	chr15:74551790-74551834	NM_198607:149	4930572J05Rik	INSIDE	0.989	1.603	1174.18	1882.01	1.585	999.82	1584.42
A_68_P23891971	chr5:92471843-92471887	NM_177270:168	Cdkl2	INSIDE	0.989	1.827	362.26	661.98	1.807	349.71	631.87
A_68_P24141815	chr5:141000477-141000521	NM_021528:18936	Chst12	INSIDE	0.989	2.683	816.95	2191.62	2.654	781.86	2074.84
A_68_P26572466	chr9:62659190-62659234	NM_010193:243	Fem1b	INSIDE	0.989	2.004	1302.10	2609.44	1.981	1173.92	2325.73
A_68_P28080241	chr11:102417779-102417823	NM_001159492:-328	Gpatch8	PROMOTER	0.989	1.658	840.79	1394.44	1.640	747.80	1226.57
A_68_P31114358	chr17:27252888-27252932	NM_080553:58662	Itpr3	INSIDE	0.989	2.351	1104.54	2596.50	2.326	798.30	1856.78
A_68_P26587427	chr9:65239407-65239451	NM_028974:31	Kbtbd13	INSIDE	0.989	1.909	3214.16	6135.23	1.888	2567.53	4848.61
A_68_P21475551	chr2:102026439-102026483	NM_178886:74	Ldlrad3	INSIDE	0.989	2.798	3455.55	9667.91	2.767	3205.43	8867.99
A_68_P26507495	chr9:50911542-50911586	NR_029654:-349	Mir34c	PROMOTER	0.989	1.836	752.30	1381.07	1.816	742.77	1349.08
A_68_P21840231	chr2:168057062-168057106	NM_001160330:963	Mocs3	INSIDE	0.989	3.064	873.74	2677.58	3.030	775.97	2351.26
A_68_P31779044	chr18:65243606-65243650	NM_031881:60448	Nedd4l	INSIDE	0.989	2.579	570.33	1470.94	2.551	530.92	1354.30
A_68_P28185956	chr11:120522369-120522413	NM_175263:-239	Notum	PROMOTER	0.989	0.606	1165.65	705.92	0.599	984.16	589.61
A_68_P20768472	chr1:162722548-162722592	NM_013862:499	Rabgap1l	INSIDE	0.989	0.603	1760.02	1061.95	0.597	1518.06	905.93

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P23701541	chr5:53980854-53980898	NM_009035:-577	Rbpj	PROMOTER	0.989	2.061	830.34	1711.25	2.039	901.43	1837.68
A_68_P27807187	chr11:53705109-53705153	NM_011396:75	Slc22a5	INSIDE	0.989	0.658	1648.46	1085.07	0.651	1324.12	862.34
A_68_P31201708	chr17:45682853-45682897	NM_001013749:3752	Tmem151b	INSIDE	0.989	1.734	1153.69	2000.09	1.714	1012.03	1734.82
A_68_P31213639	chr17:47826066-47826110	NM_001164729:-753	Tomm6	DIVERGENT_PROMOTER	0.989	1.579	5728.67	9043.05	1.561	3958.98	6180.54
A_68_P24428426	chr6:48579284-48579328	NR_027236:1141	AI854703	INSIDE	0.988	1.547	1267.20	1960.61	1.529	1086.86	1662.15
A_68_P32319552	chrX:34185014-34185058	NM_001081956:373	Akap17b	INSIDE	0.988	2.118	578.43	1225.19	2.093	337.18	705.86
A_68_P25471454	chr7:128125669-128125713	NM_007672:136	Cdr2	INSIDE	0.988	1.885	713.74	1345.06	1.861	641.60	1194.29
A_68_P25956954	chr8:73993612-73993656	NM_025600:542	Dda1	INSIDE	0.988	2.090	419.93	877.79	2.065	348.89	720.56
A_68_P29241526	chr13:96374600-96374644	NM_010169:13766	F2r	INSIDE	0.988	2.375	420.52	998.80	2.346	341.74	801.61
A_68_P21874509	chr2:174124950-174124994	NM_201617:1613	Gnas	INSIDE	0.988	1.802	1248.85	2250.76	1.780	1032.70	1838.30
A_68_P31116850	chr17:27649440-27649484	NM_001013385:-9213	Grm4	PROMOTER	0.988	0.464	1307.14	606.05	0.458	1107.42	507.50
A_68_P23415960	chr4:151383595-151383639	NM_001033352:617	Klhl21	INSIDE	0.988	2.642	365.93	966.95	2.610	381.00	994.36
A_68_P22629215	chr3:148482907-148482960	NM_001081298:134666	Lphn2	INSIDE	0.988	2.062	396.38	817.25	2.036	345.95	704.50
A_68_P30350167	chr15:76546156-76546200	NM_198119:6425	Lrrc24	INSIDE	0.988	0.557	993.26	553.73	0.551	692.99	381.75
A_68_P22312500	chr3:88018418-88018462	NR_037276:-652	Mir3093	PROMOTER	0.988	0.606	1184.88	718.54	0.599	1037.70	621.45
A_68_P24466502	chr6:54922369-54922413	NM_001171007:-735	Nod1	PROMOTER	0.988	0.532	1305.33	694.96	0.526	1238.16	651.16
A_68_P31375069	chr17:79419723-79419767	NM_001171004:412	Prkd3	INSIDE	0.988	2.266	1129.26	2559.25	2.238	1105.71	2474.92
A_68_P26629967	chr9:72704625-72704669	NM_175485:49566	Prtg	INSIDE	0.988	2.087	1229.92	2566.27	2.062	1035.26	2134.25
A_68_P26892620	chr9:122930391-122930435	NM_001164823:-31	Tmem42	PROMOTER	0.988	1.660	1637.69	2718.51	1.640	1357.42	2226.35
A_68_P24972906	chr7:13366070-13366114	NM_001017955:-5085	Zscan18	PROMOTER	0.988	1.737	885.58	1537.96	1.715	816.81	1400.82
A_68_P31219173	chr17:48925797-48925845			Unknown	0.988	2.862	1780.84	5096.60	2.828	1310.40	3705.23
A_68_P20121784	chr1:30930609-30930653	ENSMUST00000046443:-91		PROMOTER	0.988	2.362	671.98	1587.49	2.335	631.87	1475.50
A_68_P20162424	chr1:38893271-38893315	ENSMUST00000147695:-357		PROMOTER	0.988	1.663	900.96	1498.38	1.644	918.20	1509.18
A_68_P25545210	chr7:141416870-141416914	NM_007400:-112	Adam12	PROMOTER	0.987	0.527	3050.15	1608.49	0.520	2311.17	1202.90
A_68_P27100727	chr10:43230406-43230450	NM_199028:31483	Bend3	INSIDE	0.987	1.976	388.54	767.63	1.949	336.31	655.53
A_68_P23904971	chr5:96590602-96590646	NM_178854:150	Cnot6l	INSIDE	0.987	2.438	17179.15	41888.87	2.407	12504.52	30097.85
A_68_P27594243	chr11:11925830-11925874	NM_001177629:2122	Grb10	INSIDE	0.987	1.542	1367.93	2109.57	1.522	1134.56	1726.73
A_68_P27340039	chr10:90564881-90564925	NM_027078:19119	Ikbip	INSIDE	0.987	4.260	1141.69	4863.62	4.203	888.96	3736.56
A_68_P27235135	chr10:70844350-70844394	NM_027184:33832	Ipmk	INSIDE	0.987	1.742	677.75	1180.30	1.719	606.33	1041.97
A_68_P22314304	chr3:88335424-88335468	NM_001029890:-870	Mex3a	PROMOTER	0.987	1.540	2407.80	3708.04	1.520	1959.91	2979.61
A_68_P27282834	chr10:79844741-79844785	NM_198615:5634	Mex3d	INSIDE	0.987	2.711	1230.65	3336.19	2.676	1166.58	3122.22
A_68_P26381826	chr9:28210925-28210969	NM_177906:612093	Opcml	INSIDE	0.987	1.813	1215.38	2203.13	1.790	1027.37	1838.58
A_68_P30012298	chr15:10644202-10644246	NM_030690:-929	Rai14	PROMOTER	0.987	0.565	1508.75	851.97	0.557	1348.68	751.79
A_68_P31256954	chr17:56705768-56705812	NM_001029979:18216	Safb2	INSIDE	0.987	2.550	2205.86	5625.21	2.517	1821.96	4585.77
A_68_P27325551	chr10:87922155-87922200	NM_011517:-154	Sycp3	PROMOTER	0.987	2.836	1525.67	4326.28	2.798	1185.52	3317.35
A_68_P29039174	chr13:52733712-52733756	NM_011518:41484	Sykb	INSIDE	0.987	1.718	1739.03	2988.28	1.696	1396.85	2369.41
A_68_P30140502	chr15:36723196-36723240	NM_011740:1075	Ywhaz	INSIDE	0.987	0.545	1024.90	558.38	0.538	905.44	486.70
A_68_P25637837	chr8:8690176-8690220	NM_176849:339	Arglu1	INSIDE	0.986	2.475	501.48	1241.14	2.440	479.12	1169.03
A_68_P25961590	chr8:74998787-74998831	NM_138585:324	Cherp	INSIDE	0.986	0.477	1545.33	737.31	0.470	1282.48	603.28
A_68_P24122082	chr5:137041507-137041551	NM_198602:1747	Cux1	INSIDE	0.986	0.558	1320.70	736.48	0.550	1047.86	576.37
A_68_P31537508	chr18:20217493-20217537	NM_013505:492	Dsc2	INSIDE	0.986	1.542	3097.57	4775.46	1.520	2366.96	3597.67
A_68_P32152396	chr19:47939880-47939924	NM_030051:-132	Gsto2	PROMOTER	0.986	0.455	1277.20	580.60	0.448	948.67	425.33
A_68_P25004860	chr7:25217492-25217536	NM_199013:13187	Irgc1	INSIDE	0.986	3.089	315.26	973.74	3.046	319.86	974.28
A_68_P25096864	chr7:53356069-53356113	NM_010602:-483	Kcnj11	PROMOTER	0.986	1.440	1508.67	2171.80	1.419	1155.14	1639.24
A_68_P31847802	chr18:77680387-77680431	NM_172834:159712	Loxhd1	INSIDE	0.986	3.351	903.31	3027.01	3.304	787.80	2602.59
A_68_P25370886	chr7:108147189-108147233	NM_008773:13295	P2ry2	INSIDE	0.986	3.180	1765.03	5612.30	3.136	1453.99	4560.23
A_68_P28323159	chr12:30687550-30687594	NM_181395:64672	Pxdn	INSIDE	0.986	2.115	1291.19	2730.50	2.085	957.93	1997.51
A_68_P32135694	chr19:45063945-45063989	NM_011976:133	Sema4g	INSIDE	0.986	2.952	1421.68	4196.36	2.909	1054.56	3067.81
A_68_P21133066	chr2:35192576-35192620	NM_013515:-69	Stom	PROMOTER	0.986	3.443	1961.74	6753.71	3.393	1605.99	5449.21
A_68_P26785091	chr9:103207385-103207429	NM_176979:-250	Topbp1	PROMOTER	0.986	1.447	1636.94	2369.01	1.428	1412.41	2016.41
A_68_P20350605	chr1:74847285-74847329	NM_009518:8714	Wnt10a	INSIDE	0.986	1.688	608.84	1027.91	1.665	595.63	991.60

						Sham group			TiO$_2$-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27541020	chr10:127814573-127814617	NM_172790:415	Ankrd52	INSIDE	0.985	0.631	1965.33	1239.93	0.622	1591.53	989.50
A_68_P24114167	chr5:135462404-135462448	NM_009902:343	Cldn3	INSIDE	0.985	2.183	1046.48	2284.14	2.150	760.25	1634.22
A_68_P26224695	chr8:123651891-123651935	NM_008024:328	Foxl1	INSIDE	0.985	1.820	560.55	1019.98	1.792	564.55	1011.86
A_68_P21901458	chr2:179839037-179839081	NM_133849:-131	Hrh3	PROMOTER	0.985	0.618	7051.52	4360.75	0.609	5215.24	3177.94
A_68_P21309975	chr2:69423669-69423713	NM_001081088:434	Lrp2	INSIDE	0.985	0.495	1031.62	510.89	0.488	895.81	437.07
A_68_P28523609	chr12:72076112-72076156	NM_011184:525	Psma3	INSIDE	0.985	2.430	1255.42	3050.49	2.394	1012.48	2424.02
A_68_P25035179	chr7:31911519-31911563	NM_011322:424	Scn1b	INSIDE	0.985	0.534	2896.12	1547.08	0.526	2303.42	1212.61
A_68_P30465080	chr15:96530202-96530246	NM_175121:-95	Slc38a2	PROMOTER	0.985	1.470	1227.30	1804.41	1.449	1141.11	1653.36
A_68_P31096054	chr17:24343797-24343841	NM_001163847:-1311	Tbc1d24	PROMOTER	0.985	1.682	848.25	1426.70	1.657	666.97	1104.98
A_68_P26398235	chr9:30838331-30838375	NM_001115130:124	Zbtb44	INSIDE	0.985	2.720	648.26	1763.40	2.680	666.22	1785.42
A_68_P32783800	chrX:157736299-157736343	ENSMUST00000141946:10933		INSIDE	0.985	1.914	995.11	1904.90	1.885	437.04	823.86
A_68_P27212535	chr10:67011075-67011119	NM_001005419:607	Ado	INSIDE	0.984	1.617	666.68	1077.75	1.591	637.98	1014.87
A_68_P30371309	chr15:80118848-80118907	NM_001044308:1210	Cacna1i	INSIDE	0.984	5.900	779.90	4601.09	5.802	448.47	2602.24
A_68_P26129047	chr8:107064724-107064768	NM_053070:40	Car7	INSIDE	0.984	1.474	916.78	1351.33	1.450	845.35	1225.81
A_68_P20350878	chr1:74901948-74901992	NM_009872:368	Cdk5r2	INSIDE	0.984	0.588	1237.48	727.57	0.578	1135.59	656.87
A_68_P21177697	chr2:44412424-44412468	NM_172662:304696	Gtdc1	DOWNSTREAM	0.984	1.679	1570.50	2637.29	1.652	1391.55	2299.44
A_68_P23912410	chr5:97820982-97821026	NM_001033191:345	Naa11	INSIDE	0.984	2.256	490.34	1106.15	2.221	444.91	988.06
A_68_P21350021	chr2:76245111-76245155	NM_145525:538	Osbpl6	INSIDE	0.984	1.465	1364.17	1998.50	1.442	1121.09	1616.89
A_68_P27924665	chr11:74992221-74992265	NM_027136:68	Ovca2	INSIDE	0.984	1.688	562.63	949.91	1.661	630.56	1047.52
A_68_P24117610	chr5:136209906-136209950	NM_008898:44845	Por	INSIDE	0.984	2.490	1005.36	2503.21	2.450	783.90	1920.31
A_68_P24770500	chr6:115312177-115312222	NM_001127330:961	Pparg	INSIDE	0.984	2.309	1915.39	4422.92	2.273	1607.28	3653.70
A_68_P27675740	chr11:29593694-29593738	NM_194051:-57	Rtn4	PROMOTER	0.984	1.512	1435.95	2171.48	1.488	1135.39	1689.32
A_68_P31253476	chr17:56176213-56176257	NM_013664:-235	Sh3gl1	DIVERGENT_PROMOTER	0.984	0.587	1319.85	774.32	0.577	1060.50	612.42
A_68_P20156313	chr1:37921860-37921904	NM_207228:42	Tsga10	INSIDE	0.984	1.487	1303.87	1938.34	1.463	1176.17	1720.15
A_68_P25735811	chr8:28089322-28089366	NM_001101502:1537	Zfp703	INSIDE	0.984	2.211	722.22	1596.76	2.177	719.20	1565.39
A_68_P29477491	chr14:26279234-26279278	NM_183208:586	Zmiz1	INSIDE	0.984	0.604	984.40	594.36	0.594	968.91	575.69
A_68_P20644617	chr1:138112450-138112494	NM_028872:18369	5730559C18Rik	INSIDE	0.983	2.441	1365.18	3332.74	2.399	1098.98	2636.37
A_68_P25024595	chr7:29747291-29747335	NM_021895:-13	Actn4	PROMOTER	0.983	2.055	665.06	1366.71	2.021	658.59	1330.70
A_68_P21007915	chr2:11700413-11700457	NM_177268:1055	Ankrd16	INSIDE	0.983	0.592	2052.73	1215.02	0.582	1741.63	1013.63
A_68_P26126978	chr8:106666653-106666697	NM_009868:41150	Cdh5	INSIDE	0.983	3.899	1326.26	5170.47	3.831	1011.90	3876.40
A_68_P21768603	chr2:155782523-155782567	NM_001129999:251	Cep250	INSIDE	0.983	1.502	1093.14	1641.73	1.476	1008.19	1487.72
A_68_P23815279	chr5:76733734-76733778	NM_007715:-183	Clock	PROMOTER	0.983	2.763	1443.94	3990.20	2.717	1235.94	3358.32
A_68_P33007788	chr4_random:128082-128126	NM_001033326:18303	Dhrsx	INSIDE	0.983	3.352	7826.58	26236.45	3.294	5918.35	19497.41
A_68_P25547702	chr7:141862476-141862520	NM_001033420:129	Dock1	INSIDE	0.983	2.493	457.48	1140.66	2.451	472.49	1158.29
A_68_P32127591	chr19:43689143-43689187	NM_008699:2350	Nkx2-3	INSIDE	0.983	1.958	1635.82	3203.36	1.925	1398.23	2691.74
A_68_P24161581	chr5:145306987-145307031	NM_016789:253	Nptx2	INSIDE	0.983	2.154	644.33	1388.03	2.118	590.96	1251.53
A_68_P31256442	chr17:56615968-56616012	NM_011218:-87	Ptprs	PROMOTER	0.983	1.977	580.47	1147.41	1.944	511.02	993.22
A_68_P21098345	chr2:29475651-29475695	NM_001039086:433	Rapgef1	INSIDE	0.983	1.737	1341.38	2329.43	1.706	1157.13	1974.37
A_68_P23364322	chr4:141034341-141034385	NM_019763:60150	Spen	INSIDE	0.983	1.865	847.60	1580.36	1.834	654.27	1199.61
A_68_P23330842	chr4:135412186-135412230	NM_001080387:202	Srsf10	INSIDE	0.983	0.521	1242.43	647.70	0.512	1088.35	557.75
A_68_P20016448	chr1:7388275-7388319	ENSMUST00000138711:-414		PROMOTER	0.983	1.639	587.94	963.72	1.611	509.66	820.91
A_68_P26291033	chr9:8134257-8134301	NM_001045524:16	AK129341	INSIDE	0.982	1.967	652.48	1283.63	1.932	584.75	1129.52
A_68_P32316569	chrX:33565828-33565872	NM_001009947:137024	Dock11	INSIDE	0.982	2.289	707.75	1620.24	2.248	378.57	851.21
A_68_P20352250	chr1:75139665-75139709	NM_170755:327	Fam134a	INSIDE	0.982	1.521	1512.86	2300.82	1.493	1259.14	1879.97
A_68_P30514665	chr16:5255833-5255877	NM_027446:195	Fam86	INSIDE	0.982	1.983	1225.66	2430.13	1.946	1036.48	2017.19
A_68_P25371479	chr7:108257513-108257557	NM_001146010:246	Fchsd2	INSIDE	0.982	1.998	6387.90	12762.35	1.961	4591.22	9004.18
A_68_P27543732	chr10:128328704-128328748	NM_010272:48	Gdf11	INSIDE	0.982	2.630	937.32	2465.40	2.584	847.16	2189.11
A_68_P22843572	chr4:36897429-36897473	NM_001165999:1327	Lingo2	INSIDE	0.982	0.645	1435.10	925.78	0.634	1199.28	759.94
A_68_P31930680	chr19:5757972-5758016	NM_008520:17091	Ltbp3	INSIDE	0.982	1.847	483.48	893.10	1.813	444.87	806.68
A_68_P28946344	chr13:36083419-36083472	NM_201358:125781	Lyrm4	INSIDE	0.982	5.879	1093.48	6428.24	5.775	840.65	4854.98
A_68_P27971539	chr11:83258360-83258404	NM_080453:18081	Mmp28	INSIDE	0.982	1.664	670.72	1115.84	1.633	551.82	901.11

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P24161578	chr5:145306716-145306760	NM_016789:-17	Nptx2	PROMOTER	0.982	2.101	570.06	1197.44	2.062	580.45	1196.88
A_68_P31442547	chr17:91487821-91487865	NM_020252:4300	Nrxn1	INSIDE	0.982	3.202	406.13	1300.31	3.143	359.60	1130.32
A_68_P28103446	chr11:106640661-106640705	NR_027785:147	Polg2	INSIDE	0.982	1.592	592.32	942.93	1.564	572.64	895.33
A_68_P29073065	chr13:58504155-58504199	NM_001168248:219	Rmi1	INSIDE	0.982	0.545	1789.99	976.38	0.535	1472.97	788.63
A_68_P26873497	chr9:119518976-119519024	NM_001205321:109150	Scn10a	INSIDE	0.982	2.249	395.25	888.94	2.208	352.59	778.39
A_68_P26365991	chr9:25059906-25059950	NM_001205367:-111	Septin7	PROMOTER	0.982	0.432	1574.16	680.02	0.424	1299.28	551.07
A_68_P21116240	chr2:32442707-32442751	NM_011373:-281	St6galnac4	PROMOTER	0.982	1.714	3043.54	5215.76	1.683	2300.64	3871.68
A_68_P23309116	chr4:131477634-131477678	NM_001201367:-29	Tmem200b	PROMOTER	0.982	3.207	560.76	1798.08	3.147	490.19	1542.84
A_68_P25452560	chr7:124524755-124524799	NM_175645:284	Xylt1	INSIDE	0.982	5.654	1157.92	6546.38	5.552	859.09	4769.48
A_68_P31932464	chr19:6061914-6061958	NM_013859:730	Znhit2-ps	INSIDE	0.982	0.578	1225.76	708.18	0.567	1047.98	594.59
A_68_P27282330	chr10:79767570-79767614	NM_011789:3028	Apc2	INSIDE	0.981	2.687	2411.80	6480.44	2.637	2069.36	5456.03
A_68_P27298383	chr10:83111269-83111313	NM_145220:119	Appl2	INSIDE	0.981	1.653	611.68	1011.10	1.621	543.45	881.12
A_68_P20456918	chr1:95582954-95582998	NM_016778:706	Bok	INSIDE	0.981	1.672	797.07	1332.57	1.639	709.43	1163.04
A_68_P23498122	chr5:15441040-15441084	NM_001110843:554	Cacna2d1	INSIDE	0.981	3.337	461.34	1539.61	3.275	428.80	1404.37
A_68_P27543294	chr10:128242682-128242726	NM_028873:-27	Dnajc14	DIVERGENT_PROMOTER	0.981	2.385	701.76	1673.61	2.340	607.95	1422.84
A_68_P20351022	chr1:74929216-74929260	NM_153111:2744	Fev	INSIDE	0.981	2.452	1021.02	2503.69	2.406	878.87	2114.20
A_68_P26319136	chr9:14555274-14555318	NM_010242:1270	Fut4	INSIDE	0.981	1.700	938.39	1594.98	1.668	793.74	1323.68
A_68_P25842942	chr8:48759661-48759705	NM_023503:831	Ing2	INSIDE	0.981	1.818	1503.05	2733.00	1.784	1379.85	2461.33
A_68_P27843264	chr11:60290404-60290448	NM_001103171:7586	Myo15	INSIDE	0.981	2.251	944.66	2126.86	2.208	790.14	1744.35
A_68_P29700850	chr14:70751126-70751170	NM_001135152:-2908	Slc39a14	PROMOTER	0.981	1.396	3974.76	5547.45	1.369	3527.42	4830.41
A_68_P21831890	chr2:166612210-166612254	NM_023815:-7034	Trp53rk	PROMOTER	0.981	1.675	591.75	991.20	1.643	505.29	830.18
A_68_P22349909	chr3:96361476-96361535	NM_001009935:-374	Txnip	PROMOTER	0.981	2.409	240.78	579.98	2.362	193.65	457.45
A_68_P25499303	chr7:133343931-133343975	NM_028816:-30	Xpo6	PROMOTER	0.981	2.118	1438.07	3045.89	2.078	1286.10	2672.31
A_68_P28608874	chr12:87585109-87585153	NM_027405:2303	1700020O03Rik	INSIDE	0.980	2.404	1351.32	3248.52	2.355	1093.47	2575.42
A_68_P31849429	chr18:77952019-77952063	NM_178670:709	8030462N17Rik	INSIDE	0.980	1.975	1675.16	3307.91	1.935	1583.02	3062.53
A_68_P24469555	chr6:55402357-55402401	NM_001025372:405	Adcyap1r1	INSIDE	0.980	0.596	1623.90	968.08	0.584	1361.30	795.29
A_68_P32385501	chrX:50410354-50410398	NR_038184:-9	C430049B03Rik	PROMOTER	0.980	2.333	2763.72	6446.59	2.286	1385.34	3166.64
A_68_P22822458	chr4:32702338-32702382	NM_001122978:-87	Casp8ap2	PROMOTER	0.980	1.454	1112.22	1617.57	1.425	940.84	1340.41
A_68_P24122109	chr5:137044884-137044928	NM_009986:-1605	Cux1	PROMOTER	0.980	1.796	1029.52	1848.75	1.760	1002.70	1765.00
A_68_P23325563	chr4:134480163-134480207	NM_023665:645	D4Wsu53e	INSIDE	0.980	2.435	330.16	803.87	2.387	339.16	809.61
A_68_P23192161	chr4:107356258-107356302	NM_019872:487	Dmrtb1	INSIDE	0.980	2.526	702.73	1774.96	2.474	651.76	1612.74
A_68_P26319147	chr9:14556469-14556513	NM_010242:76	Fut4	INSIDE	0.980	2.217	666.39	1477.29	2.173	654.42	1421.96
A_68_P24537468	chr6:71583029-71583078	NM_001038695:-154	Kdm3a	PROMOTER	0.980	3.072	2362.22	7256.83	3.009	1491.92	4489.71
A_68_P25034847	chr7:31852339-31852383	NM_144556:7407	Lgi4	INSIDE	0.980	1.931	685.05	1322.98	1.894	571.57	1082.27
A_68_P23193224	chr4:107526867-107526911	NM_001080926:52025	Lrp8	INSIDE	0.980	1.745	678.85	1184.64	1.710	524.48	896.80
A_68_P22222512	chr3:69526351-69526395	NM_133787:396	Nmd3	INSIDE	0.980	0.562	1321.36	742.32	0.551	1101.43	606.69
A_68_P30346616	chr15:76011981-76012026	NM_201394:14137	Plec	INSIDE	0.980	3.494	444.43	1552.78	3.423	351.97	1204.88
A_68_P23984174	chr5:111611967-111612011	NM_024477:303167	Ttc28	INSIDE	0.980	1.823	494.07	900.72	1.786	446.67	797.79
A_68_P27287687	chr10:80607189-80607233	NM_010731:8195	Zbtb7a	INSIDE	0.980	2.194	1251.84	2747.00	2.150	909.51	1955.09
A_68_P20319175	chr1:69424592-69424636			Unknown	0.980	1.944	1354.40	2632.93	1.906	1157.69	2206.49
A_68_P23368579	chr4:141795272-141795316	NM_001109685:22	9030409G11Rik	INSIDE	0.979	0.536	1130.87	606.50	0.525	963.86	506.31
A_68_P26349675	chr9:21748731-21748775	NM_144935:6035	BC018242	INSIDE	0.979	2.028	2302.75	4669.95	1.986	1619.03	3214.96
A_68_P32097107	chr19:37773571-37773615	NM_007811:1295	Cyp26a1	INSIDE	0.979	0.471	1173.84	553.24	0.462	971.49	448.39
A_68_P32227249	chr19:60866612-60866656	NM_010123:-38	Eif3a	PROMOTER	0.979	1.523	952.50	1450.73	1.491	853.67	1272.68
A_68_P28865543	chr13:20183326-20183370	NM_080288:973	Elmo1	INSIDE	0.979	1.481	1756.61	2601.79	1.451	1422.94	2064.20
A_68_P25780170	chr8:36558186-36558230	NM_026067:379	Eri1	INSIDE	0.979	0.426	1745.28	743.68	0.417	1319.80	550.56
A_68_P25087552	chr7:51718008-51718052	NM_198250:20174	Lrrc4b	INSIDE	0.979	1.656	1325.45	2194.73	1.620	1247.49	2021.43
A_68_P25601671	chr7:150734944-150734988	NM_008672:29	Nap1l4	INSIDE	0.979	0.592	2591.99	1534.04	0.579	2194.30	1271.39
A_68_P30473222	chr15:97951292-97951336	NM_021514:8824	Pfkm	INSIDE	0.979	1.863	545.73	1016.79	1.823	461.51	841.56
A_68_P26203591	chr8:120114052-120114099	NM_172285:91885	Plcg2	INSIDE	0.979	3.164	265.78	841.05	3.097	227.03	703.15
A_68_P31154936	chr17:34768097-34768141	NM_030890:1488	Prrt1	INSIDE	0.979	2.065	2168.30	4478.42	2.021	1633.94	3302.25

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P30348895	chr15:76352647-76352691	NM_130893:-109	Scrt1	PROMOTER	0.979	3.249	1080.22	3510.05	3.180	978.98	3112.86
A_68_P21584533	chr2:121943910-121943954	NM_145531:190	Spg11	INSIDE	0.979	2.006	585.34	1173.93	1.963	566.39	1112.05
A_68_P23996936	chr5:113649993-113650037	NM_001033428:-5914	Tmem211	PROMOTER	0.979	0.612	2611.36	1597.81	0.599	2278.23	1364.43
A_68_P29051403	chr13:54890672-54890716	NM_028841:-71	Tspan17	PROMOTER	0.979	1.507	4407.64	6640.25	1.475	3326.99	4906.93
A_68_P23756860	chr5:65929084-65929128	NM_016786:607	Ube2k	INSIDE	0.979	0.642	2315.85	1486.66	0.629	1880.74	1182.58
A_68_P30572505	chr16:17201070-17201114	NM_009456:493	Ube2l3	INSIDE	0.979	2.566	2010.01	5156.91	2.513	1795.94	4512.98
A_68_P24007964	chr5:115577031-115577075	NM_175352:7932	Unc119b	INSIDE	0.979	2.099	973.47	2043.29	2.054	724.83	1488.77
A_68_P26891838	chr9:122775033-122775077	NM_173364:70	Zfp445	INSIDE	0.979	0.664	1036.49	687.72	0.649	953.74	619.36
A_68_P25505248	chr7:134486671-134486730	NM_146202:2128	Zfp768	INSIDE	0.979	6.394	365.83	2339.20	6.262	286.34	1792.97
A_68_P20637767	chr1:137043374-137043418	NM_026823:-14	Arl8a	PROMOTER	0.978	1.852	842.77	1561.15	1.812	798.09	1446.17
A_68_P21866714	chr2:172766163-172766207	NM_007557:-390	Bmp7	PROMOTER	0.978	1.710	2912.63	4981.20	1.672	2002.53	3348.33
A_68_P28153230	chr11:115255314-115255358	NM_001080929:12107	Cdr2l	INSIDE	0.978	2.087	1160.03	2420.95	2.041	962.20	1963.40
A_68_P28685876	chr12:102321244-102321288	NR_038047:606	D130020L05Rik	INSIDE	0.978	1.571	845.94	1329.10	1.536	916.73	1408.13
A_68_P32206764	chr19:57435985-57436029	NM_145505:508	Fam160b1	INSIDE	0.978	1.877	766.09	1437.58	1.835	641.15	1176.82
A_68_P31927963	chr19:5306888-5306932	NM_001024717:8580	Gal3st3	INSIDE	0.978	1.720	1482.12	2548.76	1.683	1307.41	2199.86
A_68_P23404326	chr4:149475854-149475898	NM_177366:14265	Gpr157	INSIDE	0.978	2.830	193.87	548.74	2.768	190.58	527.50
A_68_P28703478	chr12:105710469-105710513	NM_010351:956	Gsc	INSIDE	0.978	0.389	2081.81	810.77	0.381	1827.05	695.76
A_68_P31304340	chr17:66460894-66460938	NM_001037757:-68	ORF19	PROMOTER	0.978	0.395	1369.36	541.08	0.386	1096.00	423.59
A_68_P23322025	chr4:133842588-133842632	NM_001163794:558	Pdik1l	INSIDE	0.978	0.636	1898.42	1207.09	0.622	1390.50	864.79
A_68_P24777648	chr6:116623614-116623658	NM_178045:218	Rassf4	INSIDE	0.978	1.595	1647.73	2628.07	1.560	1354.69	2112.89
A_68_P30956056	chr16:90283863-90283907	NM_178923:786	Scaf4	INSIDE	0.978	1.505	968.35	1457.62	1.473	817.58	1204.02
A_68_P26887499	chr9:122026546-122026590	NM_001164572:185	Snrk	INSIDE	0.978	2.202	834.93	1838.70	2.155	752.48	1621.30
A_68_P22059401	chr3:36570355-36570399	NM_019510:18713	Trpc3	INSIDE	0.978	2.619	791.95	2074.36	2.561	664.29	1701.35
A_68_P31016358	chr17:5342260-5342304	NM_001085355:347209	Arid1b	INSIDE	0.977	3.958	1777.33	7034.09	3.867	1236.33	4780.80
A_68_P23440035	chr4:155068628-155068672	NM_178699:200	B930041F14Rik	INSIDE	0.977	2.625	577.01	1514.58	2.565	549.08	1408.63
A_68_P22412463	chr3:108209838-108209882	NM_001004177:8552	Celsr2	INSIDE	0.977	3.198	2283.82	7304.78	3.125	1809.95	5656.47
A_68_P21425367	chr2:91762276-91762320	NM_007699:-47	Chrm4	PROMOTER	0.977	0.585	1082.72	633.06	0.571	830.94	474.49
A_68_P25948482	chr8:72406463-72406507	NM_026818:4807	Cilp2	INSIDE	0.977	1.583	988.34	1564.68	1.547	916.61	1417.58
A_68_P29140850	chr13:73741332-73741376	NM_146047:-95	Clptm1l	PROMOTER	0.977	3.296	1111.79	3664.29	3.221	902.09	2905.54
A_68_P31150930	chr17:34048600-34048644	NM_001199733:2077	Daxx	INSIDE	0.977	2.635	446.63	1176.68	2.575	432.74	1114.31
A_68_P26581361	chr9:64189105-64189149	NM_001001295:-62	Dis3l	PROMOTER	0.977	0.556	1025.28	570.46	0.543	945.90	514.00
A_68_P21877293	chr2:174586128-174586172	NM_007903:-123	Edn3	PROMOTER	0.977	2.024	1003.70	2031.23	1.978	878.99	1738.72
A_68_P23363267	chr4:140864773-140864817	NM_010139:7640	Epha2	INSIDE	0.977	2.644	875.68	2315.66	2.584	763.89	1974.11
A_68_P29083939	chr13:60277184-60277228	NM_008086:1690	Gas1	INSIDE	0.977	0.670	2245.18	1505.13	0.655	1665.53	1090.72
A_68_P20679836	chr1:145586729-145586773	NM_001038594:-826	Glrx2	PROMOTER	0.977	0.615	1449.85	891.55	0.601	1225.25	735.82
A_68_P21338760	chr2:74520854-74520898	NM_008273:427	Hoxd11	INSIDE	0.977	2.046	572.41	1171.33	1.998	554.02	1107.19
A_68_P26674975	chr9:81525929-81525973	NM_010482:209	Htr1b	INSIDE	0.977	0.622	1087.38	676.59	0.608	832.45	506.22
A_68_P26423542	chr9:35378046-35378090	NM_029762:-414	Hyls1	PROMOTER	0.977	1.684	2019.99	3401.85	1.645	1561.96	2570.02
A_68_P25031178	chr7:31141047-31141091	NM_175478:6723	Lrfn3	INSIDE	0.977	2.315	750.13	1736.85	2.261	577.61	1306.04
A_68_P28095691	chr11:105224580-105224624	NM_172568:93447	Marchf10	INSIDE	0.977	3.035	583.50	1770.92	2.964	478.99	1419.92
A_68_P24591434	chr6:83052524-83052568	NM_026744:-6555	Mrpl53	PROMOTER	0.977	0.487	1127.49	548.90	0.476	917.90	436.65
A_68_P24974396	chr7:13639929-13639973	NM_145819:163	Mzf1	INSIDE	0.977	0.684	1426.34	975.04	0.668	1160.36	775.00
A_68_P21820162	chr2:164683144-164683188	NM_011125:42	Pltp	INSIDE	0.977	0.491	1594.58	783.21	0.480	1299.47	623.55
A_68_P27267071	chr10:76728631-76728675	NM_030262:6608	Pofut2	INSIDE	0.977	2.304	738.07	1700.60	2.251	591.94	1332.31
A_68_P32957128	chr17:8534244-8534288	NM_178774:663	Prr18	INSIDE	0.977	1.822	1223.40	2229.03	1.781	1129.82	2012.17
A_68_P26825466	chr9:110629375-110629419	NM_001083936:15718	Pth1r	INSIDE	0.977	3.170	3255.82	10320.97	3.097	2223.98	6888.59
A_68_P21843310	chr2:168575642-168575686	NM_175303:17037	Sall4	INSIDE	0.977	1.713	525.29	899.66	1.674	475.38	795.59
A_68_P21116407	chr2:32470667-32470711	NM_001025310:8208	St6galnac6	INSIDE	0.977	3.117	1219.51	3800.73	3.045	1024.38	3118.84
A_68_P27507136	chr10:121534175-121534219	NM_153059:-38	Tmem5	PROMOTER	0.977	1.616	1674.61	2706.35	1.580	1416.59	2237.63
A_68_P22059402	chr3:36570442-36570486	NM_019510:18625	Trpc3	INSIDE	0.977	2.023	1040.82	2105.14	1.976	850.40	1680.54
A_68_P30379485	chr15:81602412-81602456	NM_001081016:27157	Zc3h7b	INSIDE	0.977	2.220	1012.45	2247.43	2.168	780.10	1691.56

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27781839	chr11:49017033-49017077	NM_001024846:53	Zfp62	INSIDE	0.977	2.007	2219.29	4454.45	1.961	1945.58	3814.57
A_68_P29059922	chr13:56322977-56323021	ENSMUST00000127754:22303		DOWNSTREAM	0.977	2.973	957.88	2847.64	2.903	849.62	2466.71
A_68_P23576262	chr5:31370994-31371038	NM_023525:13833	Cad	INSIDE	0.976	1.979	1458.58	2886.34	1.932	1161.40	2243.57
A_68_P21114928	chr2:32218406-32218450	NM_028412:-325	Ciz1	DIVERGENT_PROMOTER	0.976	1.869	506.90	947.20	1.824	508.52	927.35
A_68_P27278592	chr10:79198242-79198286	NM_008226:18886	Hcn2	INSIDE	0.976	1.766	1097.74	1938.15	1.724	1007.25	1736.10
A_68_P32147194	chr19:47089078-47089122	NM_146100:-87	Ina	PROMOTER	0.976	0.523	3667.21	1916.31	0.510	3001.83	1531.16
A_68_P21147645	chr2:38207336-38207380	NM_010710:531	Lhx2	INSIDE	0.976	0.632	864.99	546.87	0.617	799.66	493.45
A_68_P32135962	chr19:45100671-45100715	NM_001130526:8068	Lzts2	INSIDE	0.976	3.964	1514.94	6005.14	3.870	1213.70	4696.96
A_68_P30370604	chr15:80003678-80003722	NM_010795:-450	Mgat3	PROMOTER	0.976	2.172	11821.68	25672.58	2.119	8110.50	17184.88
A_68_P28174637	chr11:118770429-118770473	NM_001024931:436	Rbfox3	INSIDE	0.976	0.661	4278.64	2827.43	0.645	3798.84	2451.21
A_68_P25090604	chr7:52263215-52263259	NM_001008422:8383	Scaf1	INSIDE	0.976	2.000	1363.86	2727.31	1.952	1035.03	2020.16
A_68_P28469857	chr12:60113204-60113248	NM_009147:-222	Sec23a	DIVERGENT_PROMOTER	0.976	1.644	6327.96	10405.71	1.605	4641.74	7448.01
A_68_P25049870	chr7:36322643-36322687	NM_028034:99	Tdrd12	INSIDE	0.976	3.088	6114.63	18884.77	3.015	4637.15	13983.05
A_68_P30849198	A_68_P30849198			Unknown	0.976	3.231	305.26	986.23	3.154	328.75	1036.88
A_68_P23226517	chr4:115570669-115570713	ENSMUST00000165938:7420		INSIDE	0.976	1.480	2350.66	3479.43	1.445	1926.69	2783.98
A_68_P27686041	chr11:31865736-31865780	NM_026262:126	4930524B15Rik	INSIDE	0.975	3.018	695.12	2098.16	2.944	570.19	1678.47
A_68_P30338797	chr15:74502578-74502622	NM_018790:400	Arc	INSIDE	0.975	1.540	1185.35	1825.67	1.502	1091.35	1639.54
A_68_P31067114	chr17:15867919-15867967	NM_007690:26012	Chd1	INSIDE	0.975	2.854	324.90	927.39	2.784	305.46	850.25
A_68_P29671492	chr14:65696284-65696328	NM_018788:20637	Extl3	INSIDE	0.975	2.313	280.87	649.69	2.256	233.85	527.46
A_68_P27185079	chr10:61732442-61732486	NM_001146100:70705	Hk1	INSIDE	0.975	4.017	4116.51	16537.39	3.916	2906.27	11380.05
A_68_P23637418	chr5:42154713-42154757	NM_007524:725	Nkx3-2	INSIDE	0.975	0.641	1306.67	837.10	0.624	1040.15	649.42
A_68_P30421712	chr15:88692211-88692255	NM_145478:-391	Pim3	PROMOTER	0.975	0.602	1174.67	707.32	0.587	937.72	550.57
A_68_P30346543	chr15:76003047-76003091	NM_201394:23072	Plec	INSIDE	0.975	1.828	787.27	1439.32	1.782	693.63	1235.86
A_68_P30447267	chr15:93331510-93331555	NM_001033217:94790	Prickle1	INSIDE	0.975	2.282	442.94	1010.69	2.224	375.40	835.01
A_68_P21747514	chr2:151907523-151907567	NM_001160410:280	Scrt2	INSIDE	0.975	0.649	1094.32	710.30	0.633	926.81	586.47
A_68_P26239400	chr8:125877888-125877932	NM_172287:21298	Spire2	INSIDE	0.975	3.363	569.51	1915.37	3.278	381.42	1250.24
A_68_P25425957	chr7:119823141-119823185	NM_001166584:329	Tead1	INSIDE	0.975	2.037	684.18	1393.77	1.986	652.73	1296.55
A_68_P25026078	chr7:30023443-30023487	NM_001110201:123	Yif1b	INSIDE	0.975	0.662	2872.41	1900.29	0.645	2226.40	1436.72
A_68_P24118492	chr5:136387366-136387410	NM_018871:23123	Ywhag	INSIDE	0.975	2.877	598.14	1720.58	2.805	533.54	1496.64
A_68_P24951462	chr7:4945928-4945972	NM_026741:1753	Zfp579	INSIDE	0.975	1.980	447.72	886.71	1.932	421.27	813.87
A_68_P30602964	A_68_P30602964			Unknown	0.975	3.257	472.59	1539.02	3.175	456.35	1448.71
A_68_P28094596	chr11:105026660-105026704	ENSMUST00000118770:1252		INSIDE	0.975	2.859	451.76	1291.45	2.787	369.47	1029.71
A_68_P23340288	chr4:137074524-137074568	NM_008305:49829	Hspg2	INSIDE	0.974	2.648	2867.07	7590.62	2.579	2334.33	6021.37
A_68_P25044863	chr7:35439623-35439667	NM_146188:-1784	Kctd15	PROMOTER	0.974	0.607	867.27	526.51	0.591	726.25	429.41
A_68_P29177385	chr13:81850332-81850377	NM_028372:-61	Mblac2	DIVERGENT_PROMOTER	0.974	0.339	2536.50	860.53	0.331	1973.15	652.29
A_68_P25954890	chr8:73437278-73437322	NM_173013:7428	Mtap1s	INSIDE	0.974	2.538	1489.36	3779.47	2.471	1139.43	2815.52
A_68_P29482962	chr14:27489116-27489160	NM_178668:194	Pde12	INSIDE	0.974	0.620	1054.13	653.29	0.603	913.26	551.02
A_68_P24984542	chr7:17612840-17612884	NM_011155:401	Ppp5c	INSIDE	0.974	2.416	1936.40	4678.89	2.353	1557.84	3665.03
A_68_P31311925	chr17:67704118-67704162	NM_008984:-341	Ptprm	PROMOTER	0.974	0.640	1013.74	648.50	0.623	863.34	537.95
A_68_P30365304	chr15:79082520-79082564	NM_020516:2636	Slc16a8	INSIDE	0.974	1.490	1849.42	2754.95	1.451	1669.98	2422.87
A_68_P32143399	chr19:46423459-46423503	NM_029186:-7889	Tmem180	PROMOTER	0.974	1.987	383.91	762.94	1.936	368.41	713.20
A_68_P22973922	chr4:63678515-63678559	NM_011607:29513	Tnc	INSIDE	0.974	2.302	1958.86	4509.35	2.242	1621.52	3636.18
A_68_P23204068	chr4:109723690-109723734			Unknown	0.974	2.594	696.53	1806.75	2.526	702.31	1774.22
A_68_P31623411	chr18:36508072-36508116	NM_001081365:-183	0610010O12Rik	PROMOTER	0.973	1.908	2562.23	4888.73	1.857	1780.99	3307.21
A_68_P31619440	chr18:35814836-35814880	NM_027222:-5837	2010001M09Rik	PROMOTER	0.973	0.503	1312.48	660.13	0.489	1101.28	538.76
A_68_P21037978	chr2:17969077-17969121	NM_028317:978	2810030E01Rik	INSIDE	0.973	3.426	2318.78	7943.93	3.335	1828.23	6097.29
A_68_P26521622	chr9:53418206-53418250	NM_144784:227	Acat1	INSIDE	0.973	1.614	810.98	1308.68	1.571	834.70	1311.19
A_68_P32020401	chr19:23968179-23968223	NM_177034:134835	Apba1	INSIDE	0.973	2.201	1184.79	2607.64	2.142	992.30	2125.58
A_68_P22186537	chr3:62143246-62143290	NM_001081295:570	Arhgef26	INSIDE	0.973	0.638	963.31	614.91	0.621	959.28	595.76
A_68_P31977527	chr19:16059339-16059383	NM_198019:119	Cep78	INSIDE	0.973	0.683	1481.56	1012.63	0.665	1291.48	858.95
A_68_P30511521	chr16:4679480-4679524	NM_030205:218	Coro7	INSIDE	0.973	1.445	2711.21	3917.38	1.405	2028.75	2851.38

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P30576507	chr16:17911333-17911377	NM_001081633:87	Dgcr14	INSIDE	0.973	2.101	834.08	1752.47	2.045	708.67	1448.95
A_68_P27490918	chr10:118890399-118890443	NM_133442:-949	Grip1	PROMOTER	0.973	0.502	1232.00	618.41	0.488	1005.16	490.87
A_68_P25945210	chr8:71405256-71405300	NM_008509:825	Lpl	INSIDE	0.973	0.518	2080.67	1077.04	0.503	1764.77	888.48
A_68_P26506085	chr9:50665071-50665115	NM_028614:53	Ppp2r1b	INSIDE	0.973	1.439	2614.80	3762.33	1.400	2172.63	3042.22
A_68_P21838401	chr2:167757841-167757885	NM_011201:36	Ptpn1	INSIDE	0.973	0.517	1051.70	544.18	0.503	1023.82	515.47
A_68_P24428216	chr6:48546831-48546875	NM_001079901:2971	Repin1	INSIDE	0.973	2.168	619.59	1343.25	2.108	512.76	1081.08
A_68_P27222447	chr10:68675289-68675333	NM_001081347:-94	Rhobtb1	PROMOTER	0.973	2.827	932.84	2636.79	2.751	756.59	2081.29
A_68_P30118686	chr15:32174840-32174884	NM_009154:295	Sema5a	INSIDE	0.973	0.599	910.67	545.19	0.583	707.60	412.35
A_68_P27552579	chr11:3435873-3435917	NM_001159284:3401	Smtn	INSIDE	0.973	1.752	588.70	1031.64	1.705	579.55	988.06
A_68_P20345417	chr1:73953929-73953973	NM_027884:217071	Tns1	DOWNSTREAM	0.973	2.227	855.46	1905.15	2.168	732.78	1588.49
A_68_P25506523	chr7:134758122-134758166	NM_177226:-197	Zfp629	PROMOTER	0.973	0.526	1502.29	790.72	0.512	1249.45	640.12
A_68_P30560721	chr16:14159223-14159267	NM_001081154:123	4921513D23Rik	INSIDE	0.972	1.435	2759.99	3961.06	1.395	1903.99	2655.38
A_68_P23602806	chr5:36100352-36100396	NM_001177696:-154	Ablim2	PROMOTER	0.972	1.753	649.81	1138.80	1.704	549.81	936.86
A_68_P28688688	chr12:103196108-103196152	NM_029705:323	Atxn3	INSIDE	0.972	1.468	1945.95	2856.10	1.427	1782.70	2544.49
A_68_P33015625	chr1_random:51092-51145	NM_026866:134220	Disp1	INSIDE	0.972	4.052	232.86	943.57	3.940	203.36	801.25
A_68_P27849839	chr11:61498513-61498557	NM_178618:623	Fam83g	INSIDE	0.972	1.531	2052.44	3143.21	1.489	1596.08	2376.43
A_68_P21874750	chr2:174153901-174153945	NM_001077510:-1667	Gnas	PROMOTER	0.972	1.869	1350.12	2523.31	1.816	1243.89	2259.27
A_68_P23753095	chr5:65213443-65213487	NM_008453:18703	Klf3	INSIDE	0.972	2.420	4090.97	9899.64	2.352	3096.05	7281.08
A_68_P27180706	chr10:60938993-60939037	NM_153542:434	Lrrc20	INSIDE	0.972	1.527	1138.09	1738.17	1.484	1050.16	1558.88
A_68_P26551402	chr9:58884501-58884545	NM_001042752:-274	Neo1	PROMOTER	0.972	3.181	2515.51	8000.97	3.092	2099.48	6492.63
A_68_P21823566	chr2:165213753-165213797	NM_178411:-15	Zfp334	PROMOTER	0.972	0.615	1111.51	683.48	0.598	920.96	550.71
A_68_P24951457	chr7:4945305-4945349	NM_026741:2377	Zfp579	INSIDE	0.972	1.821	1574.76	2867.78	1.770	1306.81	2312.55
A_68_P23320094	chr4:133466780-133466824	AK015234:96		INSIDE	0.972	1.863	826.65	1539.80	1.811	730.81	1323.62
A_68_P26215962	chr8:122292157-122292201	NM_028883:10138	4632415K11Rik	INSIDE	0.971	2.449	626.16	1533.72	2.378	518.40	1232.88
A_68_P27473558	chr10:115550897-115550941	NM_001161855:55	4933416C03Rik	INSIDE	0.971	1.953	1190.25	2324.22	1.897	1072.90	2035.22
A_68_P28171533	chr11:118338257-118338301	NM_172573:5	Engase	INSIDE	0.971	0.462	1195.86	552.07	0.448	1010.57	452.84
A_68_P24024962	chr5:118605340-118605384	NM_172721:105	Fbxw8	INSIDE	0.971	1.612	660.95	1065.53	1.566	626.27	980.71
A_68_P29660046	chr14:63859832-63859876	NM_008092:4243	Gata4	INSIDE	0.971	2.882	834.39	2404.36	2.798	736.16	2059.75
A_68_P21874752	chr2:174154225-174154269	NM_001077510:-1343	Gnas	PROMOTER	0.971	2.941	634.88	1867.23	2.855	572.98	1635.85
A_68_P28266914	chr12:16807531-16807575	NM_015764:140	Greb1	INSIDE	0.971	2.246	630.05	1414.97	2.181	603.58	1316.49
A_68_P21840418	chr2:168094705-168094749	NM_001081134:105	Kcng1	INSIDE	0.971	3.398	1086.03	3689.96	3.301	884.92	2920.90
A_68_P22530124	chr3:130809206-130809257	NM_010703:-4157	Lef1	PROMOTER	0.971	1.913	454.89	870.06	1.858	426.51	792.38
A_68_P32135963	chr19:45100793-45100839	NM_001130526:8192	Lzts2	INSIDE	0.971	1.825	849.89	1551.07	1.772	641.09	1135.76
A_68_P29437674	chr14:19071169-19071213	NM_011584:430	Nr1d2	INSIDE	0.971	0.578	1302.30	753.13	0.562	1184.57	665.39
A_68_P26825588	chr9:110645482-110645526	NM_001083936:-390	Pth1r	PROMOTER	0.971	0.599	3626.38	2172.34	0.582	2620.71	1525.09
A_68_P20878434	chr1:182834646-182834690	NM_133705:264	Pycr2	INSIDE	0.971	3.018	557.10	1681.11	2.930	528.81	1549.31
A_68_P32099687	chr19:38199117-38199161	NM_011255:163	Rbp4	INSIDE	0.971	0.608	907.04	551.75	0.590	788.52	465.61
A_68_P27795628	chr11:51577154-51577198	NM_025535:12	Sar1b	INSIDE	0.971	1.390	3060.05	4254.21	1.350	2587.65	3494.02
A_68_P30575738	chr16:17797523-17797567	NM_153790:170	Scarf2	INSIDE	0.971	2.068	6359.23	13153.07	2.009	4977.00	9996.54
A_68_P22286845	chr3:83570356-83570400	NM_009144:136	Sfrp2	INSIDE	0.971	1.885	816.44	1538.69	1.830	721.69	1320.64
A_68_P28116268	chr11:108873014-108873058	ENSMUST00000119655:4072		DOWNSTREAM	0.971	1.853	1103.12	2044.13	1.799	840.74	1512.54
A_68_P25087019	chr7:51615634-51615678	NM_027049:14744	1700008O03Rik	INSIDE	0.970	0.615	983.82	605.52	0.597	851.36	508.18
A_68_P28525479	chr12:72411396-72411440	NM_001190466:548	Dact1	INSIDE	0.970	1.623	5022.66	8149.95	1.573	3551.70	5587.56
A_68_P28157767	chr11:116029485-116029529	NM_172571:-14	Fbf1	PROMOTER	0.970	5.003	341.38	1707.97	4.851	315.61	1531.16
A_68_P29101872	chr13:65213921-65213965	NM_001083901:348	Hiatl1	INSIDE	0.970	2.047	374.73	766.90	1.984	340.45	675.61
A_68_P27950544	chr11:79517837-79517881	NR_029579:-7612	Mir193	PROMOTER	0.970	1.806	857.19	1547.81	1.752	653.94	1145.67
A_68_P24055453	chr5:123845311-123845355	NM_177582:505	Mlxip	INSIDE	0.970	0.648	1420.28	920.71	0.629	1159.24	729.07
A_68_P31632606	chr18:38358924-38358968	NM_029357:10470	Pcdh1	INSIDE	0.970	2.628	1795.93	4719.59	2.549	1291.78	3292.12
A_68_P32745693	chrX:147954890-147954934	NM_177201:-302	Phf8	PROMOTER	0.970	2.347	3293.57	7730.06	2.277	1522.83	3467.79
A_68_P25972617	chr8:77737759-77737803	NM_029182:-62	Rasd2	PROMOTER	0.970	2.110	1152.07	2430.50	2.047	1049.70	2149.08
A_68_P27275565	chr10:78243326-78243370	NM_009200:108	Slc1a6	INSIDE	0.970	1.966	597.28	1174.40	1.908	617.78	1178.55

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P24092031	chr5:130555095-130555139	NM_001130476:-239	Tpst1	PROMOTER	0.970	3.754	1010.19	3791.84	3.639	843.27	3068.80
A_68_P29438117	chr14:19159490-19159534	NM_009455:4846	Ube2e1	INSIDE	0.970	1.437	1631.20	2343.89	1.393	1450.95	2021.53
A_68_P20191088	chr1:43884115-43884159	NM_026430:417	Uxs1	INSIDE	0.970	1.583	1301.83	2060.39	1.535	1120.06	1719.28
A_68_P20350533	chr1:74838685-74838729	NM_009518:114	Wnt10a	INSIDE	0.970	0.740	2570.24	1900.83	0.717	2048.58	1469.73
A_68_P31939674	chr19:7491304-7491348	NM_175381:-788	2700081O15Rik	PROMOTER	0.969	1.520	965.20	1466.89	1.473	876.30	1291.04
A_68_P22150381	chr3:54703304-54703351	NM_177854:16482	6030405A18Rik	INSIDE	0.969	3.070	393.95	1209.27	2.975	324.90	966.51
A_68_P23417009	chr4:151552981-151553025	NM_001146057:-7240	Acot7	PROMOTER	0.969	1.607	1097.55	1763.26	1.556	935.98	1456.63
A_68_P27809325	chr11:54117457-54117501	NM_001033597:-227	Acsl6	PROMOTER	0.969	1.779	3088.94	5494.13	1.723	2481.90	4276.18
A_68_P21105432	chr2:30679697-30679741	NM_133346:4102	Asb6	INSIDE	0.969	2.592	539.86	1399.11	2.511	410.86	1031.65
A_68_P32536864	chrX:91226158-91226202	NR_028320:12186	AU015836	DOWNSTREAM	0.969	2.802	483.67	1355.22	2.714	255.56	693.61
A_68_P27649723	chr11:24064200-24064244	NM_001159290:83528	Bcl11a	INSIDE	0.969	2.943	1208.68	3556.93	2.851	1018.30	2903.27
A_68_P28452660	chr12:56701063-56701107	NM_020287:1181	Insm2	INSIDE	0.969	0.396	1845.14	731.48	0.384	1511.96	580.89
A_68_P32029537	chr19:25484593-25484638	NM_181404:172924	Kank1	INSIDE	0.969	3.483	2154.07	7501.80	3.374	1536.95	5185.68
A_68_P27267070	chr10:76728491-76728535	NM_030262:6468	Pofut2	INSIDE	0.969	2.232	1263.16	2819.82	2.163	1016.41	2198.40
A_68_P24428218	chr6:48547068-48547112	NM_001079901:3209	Repin1	INSIDE	0.969	2.236	1659.60	3710.07	2.165	1377.35	2982.11
A_68_P25228918	chr7:80554115-80554159	NM_177740:33731	Rgma	INSIDE	0.969	2.092	1099.96	2301.04	2.027	810.80	1643.35
A_68_P23339116	chr4:136852284-136852328	NM_009523:18757	Wnt4	INSIDE	0.969	4.338	1849.93	8025.39	4.202	1426.82	5995.50
A_68_P27287689	chr10:80607406-80607450	NM_010731:8413	Zbtb7a	INSIDE	0.969	1.930	911.26	1758.90	1.871	733.71	1372.55
A_68_P27686040	chr11:31865634-31865678	NM_026262:24	4930524B15Rik	INSIDE	0.968	2.096	2028.28	4251.89	2.029	1642.47	3332.84
A_68_P28612729	chr12:88224702-88224747	NM_145836:1040	6430527G18Rik	INSIDE	0.968	0.417	1236.63	515.22	0.403	1032.77	416.67
A_68_P28724527	chr12:109155388-109155432	NM_001079883:86214	Bcl11b	INSIDE	0.968	2.041	561.66	1146.15	1.976	454.74	898.70
A_68_P23818501	chr5:77286574-77286618	NM_001163793:16973	C530008M17Rik	INSIDE	0.968	3.192	3341.82	10666.19	3.091	2226.22	6881.31
A_68_P26844413	chr9:114299730-114299774	NM_019922:78	Crtap	INSIDE	0.968	1.794	1238.57	2222.39	1.737	1120.55	1946.50
A_68_P31227870	chr17:50432887-50432931	NM_010021:16	Dazl	INSIDE	0.968	2.598	1094.53	2843.43	2.515	1119.65	2816.38
A_68_P30642684	chr16:30601415-30601459	NM_177632:1628	Fam43a	INSIDE	0.968	1.593	696.07	1109.15	1.542	591.69	912.32
A_68_P32026433	chr19:24974465-24974509	NM_008022:1313	Foxd4	INSIDE	0.968	0.614	2497.57	1532.41	0.594	2040.07	1212.09
A_68_P24674234	chr6:97567426-97567470	NM_145148:203	Frmd4b	INSIDE	0.968	1.614	1134.36	1830.40	1.562	960.93	1501.12
A_68_P23417689	chr4:151654150-151654194	NM_178406:5702	Gpr153	INSIDE	0.968	2.088	484.12	1011.08	2.021	413.55	835.63
A_68_P31313936	chr17:68046719-68046763	NM_008480:136	Lama1	INSIDE	0.968	2.073	687.64	1425.35	2.007	726.58	1458.48
A_68_P25031177	chr7:31140943-31140987	NM_175478:6827	Lrfn3	INSIDE	0.968	2.651	681.89	1807.68	2.566	563.90	1446.71
A_68_P23326916	chr4:134708430-134708475	NM_019732:31893	Runx3	INSIDE	0.968	3.717	197.36	733.68	3.599	176.25	634.34
A_68_P21018171	chr2:13715028-13715072	NM_145838:97	St8sia6	INSIDE	0.968	0.641	2543.71	1630.95	0.620	2023.22	1255.36
A_68_P25959800	chr8:74659745-74659789	NM_001001491:576	Tpm4	INSIDE	0.968	0.745	4219.91	3142.70	0.721	3224.85	2324.62
A_68_P30363605	chr15:78813442-78813487	NM_001024716:-21	Triobp	PROMOTER	0.968	2.827	243.95	689.73	2.737	220.11	602.41
A_68_P27365512	chr10:94977939-94977984	NM_080560:166	Ube2n	INSIDE	0.968	2.585	249.26	644.23	2.502	214.67	537.14
A_68_P24168282	chr5:147197029-147197073	NM_145155:469	Wasf3	INSIDE	0.968	0.480	2103.45	1008.98	0.464	1741.66	808.88
A_68_P25008271	chr7:25866888-25866932	NM_175477:4646	Zfp574	INSIDE	0.968	1.565	762.61	1193.64	1.516	665.04	1008.12
A_68_P32565627	chrX:98989595-98989639	ENSMUST00000151231:-378		DIVERGENT_PROMOTER	0.968	4.679	438.11	2050.04	4.528	224.84	1017.97
A_68_P27899786	chr11:70068857-70068903	NM_007440:-37	Alox12	PROMOTER	0.967	3.348	1152.40	3858.56	3.238	1063.01	3441.50
A_68_P27503065	chr10:120802501-120802545	NM_029364:377	Gns	INSIDE	0.967	1.927	842.41	1623.03	1.863	818.41	1524.87
A_68_P27278589	chr10:79197977-79198021	NM_008226:18620	Hcn2	INSIDE	0.967	1.636	723.89	1184.53	1.583	647.23	1024.38
A_68_P25599895	chr7:150481208-150481262	NR_001461:1218	Kcnq1ot1	INSIDE	0.967	2.362	3496.10	8256.61	2.284	2538.78	5797.90
A_68_P21816616	chr2:163996879-163996923	NM_008435:-51	Kcns1	PROMOTER	0.967	1.663	1066.31	1773.00	1.607	941.67	1513.49
A_68_P25951933	chr8:72975932-72975976	NM_001122830:24888	Klhl26	INSIDE	0.967	2.973	391.33	1163.61	2.876	331.47	953.16
A_68_P26216538	chr8:122394181-122394225	NM_146219:7998	Klhl36	INSIDE	0.967	2.742	396.15	1086.42	2.652	320.98	851.10
A_68_P27950594	chr11:79524651-79524695	NR_029579:-798	Mir193	PROMOTER	0.967	0.620	2065.30	1280.80	0.600	1682.46	1008.83
A_68_P28055768	chr11:98200119-98200163	NM_010895:-9181	Neurod2	DIVERGENT_PROMOTER	0.967	0.422	1482.50	625.98	0.408	1382.24	564.18
A_68_P29056694	chr13:55828552-55828596	NM_028281:-154	Pcbd2	PROMOTER	0.967	3.181	542.75	1726.57	3.078	548.22	1687.25
A_68_P24994416	chr7:20214165-20214209	NM_009046:601	Relb	INSIDE	0.967	2.034	1502.25	3055.02	1.967	1131.46	2226.11
A_68_P24950762	chr7:4788423-4788469	NM_172737:7852	Shisa7	INSIDE	0.967	3.937	2138.58	8419.16	3.806	1674.67	6373.12
A_68_P26849143	chr9:115218715-115218759	NM_024222:803	Stt3b	INSIDE	0.967	1.821	859.50	1565.13	1.761	790.59	1392.07

						Sham group			TiO$_2$-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P23331726	chr4:135577649-135577693	NM_013736:-106	Tceb3	PROMOTER	0.967	1.640	2011.60	3299.36	1.587	1605.53	2547.20
A_68_P26323063	chr9:15297918-15297962	AK146267:65		INSIDE	0.967	2.930	319.57	936.38	2.833	315.23	893.07
A_68_P21326874	chr2:72472122-72472166	ENSMUST00000120282:152		INSIDE	0.967	2.729	563.77	1538.69	2.638	482.34	1272.48
A_68_P30665798	chr16:34745356-34745400	ENSMUST00000155268:83		INSIDE	0.967	2.005	1256.21	2518.85	1.938	1092.85	2118.02
A_68_P21774856	chr2:156866097-156866141	NM_001164663:38883	9830001H06Rik	INSIDE	0.966	2.841	512.26	1455.22	2.745	425.38	1167.58
A_68_P23320879	chr4:133628861-133628905	NM_001162970:4516	Aim1l	INSIDE	0.966	1.869	858.03	1603.98	1.806	718.83	1297.94
A_68_P32533284	chrX:90544387-90544431	NM_007492:12424	Arx	DOWNSTREAM	0.966	1.941	861.31	1671.88	1.874	610.59	1144.38
A_68_P27173579	chr10:59766022-59766066	NM_023370:393194	Cdh23	INSIDE	0.966	2.433	773.97	1883.27	2.351	600.60	1412.11
A_68_P25020922	chr7:29062595-29062639	NM_001177427:-108	Eid2b	PROMOTER	0.966	1.803	848.63	1530.30	1.742	688.20	1198.81
A_68_P24003588	chr5:114830147-114830191	NM_001159941:346	Kctd10	INSIDE	0.966	2.081	10672.79	22213.64	2.011	6353.84	12779.78
A_68_P31922935	chr19:4397029-4397073	NM_001001984:27	Kdm2a	INSIDE	0.966	1.675	8529.86	14284.03	1.618	5892.29	9532.24
A_68_P31601517	chr18:32322542-32322586	NM_011946:-178	Map3k2	PROMOTER	0.966	1.986	334.24	663.95	1.918	394.56	756.93
A_68_P24990477	chr7:19511769-19511813	NM_001029877:554	Nova2	INSIDE	0.966	1.589	2661.36	4228.37	1.535	1824.74	2800.68
A_68_P27181450	chr10:61088648-61088692	NM_001177511:30439	Npffr1	INSIDE	0.966	0.577	1670.78	964.19	0.557	1354.64	755.13
A_68_P25953724	chr8:73267060-73267104	NM_201607:19120	Pde4c	INSIDE	0.966	2.033	643.26	1307.89	1.965	544.13	1069.02
A_68_P22522615	chr3:129581952-129581996	NM_183423:-2127	Pla2g12a	PROMOTER	0.966	7.610	7942.28	60438.52	7.351	4845.14	35618.85
A_68_P23430799	chr4:153715942-153715986	NM_001177995:295018	Prdm16	INSIDE	0.966	5.873	4321.20	25379.65	5.673	3110.20	17644.01
A_68_P31256001	chr17:56562089-56562133	NM_011218:53793	Ptprs	INSIDE	0.966	1.883	390.47	735.39	1.819	354.17	644.21
A_68_P22523680	chr3:129763666-129763710	NM_207209:137	Sec24b	INSIDE	0.966	0.599	2451.45	1468.27	0.578	2098.65	1213.61
A_68_P32203282	chr19:56901047-56901091	NM_001002241:-4133	Tdrd1	PROMOTER	0.966	2.627	1661.33	4363.70	2.538	1401.68	3557.37
A_68_P29049666	chr13:54569805-54569849	NM_028597:375	Thoc3	INSIDE	0.966	3.584	11387.77	40816.57	3.462	7150.73	24752.26
A_68_P32700063	chrX:137133904-137133948	NM_001077364:1135	Tsc22d3	INSIDE	0.966	3.058	458.56	1402.22	2.954	315.96	933.49
A_68_P21931967	chr3:8327343-8327387			Unknown	0.966	3.401	1379.32	4691.57	3.287	1266.35	4162.24
A_68_P24944609	chr6:149310012-149310056	ENSMUST00000120260:-173		DIVERGENT_PROMOTER	0.966	2.507	614.97	1541.84	2.423	559.63	1355.90
A_68_P28184669	chr11:120319314-120319358	NM_025560:41	1810049H13Rik	INSIDE	0.965	1.683	696.59	1172.54	1.625	646.08	1049.91
A_68_P20412921	chr1:88483574-88483618	NM_172974:-78	Cops7b	DIVERGENT_PROMOTER	0.965	1.634	769.01	1256.72	1.578	612.63	966.60
A_68_P32467036	chrX:71491383-71491427	NM_010227:469	Flna	INSIDE	0.965	1.705	3377.47	5757.93	1.645	1360.61	2238.20
A_68_P22661983	chr3:153991849-153991908	NM_010713:1646	Lhx8	INSIDE	0.965	2.132	1134.10	2418.22	2.057	981.86	2019.46
A_68_P23955549	chr5:105910183-105910227	NM_001033550:65411	Lrrc8b	INSIDE	0.965	2.192	617.55	1353.45	2.116	554.46	1173.09
A_68_P24946818	chr7:3637479-3637523	NM_029934:7627	Mboat7	INSIDE	0.965	3.062	1927.97	5902.77	2.955	1574.12	4651.46
A_68_P27843267	chr11:60290696-60290740	NM_001103171:7878	Myo15	INSIDE	0.965	1.793	1689.47	3029.45	1.731	1177.08	2036.99
A_68_P29237614	chr13:95655500-95655544	NM_011021:9941	Otp	DOWNSTREAM	0.965	2.514	220.86	555.15	2.426	219.41	532.18
A_68_P26492040	chr9:48288627-48288671	NM_024233:68	Rexo2	INSIDE	0.965	0.662	3589.28	2375.05	0.639	3021.85	1929.84
A_68_P32415805	chrX:58146252-58146296	NM_009237:331	Sox3	INSIDE	0.965	2.384	899.27	2143.43	2.300	498.80	1147.02
A_68_P23416139	chr4:151406623-151406667	NM_031867:5955	Tas1r1	INSIDE	0.965	2.616	2348.04	6143.61	2.526	1773.68	4479.83
A_68_P27943938	chr11:78349603-78349647	NM_001159392:138	Tnfaip1	INSIDE	0.965	0.517	1417.60	733.32	0.499	1037.53	517.97
A_68_P24002087	chr5:114580701-114580745	NM_011677:-442	Ung	PROMOTER	0.965	0.327	1848.49	603.84	0.315	1538.96	485.30
A_68_P30511262	chr16:4640285-4640329	NM_139307:362	Vasn	INSIDE	0.965	0.597	1099.81	656.89	0.576	985.82	568.05
A_68_P29390921	chr14:9498720-9498764	NM_028934:62	4930452B06Rik	INSIDE	0.964	0.733	2147.08	1574.57	0.707	1850.66	1308.08
A_68_P23293013	chr4:128444472-128444516	NM_001009819:7993	A3galt2	INSIDE	0.964	1.601	921.37	1475.32	1.543	656.77	1013.69
A_68_P22482405	chr3:122123152-122123204	NM_013867:481	Bcar3	INSIDE	0.964	3.352	284.01	951.99	3.231	218.22	705.12
A_68_P23574101	chr5:31013677-31013721	NM_023047:-569	Dpysl5	PROMOTER	0.964	2.119	640.71	1357.36	2.042	550.25	1123.69
A_68_P27143973	chr10:53471309-53471353	NM_001081428:-615	Fam184a	PROMOTER	0.964	0.752	6136.58	4614.28	0.725	4835.20	3505.87
A_68_P28940416	chr13:34839156-34839200	NM_138746:7668	Fam50b	INSIDE	0.964	2.220	1030.54	2287.50	2.140	843.92	1805.91
A_68_P26658191	chr9:77961162-77961206	NM_019987:140	Ick	INSIDE	0.964	0.562	2159.68	1214.59	0.542	1848.77	1002.06
A_68_P33012165	chr9_random:55589-55633	NM_011154:-578	Ppp2r3d	PROMOTER	0.964	0.513	1365.48	700.53	0.495	1157.80	572.79
A_68_P20412584	chr1:88421724-88421768	NM_008972:-1564	Ptma	PROMOTER	0.964	0.590	1192.90	703.68	0.569	943.08	536.36
A_68_P23308588	chr4:131393415-131393459	NM_001083119:757	Ptpru	INSIDE	0.964	4.245	16927.72	71856.67	4.093	10362.62	42409.37
A_68_P25025681	chr7:29946628-29946672	NM_182927:7016	Spred3	INSIDE	0.964	2.362	2182.95	5156.37	2.277	1803.38	4105.54
A_68_P23395335	chr4:147966100-147966144	NM_009272:501	Srm	INSIDE	0.964	1.600	1672.56	2676.41	1.543	1587.41	2449.95
A_68_P23608584	chr5:36924656-36924700	NM_133910:368	Tbc1d14	INSIDE	0.964	1.411	11401.18	16081.94	1.359	7749.20	10534.57

						Sham group			TiO$_2$-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31092363	chr17:23694927-23694971	NM_001033496:6245	Zfp213	INSIDE	0.964	2.598	1121.66	2913.77	2.505	900.96	2256.49
A_68_P21914376	chr3:3309284-3309328			Unknown	0.964	3.811	1027.34	3915.69	3.676	868.98	3194.30
A_68_P26403086	chr9:31839692-31839736			Unknown	0.964	0.617	1749.03	1079.72	0.595	1490.88	887.49
A_68_P26017564	chr8:86525774-86525820	NM_183097:192	1700067K01Rik	INSIDE	0.963	1.930	332.98	642.60	1.859	320.28	595.36
A_68_P22314994	chr3:88448009-88448053	NM_001198912:22715	Arhgef2	INSIDE	0.963	2.591	883.10	2288.09	2.494	829.48	2069.13
A_68_P28788966	chr13:3610442-3610486	NM_134063:-110	BC016423	PROMOTER	0.963	2.094	1375.50	2880.73	2.017	1151.33	2322.70
A_68_P24055363	chr5:123823490-123823534	NM_029850:29056	Bcl7a	INSIDE	0.963	2.687	2360.30	6341.13	2.586	1809.47	4679.46
A_68_P26055369	chr8:93352945-93352989	NM_177224:233	Chd9	INSIDE	0.963	1.857	723.30	1342.95	1.788	650.44	1163.16
A_68_P26349278	chr9:21656710-21656754	NM_177030:347	Dock6	INSIDE	0.963	2.223	462.16	1027.19	2.140	412.57	883.05
A_68_P32750744	chrX:149216782-149216826	NM_010951:341	Gpr143	INSIDE	0.963	1.507	1631.26	2457.98	1.452	937.50	1360.83
A_68_P29589396	chr14:49286130-49286176	NR_029384:-2810	Otx2os1	DIVERGENT_PROMOTER	0.963	3.952	186.22	735.89	3.805	161.62	615.03
A_68_P24898887	chr6:141198621-141198665	NM_018779:853	Pde3a	INSIDE	0.963	1.821	1527.37	2781.61	1.753	1246.35	2185.34
A_68_P31127303	chr17:29459319-29459363	NM_023734:3514	Pi16	INSIDE	0.963	3.564	6569.63	23416.27	3.433	4080.06	14007.31
A_68_P29701213	chr14:70828758-70828802	NM_021308:121	Piwil2	INSIDE	0.963	1.752	1106.00	1937.24	1.687	844.62	1424.66
A_68_P24424178	chr6:47601643-47601687	NR_002841:3429	Rn4.5s	DOWNSTREAM	0.963	1.971	5917.35	11664.09	1.899	5060.23	9607.70
A_68_P30489330	chr15:100884551-100884595	NM_011323:117871	Scn8a	DOWNSTREAM	0.963	1.855	882.90	1637.64	1.786	764.43	1365.66
A_68_P27911312	chr11:72224674-72224718	NM_177776:519	Smtnl2	INSIDE	0.963	1.476	5700.32	8414.10	1.421	4051.52	5758.33
A_68_P22386748	chr3:103380204-103380248	NM_018800:1023	Syt6	INSIDE	0.963	2.268	1445.24	3277.60	2.184	1339.00	2924.00
A_68_P30370355	chr15:79963981-79964036	NM_025609:425	Tab1	INSIDE	0.963	1.930	1201.95	2319.81	1.859	863.31	1604.63
A_68_P32203280	chr19:56900735-56900779	NM_001002240:-8	Tdrd1	PROMOTER	0.963	2.616	829.11	2169.16	2.520	640.53	1614.19
A_68_P26082679	chr8:97852246-97852290	NM_024467:3582	Zfp319	INSIDE	0.963	1.545	1141.63	1763.91	1.488	943.23	1403.44
A_68_P33007655	A_68_P33007655			Unknown	0.963	1.687	3501.59	5908.89	1.625	3706.54	6023.41
A_68_P29018252	chr13:48323302-48323346	ENSMUST00000143259:34668		INSIDE	0.963	0.456	1506.78	686.38	0.439	1250.98	548.78
A_68_P27100725	chr10:43230190-43230234	NM_199028:31267	Bend3	INSIDE	0.962	1.880	643.01	1208.91	1.810	472.27	854.59
A_68_P20528694	chr1:113761142-113761186	NM_001081316:331	Dsel	INSIDE	0.962	2.025	607.10	1229.49	1.949	594.41	1158.61
A_68_P24620357	chr6:88148628-88148672	NM_008090:-7	Gata2	PROMOTER	0.962	1.839	1623.52	2985.55	1.768	1387.12	2452.93
A_68_P21874751	chr2:174154053-174154097	NM_001077510:-1515	Gnas	PROMOTER	0.962	2.056	634.46	1304.31	1.978	668.48	1322.40
A_68_P24159777	chr5:144934590-144934634	NM_001081109:73308	Lmtk2	INSIDE	0.962	2.531	1229.86	3112.97	2.436	1028.45	2505.18
A_68_P21102108	chr2:30111813-30111859	NM_177725:18548	Lrrc8a	INSIDE	0.962	2.719	527.34	1433.95	2.617	456.35	1194.17
A_68_P30961946	chr16:91270379-91270423	NM_016968:387	Olig1	INSIDE	0.962	2.180	3404.57	7422.90	2.098	2602.93	5462.02
A_68_P20474071	chr1:99873584-99873628	NM_013626:118603	Pam	INSIDE	0.962	1.860	588.27	1094.41	1.790	514.69	921.12
A_68_P32114752	chr19:41450572-41450616	NM_031376:8966	Pik3ap1	INSIDE	0.962	1.895	907.28	1719.06	1.823	776.69	1415.58
A_68_P23271481	chr4:124664358-124664402	NM_138683:707	Rspo1	INSIDE	0.962	0.580	1089.79	632.44	0.558	934.84	522.03
A_68_P31123428	chr17:28758772-28758816	NM_016795:605	Srpk1	INSIDE	0.962	0.704	2057.92	1448.38	0.677	1632.02	1104.51
A_68_P25971567	chr8:77558116-77558160	NM_001136259:554	Tom1	INSIDE	0.962	0.608	1510.12	918.48	0.585	1209.47	707.74
A_68_P21875504	chr2:174282882-174282926	NM_001080971:6709	Tubb1	INSIDE	0.962	3.783	1344.89	5087.13	3.640	1020.41	3714.05
A_68_P31301685	chr17:65962800-65962844	NM_013933:73	Vapa	INSIDE	0.962	0.710	1375.96	977.26	0.683	1181.22	807.34
A_68_P28599174	chr12:85930850-85930894	NM_007701:20071	Vsx2	INSIDE	0.962	1.642	528.35	867.58	1.579	757.69	1196.38
A_68_P24424841	chr6:47855192-47855236	NM_146175:27661	Zfp282	INSIDE	0.962	1.687	1379.08	2326.54	1.623	1051.04	1706.17
A_68_P31219171	chr17:48925588-48925633			Unknown	0.962	1.856	595.33	1105.13	1.785	492.10	878.55
A_68_P24761357	chr6:113705166-113705210	NM_001036684:136182	Atp2b2	INSIDE	0.961	2.519	525.97	1324.93	2.420	444.96	1076.97
A_68_P25272114	chr7:88600003-88600048	NM_007755:-463	Cpeb1	PROMOTER	0.961	2.508	992.10	2488.33	2.411	823.50	1985.70
A_68_P21082466	chr2:26968285-26968329	NM_175427:29691	Fam163b	INSIDE	0.961	3.705	5130.49	19006.68	3.560	3391.22	12072.19
A_68_P21621960	chr2:128718146-128718190	NM_024237:28501	Fbln7	INSIDE	0.961	1.719	1152.19	1981.03	1.653	1082.09	1788.55
A_68_P21122756	chr2:33495852-33495899	NM_010725:156	Lmx1b	INSIDE	0.961	2.376	896.77	2130.85	2.284	673.54	1538.17
A_68_P25021325	chr7:29135852-29135896	NR_028129:-684	LOC100302567	PROMOTER	0.961	1.620	1713.15	2775.30	1.556	1245.43	1938.27
A_68_P28554434	chr12:77634454-77634498	NM_153804:-70	Plekhg3	PROMOTER	0.961	0.643	1525.63	980.27	0.617	1359.06	839.04
A_68_P30447392	chr15:93349977-93350021	NM_001033217:76324	Prickle1	INSIDE	0.961	3.097	1119.09	3465.84	2.975	1056.04	3141.88
A_68_P21227529	chr2:53937298-53937342	NM_023396:643	Rprm	INSIDE	0.961	1.937	1088.69	2108.54	1.862	991.20	1845.20
A_68_P28291143	chr12:25392901-25392945	NM_009104:-196	Rrm2	PROMOTER	0.961	0.648	4211.50	2730.99	0.623	3364.06	2096.64
A_68_P28469854	chr12:60112791-60112835	NM_009147:192	Sec23a	INSIDE	0.961	0.346	1613.18	558.72	0.333	1264.54	420.80

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26752042	chr9:97266348-97266392	NM_030219:4007	Trim42	INSIDE	0.961	2.286	1445.52	3304.90	2.197	1218.61	2677.25
A_68_P22485525	chr3:122687267-122687311	NM_133857:77	Usp53	INSIDE	0.961	0.525	2546.71	1336.85	0.504	1892.18	954.49
A_68_P26494144	A_68_P26494144			Unknown	0.961	2.117	1431.31	3029.98	2.034	1248.77	2540.55
A_68_P28175548	chr11:118914534-118914580			Unknown	0.961	1.700	648.78	1103.06	1.633	538.68	879.74
A_68_P23523567	chr5:20457129-20457173	NR_030699:344	A630072M18Rik	INSIDE	0.960	2.090	944.95	1974.83	2.007	815.25	1636.07
A_68_P24617814	chr6:87681107-87681152	NM_001159697:267	Ccdc48	INSIDE	0.960	1.855	826.58	1533.44	1.782	719.54	1281.91
A_68_P27172913	chr10:59648822-59648866	NM_016803:33164	Chst3	INSIDE	0.960	2.228	451.05	1004.98	2.139	347.59	743.61
A_68_P26221740	chr8:123192627-123192671	NM_009941:459	Cox4i1	INSIDE	0.960	0.620	1248.33	774.28	0.596	962.51	573.36
A_68_P24193750	chr5:151755531-151755575	NM_013823:371	Kl	INSIDE	0.960	0.401	1398.75	560.46	0.385	1214.61	467.10
A_68_P27270908	chr10:77365226-77365270	NM_145152:33	Lrrc3	INSIDE	0.960	1.586	5274.44	8363.88	1.522	3710.46	5647.16
A_68_P21127263	chr2:34226980-34227024	NM_016768:554	Pbx3	INSIDE	0.960	0.667	1242.41	828.21	0.640	1096.85	701.82
A_68_P31207974	chr17:46766268-46766312	NM_175168:163	Ptk7	INSIDE	0.960	0.658	1815.69	1195.39	0.632	1476.68	932.97
A_68_P20370953	chr1:78306980-78307024	NM_001004173:82	Sgpp2	INSIDE	0.960	0.643	1754.94	1128.30	0.617	1602.42	989.17
A_68_P28176530	chr11:119072055-119072099	NM_172443:17737	Tbc1d16	INSIDE	0.960	18.837	1910.68	35990.56	18.076	1455.53	26310.09
A_68_P27965916	chr11:82200818-82200862	NM_023438:-1561	Tmem132e	PROMOTER	0.960	0.512	1179.51	604.47	0.492	1055.62	519.23
A_68_P26247306	chr8:127245477-127245521	NM_145607:377	Ttc13	INSIDE	0.960	0.634	1928.51	1221.94	0.608	1659.64	1009.76
A_68_P23424872	chr4:152806992-152807036	NM_001099299:49925	Ajap1	INSIDE	0.959	2.196	1927.70	4232.39	2.106	1556.44	3277.19
A_68_P27298384	chr10:83111351-83111395	NM_145220:37	Appl2	INSIDE	0.959	0.551	1183.75	652.63	0.529	955.54	505.35
A_68_P29338035	chr13:113777889-113777933	NM_001081062:-99	Ccno	PROMOTER	0.959	1.858	648.69	1205.01	1.781	623.25	1109.76
A_68_P33015621	chr1_random:50610-50662	NM_026866:134702	Disp1	INSIDE	0.959	2.720	779.42	2120.03	2.607	615.67	1605.19
A_68_P25006992	chr7:25654882-25654927	NM_027732:-171	Dmrtc2	DIVERGENT_PROMOTER	0.959	2.247	829.70	1864.04	2.155	625.27	1347.61
A_68_P23335794	chr4:136326887-136326931	NM_010142:64942	Ephb2	INSIDE	0.959	3.026	2754.47	8334.68	2.901	2143.54	6218.37
A_68_P22293166	chr3:84619656-84619700	NM_001177773:180	Fbxw7	INSIDE	0.959	0.621	2197.02	1364.24	0.595	1721.42	1025.02
A_68_P24112566	chr5:134790011-134790055	NM_001080746:584	Gtf2i	INSIDE	0.959	1.604	864.13	1385.83	1.539	782.29	1203.64
A_68_P31113975	chr17:27194456-27194500	NM_080553:230	Itpr3	INSIDE	0.959	2.019	400.59	808.86	1.937	400.96	776.62
A_68_P28547082	chr12:76277823-76277867	NM_172805:475	Kcnh5	INSIDE	0.959	4.953	805.27	3988.38	4.751	744.42	3536.76
A_68_P26346082	chr9:21038221-21038265	NM_001110305:5534	Keap1	INSIDE	0.959	2.452	324.58	796.01	2.353	286.58	674.21
A_68_P27988569	chr11:86171411-86171455	NM_001080931:-405	Med13	PROMOTER	0.959	2.829	566.59	1602.62	2.712	538.16	1459.64
A_68_P30422884	chr15:88899097-88899141	NM_001002005:8963	Panx2	INSIDE	0.959	3.241	2929.63	9493.74	3.108	2032.62	6318.18
A_68_P31868009	chr18:81171208-81171252	NM_178280:12087	Sall3	INSIDE	0.959	2.177	435.61	948.22	2.089	400.11	835.66
A_68_P27942518	chr11:78114962-78115006	NM_017407:-108	Spag5	PROMOTER	0.959	0.500	1638.13	818.31	0.479	1327.25	635.91
A_68_P32114044	chr19:41338030-41338074	NM_133352:442	Tm9sf3	INSIDE	0.959	1.935	713.01	1379.85	1.856	642.13	1191.85
A_68_P25062054	chr7:38352951-38352995	NM_172385:201799	Zfp536	INSIDE	0.959	2.206	1504.60	3319.42	2.117	1255.26	2656.78
A_68_P33007021	A_68_P33007021			Unknown	0.959	1.848	19506.44	36045.89	1.772	15585.65	27618.44
A_68_P26323069	chr9:15298668-15298712	AK146267:815		INSIDE	0.959	1.413	2726.28	3853.27	1.356	1913.02	2593.92
A_68_P32288516	chrX:20002305-20002349	ENSMUST00000115384:-487		PROMOTER	0.959	1.727	690.49	1192.30	1.656	481.95	797.99
A_68_P22455157	chr3:117278382-117278426	NM_029425:26	4833424O15Rik	INSIDE	0.958	0.575	1998.63	1148.34	0.551	1726.16	950.40
A_68_P32795516	chrX:160347102-160347146	NM_026887:33	Ap1s2	INSIDE	0.958	1.975	1139.31	2249.72	1.893	776.14	1468.95
A_68_P22338536	chr3:94167827-94167871	NM_001136117:1483	C2cd4d	INSIDE	0.958	1.814	834.22	1513.20	1.739	827.50	1438.61
A_68_P21070566	chr2:25066778-25066822	NM_021393:209	Cobra1	INSIDE	0.958	1.451	2238.87	3248.01	1.390	1853.17	2576.21
A_68_P28575259	chr12:81440889-81440933	NM_177267:96678	Dcaf5	INSIDE	0.958	2.806	1783.02	5003.84	2.690	1431.13	3849.20
A_68_P28158193	chr11:116099596-116099640	NM_025276:-213	Evpl	PROMOTER	0.958	2.085	877.97	1830.20	1.997	809.10	1615.42
A_68_P20294244	chr1:64781733-64781777	NM_001042659:2570	Fzd5	INSIDE	0.958	4.143	704.93	2920.67	3.969	559.53	2220.89
A_68_P21750610	chr2:152512595-152512639	NM_025543:-267	Mcts2	PROMOTER	0.958	2.084	1033.76	2154.25	1.997	871.73	1741.04
A_68_P27843266	chr11:60290609-60290656	NM_001103171:7792	Myo15	INSIDE	0.958	2.232	981.08	2189.87	2.137	738.41	1578.32
A_68_P28185382	chr11:120434920-120434964	NM_011032:-692	P4hb	PROMOTER	0.958	0.560	954.84	534.66	0.536	717.26	384.58
A_68_P24117612	chr5:136210056-136210100	NM_008898:44995	Por	INSIDE	0.958	2.450	458.74	1123.78	2.346	371.55	871.64
A_68_P25728673	chr8:26830531-26830575	NM_028000:33	Ppapdc1b	INSIDE	0.958	3.163	1901.11	6013.56	3.031	1711.61	5187.95
A_68_P21817577	chr2:164219124-164219168	NM_009036:-9547	Rbpjl	PROMOTER	0.958	1.762	479.37	844.54	1.688	438.85	740.97
A_68_P21750312	chr2:152460407-152460451	NM_009047:7685	Rem1	INSIDE	0.958	2.295	837.19	1921.38	2.199	827.94	1820.40
A_68_P26539387	chr9:56775942-56775986	NM_175483:214	Snx33	INSIDE	0.958	0.526	1225.75	644.99	0.504	1010.84	509.51

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P30498346	chr15:102348908-102348952	NM_009319:254	Tarbp2	INSIDE	0.958	1.938	3148.64	6103.39	1.856	2604.36	4834.94
A_68_P23317934	chr4:133053638-133053682	NM_001081156:805	Trnp1	INSIDE	0.958	1.567	1644.13	2576.55	1.501	1268.42	1903.77
A_68_P29477492	chr14:26279368-26279412	NM_183208:720	Zmiz1	INSIDE	0.958	0.534	1044.11	557.57	0.512	755.70	386.78
A_68_P25357072	chr7:105804387-105804431	NM_172280:671	2210018M11Rik	INSIDE	0.957	0.434	1612.29	699.63	0.415	1309.20	543.56
A_68_P25730019	chr8:27096869-27096915	NM_029037:7701	4930444A02Rik	INSIDE	0.957	3.339	2049.67	6843.96	3.196	1564.71	5001.28
A_68_P24127312	chr5:138182456-138182500	NM_175521:-1252	6430598A04Rik	DIVERGENT_PROMOTER	0.957	2.453	6825.66	16740.28	2.347	4518.49	10605.07
A_68_P28696863	chr12:104563389-104563437	NM_023049:30799	Asb2	INSIDE	0.957	2.091	465.93	974.27	2.000	430.02	860.18
A_68_P25047622	chr7:35905690-35905734	NM_007678:1401	Cebpa	INSIDE	0.957	0.662	1425.63	943.10	0.633	1083.91	685.89
A_68_P20884269	chr1:183853674-183853718	NM_001083120:96415	Enah	INSIDE	0.957	1.579	1538.17	2428.25	1.511	1161.41	1754.80
A_68_P20941838	chr1:193960926-193960970	NR_033536:169	Gm10516	INSIDE	0.957	0.596	1299.74	774.12	0.570	1083.37	617.57
A_68_P32119985	chr19:42330579-42330623	NM_027694:372	Golga7b	INSIDE	0.957	1.869	2309.86	4317.51	1.790	1858.20	3325.41
A_68_P29616393	chr14:55732216-55732260	NM_177049:3534	Jph4	INSIDE	0.957	2.803	686.73	1925.01	2.683	683.02	1832.50
A_68_P20864297	chr1:180458955-180458999	NM_001161665:-279	Kif26b	PROMOTER	0.957	1.631	665.77	1086.07	1.561	596.48	931.03
A_68_P21071165	chr2:25146200-25146244	NM_146117:792	Lrrc26	INSIDE	0.957	0.630	1622.06	1022.20	0.603	1199.75	723.67
A_68_P22006136	chr3:26230775-26230819	NM_138666:35	Nlgn1	INSIDE	0.957	0.672	2414.71	1621.73	0.642	1915.82	1230.87
A_68_P30139533	chr15:36539361-36539405	NM_008774:-654	Pabpc1	PROMOTER	0.957	2.235	744.22	1663.29	2.139	709.18	1517.28
A_68_P28957530	chr13:38022811-38022855	NM_001177869:42093	Rreb1	INSIDE	0.957	1.650	2230.16	3680.80	1.580	1744.40	2756.46
A_68_P30953522	chr16:89885052-89885096	NM_009384:75998	Tiam1	INSIDE	0.957	2.368	1041.42	2466.41	2.266	930.20	2107.46
A_68_P24974196	chr7:13610514-13610558	NM_011588:1036	Trim28	INSIDE	0.957	1.517	1684.95	2555.76	1.452	1209.98	1757.00
A_68_P31119041	chr17:28024335-28024379	NM_001080769:30905	Uhrf1bp1	INSIDE	0.957	3.042	909.15	2765.72	2.913	785.87	2289.00
A_68_P32241860	chrX:7706225-7706269	NR_029428:3727	Wdr13	INSIDE	0.957	3.661	1399.37	5123.30	3.502	630.03	2206.64
A_68_P25029972	chr7:30906920-30906964	NM_001081007:-24	Zfp382	PROMOTER	0.957	1.598	936.59	1496.75	1.529	802.25	1226.46
A_68_P25506496	chr7:134754584-134754628	NM_177226:3341	Zfp629	INSIDE	0.957	2.684	517.66	1389.16	2.568	466.53	1198.11
A_68_P30959217	chr16:90830454-90830498	NM_001199210:-627	4931408A02Rik	PROMOTER	0.956	1.735	2441.84	4235.63	1.659	1940.22	3218.64
A_68_P22831245	chr4:34498019-34498063	NM_001007589:177	Akirin2	INSIDE	0.956	2.089	599.92	1253.27	1.997	582.67	1163.50
A_68_P26813123	chr9:108017642-108017686	NM_007567:75050	Bsn	INSIDE	0.956	3.257	2356.65	7676.63	3.114	1652.23	5145.64
A_68_P27565934	chr11:5872237-5872281	NM_001174053:93493	Camk2b	INSIDE	0.956	1.725	1149.19	1982.17	1.649	892.23	1471.31
A_68_P25186368	chr7:73253968-73254012	NM_001081163:-410	Chsy1	PROMOTER	0.956	1.555	1168.42	1816.54	1.487	970.19	1442.53
A_68_P31951462	chr19:10651912-10651957	NM_201351:-278	Cybasc3	DIVERGENT_PROMOTER	0.956	0.607	969.01	588.52	0.580	831.83	482.73
A_68_P23366443	chr4:141430949-141430993	NM_025994:-135	Efhd2	PROMOTER	0.956	2.508	640.76	1606.84	2.397	569.55	1365.24
A_68_P21229088	chr2:54288519-54288563	NM_173030:-257	Galnt13	PROMOTER	0.956	0.722	1814.71	1311.03	0.691	1669.13	1153.38
A_68_P27290411	chr10:81007514-81007558	NM_010301:255	Gna11	INSIDE	0.956	2.305	2034.66	4690.58	2.204	1745.69	3846.83
A_68_P22344500	chr3:95363378-95363422	NM_026489:-198	Hormad1	PROMOTER	0.956	1.949	602.46	1174.31	1.864	522.17	973.35
A_68_P32537944	chrX:91480391-91480435	NM_001039059:144	Klhl15	INSIDE	0.956	1.934	1279.09	2473.33	1.848	728.56	1346.52
A_68_P22659609	chr3:153568957-153569001	NM_031870:124	Msh4	INSIDE	0.956	2.029	1639.52	3326.21	1.939	1324.55	2568.78
A_68_P32319272	chrX:34138495-34138539	NM_016783:297	Pgrmc1	INSIDE	0.956	2.274	2937.00	6678.02	2.173	1297.31	2819.63
A_68_P21843325	chr2:168577925-168577969	NM_175303:14755	Sall4	INSIDE	0.956	2.520	1293.03	3258.06	2.409	1032.64	2487.51
A_68_P22207890	chr3:66785065-66785109	NM_013665:607	Shox2	INSIDE	0.956	7.540	600.45	4527.71	7.207	538.83	3883.61
A_68_P20723684	chr1:154750088-154750132	NM_001005507:-334	Smg7	PROMOTER	0.956	3.453	995.18	3436.09	3.302	963.71	3181.71
A_68_P28607920	chr12:87420588-87420632	NM_009368:-619	Tgfb3	DIVERGENT_PROMOTER	0.956	0.485	1808.96	877.50	0.464	1498.61	695.11
A_68_P23463653	chr5:7344782-7344826	NM_001163223:-426	Zfp804b	PROMOTER	0.956	1.985	832.43	1651.99	1.898	889.98	1689.06
A_68_P26304291	chr9:11277863-11277907			Unknown	0.956	2.403	510.57	1227.14	2.298	451.74	1038.07
A_68_P28178206	chr11:119352324-119352368	NM_001164636:-314	A730011L01Rik	PROMOTER	0.955	0.510	1544.29	787.09	0.487	1180.90	574.55
A_68_P27533697	chr10:126486074-126486118	NM_010009:795	Cyp27b1	INSIDE	0.955	0.621	1069.91	664.84	0.594	917.02	544.42
A_68_P24156008	chr5:144077206-144077250	NM_172726:-189	E130309D02Rik	PROMOTER	0.955	0.616	1817.82	1119.85	0.589	1371.11	807.03
A_68_P28748275	chr12:113399969-113400013	NM_001097621:15572	Kif26a	INSIDE	0.955	3.309	2655.44	8786.70	3.160	2009.42	6350.13
A_68_P21137730	chr2:35947180-35947224	NM_001083126:12378	Lhx6	INSIDE	0.955	1.893	979.93	1854.85	1.808	824.89	1491.21
A_68_P26709438	chr9:88221992-88222036	NM_011851:-432	Nt5e	PROMOTER	0.955	1.607	1083.63	1741.06	1.535	929.26	1426.31
A_68_P26242532	chr8:126472872-126472916	NM_172288:271	Nup133	INSIDE	0.955	1.490	1427.66	2126.63	1.422	1213.57	1725.67
A_68_P24381545	chr6:39068163-39068207	NM_172893:164	Parp12	INSIDE	0.955	3.098	338.47	1048.60	2.957	338.51	1001.13
A_68_P31097497	chr17:24607518-24607562	NM_025954:123	Pgp	INSIDE	0.955	0.536	1698.35	910.79	0.512	1297.88	664.88

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25505712	chr7:134615346-134615390	NM_145589:241	Prr14	INSIDE	0.955	0.447	1552.59	693.42	0.427	1363.49	581.63
A_68_P28863269	chr13:19715200-19715245	NM_016687:179	Sfrp4	INSIDE	0.955	2.584	369.66	955.19	2.467	289.85	715.04
A_68_P23158194	chr4:101760223-101760267	ENSMUST00000106911:97		INSIDE	0.955	0.667	1763.67	1177.15	0.637	1724.37	1098.96
A_68_P25090215	chr7:52185401-52185445	NM_001077264:-562	Ap2a1	PROMOTER	0.954	0.460	1559.85	717.83	0.439	1358.75	596.73
A_68_P29523393	chr14:34133081-34133125	NM_153800:103094	Arhgap22	INSIDE	0.954	0.534	1814.67	968.68	0.509	1356.39	690.72
A_68_P32233092	chrX:5660427-5660471	NM_001033211:90	AU022751	INSIDE	0.954	2.287	618.24	1413.85	2.182	293.52	640.38
A_68_P27892695	chr11:68853469-68853515	NM_011496:-5652	Aurkb	PROMOTER	0.954	1.516	1056.03	1600.72	1.447	832.58	1204.37
A_68_P28047197	chr11:96723274-96723318	NM_019877:12107	Copz2	DOWNSTREAM	0.954	1.615	2150.86	3473.84	1.541	1550.99	2389.77
A_68_P24383682	chr6:39507280-39507324	NM_172477:531	Dennd2a	INSIDE	0.954	0.501	2609.72	1308.07	0.478	2051.52	981.46
A_68_P31927972	chr19:5307824-5307868	NM_001024717:9516	Gal3st3	INSIDE	0.954	1.799	1078.67	1940.44	1.717	883.85	1517.30
A_68_P26270752	chr8:131210063-131210107	NM_010578:531	Itgb1	INSIDE	0.954	0.456	2072.96	944.76	0.435	1898.93	825.54
A_68_P25031210	chr7:31145533-31145577	NM_175478:2237	Lrfn3	INSIDE	0.954	2.155	555.19	1196.53	2.056	473.92	974.43
A_68_P30477058	chr15:98702295-98702339	NM_001033276:-702	Mll2	PROMOTER	0.954	1.816	978.69	1777.24	1.733	830.55	1439.58
A_68_P20075274	chr1:20925596-20925640	NM_028829:44916	Paqr8	INSIDE	0.954	2.264	1098.57	2487.55	2.160	799.23	1726.58
A_68_P28583198	chr12:82961466-82961510	NM_018814:472	Pcnx	INSIDE	0.954	0.677	1769.84	1197.56	0.646	1493.74	964.70
A_68_P21871014	chr2:173485531-173485575	NM_024436:207	Rab22a	INSIDE	0.954	1.968	3089.01	6079.67	1.878	2650.30	4976.20
A_68_P21142185	chr2:37307958-37308002	NM_001033960:207	Rabgap1	INSIDE	0.954	0.531	1686.60	896.29	0.507	1461.38	740.76
A_68_P23415822	chr4:151362674-151362718	NM_001145929:399	Thap3	INSIDE	0.954	0.720	1816.31	1308.55	0.687	1408.32	967.60
A_68_P24431877	chr6:49214057-49214101	NM_198102:-27	Tra2a	PROMOTER	0.954	0.660	1099.37	725.21	0.629	994.06	625.68
A_68_P30094307	chr15:27677421-27677465	NM_001081302:278161	Trio	INSIDE	0.954	3.859	3487.62	13459.28	3.680	2485.40	9146.76
A_68_P28693529	chr12:103996499-103996543	NM_025666:336	Ubr7	INSIDE	0.954	0.483	1510.97	730.41	0.461	1248.64	575.72
A_68_P28202958	chr12:4913875-4913919	NM_145441:430	Ubxn2a	INSIDE	0.954	2.060	1176.76	2424.71	1.965	1060.07	2083.33
A_68_P24123997	chr5:137463625-137463669	NM_027318:106	Znhit1	INSIDE	0.954	0.685	1397.38	957.66	0.654	1122.40	733.96
A_68_P24159892	chr5:144952166-144952210	NM_010800:1034	Bhlha15	INSIDE	0.953	1.540	1328.00	2045.23	1.468	953.73	1399.66
A_68_P21483578	chr2:103325096-103325140	NM_009804:192	Cat	INSIDE	0.953	0.627	1379.71	864.72	0.597	1074.01	641.70
A_68_P31919589	chr19:3852192-3852236	NM_001025566:442	Chka	INSIDE	0.953	0.554	1239.57	687.30	0.528	1117.50	590.59
A_68_P31227866	chr17:50432495-50432539	NM_010021:408	Dazl	INSIDE	0.953	1.651	656.14	1083.06	1.573	638.53	1004.26
A_68_P28221326	chr12:8308667-8308711	NM_013527:72	Gdf7	INSIDE	0.953	2.106	446.54	940.46	2.007	388.19	779.04
A_68_P25512009	chr7:135831848-135831892	NM_178641:76992	Inpp5f	INSIDE	0.953	1.530	1504.42	2302.15	1.459	1268.63	1850.90
A_68_P25004857	chr7:25217107-25217151	NM_199013:13573	Irgc1	INSIDE	0.953	2.736	980.10	2681.66	2.607	728.21	1898.59
A_68_P25088775	chr7:51926026-51926070	NM_028021:-5175	Myh14	PROMOTER	0.953	0.676	1210.01	818.09	0.644	1067.81	687.88
A_68_P20412597	chr1:88423071-88423115	NM_008972:-218	Ptma	PROMOTER	0.953	0.442	1205.24	533.08	0.421	928.24	391.11
A_68_P29751623	chr14:79881191-79881235	NM_018765:-137	Wbp4	PROMOTER	0.953	2.138	413.32	883.59	2.037	297.03	604.94
A_68_P24951675	chr7:4982142-4982186	NM_001033383:10187	Zfp865	INSIDE	0.953	2.251	2039.47	4591.47	2.145	1611.87	3457.32
A_68_P26663736	chr9:79190551-79190595			Unknown	0.953	2.576	592.54	1526.10	2.455	570.51	1400.47
A_68_P24159893	chr5:144952289-144952338	NM_010800:1159	Bhlha15	INSIDE	0.952	2.218	774.51	1717.66	2.111	642.24	1356.00
A_68_P31977525	chr19:16059111-16059155	NM_198019:347	Cep78	INSIDE	0.952	0.619	1873.65	1160.34	0.590	1556.63	918.11
A_68_P21911108	chr2:181255242-181255287	NM_016775:55	Dnajc5	INSIDE	0.952	2.089	1414.50	2954.99	1.989	1199.12	2385.43
A_68_P32092667	chr19:36993325-36993369	NM_028263:743	Fgfbp3	INSIDE	0.952	2.674	602.46	1610.76	2.546	538.83	1371.93
A_68_P23283635	chr4:126803524-126803568	NM_001099319:257	Gm12942	INSIDE	0.952	2.539	521.49	1323.85	2.418	465.84	1126.25
A_68_P27235136	chr10:70844509-70844565	NM_027184:33996	Ipmk	INSIDE	0.952	1.625	774.29	1258.02	1.547	586.96	907.95
A_68_P21583617	chr2:121781672-121781716	NM_008545:134	Mageb3	INSIDE	0.952	2.052	920.31	1888.65	1.953	861.95	1683.21
A_68_P23278934	chr4:125911232-125911279	NM_001145970:22308	Mtap7d1	INSIDE	0.952	4.289	283.33	1215.24	4.082	230.80	942.10
A_68_P24171760	chr5:147889385-147889429	NM_181730:263	Polr1d	INSIDE	0.952	1.454	2501.83	3638.73	1.384	2189.87	3031.72
A_68_P25481817	chr7:130113128-130113172	NM_175023:-927	Rbbp6	PROMOTER	0.952	0.619	2123.82	1313.92	0.589	1730.51	1019.23
A_68_P26248944	chr8:127536746-127536790	NM_016909:-128	Tsnax	PROMOTER	0.952	0.690	1878.23	1295.18	0.657	1486.63	976.34
A_68_P27932455	chr11:76308282-76308326	NM_198018:14617	Abr	INSIDE	0.951	1.907	1602.66	3056.94	1.814	1368.07	2482.01
A_68_P27804993	chr11:53293588-53293632	NM_183173:87	Ankrd43	INSIDE	0.951	0.662	1292.64	856.03	0.630	1097.01	690.96
A_68_P26169910	chr8:114255749-114255793	NM_001198839:266	Bcar1	INSIDE	0.951	2.050	805.29	1650.51	1.948	787.49	1534.13
A_68_P26336206	chr9:18096974-18097018	NM_025844:286	Chordc1	INSIDE	0.951	1.479	2032.93	3006.03	1.406	1760.63	2475.95
A_68_P23284714	chr4:127003444-127003488	NM_008126:2903	Gjb3	INSIDE	0.951	1.869	1017.67	1902.08	1.777	853.97	1517.74

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27339938	chr10:90545771-90545815	NM_026166:9	Ikbip	INSIDE	0.951	2.719	1586.47	4314.39	2.587	1367.46	3537.94
A_68_P26700781	chr9:86589673-86589717	NM_001198933:-8488	Me1	PROMOTER	0.951	1.841	799.09	1470.86	1.750	812.26	1421.83
A_68_P25285295	chr7:91032191-91032235	NM_030705:639	Mesdc1	INSIDE	0.951	2.221	496.80	1103.61	2.112	431.29	910.98
A_68_P29612018	chr14:54980756-54980800	NM_026936:254	Oxa1l	INSIDE	0.951	1.774	864.11	1532.91	1.687	718.72	1212.76
A_68_P23401742	chr4:149029621-149029665	NM_001164052:7783	Pik3cd	INSIDE	0.951	2.400	2923.05	7015.79	2.283	2391.86	5460.81
A_68_P24025453	chr5:118687359-118687403	NM_172998:7490	Rnft2	INSIDE	0.951	2.926	589.17	1724.16	2.784	607.63	1691.77
A_68_P31257220	chr17:56743025-56743069	NM_001163300:18642	Safb	INSIDE	0.951	1.909	1289.90	2462.09	1.815	1019.44	1850.18
A_68_P21099539	chr2:29658324-29658368	NM_011989:147	Slc27a4	INSIDE	0.951	0.619	2874.42	1779.42	0.589	2197.48	1293.98
A_68_P27287199	chr10:80532582-80532627	NM_022653:-223	Thop1	DIVERGENT_PROMOTER	0.951	2.961	231.60	685.65	2.816	225.48	634.86
A_68_P23984450	chr5:111652272-111652316	NM_024477:343473	Ttc28	INSIDE	0.951	1.731	647.17	1120.45	1.646	552.58	909.65
A_68_P25805587	chr8:41508783-41508827	NM_178395:-364	Zdhhc2	PROMOTER	0.951	0.625	1129.17	706.27	0.595	942.09	560.54
A_68_P29614459	chr14:55433246-55433296	ENSMUST00000095853:-2053		PROMOTER	0.951	3.890	420.99	1637.70	3.698	486.05	1797.33
A_68_P28680132	chr12:101369299-101369345	NM_183155:28541	BC002230	INSIDE	0.950	2.143	523.21	1121.15	2.036	411.71	838.16
A_68_P24120339	chr5:136751005-136751049	NM_198602:292249	Cux1	INSIDE	0.950	1.844	1299.39	2395.50	1.752	1079.89	1891.46
A_68_P27188599	chr10:62409837-62409881	NM_177372:82	Dna2	INSIDE	0.950	1.689	1171.92	1979.90	1.605	1063.89	1707.23
A_68_P28947123	chr13:36209265-36209309	NM_001039189:7	Fars2	INSIDE	0.950	1.652	618.92	1022.24	1.570	650.19	1020.61
A_68_P22209918	chr3:67234256-67234300	NM_138591:242	Gfm1	INSIDE	0.950	1.607	1082.84	1740.46	1.527	932.35	1423.71
A_68_P24143542	chr5:141305948-141305992	NM_010302:415	Gna12	INSIDE	0.950	0.560	1264.38	707.97	0.532	1040.87	553.58
A_68_P26085826	chr8:98412091-98412135	NM_010325:153	Got2	INSIDE	0.950	0.630	953.08	600.12	0.598	794.94	475.58
A_68_P29616397	chr14:55732548-55732592	NM_177049:3202	Jph4	INSIDE	0.950	2.187	675.81	1478.30	2.078	644.51	1339.45
A_68_P25954895	chr8:73437847-73437891	NM_173013:7996	Mtap1s	INSIDE	0.950	2.055	878.16	1805.04	1.953	758.42	1481.49
A_68_P29116251	chr13:69672583-69672627	NM_001169131:138	Papd7	INSIDE	0.950	4.069	298.07	1212.90	3.865	319.70	1235.70
A_68_P22614374	chr3:146068079-146068128	NM_138744:453	Ssx2ip	INSIDE	0.950	1.775	2065.99	3667.38	1.687	1556.20	2624.72
A_68_P26948303	chr10:12661129-12661173	NM_001163590:22915	Stx11	INSIDE	0.950	1.690	839.17	1418.24	1.605	735.18	1179.75
A_68_P28755249	chr12:114427080-114427124	NM_153776:2989	Tmem121	INSIDE	0.950	2.139	520.04	1112.54	2.032	460.61	936.02
A_68_P23316766	chr4:132833535-132833579	NM_025667:149	Tmem222	INSIDE	0.950	1.648	1050.47	1731.49	1.565	910.33	1424.80
A_68_P21610507	chr2:126702013-126702057	NM_001164325:-37	Trpm7	PROMOTER	0.950	0.682	1252.94	854.32	0.647	1117.65	723.63
A_68_P32978434	A_68_P32978434			Unknown	0.950	2.538	1628.55	4133.13	2.412	1362.62	3286.50
A_68_P26742255	chr9:95412044-95412088	NM_001114977:349	2610101N10Rik	INSIDE	0.949	0.503	1420.62	714.88	0.477	1209.80	577.56
A_68_P22314995	chr3:88448116-88448160	NM_001198912:22823	Arhgef2	INSIDE	0.949	2.164	488.16	1056.49	2.054	483.02	991.95
A_68_P28051740	chr11:97490459-97490503	NM_175332:550	E130012A19Rik	INSIDE	0.949	2.035	1804.19	3671.74	1.932	1676.51	3238.19
A_68_P21874502	chr2:174124098-174124142	NM_201617:761	Gnas	INSIDE	0.949	1.663	2169.11	3608.23	1.578	1782.20	2813.05
A_68_P32748068	chrX:148579482-148579526	NM_001114664:694	Iqsec2	INSIDE	0.949	1.801	1310.24	2359.55	1.709	738.33	1261.54
A_68_P31150605	chr17:33954480-33954524	NM_030697:7035	Kank3	INSIDE	0.949	2.462	404.17	995.07	2.337	345.74	807.85
A_68_P23752950	chr5:65195357-65195401	NM_008453:617	Klf3	INSIDE	0.949	0.565	948.37	536.21	0.537	780.04	418.58
A_68_P25048197	chr7:35988690-35988734	NM_001024707:11652	Lrp3	INSIDE	0.949	1.793	1306.48	2342.27	1.702	978.70	1665.35
A_68_P31828826	chr18:74130007-74130051	NM_172632:94575	Mapk4	INSIDE	0.949	2.051	603.40	1237.87	1.946	501.29	975.45
A_68_P24090499	chr5:130221338-130221382	NM_025450:-42	Mrps17	DIVERGENT_PROMOTER	0.949	2.952	684.66	2021.29	2.801	646.85	1811.85
A_68_P25360747	chr7:106416712-106416756	NM_001043355:-121	Mtap6	PROMOTER	0.949	1.784	654.16	1166.75	1.693	577.95	978.30
A_68_P25091030	chr7:52331941-52331985	NM_001163684:14164	Nosip	INSIDE	0.949	2.088	934.96	1951.95	1.982	747.48	1481.39
A_68_P23198685	chr4:108673245-108673289	NM_146150:-143	Nrd1	PROMOTER	0.949	1.625	1514.57	2461.00	1.543	1281.69	1977.19
A_68_P27709961	chr11:35821845-35821890	NM_011856:935878	Odz2	INSIDE	0.949	1.790	925.66	1656.62	1.698	763.42	1296.14
A_68_P28224326	chr12:8779101-8779145	NM_011519:921	Sdc1	INSIDE	0.949	0.592	1117.41	661.81	0.562	940.49	528.65
A_68_P26316375	chr9:14081197-14081241	NM_030261:474	Sesn3	INSIDE	0.949	1.473	3222.18	4745.89	1.398	2368.00	3310.02
A_68_P26540064	chr9:56920273-56920317	NM_001110350:-3888	Sin3a	PROMOTER	0.949	1.901	721.72	1371.67	1.803	668.74	1205.53
A_68_P27468584	chr10:114688310-114688354	NM_025706:217	Tbc1d15	INSIDE	0.949	0.726	1912.87	1388.53	0.689	1706.58	1175.99
A_68_P32288520	chrX:20002860-20002904	ENSMUST00000136093:-31		PROMOTER	0.949	2.872	1179.57	3388.24	2.725	868.15	2365.54
A_68_P31939730	chr19:7498138-7498182	NM_175381:6046	2700081O15Rik	INSIDE	0.948	0.539	969.76	522.24	0.510	837.73	427.62
A_68_P29450644	chr14:21895153-21895197	NM_134079:23320	Adk	INSIDE	0.948	1.986	861.34	1710.25	1.882	737.54	1387.95
A_68_P26822031	chr9:110019702-110019746	NM_133347:-1638	Dhx30	PROMOTER	0.948	1.768	1211.54	2142.19	1.676	1108.21	1857.76
A_68_P23553583	chr5:27144126-27144170	NM_010075:252	Dpp6	INSIDE	0.948	0.484	1113.86	538.90	0.459	945.83	433.82

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P32408596	chrX:56387279-56387323	NM_010200:313	Fgf13	INSIDE	0.948	2.347	2716.44	6374.24	2.225	1557.16	3464.98
A_68_P25087544	chr7:51716906-51716950	NM_198250:19072	Lrrc4b	INSIDE	0.948	2.165	1247.86	2701.19	2.053	985.60	2023.04
A_68_P23536419	chr5:22940563-22940607	NM_026984:338	Mll5	INSIDE	0.948	0.610	1181.44	720.77	0.579	936.20	541.73
A_68_P27278628	chr10:79202047-79202091	NM_172551:7258	Polrmt	INSIDE	0.948	2.075	1313.39	2725.53	1.968	1085.54	2136.67
A_68_P31862907	chr18:80397180-80397224	NM_199197:156	Rbfa	INSIDE	0.948	1.621	828.14	1342.67	1.537	713.65	1096.65
A_68_P31196988	chr17:44872166-44872210	NM_001145920:1409	Runx2	INSIDE	0.948	0.593	1390.44	824.05	0.562	1029.09	578.09
A_68_P27228616	chr10:69707646-69707690	NM_025807:-355	Slc16a9	PROMOTER	0.948	0.436	1218.78	531.92	0.414	1025.53	424.23
A_68_P25075290	chr7:48158061-48158105	NM_021387:3435	Vstm2b	INSIDE	0.948	1.871	1151.28	2154.08	1.775	958.72	1701.34
A_68_P28729930	chr12:110032477-110032521	NM_009537:978	Yy1	INSIDE	0.948	1.817	1001.90	1820.51	1.723	872.94	1504.05
A_68_P24631963	chr6:90319610-90319654	NM_030260:145	Zxdc	INSIDE	0.948	1.656	650.36	1077.09	1.570	636.97	1000.00
A_68_P25730016	chr8:27096591-27096635	NM_029037:7981	4930444A02Rik	INSIDE	0.947	2.557	802.93	2053.10	2.420	671.46	1625.27
A_68_P30357051	chr15:77825627-77825674	NM_007583:124060	Cacng2	INSIDE	0.947	3.122	698.41	2180.23	2.958	746.80	2208.75
A_68_P24798777	chr6:120442544-120442588	NM_033567:1259	Cecr6	INSIDE	0.947	0.623	1083.29	674.47	0.589	945.78	557.54
A_68_P21221950	chr2:52717844-52717888	NM_172409:965	Fmnl2	INSIDE	0.947	0.511	1484.84	758.85	0.484	1205.24	583.53
A_68_P31978255	chr19:16207934-16207978	NM_008139:636	Gnaq	INSIDE	0.947	2.497	3619.36	9037.74	2.366	3063.27	7246.82
A_68_P26220842	chr8:123060303-123060347	NM_001145896:-984	Gse1	PROMOTER	0.947	0.653	2028.37	1324.77	0.619	1745.02	1079.87
A_68_P32378027	chrX:49034445-49034489	NM_015819:-812	Hs6st2	PROMOTER	0.947	1.945	846.63	1646.45	1.841	582.14	1071.84
A_68_P23252661	chr4:120370848-120370892	NM_001081142:48911	Kcnq4	INSIDE	0.947	3.449	3645.73	12574.45	3.267	2683.92	8768.79
A_68_P32697224	chrX:136596652-136596696	NM_001081668:433	Nup62cl	INSIDE	0.947	2.098	2824.97	5927.37	1.987	1577.19	3134.01
A_68_P24697527	chr6:101327639-101327683	NM_018884:231	Pdzrn3	INSIDE	0.947	1.637	703.14	1151.28	1.551	652.32	1011.68
A_68_P28100896	chr11:106181914-106181958	NM_133199:28768	Scn4a	INSIDE	0.947	2.129	476.92	1015.42	2.016	381.97	770.16
A_68_P23893507	chr5:92739062-92739106	NM_172713:-34	Sdad1	PROMOTER	0.947	0.613	1081.42	662.41	0.580	898.38	520.93
A_68_P22031740	chr3:30993764-30993808	NM_001039090:-196	Skil	PROMOTER	0.947	2.467	473.40	1167.79	2.336	458.60	1071.50
A_68_P30015973	chr15:11313872-11313916	NM_033074:15519	Tars	INSIDE	0.947	1.980	419.00	829.46	1.874	312.13	585.04
A_68_P32226231	chr19:60657044-60657088	NM_001172096:-140	2700078E11Rik	PROMOTER	0.946	0.663	1307.06	866.11	0.627	1010.77	633.57
A_68_P22142067	chr3:53283022-53283066	NM_173382:15306	2810046L04Rik	INSIDE	0.946	2.409	818.74	1972.34	2.278	753.75	1717.07
A_68_P31096787	chr17:24488644-24488688	NM_001039581:-324	Abca3	DIVERGENT_PROMOTER	0.946	0.612	908.95	556.50	0.579	715.47	414.61
A_68_P24980794	chr7:16899349-16899393	NM_133234:4439	Bbc3	INSIDE	0.946	0.403	1364.78	550.52	0.382	1106.48	422.27
A_68_P27933408	chr11:76486478-76486522	NM_177182:529	Bhlha9	INSIDE	0.946	0.455	1610.89	733.29	0.431	1333.24	574.16
A_68_P26022160	chr8:87356049-87356093	NM_201227:-9348	Dand5	PROMOTER	0.946	0.503	1731.61	871.30	0.476	1431.56	681.49
A_68_P28036777	chr11:94982683-94982727	NM_010055:1274	Dlx3	INSIDE	0.946	0.596	1243.10	740.84	0.564	1090.73	614.81
A_68_P27093483	chr10:41917159-41917203	NM_019740:79368	Foxo3	INSIDE	0.946	1.894	1674.37	3170.51	1.792	1248.38	2236.58
A_68_P31515587	chr18:15222623-15222667	NM_001142731:-553	Kctd1	PROMOTER	0.946	2.206	1302.36	2873.42	2.087	1080.43	2254.95
A_68_P24921913	chr6:145198164-145198208	NM_021284:565	Kras	INSIDE	0.946	0.713	1827.39	1302.38	0.674	1510.40	1018.27
A_68_P25025265	chr7:29870930-29870974	NR_035489:-2239	Mir1963	PROMOTER	0.946	2.665	705.36	1879.64	2.521	621.96	1567.73
A_68_P28961841	chr13:38726802-38726846	NM_139063:154	Muted	INSIDE	0.946	0.497	2137.73	1061.59	0.470	1669.08	784.06
A_68_P31110246	chr17:26576080-26576124	NM_001081656:24193	Neurl1b	INSIDE	0.946	1.773	745.70	1322.39	1.677	688.70	1154.89
A_68_P27261657	chr10:75837670-75837714	NM_008787:67965	Pcnt	INSIDE	0.946	3.115	792.24	2468.18	2.948	773.42	2280.40
A_68_P25169318	chr7:69609337-69609381	NM_013788:38	Peg12	INSIDE	0.946	3.281	735.56	2413.63	3.106	744.26	2311.47
A_68_P21005392	chr2:11212245-11212289	NM_008859:118258	Prkcq	INSIDE	0.946	2.137	735.89	1572.82	2.023	631.92	1278.11
A_68_P28159661	chr11:116351482-116351526	NM_026364:156	Prpsap1	INSIDE	0.946	3.643	7548.92	27497.03	3.446	5932.00	20439.50
A_68_P26540069	chr9:56920831-56920875	NM_001110350:-3330	Sin3a	PROMOTER	0.946	1.459	2615.39	3815.11	1.380	2020.45	2788.38
A_68_P21682258	chr2:139892550-139892594	NM_001159640:-51	Tasp1	PROMOTER	0.946	0.610	1467.19	894.95	0.577	1226.02	707.29
A_68_P21747902	chr2:151968924-151968968	NM_009328:-398	Tcf15	PROMOTER	0.946	0.621	1002.71	622.91	0.587	803.39	471.93
A_68_P22860681	chr4:41082365-41082409	NM_026275:-667	Ube2r2	PROMOTER	0.946	2.082	2362.25	4917.10	1.970	2012.58	3964.55
A_68_P32753662	chrX:149932604-149932648	NM_018798:-148	Ubqln2	PROMOTER	0.946	2.655	486.17	1291.01	2.511	283.40	711.64
A_68_P31087860	chr17:22058016-22058060	NM_001199048:41393	Zfp942	DOWNSTREAM	0.946	2.173	1132.14	2460.65	2.055	1150.69	2364.87
A_68_P24449794	chr6:52256292-52256336	NR_038163:8512	5730457N03Rik	DOWNSTREAM	0.945	0.588	1786.96	1051.20	0.556	1363.13	758.06
A_68_P25430230	chr7:120513248-120513292	NM_133700:-417	Btbd10	PROMOTER	0.945	2.884	1010.02	2912.97	2.725	953.11	2597.00
A_68_P26581355	chr9:64188489-64188533	NM_172519:-246	Dis3l	PROMOTER	0.945	0.524	1460.70	765.96	0.496	1186.66	588.05
A_68_P30588851	chr16:20672864-20672908	NM_001005331:65	Eif4g1	INSIDE	0.945	0.596	2425.81	1445.29	0.563	1983.47	1116.34

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26224694	chr8:123651817-123651861	NM_008024:254	Foxl1	INSIDE	0.945	0.587	1549.82	910.50	0.555	1383.76	768.08
A_68_P20679834	chr1:145586536-145586580	NM_001038592:-139	Glrx2	PROMOTER	0.945	2.550	1450.77	3699.63	2.410	1244.38	2999.39
A_68_P24131923	chr5:139297423-139297474	NM_001195128:1415	Gm5294	INSIDE	0.945	0.615	3755.96	2308.38	0.581	2559.10	1486.48
A_68_P24176695	chr5:148768968-148769012	NM_029920:95	Mtus2	INSIDE	0.945	0.506	1537.91	777.52	0.478	1269.36	606.38
A_68_P21078907	chr2:26321004-26321048	NM_008714:38316	Notch1	INSIDE	0.945	2.106	1488.18	3134.76	1.991	1104.51	2199.57
A_68_P27833619	chr11:58752222-58752266	NM_022423:164	Rnf187	INSIDE	0.945	2.634	464.91	1224.41	2.490	437.20	1088.45
A_68_P22049380	chr3:34548131-34548175	NM_011443:-774	Sox2	PROMOTER	0.945	1.760	839.32	1476.83	1.663	656.92	1092.73
A_68_P27985859	chr11:85699856-85699900	NM_011536:-3686	Tbx4	PROMOTER	0.945	1.881	2279.64	4287.94	1.777	1920.82	3413.98
A_68_P21612304	chr2:127073616-127073660	NM_175145:-72	Tmem127	DIVERGENT_PROMOTER	0.945	24.852	5414.66	134564.50	23.497	3681.31	86499.55
A_68_P31155255	chr17:34817289-34817333	NM_031176:9831	Tnxb	INSIDE	0.945	1.721	1001.58	1723.96	1.627	759.94	1236.25
A_68_P22168172	chr3:58220477-58220521	NM_001081229:888	Tsc22d2	INSIDE	0.945	1.751	807.72	1414.13	1.655	739.43	1223.44
A_68_P29081872	chr13:59924315-59924359	NM_153538:172	Zcchc6	INSIDE	0.945	1.601	1031.74	1651.67	1.513	928.02	1403.84
A_68_P26233343	chr8:124956522-124956566	NM_007806:296	Cyba	INSIDE	0.944	1.813	777.61	1409.71	1.711	731.03	1250.78
A_68_P26659375	chr9:78243556-78243600	NM_001191044:-5	Ddx43	PROMOTER	0.944	3.376	724.26	2445.23	3.186	759.30	2419.45
A_68_P24795426	chr6:119797651-119797695	NM_053204:496	Erc1	INSIDE	0.944	1.456	6328.99	9215.64	1.375	4864.59	6689.62
A_68_P24990861	chr7:19590354-19590398	NM_178757:963	Irf2bp1	INSIDE	0.944	2.185	636.71	1391.04	2.062	461.79	952.33
A_68_P28185783	chr11:120494397-120494441	NM_010756:443	Mafg	INSIDE	0.944	1.615	805.42	1300.70	1.524	836.72	1275.08
A_68_P28875768	chr13:22097992-22098036	NM_019429:3596	Prss16	INSIDE	0.944	1.533	1141.69	1749.83	1.447	996.14	1441.49
A_68_P21115159	chr2:32252005-32252049	NM_133783:617	Ptges2	INSIDE	0.944	2.056	756.72	1555.81	1.942	694.65	1348.76
A_68_P30496912	chr15:102087767-102087811	NM_011244:126	Rarg	INSIDE	0.944	1.689	1292.35	2182.69	1.594	1127.42	1796.95
A_68_P25499765	chr7:133435758-133435803	NM_145587:19648	Sbk1	INSIDE	0.944	2.339	468.23	1095.39	2.208	434.13	958.77
A_68_P29699984	chr14:70605667-70605711	NM_011366:1756	Sorbs3	INSIDE	0.944	1.707	797.44	1361.28	1.611	627.37	1010.57
A_68_P30250398	chr15:58654714-58654758	NM_175212:246	Tmem65	INSIDE	0.944	2.123	577.90	1227.09	2.005	528.23	1059.01
A_68_P24956428	chr7:6649272-6649316	NM_011769:-151	Zim1	PROMOTER	0.944	1.981	468.49	927.94	1.870	433.58	810.59
A_68_P23093077	chr4:88583855-88583899			Unknown	0.944	1.678	1118.47	1876.96	1.584	903.53	1431.23
A_68_P23747547	chr5:64203832-64203876	NM_029554:121	0610040J01Rik	INSIDE	0.943	2.505	463.36	1160.70	2.362	410.75	970.19
A_68_P22832217	chr4:34663673-34663717	NM_027041:13761	1700003M02Rik	INSIDE	0.943	2.878	323.36	930.79	2.715	270.54	734.41
A_68_P31124400	chr17:28943442-28943486	NM_001081315:5394	Brpf3	INSIDE	0.943	1.609	1023.69	1647.24	1.518	758.95	1151.74
A_68_P24610262	chr6:86422458-86422502	NR_027370:33841	C87436	DOWNSTREAM	0.943	1.442	3397.02	4898.03	1.360	2426.23	3299.22
A_68_P27172918	chr10:59649296-59649341	NM_016803:32690	Chst3	INSIDE	0.943	1.922	663.70	1275.84	1.813	487.75	884.24
A_68_P26017804	chr8:86566375-86566419	NM_016671:78	Il27ra	INSIDE	0.943	0.695	1628.08	1131.01	0.655	1304.68	854.36
A_68_P33007165	chr8:121970673-121970717	NM_054095:76	Necab2	INSIDE	0.943	0.679	1627.56	1104.46	0.640	1443.05	923.56
A_68_P21098346	chr2:29475741-29475785	NM_001039086:523	Rapgef1	INSIDE	0.943	0.431	1349.14	581.07	0.406	1137.69	462.01
A_68_P26823381	chr9:110283194-110283238	NM_001001144:47420	Scap	INSIDE	0.943	2.046	2323.51	4752.96	1.929	1818.29	3507.89
A_68_P22323187	chr3:89856233-89856277	NM_028475:143	Ubap2l	INSIDE	0.943	1.791	883.68	1583.05	1.689	550.99	930.46
A_68_P32462209	chrX:70599489-70599533	NM_001160229:11551	Zfp275	INSIDE	0.943	2.784	440.74	1227.21	2.625	246.32	646.50
A_68_P24955007	chr7:6282885-6282929	NM_001033249:-870	Zfp583	PROMOTER	0.943	0.413	1286.23	531.11	0.389	1166.04	453.82
A_68_P23593510	chr5:34631368-34631412	NM_001015039:-417	Zfyve28	PROMOTER	0.943	0.487	1090.78	531.29	0.459	924.19	424.44
A_68_P28175593	chr11:118919618-118919662			Unknown	0.943	0.513	1413.07	724.85	0.484	1174.46	568.05
A_68_P29998441	chr15:8118989-8119033	NM_001162906:-95	2410089E03Rik	PROMOTER	0.942	3.178	846.38	2689.70	2.995	756.40	2265.47
A_68_P27262974	chr10:76059438-76059482	NM_146007:26689	Col6a2	INSIDE	0.942	2.102	2516.49	5290.32	1.980	1808.44	3580.44
A_68_P31227872	chr17:50433053-50433097	NM_010021:-150	Dazl	PROMOTER	0.942	1.816	1051.38	1909.44	1.710	818.52	1399.97
A_68_P27612237	chr11:16652694-16652738	NM_007912:511	Egfr	INSIDE	0.942	0.501	1344.60	673.73	0.472	1170.83	552.86
A_68_P20644879	chr1:138157097-138157141	NM_001101516:332	Gpr25	INSIDE	0.942	2.683	228.53	613.12	2.528	235.83	596.15
A_68_P23753094	chr5:65213362-65213406	NM_008453:18623	Klf3	INSIDE	0.942	2.863	2103.00	6021.37	2.697	1693.60	4567.94
A_68_P31130219	chr17:29989367-29989411	NM_001081160:35439	Mdga1	INSIDE	0.942	2.105	2321.67	4886.79	1.982	1727.19	3422.96
A_68_P22373051	chr3:100881021-100881065	NM_011197:33047	Ptgfrn	INSIDE	0.942	2.037	1378.53	2807.74	1.919	1035.87	1988.00
A_68_P23457020	chr5:5694251-5694295	NM_001103156:-195	Steap2	PROMOTER	0.942	0.688	3441.84	2368.77	0.648	2758.68	1788.69
A_68_P32700064	chrX:137133979-137134023	NM_001077364:1061	Tsc22d3	INSIDE	0.942	1.946	760.45	1480.05	1.833	494.69	906.81
A_68_P30716739	chr16:43618530-43618574	NM_019778:371156	Zbtb20	INSIDE	0.942	2.334	388.90	907.50	2.199	345.38	759.57
A_68_P25264699	chr7:87226574-87226619	NM_175433:55483	Zfp710	INSIDE	0.942	4.519	1354.71	6122.23	4.259	939.94	4003.00

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P32975877	A_68_P32975877			Unknown	0.942	1.893	1860.06	3521.33	1.784	1384.30	2469.45
A_68_P28741419	chr12:112215560-112215604	NM_175207:1649	Ankrd9	INSIDE	0.941	1.626	793.35	1289.94	1.531	611.01	935.23
A_68_P27143036	chr10:53317089-53317133	NM_025541:344	Asf1a	INSIDE	0.941	1.458	2012.07	2934.53	1.372	1630.53	2237.28
A_68_P28525477	chr12:72411137-72411181	NM_001190466:288	Dact1	INSIDE	0.941	2.192	619.26	1357.53	2.063	506.29	1044.40
A_68_P32006563	chr19:21547067-21547111	NM_010266:63	Gda	INSIDE	0.941	1.768	627.23	1108.87	1.664	557.66	928.16
A_68_P24636903	chr6:91066915-91066959	NM_018815:-116	Nup210	PROMOTER	0.941	0.454	1336.05	606.29	0.427	1065.66	454.90
A_68_P30587014	chr16:20302209-20302253	NM_001005767:205	Parl	INSIDE	0.941	0.437	1815.83	792.98	0.411	1510.87	621.17
A_68_P24759852	chr6:113445089-113445133	NM_172487:6702	Prrt3	INSIDE	0.941	1.771	1120.24	1984.17	1.667	949.71	1582.89
A_68_P20427304	chr1:90967161-90967205	NM_133816:146	Sh3bp4	INSIDE	0.941	0.657	988.01	648.98	0.618	945.76	584.65
A_68_P24111847	chr5:134652378-134652422	NM_033572:237	Wbscr16	INSIDE	0.941	0.528	1901.87	1003.70	0.497	1656.34	822.63
A_68_P28553591	chr12:77470382-77470426	NM_001172104:47	Zbtb25	INSIDE	0.941	2.515	892.11	2243.53	2.368	891.52	2110.76
A_68_P29224475	chr13:93300495-93300539	NM_173392:249	Zfyve16	INSIDE	0.941	0.704	2025.36	1426.24	0.662	1802.78	1194.08
A_68_P33005898	A_68_P33005898			Unknown	0.941	3.460	240.81	833.25	3.256	260.17	847.15
A_68_P27883391	chr11:67269235-67269279	ENSMUST00000136796:31		INSIDE	0.941	0.385	1467.72	564.62	0.362	1146.14	414.74
A_68_P25594226	chr7:149558251-149558295	NM_177265:-108	6330512M04Rik	PROMOTER	0.940	3.184	425.70	1355.52	2.993	390.45	1168.47
A_68_P28050586	chr11:97301883-97301927	NM_021493:-9569	Arhgap23	PROMOTER	0.940	1.598	1122.42	1794.16	1.502	997.97	1499.32
A_68_P24098743	chr5:132014457-132014501	NM_177047:1003735	Auts2	INSIDE	0.940	0.583	1364.72	795.42	0.548	1102.83	604.53
A_68_P27254388	chr10:74523771-74523815	NM_001081412:152	Bcr	INSIDE	0.940	3.177	694.76	2207.09	2.987	739.58	2209.46
A_68_P27100736	chr10:43231246-43231290	NM_199028:32323	Bend3	INSIDE	0.940	3.083	694.43	2140.99	2.897	666.21	1930.18
A_68_P28743718	chr12:112615438-112615482	NM_183016:469	Cdc42bpb	INSIDE	0.940	1.894	626.13	1185.97	1.781	532.96	949.31
A_68_P26224343	chr8:123606757-123606801	NM_010426:-1595	Foxf1a	PROMOTER	0.940	0.497	2217.09	1100.96	0.467	1745.45	814.80
A_68_P25151569	chr7:64846153-64846197	NM_008071:-368	Gabrb3	PROMOTER	0.940	0.518	2187.00	1132.17	0.486	1706.30	830.00
A_68_P25891572	chr8:59990950-59990994	NM_008252:333	Hmgb2	INSIDE	0.940	2.112	1066.80	2253.47	1.985	881.81	1750.02
A_68_P23985682	chr5:111849354-111849398	NM_001081235:2191	Mn1	INSIDE	0.940	2.106	673.48	1418.48	1.979	605.51	1198.55
A_68_P23429470	chr4:153534460-153534504	NM_026388:311	Tprgl	INSIDE	0.940	2.046	9904.95	20266.06	1.922	7726.65	14853.14
A_68_P30665800	chr16:34745530-34745574	ENSMUST00000155268:257		INSIDE	0.940	2.629	260.28	684.36	2.472	242.63	599.77
A_68_P24172798	chr5:148086398-148086442	NR_038157:-3323	2210019I11Rik	PROMOTER	0.939	0.494	1607.45	794.38	0.464	1341.10	622.45
A_68_P27288887	chr10:80787956-80788000	NM_027381:4131	2510012J08Rik	INSIDE	0.939	1.794	766.38	1374.67	1.684	580.83	977.83
A_68_P21646214	chr2:133377926-133377970	NM_007553:-986	Bmp2	PROMOTER	0.939	3.550	300.44	1066.54	3.335	307.00	1023.73
A_68_P30404602	chr15:85861703-85861747	NM_009886:2483	Celsr1	INSIDE	0.939	1.756	734.87	1290.40	1.648	577.03	951.18
A_68_P26526448	chr9:54407958-54408002	NM_019686:-94	Cib2	PROMOTER	0.939	2.155	860.64	1854.25	2.023	754.91	1527.00
A_68_P22317611	chr3:88972711-88972761	NM_001163432:4010	Clk2	INSIDE	0.939	2.947	1251.65	3688.96	2.767	898.68	2486.30
A_68_P28576092	chr12:81620747-81620791	NM_001081421:792	Galntl1	INSIDE	0.939	0.571	1472.51	840.98	0.536	1193.43	639.99
A_68_P26035032	chr8:89996819-89996863	NR_033430:130	Gm2694	INSIDE	0.939	0.691	1843.43	1273.49	0.649	1475.11	957.12
A_68_P25394035	chr7:112885416-112885460	NM_010562:200	Ilk	INSIDE	0.939	0.617	1056.24	652.07	0.580	746.90	433.14
A_68_P22129521	chr3:51220268-51220312	NM_053089:353	Naa15	INSIDE	0.939	0.554	1466.45	812.38	0.520	1114.27	579.70
A_68_P32147396	chr19:47124826-47124870	NM_027654:487	Pcgf6	INSIDE	0.939	0.644	1518.78	977.47	0.604	1259.92	761.24
A_68_P31121662	chr17:28434204-28434248	NM_011145:64528	Ppard	INSIDE	0.939	2.365	562.99	1331.48	2.220	509.14	1130.42
A_68_P32183828	chr19:53752058-53752102	NM_001170847:285	Rbm20	INSIDE	0.939	2.127	508.92	1082.35	1.997	425.19	849.10
A_68_P25588800	chr7:148623401-148623445	NM_001177576:-2929	Slc25a22	PROMOTER	0.939	0.650	1965.89	1277.03	0.610	1442.70	879.97
A_68_P24320421	chr6:28430461-28430505	NM_019776:135	Snd1	INSIDE	0.939	1.776	1401.21	2488.93	1.667	1109.64	1850.05
A_68_P29478589	chr14:26426247-26426291	NM_183208:147598	Zmiz1	INSIDE	0.939	0.609	1480.53	900.95	0.571	1087.21	621.27
A_68_P27360776	chr10:94151341-94151385	NR_015524:-4	4932415G12Rik	DIVERGENT_PROMOTER	0.938	6.981	1292.11	9020.13	6.550	1011.53	6625.23
A_68_P29049158	chr13:54472997-54473041	NM_009946:306	Cplx2	INSIDE	0.938	0.694	1999.40	1387.98	0.651	1800.75	1172.88
A_68_P29611636	chr14:54873516-54873560	NM_001113358:66	Dad1	INSIDE	0.938	0.385	1904.44	733.75	0.361	1358.99	491.17
A_68_P23365989	chr4:141346549-141346593	NM_172338:-11	Dnajc16	DIVERGENT_PROMOTER	0.938	2.433	490.62	1193.88	2.283	512.72	1170.76
A_68_P28329060	chr12:31758731-31758776	NM_027828:-79	Fam110c	PROMOTER	0.938	0.704	1708.18	1202.26	0.660	1320.20	871.64
A_68_P23320288	chr4:133523806-133523851	NM_016957:78	Hmgn2	INSIDE	0.938	2.021	591.76	1196.07	1.896	465.46	882.40
A_68_P28204868	chr12:5216846-5216890	NM_001164493:165620	Klhl29	INSIDE	0.938	2.283	1485.62	3391.05	2.141	1312.03	2809.20
A_68_P25031175	chr7:31140774-31140818	NM_175478:6995	Lrfn3	INSIDE	0.938	2.359	656.86	1549.79	2.213	559.69	1238.72
A_68_P21776626	chr2:157193205-157193256	NM_026968:-99	Manbal	PROMOTER	0.938	2.343	438.75	1027.93	2.198	324.14	712.58

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P30425291	chr15:89288179-89288223	NM_021921:3859	Mapk8ip2	INSIDE	0.938	2.722	1156.29	3147.71	2.554	1011.50	2582.99
A_68_P27787485	chr11:50048388-50048432	NM_145926:9574	Mgat4b	INSIDE	0.938	2.287	658.22	1505.65	2.145	588.42	1262.21
A_68_P23439845	chr4:155027518-155027562	NM_011985:-47	Mmp23	PROMOTER	0.938	0.658	1282.06	843.71	0.617	1014.34	625.97
A_68_P21818281	chr2:164332907-164332953	NM_133779:9906	Pigt	INSIDE	0.938	3.599	2072.70	7458.85	3.374	1373.13	4633.39
A_68_P30423624	chr15:88998188-88998232	NM_001159521:6070	Plxnb2	INSIDE	0.938	2.078	394.84	820.55	1.949	398.88	777.55
A_68_P21261714	chr2:60800138-60800182	NM_020296:1101	Rbms1	INSIDE	0.938	0.649	1591.36	1032.82	0.609	1264.91	769.77
A_68_P31067775	chr17:15968105-15968150	NM_178615:-4577	Rgmb	PROMOTER	0.938	1.714	1439.57	2467.33	1.608	1291.47	2076.14
A_68_P20165363	chr1:39424634-39424678	NM_053257:-39	Rpl31	PROMOTER	0.938	0.592	3993.95	2363.20	0.555	3084.49	1711.13
A_68_P29614999	chr14:55531847-55531891	NM_021551:101	Slc22a17	INSIDE	0.938	0.679	1894.38	1287.19	0.637	1647.96	1050.22
A_68_P30964218	chr16:91660311-91660368	NM_019973:12271	Son	INSIDE	0.938	3.343	421.83	1410.38	3.137	362.66	1137.51
A_68_P26363428	chr9:24578465-24578509	NM_194263:261	Tbx20	INSIDE	0.938	1.490	1627.26	2424.94	1.397	1295.62	1810.08
A_68_P23240688	chr4:118159059-118159103	NM_011587:3374	Tie1	INSIDE	0.938	2.368	1221.78	2893.54	2.222	997.05	2215.06
A_68_P27056140	chr10:34001966-34002010	NM_009433:-7	Tspyl1	PROMOTER	0.938	1.563	1500.06	2344.63	1.466	1331.59	1951.57
A_68_P27186305	chr10:61949424-61949468	NM_001113355:-100	Vps26a	PROMOTER	0.938	0.550	1760.19	968.97	0.516	1636.84	845.10
A_68_P24424641	chr6:47816485-47816534	NM_027477:30850	Zfp398	INSIDE	0.938	2.112	455.96	962.78	1.981	379.81	752.54
A_68_P24424642	chr6:47816553-47816601	NM_027477:30917	Zfp398	INSIDE	0.938	2.422	373.19	903.88	2.273	305.03	693.27
A_68_P30796632	chr16:59600772-59600816			Unknown	0.938	3.041	295.36	898.13	2.852	286.72	817.81
A_68_P24541219	chr6:72297667-72297711	NM_026696:378	0610030E20Rik	INSIDE	0.937	0.668	4380.83	2925.49	0.626	3699.06	2314.44
A_68_P30941181	chr16:87699207-87699251	NM_007520:30	Bach1	INSIDE	0.937	0.725	4884.89	3542.67	0.680	4048.14	2751.72
A_68_P27489857	chr10:118677199-118677243	NM_027994:-109	Cand1	PROMOTER	0.937	0.577	1470.72	847.95	0.540	1333.66	720.51
A_68_P31125929	chr17:29231859-29231903	NM_007669:1164	Cdkn1a	INSIDE	0.937	0.527	1029.13	542.00	0.493	822.09	405.52
A_68_P27263123	chr10:76077247-76077291	NM_146007:8881	Col6a2	INSIDE	0.937	2.296	1694.67	3891.28	2.152	1389.29	2990.21
A_68_P26715672	chr9:89949316-89949360	NM_007801:234	Ctsh	INSIDE	0.937	0.723	2180.24	1576.89	0.678	1842.92	1248.80
A_68_P27271712	chr10:77497354-77497398	NM_001081695:-7655	Dnmt3l	PROMOTER	0.937	3.002	1086.70	3261.85	2.812	968.73	2724.14
A_68_P25641011	chr8:9207733-9207777	NM_173446:563269	Fam155a	INSIDE	0.937	3.319	310.90	1031.91	3.109	278.82	866.98
A_68_P32241740	chrX:7674050-7674094	NR_003632:-140	Gm6787	DIVERGENT_PROMOTER	0.937	1.980	1381.70	2735.60	1.856	733.67	1361.36
A_68_P29356808	chr13:117099881-117099929	NM_021459:-8	Isl1	PROMOTER	0.937	0.512	1546.76	791.45	0.479	1258.06	603.15
A_68_P29054505	chr13:55452830-55452879	NM_025828:11290	Lman2	INSIDE	0.937	2.208	562.31	1241.77	2.070	513.04	1062.09
A_68_P24990780	chr7:19576294-19576338	NM_145579:-277	Mypop	PROMOTER	0.937	2.314	374.98	867.62	2.169	355.93	772.02
A_68_P26824898	chr9:110540931-110540975	NM_183276:15713	Nbeal2	INSIDE	0.937	1.873	693.29	1298.55	1.755	637.89	1119.29
A_68_P31629941	chr18:37926527-37926571	NM_033595:1315	Pcdhga12	INSIDE	0.937	1.884	771.43	1453.18	1.765	703.20	1241.41
A_68_P31236181	chr17:51952553-51952597	NM_001163630:-1195	Satb1	PROMOTER	0.937	2.753	402.23	1107.43	2.581	394.86	1019.18
A_68_P30979599	chr16:94347306-94347350	NM_011377:261824	Sim2	INSIDE	0.937	3.122	497.54	1553.49	2.927	515.43	1508.75
A_68_P22324940	chr3:90193568-90193612	NM_011988:259	Slc27a3	INSIDE	0.937	2.306	459.79	1060.23	2.160	506.46	1094.18
A_68_P28550370	chr12:76919981-76920025	NM_001005510:698	Syne2	INSIDE	0.937	0.376	2522.86	949.35	0.353	2087.13	736.02
A_68_P31926782	chr19:5082847-5082891	NM_001001885:2609	Tmem151a	INSIDE	0.937	3.548	882.26	3130.47	3.326	808.60	2689.12
A_68_P25393299	chr7:112766364-112766408	NM_018880:15627	Trim3	INSIDE	0.937	2.642	851.71	2250.06	2.476	718.54	1778.87
A_68_P32791134	chrX:159266854-159266898	NM_178935:455	Txlng	INSIDE	0.937	2.277	6885.64	15678.71	2.133	3336.07	7114.19
A_68_P24630035	chr6:89785240-89785284	NM_053221:10269	Vmn1r42	DOWNSTREAM	0.937	3.436	600.88	2064.41	3.220	554.95	1786.73
A_68_P23244792	chr4:118967244-118967289	NM_011732:-148	Ybx1	PROMOTER	0.937	1.855	3083.95	5719.25	1.737	1938.79	3368.39
A_68_P24118629	chr5:136410508-136410552	NM_018871:-19	Ywhag	PROMOTER	0.937	2.420	1234.43	2987.44	2.267	985.74	2234.22
A_68_P25030073	chr7:30928817-30928863	NM_001081007:21874	Zfp382	DOWNSTREAM	0.937	3.328	614.01	2043.25	3.119	441.65	1377.62
A_68_P24142834	chr5:141180937-141180981	NM_172724:-18	Baat1	DIVERGENT_PROMOTER	0.936	1.705	2460.35	4194.40	1.596	1895.74	3025.52
A_68_P31158872	chr17:35457951-35457995	NM_010390:470	H2-Q1	INSIDE	0.936	0.566	1044.41	590.81	0.529	918.60	486.28
A_68_P27285763	chr10:80298067-80298111	NM_001013758:8696	Lingo3	INSIDE	0.936	2.028	638.15	1294.23	1.898	564.92	1072.28
A_68_P25031174	chr7:31140698-31140742	NM_175478:7071	Lrfn3	INSIDE	0.936	2.191	464.69	1017.98	2.050	428.31	878.23
A_68_P24008162	chr5:115607960-115608004	NM_175403:203	Mlec	INSIDE	0.936	2.904	7081.42	20564.08	2.717	5209.97	14154.52
A_68_P27854122	chr11:62270378-62270422	NM_011308:434	Ncor1	INSIDE	0.936	0.686	2475.11	1697.00	0.642	1891.41	1213.61
A_68_P23253519	chr4:120498120-120498164	NM_008692:178	Nfyc	INSIDE	0.936	0.647	963.60	623.07	0.605	831.37	502.91
A_68_P28683723	chr12:101962977-101963021	NM_153587:240	Rps6ka5	INSIDE	0.936	0.630	1066.04	671.42	0.590	909.81	536.44
A_68_P26783276	chr9:102911099-102911143	NM_033314:302	Slco2a1	INSIDE	0.936	0.589	1020.16	601.37	0.552	903.70	498.77

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27098030	chr10:42741219-42741263	NM_175407:153096	Sobp	INSIDE	0.936	5.340	375.61	2005.75	4.998	362.83	1813.31
A_68_P28614749	chr12:88541116-88541160	NM_001033475:41	Tmed8	INSIDE	0.936	2.255	472.30	1065.01	2.110	453.31	956.47
A_68_P26894029	chr9:123169283-123169327	NM_001002267:603	Tmem158	INSIDE	0.936	2.848	821.54	2339.84	2.665	868.02	2313.21
A_68_P29260159	chr13:99660900-99660944	NM_001048267:75	Tnpo1	INSIDE	0.936	1.803	1558.28	2810.13	1.688	1428.62	2410.99
A_68_P27779788	chr11:48567252-48567296	ENSMUST00000120566:-58		PROMOTER	0.936	2.510	1291.20	3241.30	2.350	1089.83	2560.82
A_68_P24648069	chr6:92893420-92893464	NR_015530:2867	9530026P05Rik	INSIDE	0.935	2.223	648.74	1442.12	2.078	649.95	1350.92
A_68_P28731507	chr12:110272513-110272557	NM_001163175:33893	Begain	INSIDE	0.935	1.815	1673.06	3036.33	1.698	1227.85	2084.55
A_68_P28175417	chr11:118898832-118898876	NM_013926:3373	Cbx8	DOWNSTREAM	0.935	1.706	1775.60	3028.48	1.595	1676.58	2673.53
A_68_P23343156	chr4:137550305-137550349	NM_172703:942	Eif4g3	INSIDE	0.935	1.938	527.20	1021.48	1.812	402.54	729.51
A_68_P23335793	chr4:136326759-136326803	NM_010142:65070	Ephb2	INSIDE	0.935	2.346	1211.20	2841.44	2.193	1012.31	2219.81
A_68_P22324052	chr3:90035906-90035950	NM_206924:410	Jtb	INSIDE	0.935	1.731	1141.67	1975.86	1.618	940.23	1521.04
A_68_P21842277	chr2:168397045-168397089	NM_001136073:18625	Nfatc2	INSIDE	0.935	1.905	620.83	1182.57	1.781	499.77	890.31
A_68_P24209922	chr6:5248441-5248485	NM_183308:-89	Pon2	PROMOTER	0.935	0.470	3231.83	1519.48	0.439	2566.20	1127.64
A_68_P23974099	chr5:109203826-109203870	NM_026109:20534	Tmed11	DOWNSTREAM	0.935	2.850	1603.10	4568.82	2.666	1266.35	3375.87
A_68_P26154297	chr8:111474389-111474435	NM_007496:235869	Zfhx3	INSIDE	0.935	1.628	1147.23	1867.33	1.522	809.30	1232.06
A_68_P24428349	chr6:48570036-48570080	NM_173429:6880	Zfp775	INSIDE	0.935	1.984	1028.78	2041.22	1.855	703.44	1304.96
A_68_P31461137	chr18:4052694-4052738			Unknown	0.935	2.136	793.43	1694.72	1.998	711.94	1422.47
A_68_P23999131	chr5:114064213-114064257	NM_008153:36165	Cmklr1	INSIDE	0.934	5.924	1827.40	10825.68	5.532	1166.26	6451.88
A_68_P31927966	chr19:5307193-5307237	NM_001024717:8884	Gal3st3	INSIDE	0.934	1.984	1127.02	2235.73	1.852	899.33	1665.99
A_68_P26804349	chr9:106549876-106549920	NM_001160353:8542	Grm2	INSIDE	0.934	3.614	2231.27	8064.18	3.377	1690.72	5709.25
A_68_P26346083	chr9:21038393-21038437	NM_001110305:5362	Keap1	INSIDE	0.934	2.544	1105.00	2811.50	2.376	919.04	2183.83
A_68_P25595364	chr7:149718822-149718866	NM_011288:-177	Mrpl23	PROMOTER	0.934	1.724	6237.18	10749.81	1.609	4530.69	7289.82
A_68_P30346546	chr15:76003525-76003570	NM_201394:22593	Plec	INSIDE	0.934	2.739	704.59	1930.14	2.560	676.47	1731.43
A_68_P32467532	chrX:71574336-71574380	NM_008883:-46	Plxna3	PROMOTER	0.934	1.948	691.33	1346.47	1.819	358.24	651.48
A_68_P25090600	chr7:52262845-52262889	NM_001008422:8753	Scaf1	INSIDE	0.934	2.426	1818.93	4413.07	2.267	1230.69	2790.08
A_68_P20354814	chr1:75542871-75542915	NM_009208:52	Slc4a3	INSIDE	0.934	4.528	2101.91	9518.27	4.228	1820.53	7696.53
A_68_P27355934	chr10:93296766-93296810	NM_183199:2489	Usp44	INSIDE	0.934	0.552	1809.82	999.40	0.516	1590.17	820.14
A_68_P27287690	chr10:80607523-80607567	NM_010731:8529	Zbtb7a	INSIDE	0.934	2.216	1502.36	3329.37	2.070	1182.19	2447.57
A_68_P24155560	chr5:143997116-143997160	NM_177681:252	Zfp12	INSIDE	0.934	0.686	1519.94	1042.31	0.641	1238.68	793.61
A_68_P25063505	chr7:38555583-38555627	NM_172385:-833	Zfp536	PROMOTER	0.934	0.725	3633.79	2632.87	0.676	3039.66	2056.33
A_68_P28202317	chr12:4775790-4775834	NM_175431:261	A830093I24Rik	INSIDE	0.933	1.687	661.19	1115.10	1.574	651.77	1025.80
A_68_P23145841	chr4:99382126-99382170	NM_001081264:-172	Alg6	PROMOTER	0.933	0.698	3490.44	2436.86	0.651	2894.75	1884.59
A_68_P30647300	chr16:31430146-31430190	NM_001122683:1330	Bdh1	INSIDE	0.933	0.572	1685.85	963.80	0.533	1290.62	688.28
A_68_P31096346	chr17:24388277-24388321	NM_007634:56	Ccnf	INSIDE	0.933	2.667	523.87	1397.08	2.487	511.19	1271.30
A_68_P25272110	chr7:88599409-88599453	NM_007755:132	Cpeb1	INSIDE	0.933	0.707	1233.45	872.65	0.660	1098.16	725.09
A_68_P26165985	chr8:113521608-113521652	NM_007916:93	Ddx19a	INSIDE	0.933	0.613	1696.24	1039.05	0.572	1386.22	792.50
A_68_P26458701	chr9:42752890-42752934	NM_175481:-458	Grik4	PROMOTER	0.933	1.654	1478.80	2446.64	1.543	1277.31	1970.99
A_68_P28751166	chr12:113838256-113838300	NM_198411:11284	Inf2	INSIDE	0.933	2.107	1940.99	4090.03	1.966	1420.36	2791.97
A_68_P28998905	chr13:44998485-44998530	NM_001205043:171868	Jarid2	INSIDE	0.933	1.880	625.81	1176.60	1.754	509.95	894.22
A_68_P25004550	chr7:25162275-25162319	NM_001163510:7015	Kcnn4	INSIDE	0.933	1.625	1515.69	2463.23	1.517	1195.10	1812.96
A_68_P30422457	chr15:88813275-88813319	NM_031260:-127	Mov10l1	DIVERGENT_PROMOTER	0.933	2.528	492.30	1244.42	2.358	425.08	1002.55
A_68_P31029176	chr17:8995030-8995074	NM_011866:443	Pde10a	INSIDE	0.933	1.958	2235.98	4378.14	1.827	1809.79	3306.25
A_68_P21911589	chr2:181335871-181335915	NM_133701:-131	Prpf6	DIVERGENT_PROMOTER	0.933	0.415	1426.10	591.41	0.387	1053.17	407.30
A_68_P24090824	chr5:130292894-130292938	NM_133900:213	Psph	INSIDE	0.933	0.445	1349.08	599.96	0.415	1179.34	489.59
A_68_P26022784	chr8:87469901-87469945	NM_144929:-967	Rtbdn	DIVERGENT_PROMOTER	0.933	0.673	1056.43	711.02	0.628	927.78	582.88
A_68_P27550650	chr11:3093527-3093573	NM_030207:-84	Sfi1	DIVERGENT_PROMOTER	0.933	1.890	1565.66	2958.66	1.764	1376.07	2427.19
A_68_P23278806	chr4:125879586-125879630	NM_146153:346	Thrap3	INSIDE	0.933	0.483	2144.94	1036.48	0.451	1968.26	887.61
A_68_P31771010	chr18:63852103-63852147	NM_016792:-111	Txnl1	PROMOTER	0.933	0.627	1325.06	830.80	0.585	1097.23	642.18
A_68_P21977355	chr3:19794775-19794819	NR_027985:-74	4632415L05Rik	PROMOTER	0.932	0.579	1746.18	1011.07	0.539	1473.29	794.74
A_68_P28182256	chr11:119948049-119948093	NM_009734:71	Azi1	INSIDE	0.932	2.022	479.20	968.95	1.884	462.83	871.98
A_68_P26156363	chr8:111864572-111864616	NR_002928:214	Gm1943	INSIDE	0.932	1.848	692.34	1279.78	1.723	525.75	905.69

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26804350	chr9:106549989-106550033	NM_001160353:8430	Grm2	INSIDE	0.932	4.656	2018.50	9397.18	4.339	1393.34	6045.26
A_68_P29628537	chr14:58161247-58161291	NM_145837:17603	Il17d	INSIDE	0.932	1.992	854.92	1702.76	1.857	778.25	1445.41
A_68_P32319267	chrX:34137999-34138043	NM_016783:-199	Pgrmc1	PROMOTER	0.932	1.816	949.99	1725.34	1.693	489.37	828.28
A_68_P22825907	chr4:33335613-33335657	NM_001033225:128	Pnrc1	INSIDE	0.932	0.537	1116.26	599.04	0.500	856.03	428.22
A_68_P23373725	chr4:142752302-142752346	NM_001081355:50288	Prdm2	INSIDE	0.932	0.401	1598.97	640.41	0.373	1364.42	509.43
A_68_P31251406	chr17:55621810-55621854	NM_172829:36818	St6gal2	INSIDE	0.932	3.147	180.23	567.20	2.932	193.92	568.55
A_68_P29056640	chr13:55819313-55819357	NM_175150:3324	Txndc15	INSIDE	0.932	2.212	703.56	1556.21	2.062	581.00	1198.22
A_68_P29023550	chr13:49243481-49243525	NM_029361:-119	Wnk2	PROMOTER	0.932	1.551	985.13	1528.36	1.446	875.99	1266.83
A_68_P21105204	chr2:30640432-30640476	ENSMUST00000139968:18701		DOWNSTREAM	0.932	1.983	782.44	1551.78	1.848	749.69	1385.48
A_68_P26559432	chr9:60369799-60369843	ENSMUST00000140824:33		INSIDE	0.932	3.850	666.42	2566.04	3.589	542.76	1947.87
A_68_P24059291	chr5:124545373-124545417	NM_019875:413	Abcb9	INSIDE	0.931	0.612	1460.57	893.62	0.570	1181.60	673.24
A_68_P24925494	chr6:145814701-145814745	NM_024469:-862	Bhlhe41	PROMOTER	0.931	0.659	2763.85	1820.61	0.614	2089.35	1282.03
A_68_P23397715	chr4:148326702-148326746	NM_001159344:148224	Casz1	INSIDE	0.931	0.597	1184.56	707.77	0.556	1037.62	576.89
A_68_P31157314	chr17:35196243-35196287	NM_001190449:285	Ddah2	INSIDE	0.931	1.471	3333.08	4902.54	1.369	2560.89	3505.95
A_68_P25678286	chr8:15027955-15027999	NM_029116:16952	Kbtbd11	INSIDE	0.931	1.887	642.03	1211.62	1.757	630.98	1108.63
A_68_P29629403	chr14:58310348-58310392	NM_015771:54590	Lats2	INSIDE	0.931	2.836	1282.63	3637.22	2.641	985.18	2601.76
A_68_P25034848	chr7:31852435-31852479	NM_144556:7503	Lgi4	INSIDE	0.931	3.337	754.59	2518.40	3.107	693.17	2153.84
A_68_P23912412	chr5:97821337-97821381	NM_001033191:-9	Naa11	PROMOTER	0.931	3.327	1216.16	4045.88	3.096	1061.21	3285.11
A_68_P22859777	chr4:40918239-40918283	NM_023739:285	Nfx1	INSIDE	0.931	1.798	497.02	893.71	1.674	475.58	796.10
A_68_P31862859	chr18:80389409-80389453	NM_199197:7928	Rbfa	INSIDE	0.931	2.547	525.61	1338.69	2.372	416.05	986.71
A_68_P24085131	chr5:129287972-129288016	NM_001081388:171243	Rimbp2	INSIDE	0.931	2.217	1299.57	2881.31	2.065	1058.34	2185.31
A_68_P29244710	chr13:96901056-96901100	NM_029210:1454	Sv2c	INSIDE	0.931	0.654	3816.22	2494.89	0.608	3071.71	1868.66
A_68_P30370136	chr15:79922200-79922244	NM_009303:459	Syngr1	INSIDE	0.931	0.521	1226.39	639.08	0.485	1012.89	491.51
A_68_P24118489	chr5:136387042-136387086	NM_018871:23447	Ywhag	INSIDE	0.931	1.985	1221.53	2424.51	1.849	816.05	1508.54
A_68_P23590587	chr5:34038039-34038083	AK172441:87326		INSIDE	0.931	1.916	856.24	1640.37	1.783	841.39	1500.23
A_68_P24513209	chr6:65622803-65622847	NM_172399:1220	A930038C07Rik	INSIDE	0.930	1.907	1171.40	2234.16	1.773	1043.11	1849.37
A_68_P29050152	chr13:54676736-54676780	NM_019968:385	Arl10	INSIDE	0.930	0.707	1562.67	1104.27	0.657	1288.45	847.01
A_68_P22716231	chr4:8679020-8679064	NM_001081417:60975	Chd7	INSIDE	0.930	2.694	1432.17	3858.30	2.506	1180.21	2958.14
A_68_P33007790	chr4_random:128337-128381	NM_001033326:18557	Dhrsx	INSIDE	0.930	3.315	8590.18	28473.79	3.083	6402.68	19739.27
A_68_P20416040	chr1:89052463-89052507	NM_021306:-882	Ecel1	PROMOTER	0.930	1.703	2901.99	4942.58	1.583	2632.76	4168.89
A_68_P27497201	chr10:119851658-119851707	NM_010441:62309	Hmga2	INSIDE	0.930	4.452	413.71	1841.97	4.142	321.53	1331.82
A_68_P23527252	chr5:21181527-21181571	NM_178728:25615	Napepld	INSIDE	0.930	2.249	1264.18	2843.54	2.093	928.53	1943.21
A_68_P28433223	chr12:53198848-53198892	NM_029760:138	Nubpl	INSIDE	0.930	2.245	1770.08	3973.89	2.087	1560.57	3257.11
A_68_P25021461	chr7:29156631-29156675	NM_001083912:1029	Plekhg2	INSIDE	0.930	0.351	1825.35	640.18	0.326	1453.40	474.25
A_68_P23374048	chr4:142802256-142802300	NM_001081355:334	Prdm2	INSIDE	0.930	0.538	1431.28	770.08	0.501	1201.33	601.28
A_68_P23232473	chr4:116782119-116782163	NM_008958:13180	Ptch2	INSIDE	0.930	2.186	926.65	2025.30	2.033	800.17	1626.93
A_68_P25090596	chr7:52262461-52262505	NM_001008422:9137	Scaf1	INSIDE	0.930	2.752	1095.77	3015.02	2.559	862.57	2207.06
A_68_P27259388	chr10:75383953-75383997	NM_001161853:385	Smarcb1	INSIDE	0.930	1.947	669.46	1303.24	1.811	679.70	1230.63
A_68_P31357836	A_68_P31357836			Unknown	0.930	0.736	4229.64	3111.36	0.684	3439.40	2353.71
A_68_P27534320	chr10:126602342-126602386	NM_027739:-522	B4galnt1	PROMOTER	0.929	0.363	1781.55	646.66	0.337	1241.86	418.56
A_68_P28743216	chr12:112537725-112537769	NM_183016:78183	Cdc42bpb	INSIDE	0.929	2.500	824.77	2061.80	2.322	701.96	1630.17
A_68_P26699344	chr9:86361211-86361255	NM_177208:472	Dopey1	INSIDE	0.929	1.839	831.39	1528.75	1.709	764.75	1306.93
A_68_P28069617	chr11:100570105-100570149	NM_001038010:3655	Kat2a	INSIDE	0.929	3.539	1048.39	3710.05	3.288	958.51	3151.62
A_68_P27281281	chr10:79610845-79610889	NM_021565:-168	Midn	PROMOTER	0.929	0.590	1110.44	654.95	0.548	830.43	454.82
A_68_P26877097	chr9:120213366-120213410	NM_144557:198	Myrip	INSIDE	0.929	0.546	942.90	514.81	0.507	826.47	419.10
A_68_P27931785	chr11:76212519-76212563	NM_008750:103	Nxn	INSIDE	0.929	1.568	1469.67	2303.85	1.457	1224.93	1784.29
A_68_P24324978	chr6:29121084-29121128	NM_001101443:8478	Prrt4	INSIDE	0.929	2.009	875.60	1758.77	1.866	818.63	1527.59
A_68_P31924141	chr19:4625447-4625491	NM_023131:149	Rce1	INSIDE	0.929	0.536	1535.67	823.65	0.498	1258.35	627.22
A_68_P22342626	chr3:94976422-94976466	NM_011351:8149	Sema6c	INSIDE	0.929	1.749	1088.72	1904.39	1.625	863.85	1403.55
A_68_P20618599	chr1:133859814-133859858	NM_145977:-7349	Slc45a3	PROMOTER	0.929	1.697	964.00	1636.14	1.576	936.57	1476.01
A_68_P30546007	chr16:11066704-11066748	NM_009223:336	Snn	INSIDE	0.929	0.652	1869.64	1218.92	0.606	1336.51	809.76

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P30351139	chr15:76741794-76741838	NM_001168276:14062	Zfp647	INSIDE	0.929	2.321	725.82	1684.29	2.156	593.98	1280.38
A_68_P31256677	chr17:56651893-56651937	NM_011483:-8	Znrf4	PROMOTER	0.929	2.174	382.88	832.54	2.019	365.16	737.28
A_68_P23498118	chr5:15440585-15440629	NM_001110843:98	Cacna2d1	INSIDE	0.928	2.072	602.76	1249.19	1.923	588.45	1131.86
A_68_P27489859	chr10:118677390-118677434	NM_027994:-301	Cand1	PROMOTER	0.928	2.069	740.55	1531.99	1.920	574.47	1103.04
A_68_P22318561	chr3:89124750-89124794	NM_010108:2029	Efna3	INSIDE	0.928	0.668	1025.98	685.77	0.620	851.48	527.99
A_68_P28924077	chr13:31718533-31718577	NM_010225:870	Foxf2	INSIDE	0.928	0.496	1489.10	738.07	0.460	1143.83	526.10
A_68_P32539665	chrX:91881517-91881561	NM_008179:131	Gspt2	INSIDE	0.928	1.689	1639.76	2769.73	1.567	971.22	1522.34
A_68_P21339292	chr2:74584954-74584998	NM_010468:34927	Hoxd3	INSIDE	0.928	0.624	3452.72	2153.79	0.579	2887.64	1671.32
A_68_P28060086	chr11:98903124-98903168	NM_010517:573	Igfbp4	INSIDE	0.928	0.563	993.45	559.50	0.523	775.11	405.05
A_68_P22540996	chr3:132754802-132754846	NM_027927:-92	Ints12	DIVERGENT_PROMOTER	0.928	0.517	1457.16	752.89	0.480	1148.49	550.95
A_68_P30619233	chr16:26105938-26105982	NM_173379:-90	Leprel1	PROMOTER	0.928	1.709	1075.12	1837.55	1.586	946.38	1500.80
A_68_P32024331	chr19:24630850-24630894	NM_008846:-555	Pip5k1b	PROMOTER	0.928	0.456	1485.31	677.37	0.423	1114.58	471.79
A_68_P21395217	chr2:84726953-84726997	NM_199223:-125	Rtn4rl2	PROMOTER	0.928	2.484	408.60	1014.77	2.305	449.17	1035.33
A_68_P27926564	chr11:75329061-75329105	NM_001004157:2040	Scarf1	INSIDE	0.928	2.616	981.75	2567.92	2.426	735.34	1784.28
A_68_P25661263	chr8:12397648-12397692	NM_009233:2152	Sox1	INSIDE	0.928	0.677	1109.99	751.95	0.628	947.23	595.23
A_68_P30296513	chr15:67008341-67008385	NM_009177:82	St3gal1	INSIDE	0.928	0.665	1619.75	1076.98	0.617	1409.80	869.46
A_68_P26154294	chr8:111474065-111474109	NM_007496:235543	Zfhx3	INSIDE	0.928	2.331	788.56	1838.29	2.164	617.30	1335.93
A_68_P20135161	chr1:33871021-33871065	NM_133817:230	Zfp451	INSIDE	0.928	0.714	2008.21	1433.43	0.662	1487.99	985.37
A_68_P25956909	chr8:73985635-73985679	NM_022419:1900	Abhd8	INSIDE	0.927	2.496	2338.73	5837.75	2.315	1796.08	4157.61
A_68_P29613379	chr14:55250870-55250914	NM_199470:9309	Cdh24	INSIDE	0.927	1.651	1360.45	2245.70	1.531	1158.87	1773.77
A_68_P29241611	chr13:96388009-96388053	NM_010169:358	F2r	INSIDE	0.927	0.543	1303.58	708.17	0.504	1181.02	595.02
A_68_P27897169	chr11:69615077-69615121	NM_010198:29	Fgf11	INSIDE	0.927	0.651	1935.64	1260.82	0.604	1357.33	819.78
A_68_P21091204	chr2:28302022-28302066	NM_001005420:-1416	Gm347	PROMOTER	0.927	0.715	1716.94	1227.65	0.663	1625.41	1076.85
A_68_P25004864	chr7:25218003-25218050	NM_199013:12675	Irgc1	INSIDE	0.927	2.427	637.91	1548.09	2.249	502.25	1129.74
A_68_P26644019	chr9:75289708-75289753	NM_001039522:400	Leo1	INSIDE	0.927	2.108	671.27	1414.83	1.954	588.84	1150.66
A_68_P22878699	chr4:44723813-44723857	NM_008782:-522	Pax5	PROMOTER	0.927	0.628	1207.35	757.62	0.582	984.37	572.80
A_68_P25377918	chr7:109399091-109399135	NM_019566:-480	Rhog	PROMOTER	0.927	1.740	1309.38	2278.08	1.612	989.03	1594.61
A_68_P21843353	chr2:168581710-168581754	NM_175303:10969	Sall4	INSIDE	0.927	2.251	288.60	649.77	2.086	270.97	565.35
A_68_P30348872	chr15:76349910-76349954	NM_130893:2627	Scrt1	INSIDE	0.927	2.304	1037.55	2390.39	2.136	935.21	1997.37
A_68_P26885414	chr9:121671950-121671994	NM_001166644:2822	Zfp651	INSIDE	0.927	2.660	602.31	1602.43	2.467	441.37	1088.84
A_68_P29308209	chr13:108681343-108681387	NM_145456:-1106	Zswim6	PROMOTER	0.927	1.590	963.81	1532.68	1.475	822.39	1212.89
A_68_P32473670	chrX:73211772-73211816	ENSMUST00000121090:-7487		PROMOTER	0.927	1.530	2064.85	3159.89	1.419	1011.59	1434.99
A_68_P21901912	chr2:179906060-179906104	NM_019822:-210	Adrm1	PROMOTER	0.926	3.610	757.83	2735.99	3.341	669.25	2236.27
A_68_P27899784	chr11:70068702-70068746	NM_007440:119	Alox12	INSIDE	0.926	0.627	1208.42	758.19	0.581	1002.89	582.54
A_68_P29056517	chr13:55794620-55794664	NM_181278:158	B230219D22Rik	INSIDE	0.926	1.805	391.42	706.59	1.671	477.72	798.38
A_68_P26221735	chr8:123191978-123192022	NM_010926:12	Cox4nb	INSIDE	0.926	0.674	1815.53	1223.91	0.625	1463.23	913.79
A_68_P24602880	chr6:85019421-85019465	NM_177077:65	Exoc6b	INSIDE	0.926	1.706	1531.81	2613.24	1.579	1418.22	2239.40
A_68_P25835331	chr8:47377554-47377598	NM_173789:2449	Helt	INSIDE	0.926	2.060	1321.32	2721.37	1.907	1003.71	1914.36
A_68_P26258434	chr8:129118421-129118465	NM_001164598:-1106	Irf2bp2	PROMOTER	0.926	2.005	609.11	1221.10	1.857	550.31	1021.94
A_68_P29054504	chr13:55452758-55452802	NM_025828:11364	Lman2	INSIDE	0.926	2.259	732.69	1655.06	2.091	598.16	1250.98
A_68_P27787411	chr11:50039460-50039504	NM_145926:646	Mgat4b	INSIDE	0.926	5.290	410.60	2172.16	4.897	343.75	1683.29
A_68_P29044154	chr13:53571404-53571448	NM_013601:-3277	Msx2	PROMOTER	0.926	1.539	3706.05	5702.14	1.425	3328.32	4743.76
A_68_P25954893	chr8:73437576-73437620	NM_173013:7726	Mtap1s	INSIDE	0.926	3.681	528.86	1946.62	3.407	419.85	1430.30
A_68_P26991388	chr10:20880481-20880525	NM_001198914:288	Myb	INSIDE	0.926	1.571	985.08	1548.04	1.455	930.29	1353.33
A_68_P20189690	chr1:43610952-43610996	NM_010879:108379	Nck2	INSIDE	0.926	1.909	809.49	1545.16	1.767	636.36	1124.56
A_68_P28621835	chr12:90498748-90498792	NM_172544:306937	Nrxn3	INSIDE	0.926	2.186	1067.40	2333.15	2.023	884.84	1790.11
A_68_P22309972	chr3:87587929-87587973	NM_001033124:11134	Ntrk1	INSIDE	0.926	3.167	1827.72	5788.41	2.932	1500.15	4398.10
A_68_P30346561	chr15:76005231-76005275	NM_201394:20888	Plec	INSIDE	0.926	2.334	1017.33	2373.96	2.161	788.14	1702.87
A_68_P24324924	chr6:29114488-29114532	NM_133925:214	Rbm28	INSIDE	0.926	0.629	3325.73	2091.72	0.582	2489.29	1449.67
A_68_P24428219	chr6:48547191-48547235	NM_001079901:3331	Repin1	INSIDE	0.926	2.259	1449.45	3274.75	2.092	1083.81	2267.57
A_68_P32694935	chrX:136145294-136145338	NM_023270:158	Rnf128	INSIDE	0.926	3.100	899.92	2789.55	2.871	675.38	1938.79

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P24604452	chr6:85283101-85283145	NM_178639:294	Sfxn5	INSIDE	0.926	0.643	875.11	562.71	0.595	756.02	450.19
A_68_P28151703	chr11:115025252-115025296	NM_012030:620	Slc9a3r1	INSIDE	0.926	0.600	1635.43	981.75	0.556	1136.03	631.70
A_68_P25183829	chr7:72789715-72789759	NM_172310:-47	Tarsl2	PROMOTER	0.926	2.044	13789.93	28181.66	1.892	9572.49	18111.79
A_68_P21105306	chr2:30656954-30656998	NM_198000:251	1700001O22Rik	INSIDE	0.925	2.505	2026.51	5076.77	2.316	1721.46	3987.51
A_68_P27033724	chr10:28916766-28916810	NM_026138:52987	6330407J23Rik	INSIDE	0.925	2.092	1805.80	3777.61	1.936	1478.82	2862.56
A_68_P30371903	chr15:80202683-80202727	NM_001044308:85037	Cacna1i	INSIDE	0.925	2.667	998.46	2662.87	2.468	786.47	1941.09
A_68_P20910363	chr1:188791777-188791821	NM_033077:504	D1Pas1	INSIDE	0.925	1.733	689.41	1194.66	1.604	577.34	925.83
A_68_P20149760	chr1:36739833-36739877	NM_001126046:174	Fam178b	INSIDE	0.925	2.814	1267.41	3566.45	2.602	1126.79	2932.09
A_68_P31927961	chr19:5306691-5306735	NM_001024717:8382	Gal3st3	INSIDE	0.925	2.240	1301.78	2915.80	2.073	1039.13	2153.91
A_68_P21874743	chr2:174152892-174152936	NR_003258:-500	Gnas	PROMOTER	0.925	3.703	4265.92	15798.12	3.427	2818.28	9657.38
A_68_P21339005	chr2:74550245-74550289	NM_010468:217	Hoxd3	INSIDE	0.925	0.601	2203.74	1323.68	0.556	1732.19	962.30
A_68_P27865441	chr11:64249280-64249324	NM_178870:469	Hs3st3a1	INSIDE	0.925	0.549	1280.62	703.58	0.508	985.05	500.45
A_68_P26258420	chr8:129116753-129116797	NM_001164598:562	Irf2bp2	INSIDE	0.925	1.589	1252.23	1989.99	1.471	1071.28	1575.59
A_68_P24428220	chr6:48547266-48547310	NM_001079901:3407	Repin1	INSIDE	0.925	2.499	661.65	1653.19	2.310	576.30	1331.30
A_68_P21081267	chr2:26788591-26788635	NM_011512:419	Surf4	INSIDE	0.925	0.675	1431.85	965.83	0.624	1350.10	842.51
A_68_P31950560	chr19:10500789-10500833	NM_018801:37231	Syt7	INSIDE	0.925	1.812	1635.94	2963.67	1.675	1198.81	2008.51
A_68_P26883519	chr9:121363673-121363717	NM_175114:87619	Trak1	INSIDE	0.925	2.819	989.40	2788.91	2.608	705.00	1838.77
A_68_P27466130	chr10:114238213-114238257	NM_146241:192	Trhde	INSIDE	0.925	0.675	1117.27	754.17	0.624	895.70	559.19
A_68_P26513689	chr9:51976512-51976556	NM_001162921:-318	Zc3h12c	PROMOTER	0.925	2.048	839.46	1719.39	1.895	710.91	1347.18
A_68_P26238819	chr8:125778613-125778657	NM_020497:540	Zfp276	INSIDE	0.925	0.601	1523.49	915.89	0.556	1187.33	660.04
A_68_P23253637	chr4:120527431-120527475	ENSMUST00000106283:-6929		PROMOTER	0.925	1.768	1223.90	2163.39	1.635	1053.28	1722.40
A_68_P32151687	chr19:47805901-47805945	NM_026377:-323	6330577E15Rik	PROMOTER	0.924	0.610	1914.37	1167.07	0.563	1715.17	966.13
A_68_P28053987	chr11:97883567-97883611	NM_001159320:-3902	Cacnb1	PROMOTER	0.924	0.549	1904.28	1044.56	0.507	1410.05	714.97
A_68_P27563899	chr11:5441997-5442041	NM_134033:202	Ccdc117	INSIDE	0.924	1.617	915.50	1480.74	1.495	799.03	1194.48
A_68_P26844379	chr9:114294023-114294067	NM_019922:5786	Crtap	INSIDE	0.924	1.663	982.86	1634.68	1.537	846.08	1300.38
A_68_P28170155	chr11:118108984-118109028	NM_001112699:900	Cyth1	INSIDE	0.924	0.568	1606.36	911.99	0.525	1191.10	624.81
A_68_P31794503	chr18:68093621-68093666	NM_172631:733	D18Ertd653e	INSIDE	0.924	1.920	1540.79	2958.23	1.774	1194.60	2119.18
A_68_P31058441	chr17:14340236-14340280	NM_172826:580	Dact2	INSIDE	0.924	0.624	1288.87	803.71	0.576	1079.74	622.11
A_68_P22019077	chr3:28680006-28680050	NM_177586:-204	Eif5a2	PROMOTER	0.924	0.492	1295.33	637.57	0.455	1061.91	482.74
A_68_P28940412	chr13:34838589-34838633	NM_138746:7100	Fam50b	INSIDE	0.924	2.203	651.73	1435.87	2.037	544.01	1107.91
A_68_P27093485	chr10:41917381-41917425	NM_019740:79146	Foxo3	INSIDE	0.924	1.936	2076.54	4020.95	1.790	1616.27	2893.07
A_68_P20969135	chr2:4525120-4525164	NM_001177844:44343	Frmd4a	INSIDE	0.924	2.158	1092.22	2356.97	1.993	983.41	1960.07
A_68_P22204191	chr3:66024790-66024834	NM_008987:1004	Ptx3	INSIDE	0.924	2.248	411.46	924.91	2.077	392.56	815.37
A_68_P21116405	chr2:32470425-32470469	NM_001025310:7966	St6galnac6	INSIDE	0.924	2.819	1322.82	3729.64	2.605	1030.62	2684.68
A_68_P23337641	chr4:136604483-136604527	NM_198248:106	Zbtb40	INSIDE	0.924	2.449	759.46	1860.03	2.262	671.94	1519.87
A_68_P21775102	chr2:156905117-156905161	NM_001164663:-137	9830001H06Rik	DIVERGENT_PROMOTER	0.923	1.567	1177.07	1844.63	1.446	1140.98	1649.65
A_68_P26466976	chr9:44127791-44127835	NM_027909:553	C2cd2l	INSIDE	0.923	0.421	1601.40	673.48	0.388	1416.07	549.95
A_68_P26140463	chr8:109127687-109127731	NM_009864:441	Cdh1	INSIDE	0.923	2.015	777.32	1566.55	1.860	679.54	1263.96
A_68_P21144179	chr2:37648980-37649024	NM_001163566:17234	Crb2	INSIDE	0.923	1.520	1714.39	2605.17	1.402	1444.54	2025.88
A_68_P26885587	chr9:121697963-121698007	NR_027967:2254	Hhatl	INSIDE	0.923	2.123	346.73	736.06	1.960	310.70	608.94
A_68_P21840386	chr2:168088202-168088246	NM_001081134:6607	Kcng1	INSIDE	0.923	1.912	410.37	784.49	1.764	397.74	701.74
A_68_P23297927	chr4:129349792-129349836	NM_008468:197	Kpna6	INSIDE	0.923	0.456	2193.16	999.59	0.421	1728.92	727.21
A_68_P23264336	chr4:123364187-123364231	NM_001199136:-2605	Macf1	PROMOTER	0.923	0.647	880.14	569.05	0.597	781.60	466.56
A_68_P23542978	chr5:24108266-24108310	NM_025891:-468	Smarcd3	PROMOTER	0.923	2.188	676.38	1480.03	2.020	578.55	1168.40
A_68_P20005806	chr1:4483262-4483306	NM_011441:3210	Sox17	INSIDE	0.923	0.554	1089.43	604.00	0.512	873.68	447.25
A_68_P27502796	chr10:120748000-120748044	NM_029057:223	Tbc1d30	INSIDE	0.923	0.576	918.78	528.83	0.531	838.23	445.13
A_68_P26564384	chr9:61220668-61220712	NM_001083927:518	Tle3	INSIDE	0.923	0.685	2351.62	1611.64	0.633	1823.98	1154.16
A_68_P26373639	chr9:26837630-26837674	NM_178027:27	Vps26b	INSIDE	0.923	0.693	1163.43	806.21	0.640	1047.73	670.29
A_68_P24994121	chr7:20163073-20163117	NM_022409:459	Zfp296	INSIDE	0.923	0.624	1155.04	720.23	0.576	953.90	549.13
A_68_P29477473	chr14:26277283-26277327	NM_183208:-1366	Zmiz1	PROMOTER	0.923	0.536	1061.53	569.14	0.495	909.18	450.08
A_68_P23990398	chr5:112583018-112583062	AK006010:-2216		PROMOTER	0.923	0.662	1508.11	998.75	0.611	1096.29	670.34

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P24127507	chr5:138220239-138220283	NM_027242:115	2010007H12Rik	INSIDE	0.922	0.600	1014.62	608.72	0.553	967.60	535.52
A_68_P28083320	chr11:102962675-102962719	NM_152813:276	Plcd3	INSIDE	0.922	0.649	1279.19	830.60	0.598	1018.30	609.38
A_68_P29055171	chr13:55565839-55565883	NM_001030296:233	Prr7	INSIDE	0.922	0.514	1205.22	619.86	0.474	1011.87	479.77
A_68_P31868008	chr18:81171137-81171181	NM_178280:12159	Sall3	INSIDE	0.922	2.704	724.41	1958.57	2.492	821.88	2047.98
A_68_P27631988	chr11:20443335-20443379	NM_021372:101	Sertad2	INSIDE	0.922	1.936	4953.85	9591.84	1.785	3999.43	7138.26
A_68_P21901054	chr2:179777765-179777809	NM_178750:599	Ss18l1	INSIDE	0.922	2.119	1100.80	2333.01	1.954	931.45	1819.68
A_68_P28037690	chr11:95120921-95120965	NM_053093:-1900	Tac4	PROMOTER	0.922	2.320	653.20	1515.62	2.140	608.61	1302.34
A_68_P24427168	chr6:48388705-48388749	NM_001085415:6363	Zfp467	INSIDE	0.922	1.820	2146.73	3907.02	1.678	1664.83	2793.47
A_68_P23470208	chr5:8912735-8912783	NM_008830:19038	Abcb4	INSIDE	0.921	3.070	683.03	2096.73	2.827	568.93	1608.38
A_68_P20395058	chr1:82836029-82836073	NM_010472:-7	Agfg1	PROMOTER	0.921	2.685	501.22	1345.70	2.472	466.34	1152.64
A_68_P28859760	chr13:19040273-19040317	NM_175007:55	Amph	INSIDE	0.921	0.646	900.90	581.85	0.595	743.02	442.05
A_68_P31932937	chr19:6141281-6141325	NM_019722:-165	Arl2	PROMOTER	0.921	3.505	455.29	1595.64	3.229	409.41	1321.83
A_68_P28731505	chr12:110272292-110272336	NM_001163175:34113	Begain	INSIDE	0.921	2.646	811.72	2147.78	2.438	730.43	1780.89
A_68_P31103374	chr17:25522637-25522681	NM_001163691:48070	Cacna1h	INSIDE	0.921	2.261	1944.76	4396.13	2.081	1563.35	3253.84
A_68_P24114171	chr5:135462844-135462888	NM_009902:783	Cldn3	INSIDE	0.921	1.729	2960.72	5119.20	1.593	2373.01	3780.02
A_68_P22398586	chr3:105490205-105490249	NM_017397:263	Ddx20	INSIDE	0.921	2.017	392.44	791.43	1.857	423.60	786.51
A_68_P25957754	chr8:74126853-74126897	NM_001166213:5330	Fam129c	INSIDE	0.921	2.138	12168.65	26011.80	1.969	8217.01	16177.09
A_68_P31123770	chr17:28829032-28829076	NM_001168513:-458	Mapk14	PROMOTER	0.921	0.641	1683.02	1078.68	0.590	1428.15	843.26
A_68_P25025269	chr7:29871316-29871362	NR_035489:-2625	Mir1963	PROMOTER	0.921	3.396	613.42	2083.33	3.129	507.96	1589.35
A_68_P21722744	chr2:147011624-147011668	NM_001077632:492	Nkx2-2	INSIDE	0.921	1.968	727.42	1431.29	1.813	595.33	1079.31
A_68_P32218816	chr19:59419677-59419721	NM_001033222:572	Pdzd8	INSIDE	0.921	0.523	1170.46	611.96	0.481	929.73	447.62
A_68_P23593814	chr5:34679655-34679699	NM_011278:638	Rnf4	INSIDE	0.921	0.482	1158.62	559.03	0.444	1094.18	485.99
A_68_P24320418	chr6:28429971-28430015	NM_019776:-355	Snd1	PROMOTER	0.921	0.612	904.85	553.79	0.564	814.37	458.93
A_68_P32562268	chrX:98255023-98255069	NM_031384:-68	Tex11	PROMOTER	0.921	2.023	1132.45	2290.77	1.862	442.25	823.68
A_68_P27845262	chr11:60691840-60691884	NM_001168507:678	Tmem11	INSIDE	0.921	0.622	3974.17	2471.33	0.573	3224.08	1846.28
A_68_P22889233	chr4:46548820-46548864	NM_029077:174	Trim14	INSIDE	0.921	1.728	1082.48	1870.15	1.591	913.12	1452.64
A_68_P24836602	chr6:127984334-127984378	NM_175414:109240	Tspan9	INSIDE	0.921	1.910	1058.84	2022.13	1.759	943.96	1660.64
A_68_P29256602	chr13:99032998-99033042	NM_178918:-73	Utp15	DIVERGENT_PROMOTER	0.921	1.797	514.75	925.17	1.655	497.54	823.52
A_68_P32977629	A_68_P32977629			Unknown	0.921	2.962	2336.85	6921.36	2.728	1541.95	4207.14
A_68_P28092301	chr11:104547023-104547067	ENSMUST00000148007:24		INSIDE	0.921	1.836	938.30	1723.10	1.692	867.86	1468.51
A_68_P28574820	chr12:81360887-81360931	NM_134156:450	Actn1	INSIDE	0.920	1.792	1836.91	3291.99	1.648	1515.90	2498.01
A_68_P24325868	chr6:29297894-29297938	NM_007594:-202	Calu	PROMOTER	0.920	0.629	1414.62	889.23	0.578	1340.39	774.96
A_68_P30778319	chr16:55905763-55905807	NM_028815:29177	Cep97	INSIDE	0.920	2.708	864.84	2341.89	2.492	772.19	1924.47
A_68_P20148455	chr1:36528583-36528627	NM_033570:163	Cnnm4	INSIDE	0.920	1.936	859.43	1663.84	1.781	774.69	1379.84
A_68_P25005643	chr7:25370538-25370582	NM_023154:-2001	Ethe1	PROMOTER	0.920	2.028	1563.68	3170.59	1.865	1194.52	2227.83
A_68_P23145550	chr4:99323204-99323248	NM_010425:237	Foxd3	INSIDE	0.920	0.511	1677.83	857.45	0.470	1431.85	673.51
A_68_P24133860	chr5:139625951-139625996	NM_001081265:-203	Heatr2	PROMOTER	0.920	3.659	8339.11	30511.15	3.366	4849.44	16322.30
A_68_P26228653	chr8:124277085-124277129	NM_020605:22648	Jph3	INSIDE	0.920	3.301	272.80	900.46	3.037	203.59	618.29
A_68_P31113143	chr17:27053838-27053882	NM_053173:-175	Kifc5b	PROMOTER	0.920	0.578	1304.57	753.65	0.531	985.08	523.54
A_68_P24324309	chr6:29010153-29010197	NM_008493:-46	Lep	PROMOTER	0.920	2.123	2161.27	4589.25	1.954	1707.95	3337.86
A_68_P28565711	chr12:79849726-79849770	NM_019579:-185	Mpp5	PROMOTER	0.920	1.769	700.74	1239.95	1.629	663.69	1080.89
A_68_P31256052	chr17:56568252-56568296	NM_011218:47629	Ptprs	INSIDE	0.920	3.075	561.43	1726.20	2.829	522.54	1478.44
A_68_P31947894	chr19:10092837-10092881	NM_144538:141	Rab3il1	INSIDE	0.920	0.690	3336.68	2303.44	0.635	2711.30	1721.75
A_68_P32070014	chr19:32462198-32462242	NM_144792:724	Sgms1	INSIDE	0.920	0.712	2112.33	1503.37	0.655	1594.68	1044.16
A_68_P24979911	chr7:16730509-16730553	NM_148946:14882	Slc8a2	INSIDE	0.920	1.764	1388.49	2449.16	1.623	1108.67	1799.57
A_68_P23650101	chr5:44617682-44617726	NM_173764:141	Tapt1	INSIDE	0.920	1.921	750.67	1442.21	1.767	714.94	1263.53
A_68_P26940975	chr10:11211781-11211825			Unknown	0.920	3.073	1680.13	5162.79	2.828	1400.89	3961.28
A_68_P30671438	A_68_P30671438			Unknown	0.920	1.812	1071.22	1941.35	1.667	961.31	1602.97
A_68_P25730018	chr8:27096782-27096826	NM_029037:7789	4930444A02Rik	INSIDE	0.919	2.917	1340.66	3911.08	2.682	1135.86	3046.79
A_68_P20086661	chr1:23108998-23109042	NM_025746:72	4933415F23Rik	INSIDE	0.919	2.250	473.59	1065.65	2.068	431.60	892.56
A_68_P25677778	chr8:14962588-14962634	NM_001037736:50894	Arhgef10	INSIDE	0.919	2.919	990.48	2891.20	2.682	718.70	1927.50

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25957004	chr8:74000092-74000136	NM_025600:7022	Dda1	INSIDE	0.919	1.657	3085.78	5112.48	1.523	2569.43	3912.55
A_68_P30361554	chr15:78502409-78502453	NM_183141:46113	Elfn2	INSIDE	0.919	1.906	780.06	1486.59	1.752	708.23	1240.82
A_68_P26885589	chr9:121698137-121698187	NR_027967:2076	Hhatl	INSIDE	0.919	3.102	802.68	2489.87	2.849	625.77	1783.02
A_68_P31828823	chr18:74129671-74129715	NM_172632:94911	Mapk4	INSIDE	0.919	1.826	692.70	1265.01	1.678	590.55	990.84
A_68_P28621837	chr12:90498937-90498981	NM_172544:307125	Nrxn3	INSIDE	0.919	2.469	1976.42	4878.99	2.269	1430.31	3245.83
A_68_P22309970	chr3:87587747-87587797	NM_001033124:11312	Ntrk1	INSIDE	0.919	2.231	527.81	1177.69	2.051	428.47	878.99
A_68_P22165658	chr3:57651977-57652021	NM_019410:-319	Pfn2	PROMOTER	0.919	0.648	2123.25	1375.69	0.595	1737.79	1034.59
A_68_P23361257	chr4:140517377-140517421	NM_023374:213	Sdhb	INSIDE	0.919	1.651	757.26	1250.61	1.518	665.89	1011.16
A_68_P21054133	chr2:21127231-21127275	NM_001001297:-98	Thnsl1	DIVERGENT_PROMOTER	0.919	0.730	2338.84	1706.39	0.671	1924.01	1290.21
A_68_P32683274	chrX:133462451-133462502	NM_027067:613	1700014N06Rik	INSIDE	0.918	2.891	585.23	1692.17	2.655	289.14	767.62
A_68_P30484701	chr15:100058334-100058378	NM_007497:67	Atf1	INSIDE	0.918	0.649	794.37	515.70	0.596	714.51	425.61
A_68_P30337697	chr15:74359726-74359770	NM_174991:13123	Bai1	INSIDE	0.918	2.542	3558.01	9045.16	2.333	2257.02	5265.51
A_68_P27228309	chr10:69651754-69651798	NM_001111121:91908	Ccdc6	INSIDE	0.918	1.657	1587.61	2631.07	1.521	1246.15	1895.54
A_68_P24376401	chr6:38203728-38203772	NM_194061:259	D630045J12Rik	INSIDE	0.918	1.605	3985.68	6398.21	1.473	3028.58	4461.45
A_68_P24046892	chr5:122303021-122303065	NM_175474:4006	Fam109a	INSIDE	0.918	2.456	1651.48	4056.63	2.255	1259.89	2840.97
A_68_P26065154	chr8:94883835-94883879	NM_018826:2162	Irx5	INSIDE	0.918	0.643	1283.13	824.75	0.590	1241.43	732.50
A_68_P21842274	chr2:168396695-168396739	NM_001136073:18975	Nfatc2	INSIDE	0.918	3.193	485.87	1551.40	2.930	526.18	1541.56
A_68_P24643141	chr6:92041701-92041746	NM_011630:312	Nr2c2	INSIDE	0.918	2.773	368.84	1022.84	2.545	354.06	901.20
A_68_P28159702	chr11:116360052-116360096	NM_026364:-8414	Prpsap1	PROMOTER	0.918	1.562	1892.27	2956.49	1.434	1514.92	2172.83
A_68_P21635428	chr2:131346491-131346535	NM_001177833:28915	Smox	INSIDE	0.918	1.877	1749.46	3284.60	1.723	1417.18	2442.32
A_68_P24912679	chr6:143782088-143782132	NM_001113559:375968	Sox5	INSIDE	0.918	2.312	1433.26	3314.02	2.122	1134.07	2407.00
A_68_P21431326	chr2:92755177-92755221	NM_030725:-59	Syt13	PROMOTER	0.918	0.484	1817.99	880.42	0.445	1664.21	739.91
A_68_P32147506	chr19:47149599-47149649	NM_177342:7387	Taf5	INSIDE	0.918	2.631	599.92	1578.10	2.414	528.51	1275.59
A_68_P28524377	chr12:72212495-72212539	NM_029227:102	Tomm20l	INSIDE	0.918	1.551	1591.20	2468.23	1.424	1402.54	1997.90
A_68_P24951591	chr7:4969560-4969604	NM_025324:2473	Zfp524	INSIDE	0.918	2.127	1471.39	3129.84	1.953	1061.33	2072.31
A_68_P25027730	chr7:30304085-30304129	ENSMUST00000141713:-117		PROMOTER	0.918	2.141	593.13	1270.08	1.965	539.71	1060.76
A_68_P31632916	chr18:38409853-38409897	NR_015475:-22	1700086O06Rik	DIVERGENT_PROMOTER	0.917	0.416	1355.48	563.97	0.381	1069.20	407.73
A_68_P21566910	chr2:118741704-118741748	NM_001045523:14376	Bahd1	INSIDE	0.917	1.807	970.43	1753.47	1.658	736.05	1220.16
A_68_P21821741	chr2:164941626-164941673	NM_174988:118588	Cdh22	INSIDE	0.917	2.649	398.23	1054.83	2.428	331.88	805.89
A_68_P21605248	chr2:125684747-125684791	NM_009939:-14	Cops2	DIVERGENT_PROMOTER	0.917	2.064	4036.12	8328.99	1.892	3090.50	5847.58
A_68_P23284203	chr4:126911090-126911134	NM_198618:64598	Dlgap3	INSIDE	0.917	3.055	949.79	2902.01	2.802	867.32	2429.83
A_68_P30981935	chr16:94748214-94748258	NM_007834:0	Dscr3	INSIDE	0.917	1.851	1196.58	2215.01	1.698	912.55	1549.24
A_68_P26585941	chr9:64971903-64971947	NM_020043:22623	Igdcc4	INSIDE	0.917	1.778	654.85	1164.43	1.631	592.66	966.37
A_68_P26546334	chr9:58046265-58046309	NM_001161535:3236	Islr2	INSIDE	0.917	0.582	2192.49	1276.24	0.534	1704.50	909.84
A_68_P23303541	chr4:130506143-130506190	NM_010769:5867	Matn1	INSIDE	0.917	4.825	771.32	3721.94	4.425	633.88	2805.09
A_68_P23088454	chr4:87679337-87679381	NM_027326:-47	Mllt3	PROMOTER	0.917	0.673	1179.48	793.40	0.617	1042.83	643.36
A_68_P29619205	chr14:56290728-56290772	NM_008683:-7	Nedd8	DIVERGENT_PROMOTER	0.917	0.531	1414.85	751.63	0.487	1021.37	497.47
A_68_P28514077	chr12:70457809-70457853	NM_025441:323	Nemf	INSIDE	0.917	0.674	1301.03	877.22	0.618	1102.99	682.05
A_68_P25090602	chr7:52263044-52263088	NM_001008422:8553	Scaf1	INSIDE	0.917	2.656	1165.01	3094.49	2.435	904.05	2201.41
A_68_P26540061	chr9:56919951-56919995	NM_001110350:-4210	Sin3a	PROMOTER	0.917	2.642	936.69	2475.05	2.422	713.46	1728.21
A_68_P21986758	chr3:21974743-21974787	NM_030732:-809	Tbl1xr1	PROMOTER	0.917	2.090	871.44	1821.59	1.916	889.85	1705.01
A_68_P22168164	chr3:58219493-58219537	NM_001081229:-96	Tsc22d2	PROMOTER	0.917	0.522	1104.35	576.37	0.479	1013.28	484.90
A_68_P32203591	chr19:56949104-56949148	NM_172840:221	Vwa2	INSIDE	0.917	0.442	1255.21	554.21	0.405	1057.06	427.97
A_68_P25021517	chr7:29163975-29164019	NM_011756:251	Zfp36	INSIDE	0.917	0.578	1544.11	893.06	0.530	1323.56	701.65
A_68_P27288262	chr10:80702920-80702964	NM_001034895:7035	Zfr2	INSIDE	0.917	1.944	698.85	1358.24	1.783	681.95	1215.59
A_68_P24631966	chr6:90319994-90320038	NM_030260:529	Zxdc	INSIDE	0.917	0.578	1009.86	583.85	0.530	867.87	459.88
A_68_P22185882	chr3:61963377-61963421			Unknown	0.917	3.084	657.13	2026.33	2.829	540.90	1530.11
A_68_P25190566	chr7:73985093-73985137	NM_001033877:494	Adamts17	INSIDE	0.916	2.066	1073.93	2218.32	1.892	931.62	1762.53
A_68_P28741429	chr12:112216865-112216909	NM_175207:345	Ankrd9	INSIDE	0.916	1.627	678.59	1104.03	1.491	698.10	1040.77
A_68_P29484378	chr14:27783198-27783242	NM_145221:517	Appl1	INSIDE	0.916	0.628	3298.86	2071.03	0.575	2583.83	1485.80
A_68_P27100734	chr10:43231084-43231128	NM_199028:32161	Bend3	INSIDE	0.916	1.797	615.40	1106.09	1.646	512.34	843.26

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25430225	chr7:120512643-120512687	NM_133700:189	Btbd10	INSIDE	0.916	0.561	1769.13	992.57	0.514	1503.52	772.39
A_68_P28171198	chr11:118280168-118280212	NM_001025617:176	Cant1	INSIDE	0.916	0.647	2755.70	1783.83	0.593	2199.21	1304.61
A_68_P24820867	chr6:125444742-125444786	NM_007657:9	Cd9	INSIDE	0.916	2.147	2772.20	5951.48	1.967	2263.15	4451.33
A_68_P27266462	chr10:76628409-76628453	NM_009929:845	Col18a1	INSIDE	0.916	0.616	1428.79	880.26	0.565	1250.35	705.97
A_68_P29698998	chr14:70474791-70474835	NM_018781:-2439	Egr3	PROMOTER	0.916	0.521	1351.15	703.35	0.477	1329.65	634.18
A_68_P20442328	chr1:93309360-93309404	NM_019479:417	Hes6	INSIDE	0.916	0.688	1596.55	1098.15	0.630	1328.47	836.90
A_68_P28293526	chr12:25783349-25783393	NM_010496:-2413	Id2	PROMOTER	0.916	1.739	3890.73	6767.63	1.593	3011.29	4796.95
A_68_P20556966	chr1:121317400-121317444	NM_008381:1403	Inhbb	INSIDE	0.916	0.693	1725.04	1195.27	0.634	1378.94	874.78
A_68_P21812069	chr2:163201531-163201575	NM_021566:22157	Jph2	INSIDE	0.916	2.714	715.06	1940.86	2.485	678.76	1687.06
A_68_P25960691	chr8:74843873-74843917	NM_008452:934	Klf2	INSIDE	0.916	1.986	675.18	1340.86	1.819	596.70	1085.18
A_68_P27880946	chr11:66908183-66908227	NM_001099635:16403	Myh3	INSIDE	0.916	2.908	275.28	800.52	2.665	275.51	734.13
A_68_P32552416	chrX:96086453-96086497	NM_052976:-150	Ophn1	PROMOTER	0.916	2.159	790.82	1707.24	1.978	565.28	1118.07
A_68_P27553983	chr11:3674675-3674719	NM_152818:89210	Osbp2	INSIDE	0.916	2.192	1166.26	2556.72	2.008	993.25	1994.00
A_68_P23234765	chr4:117168524-117168568	NM_025739:974	Rnf220	INSIDE	0.916	0.675	1152.63	778.22	0.618	969.97	599.77
A_68_P25016961	chr7:28152919-28152968	NM_001199235:26582	Spnb4	INSIDE	0.916	4.566	1382.05	6310.84	4.181	998.02	4172.60
A_68_P20191095	chr1:43884838-43884882	NM_026430:-307	Uxs1	PROMOTER	0.916	0.521	1162.04	605.62	0.477	941.87	449.59
A_68_P25805594	chr8:41509577-41509621	NM_178395:430	Zdhhc2	INSIDE	0.916	0.473	1937.26	915.80	0.433	1596.11	690.88
A_68_P25004348	chr7:25118652-25118696	NM_001163810:310	1700008P20Rik	INSIDE	0.915	1.962	772.49	1515.53	1.794	615.01	1103.54
A_68_P25260060	chr7:86418215-86418259	NM_018811:85	Abhd2	INSIDE	0.915	0.580	878.58	509.34	0.530	794.98	421.51
A_68_P32233080	chrX:5659260-5659304	NM_001033211:1256	AU022751	INSIDE	0.915	2.228	799.75	1782.09	2.038	347.59	708.37
A_68_P27183499	chr10:61440751-61440795	NM_007731:1084	Col13a1	INSIDE	0.915	0.683	5777.62	3943.80	0.625	4263.72	2663.04
A_68_P25755967	chr8:32200134-32200178	NM_025869:23	Dusp26	INSIDE	0.915	3.055	317.69	970.63	2.797	319.89	894.73
A_68_P27640628	chr11:22186580-22186624	NM_153078:-761	Ehbp1	PROMOTER	0.915	0.588	1787.92	1051.22	0.538	1426.37	767.05
A_68_P29702035	chr14:70954292-70954336	NM_021877:452	Hr	INSIDE	0.915	0.592	1273.02	753.64	0.542	941.22	510.03
A_68_P28149754	chr11:114647920-114647964	NM_001102615:21240	Kif19a	INSIDE	0.915	2.153	384.92	828.78	1.970	379.74	748.13
A_68_P26919699	chr10:7309827-7309871	NM_172784:251	Lrp11	INSIDE	0.915	2.778	188.46	523.47	2.541	237.78	604.10
A_68_P27356288	chr10:93352563-93352607	NM_019648:1363	Metap2	INSIDE	0.915	0.516	1843.03	951.06	0.472	1732.10	818.08
A_68_P27857774	chr11:62945885-62945929	NM_008885:895	Pmp22	INSIDE	0.915	0.587	1384.16	811.85	0.537	1023.54	549.40
A_68_P25025139	chr7:29849652-29849696	NM_009109:60496	Ryr1	INSIDE	0.915	2.309	420.88	971.83	2.112	385.55	814.32
A_68_P26872706	chr9:119395898-119395942	NM_021544:92214	Scn5a	INSIDE	0.915	2.434	538.01	1309.61	2.227	409.24	911.22
A_68_P25588801	chr7:148623566-148623613	NM_001177576:-3096	Slc25a22	PROMOTER	0.915	2.258	927.83	2094.59	2.065	791.15	1633.90
A_68_P24593031	chr6:83318401-83318445	NM_183138:73250	Tet3	INSIDE	0.915	2.163	2635.46	5701.62	1.979	1852.19	3666.35
A_68_P27537442	chr10:127114141-127114185	NM_173732:42	Tmem194	INSIDE	0.915	0.405	5104.16	2065.48	0.370	3901.48	1445.03
A_68_P20354370	chr1:75479524-75479568	NM_177056:3440	Tmem198	INSIDE	0.915	2.226	1183.36	2633.61	2.036	891.58	1815.56
A_68_P26743635	chr9:95650332-95650376	NM_011643:423	Trpc1	INSIDE	0.915	0.635	1640.21	1041.39	0.581	1449.49	842.05
A_68_P22038455	chr3:32409802-32409846	NM_144519:311	Zfp639	INSIDE	0.915	2.020	348.30	703.67	1.848	356.15	658.24
A_68_P33007654	A_68_P33007654			Unknown	0.915	2.377	1514.86	3600.31	2.175	1622.01	3527.90
A_68_P28194146	chr12:3235815-3235859	NR_015551:46	1700012B15Rik	INSIDE	0.914	0.691	1237.93	855.77	0.632	1004.35	634.45
A_68_P22376196	chr3:101408366-101408410	NM_144900:192	Atp1a1	INSIDE	0.914	2.095	624.80	1308.72	1.915	553.33	1059.59
A_68_P28731503	chr12:110272067-110272111	NM_001163175:34339	Begain	INSIDE	0.914	3.240	566.15	1834.45	2.963	529.39	1568.50
A_68_P25585266	chr7:148042623-148042667	NM_018742:-362	Bet1l	DIVERGENT_PROMOTER	0.914	0.608	3728.44	2266.10	0.556	2848.61	1582.93
A_68_P26475229	chr9:45480644-45480688	NM_001081270:242291	Dscaml1	INSIDE	0.914	1.947	485.53	945.16	1.778	388.13	690.22
A_68_P31961135	chr19:12575854-12575898	NM_172442:610	Dtx4	INSIDE	0.914	2.018	1040.25	2099.57	1.844	920.23	1697.29
A_68_P29625742	chr14:57655527-57655571	NM_016975:21234	Gja3	INSIDE	0.914	3.116	2408.74	7505.58	2.847	1902.11	5415.66
A_68_P27594323	chr11:11936669-11936713	NM_001177629:-8716	Grb10	PROMOTER	0.914	1.988	1197.26	2379.78	1.817	1118.25	2031.78
A_68_P23080768	chr4:86257578-86257622	NM_173400:326	Haus6	INSIDE	0.914	0.692	1172.91	812.12	0.633	1036.91	656.16
A_68_P27828619	chr11:57823508-57823552	NM_028451:965	Larp1	INSIDE	0.914	2.673	2151.18	5750.12	2.443	1850.51	4520.88
A_68_P23229425	chr4:116136181-116136225	NM_001042743:586	Mast2	INSIDE	0.914	3.392	19747.02	66976.33	3.100	12848.53	39828.77
A_68_P27995000	chr11:87409082-87409126	NM_133215:3386	Mtmr4	INSIDE	0.914	1.967	515.81	1014.43	1.798	453.49	815.55
A_68_P21909034	chr2:180922268-180922312	NM_025598:243	Ppdpf	INSIDE	0.914	0.597	1292.55	771.74	0.546	1078.22	588.64
A_68_P27841039	chr11:59953284-59953328	NM_001037764:-277	Rai1	PROMOTER	0.914	0.413	1677.63	693.21	0.378	1332.67	503.35

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27943625	chr11:78301348-78301392	NM_001168521:9886	Sarm1	INSIDE	0.914	2.161	684.88	1480.18	1.975	660.90	1305.19
A_68_P32116949	chr19:41817858-41817902	NM_015748:466	Slit1	INSIDE	0.914	0.633	1233.86	781.56	0.579	1014.56	587.63
A_68_P21635427	chr2:131346365-131346409	NM_001177833:28789	Smox	INSIDE	0.914	1.979	427.09	845.07	1.809	401.49	726.30
A_68_P22829978	chr4:34137124-34137168	NM_026293:-104	Spaca1	PROMOTER	0.914	2.080	1572.08	3270.31	1.902	1197.05	2276.96
A_68_P21370051	chr2:79475802-79475846	NM_080558:243	Ssfa2	INSIDE	0.914	0.666	924.67	615.91	0.609	797.06	485.14
A_68_P26948442	chr10:12684445-12684489	NM_001163590:-401	Stx11	PROMOTER	0.914	0.344	1753.27	602.35	0.314	1441.73	452.60
A_68_P23240955	chr4:118214466-118214510	NM_172383:1843	Tmem125	INSIDE	0.914	2.009	918.78	1845.82	1.835	837.11	1536.48
A_68_P24092032	chr5:130555232-130555276	NM_001130476:-101	Tpst1	PROMOTER	0.914	1.707	2098.62	3581.88	1.560	1867.56	2912.99
A_68_P31862936	chr18:80403608-80403652	NM_001042408:25	Txnl4a	INSIDE	0.914	0.452	1296.66	586.40	0.414	1071.83	443.25
A_68_P26217006	chr8:122480748-122480792	NM_009462:46019	Usp10	INSIDE	0.914	4.372	543.87	2377.79	3.997	496.70	1985.08
A_68_P24425593	chr6:48014031-48014075	NM_001163475:22540	Zfp746	INSIDE	0.914	1.687	1279.20	2157.94	1.542	867.90	1338.47
A_68_P25992688	chr8:81636396-81636453	NM_178267:84089	Zfp827	INSIDE	0.914	2.145	621.65	1333.70	1.960	565.72	1108.89
A_68_P23971471	chr5:108796094-108796138	ENSMUST00000100944:-2760		PROMOTER	0.914	0.503	1333.30	670.04	0.460	1135.89	521.95
A_68_P27670840	chr11:28483846-28483890	NM_001166661:428	Ccdc85a	INSIDE	0.913	1.875	1347.24	2526.48	1.711	1118.10	1913.35
A_68_P23936790	chr5:102193955-102193999	NM_173370:-172	Cds1	PROMOTER	0.913	2.051	460.31	943.91	1.873	389.65	729.83
A_68_P20938884	chr1:193399786-193399830	NM_178632:196	Ints7	INSIDE	0.913	0.605	905.88	548.13	0.552	698.91	386.01
A_68_P24517582	chr6:66485182-66485226	NM_019499:-257	Mad2l1	PROMOTER	0.913	1.605	1635.32	2625.02	1.465	1352.44	1981.72
A_68_P29618280	chr14:56139420-56139464	NM_008736:3586	Nrl	INSIDE	0.913	2.239	658.22	1473.69	2.044	644.40	1317.06
A_68_P31632605	chr18:38358832-38358876	NM_029357:10562	Pcdh1	INSIDE	0.913	2.962	3588.90	10630.72	2.704	2750.09	7435.50
A_68_P31924876	chr19:4756468-4756512	NM_025717:-34	Rbm4b	PROMOTER	0.913	3.544	477.60	1692.55	3.235	498.05	1610.97
A_68_P23523568	chr5:20457296-20457340	NM_001080977:322	Rsbn1l	INSIDE	0.913	0.553	1654.69	915.68	0.505	1401.61	708.14
A_68_P27804720	chr11:53244141-53244185	NM_025352:171	Uqcrq	INSIDE	0.913	0.554	1948.20	1078.99	0.506	1537.84	777.74
A_68_P23244789	chr4:118966777-118966821	NM_011732:320	Ybx1	INSIDE	0.913	5.471	1792.55	9806.91	4.995	1327.80	6632.44
A_68_P26154271	chr8:111471277-111471321	NM_007496:232755	Zfhx3	INSIDE	0.913	2.178	895.93	1951.03	1.989	812.63	1616.01
A_68_P25009109	chr7:26011119-26011163	NM_175436:4671	Zfp526	INSIDE	0.913	4.032	1513.46	6101.83	3.683	1116.70	4112.43
A_68_P25992137	chr8:81554288-81554333	NM_178267:1975	Zfp827	INSIDE	0.913	0.533	1115.14	593.96	0.486	976.80	475.19
A_68_P26345262	chr9:20871580-20871624	NM_001103168:-65	Zglp1	PROMOTER	0.913	2.273	1245.74	2831.65	2.075	1027.99	2133.35
A_68_P25022915	chr7:29415604-29415648	NM_175319:408	C330005M16Rik	INSIDE	0.912	0.651	1298.54	845.58	0.594	1163.18	690.56
A_68_P26699343	chr9:86361138-86361182	NM_177208:400	Dopey1	INSIDE	0.912	2.230	398.53	888.65	2.033	465.42	946.08
A_68_P29142607	chr13:73984759-73984803	NM_028186:299	Nkd2	INSIDE	0.912	0.701	2323.13	1627.44	0.639	1701.10	1087.35
A_68_P20088278	chr1:23389719-23389763	NM_001081079:274	Ogfrl1	INSIDE	0.912	2.155	479.67	1033.64	1.965	435.94	856.55
A_68_P23415894	chr4:151370837-151370881	NM_172705:-570	Phf13	PROMOTER	0.912	0.577	1258.98	726.71	0.527	968.80	510.13
A_68_P24428217	chr6:48546955-48546999	NM_001079901:3095	Repin1	INSIDE	0.912	2.121	1402.80	2975.10	1.934	1375.97	2660.65
A_68_P28530875	chr12:73337837-73337881	NM_001007596:-147	Rtn1	PROMOTER	0.912	0.539	1114.54	601.20	0.492	836.05	411.21
A_68_P32182248	chr19:53464624-53464668	NM_172429:417	Smndc1	INSIDE	0.912	0.613	1466.11	899.21	0.560	1378.24	771.32
A_68_P31834367	chr18:75160274-75160318	NR_028552:-425	Snord58b	PROMOTER	0.912	0.653	1017.14	664.69	0.596	894.02	532.84
A_68_P26398840	chr9:30939131-30939175	NM_011176:232	St14	INSIDE	0.912	0.608	1464.50	889.92	0.554	1174.70	651.04
A_68_P21266476	chr2:61654143-61654187	NM_009322:11655	Tbr1	DOWNSTREAM	0.912	2.241	595.49	1334.19	2.044	707.44	1445.73
A_68_P32393596	chrX:52896212-52896256	ENSMUST00000163353:91502		INSIDE	0.912	2.117	2437.75	5160.65	1.931	881.98	1703.23
A_68_P22510980	chr3:127540779-127540823	NM_145964:-390	Ap1ar	PROMOTER	0.911	3.221	314.24	1012.20	2.933	333.22	977.43
A_68_P26781225	chr9:102528131-102528175	NM_001081122:302	Cep63	INSIDE	0.911	3.181	2230.97	7096.27	2.897	1829.44	5299.82
A_68_P27261496	chr10:75807584-75807628	NM_001081419:401	Dip2a	INSIDE	0.911	1.795	1383.18	2482.49	1.636	1131.51	1850.90
A_68_P28054686	chr11:98010707-98010751	NM_028149:202	Fbxl20	INSIDE	0.911	1.890	2035.27	3846.59	1.723	1624.25	2797.78
A_68_P25004863	chr7:25217918-25217962	NM_199013:12761	Irgc1	INSIDE	0.911	2.087	327.08	682.46	1.901	307.40	584.23
A_68_P29863084	chr14:103380991-103381035	NM_177715:842	Kctd12	INSIDE	0.911	1.894	528.55	1001.18	1.725	511.94	883.02
A_68_P31827982	chr18:73974763-73974807	NM_145494:262	Me2	INSIDE	0.911	0.498	1563.41	777.81	0.453	1366.81	619.14
A_68_P21840223	chr2:168056306-168056350	NM_001160330:207	Mocs3	INSIDE	0.911	2.755	525.13	1446.59	2.509	439.79	1103.43
A_68_P26821058	chr9:109833931-109833975	NM_001205331:-325	Mtap4	PROMOTER	0.911	2.030	1203.28	2442.62	1.849	1202.70	2224.21
A_68_P22741777	chr4:13670508-13670552	NM_001111027:-7913	Runx1t1	PROMOTER	0.911	2.605	1098.61	2861.99	2.373	870.09	2064.83
A_68_P24215193	chr6:6166905-6166949	NM_001177572:247	Slc25a13	INSIDE	0.911	0.546	1122.71	613.06	0.498	919.27	457.45
A_68_P26978752	chr10:18735310-18735354	NM_009397:-116	Tnfaip3	PROMOTER	0.911	1.689	879.64	1485.94	1.539	860.43	1323.78

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31156690	chr17:35089452-35089496	NR_015536:-58	1110038B12Rik	PROMOTER	0.910	0.466	1142.58	532.88	0.425	1012.88	430.05
A_68_P21537142	chr2:113688722-113688766	NM_181416:74	Arhgap11a	INSIDE	0.910	0.679	2069.45	1405.16	0.618	1635.40	1010.55
A_68_P22338537	chr3:94167894-94167938	NM_001136117:1551	C2cd4d	INSIDE	0.910	1.686	821.80	1385.84	1.534	695.46	1067.17
A_68_P27275480	chr10:78215153-78215197	NM_027630:638	Ccdc105	INSIDE	0.910	0.525	1019.24	534.96	0.478	818.26	390.88
A_68_P30331033	chr15:73377952-73378002	NM_001081066:34987	Dennd3	INSIDE	0.910	1.866	798.39	1490.00	1.698	668.94	1135.73
A_68_P25507079	chr7:134895761-134895805	NM_172748:5494	Fbxl19	INSIDE	0.910	1.923	1984.65	3817.08	1.751	1680.12	2941.83
A_68_P28080761	chr11:102527193-102527237	NM_001127576:313	Gm1564	INSIDE	0.910	2.213	643.54	1424.34	2.013	620.00	1248.19
A_68_P23321826	chr4:133808110-133808154	NM_001099296:1889	Grrp1	INSIDE	0.910	0.591	929.60	549.80	0.538	732.35	394.12
A_68_P28748276	chr12:113400089-113400133	NM_001097621:15692	Kif26a	INSIDE	0.910	3.526	3820.00	13468.84	3.207	2800.83	8981.82
A_68_P24563506	chr6:77193106-77193150	NM_028880:418	Lrrtm1	INSIDE	0.910	0.392	1593.82	624.59	0.357	1187.55	423.71
A_68_P27279614	chr10:79365826-79365870	NM_001163276:5835	Med16	INSIDE	0.910	2.087	2603.62	5433.87	1.900	1788.88	3399.11
A_68_P22785945	chr4:24423615-24423659	NM_199467:28	Mms22l	INSIDE	0.910	1.637	981.98	1607.63	1.489	825.95	1230.23
A_68_P28189462	chr11:121098436-121098480	NM_026272:-91	Narf	DIVERGENT_PROMOTER	0.910	1.511	2766.99	4180.81	1.376	2032.38	2795.90
A_68_P27262051	chr10:75905675-75905719	NM_008787:-39	Pcnt	DIVERGENT_PROMOTER	0.910	0.519	1174.90	609.59	0.472	841.86	397.48
A_68_P21630861	chr2:130460763-130460807	NM_197945:7755	Prosapip1	INSIDE	0.910	1.758	3024.45	5317.67	1.599	2429.11	3885.29
A_68_P26585375	chr9:64868889-64868933	NM_021345:614	Ptplad1	INSIDE	0.910	0.530	1701.69	902.59	0.482	1509.48	728.27
A_68_P32050980	chr19:29175604-29175648	NM_021525:-238	Rcl1	PROMOTER	0.910	0.603	1026.50	619.10	0.549	902.23	495.32
A_68_P24979891	chr7:16726357-16726401	NM_148946:10730	Slc8a2	INSIDE	0.910	1.947	710.34	1383.30	1.772	565.83	1002.69
A_68_P27673285	chr11:29073225-29073269	NM_134034:340	Smek2	INSIDE	0.910	0.600	940.64	564.26	0.546	688.87	376.24
A_68_P23814579	chr5:76612836-76612880	NM_011626:-46	Tmem165	PROMOTER	0.910	1.780	983.59	1750.47	1.620	848.78	1374.83
A_68_P31161191	chr17:35974038-35974082	NM_011655:1186	Tubb5	INSIDE	0.910	2.097	798.25	1673.90	1.909	767.73	1465.82
A_68_P20827835	chr1:173341606-173341650	NM_009480:-183	Usf1	PROMOTER	0.910	2.674	926.55	2477.22	2.434	905.46	2204.16
A_68_P24992397	chr7:19857058-19857102	NM_009499:123	Vasp	INSIDE	0.910	0.442	1371.75	606.21	0.402	1152.11	463.28
A_68_P24864287	chr6:134876970-134877014	NR_037955:-2117	1190002F15Rik	PROMOTER	0.909	0.666	2170.95	1445.29	0.605	1924.43	1164.33
A_68_P30927369	chr16:85080522-85080569	NM_001198823:93407	App	INSIDE	0.909	6.198	8581.05	53183.60	5.631	5463.68	30767.67
A_68_P21843263	chr2:168567207-168567251	NM_015731:72	Atp9a	INSIDE	0.909	2.755	438.76	1208.83	2.505	434.09	1087.42
A_68_P28752187	chr12:113977286-113977330	NM_001024602:16924	AW555464	INSIDE	0.909	2.120	2107.47	4467.78	1.928	1826.84	3521.44
A_68_P22775355	chr4:21807011-21807055	NM_172687:211	Coq3	INSIDE	0.909	1.753	1012.28	1774.71	1.594	884.00	1409.17
A_68_P25542608	chr7:140968333-140968377	NM_133941:132	Dhx32	INSIDE	0.909	1.950	556.22	1084.43	1.773	565.66	1002.75
A_68_P25020568	chr7:28964442-28964486	NM_001037957:-37	Dyrk1b	PROMOTER	0.909	1.761	985.77	1735.57	1.600	798.92	1278.50
A_68_P26161391	chr8:112741858-112741902	NM_146215:21	Ftsjd1	INSIDE	0.909	1.633	1996.24	3260.66	1.484	1509.42	2240.03
A_68_P29625743	chr14:57655656-57655700	NM_016975:21104	Gja3	INSIDE	0.909	3.413	1377.89	4702.19	3.101	1178.94	3655.34
A_68_P26972773	chr10:17667513-17667557	NM_001033432:339	Heca	INSIDE	0.909	1.907	736.48	1404.12	1.732	745.59	1291.66
A_68_P31114337	chr17:27250538-27250582	NM_080553:56312	Itpr3	INSIDE	0.909	1.969	1001.53	1972.40	1.790	941.90	1685.78
A_68_P22530128	chr3:130809594-130809638	NM_010703:-3772	Lef1	PROMOTER	0.909	1.676	908.56	1522.81	1.523	779.62	1187.66
A_68_P21817705	chr2:164240088-164240132	NM_013592:-9996	Matn4	PROMOTER	0.909	2.218	2413.48	5353.73	2.017	1752.76	3535.70
A_68_P32466325	chrX:71330416-71330460	NM_010788:494	Mecp2	INSIDE	0.909	2.086	2623.90	5474.29	1.896	1715.46	3252.78
A_68_P27944883	chr11:78510477-78510521	NM_008702:429	Nlk	INSIDE	0.909	1.523	2650.19	4035.83	1.384	2052.07	2839.85
A_68_P30558434	chr16:13668204-13668248	NM_028761:37	Parn	INSIDE	0.909	0.668	1822.33	1217.49	0.607	1324.03	803.90
A_68_P24983897	chr7:17492695-17492739	NM_008967:878	Ptgir	INSIDE	0.909	2.573	547.58	1408.99	2.338	467.01	1092.00
A_68_P28322713	chr12:30623311-30623355	NM_181395:432	Pxdn	INSIDE	0.909	2.156	1897.49	4091.68	1.961	1481.79	2905.50
A_68_P22347939	chr3:95976249-95976293	NM_153053:-202	Sf3b4	PROMOTER	0.909	0.535	1186.04	634.86	0.487	872.25	424.46
A_68_P25962756	chr8:75273840-75273884	NM_009188:26676	Sin3b	INSIDE	0.909	3.118	851.47	2655.29	2.835	739.59	2097.00
A_68_P27833774	chr11:58775271-58775315	NM_031172:-1990	Trim17	PROMOTER	0.909	1.774	1945.03	3450.16	1.613	1429.05	2304.92
A_68_P23984176	chr5:111612120-111612164	NM_024477:303321	Ttc28	INSIDE	0.909	2.073	899.00	1863.63	1.884	771.92	1454.45
A_68_P30668283	chr16:35156994-35157038	NM_001012765:1295	Adcy5	INSIDE	0.908	1.952	933.76	1822.48	1.772	761.45	1349.46
A_68_P28115698	chr11:108783986-108784030	NM_015732:2346	Axin2	INSIDE	0.908	0.551	1565.96	863.45	0.501	1274.13	638.17
A_68_P26170009	chr8:114267322-114267366	NM_009954:405	Bcar1	INSIDE	0.908	0.713	2571.24	1832.86	0.647	2060.27	1333.80
A_68_P28778249	chr12:119437163-119437207	NM_010060:332	Dnahc11	INSIDE	0.908	0.645	1768.75	1140.10	0.585	1504.64	880.82
A_68_P24591568	chr6:83072012-83072056	NM_023547:2989	Ino80b	INSIDE	0.908	0.613	2332.76	1430.36	0.557	1833.55	1020.97
A_68_P21019040	chr2:13976882-13976926	NM_001012396:758	Ptpla	INSIDE	0.908	0.725	2669.08	1935.24	0.658	2280.55	1501.13

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25090599	chr7:52262741-52262785	NM_001008422:8857	Scaf1	INSIDE	0.908	2.559	2295.19	5874.15	2.324	1620.01	3765.56
A_68_P28184908	chr11:120353660-120353704	NM_013770:532	Slc25a10	INSIDE	0.908	0.616	1668.99	1027.60	0.559	1251.74	699.69
A_68_P23541736	chr5:23931307-23931351	NM_009207:279	Slc4a2	INSIDE	0.908	0.395	1683.88	665.86	0.359	1530.19	549.44
A_68_P23364328	chr4:141035058-141035110	NM_019763:59428	Spen	INSIDE	0.908	2.938	388.35	1140.81	2.667	331.92	885.26
A_68_P28034316	chr11:94538398-94538442	NM_145828:387	Xylt2	INSIDE	0.908	2.566	1878.56	4820.87	2.330	1638.79	3818.57
A_68_P26037061	chr8:90304956-90305000	NM_033327:178516	Zfp423	INSIDE	0.908	2.265	742.47	1681.34	2.057	693.16	1426.02
A_68_P21812331	chr2:163245232-163245276	NM_025699:-48	3230401D17Rik	PROMOTER	0.907	0.663	1874.69	1243.38	0.602	1543.60	928.67
A_68_P31939556	chr19:7457214-7457258	NM_001033139:280	AI846148	INSIDE	0.907	0.396	1586.15	628.36	0.359	1246.60	447.79
A_68_P24248437	chr6:13627972-13628016	NM_175312:-28	B630005N14Rik	PROMOTER	0.907	0.692	2585.36	1789.63	0.628	1903.83	1195.83
A_68_P23391997	chr4:147412754-147412798	NM_011929:100	Clcn6	INSIDE	0.907	2.323	8775.74	20383.07	2.107	6035.76	12718.59
A_68_P25951438	chr8:72898648-72898692	NM_016685:1224	Comp	INSIDE	0.907	2.032	1190.57	2419.66	1.843	1090.65	2010.15
A_68_P24138652	chr5:140448047-140448091	NM_175522:64172	Elfn1	INSIDE	0.907	1.636	1748.14	2860.58	1.484	1296.65	1923.62
A_68_P25181442	chr7:72300864-72300908	NM_183087:528	Fam189a1	INSIDE	0.907	1.704	1346.92	2294.50	1.545	1256.31	1940.80
A_68_P22325240	chr3:90237336-90237380	NM_145540:200	Ints3	INSIDE	0.907	0.731	3096.03	2264.53	0.663	2335.88	1549.27
A_68_P30346608	chr15:76011006-76011051	NM_201394:15112	Plec	INSIDE	0.907	3.573	300.62	1074.11	3.240	271.39	879.35
A_68_P21870545	chr2:173412385-173412429	NR_027957:72634	Ppp4r1l-ps	INSIDE	0.907	2.570	582.18	1495.94	2.330	563.48	1312.99
A_68_P31209386	chr17:47026859-47026903	NM_178385:-689	Tbcc	PROMOTER	0.907	0.685	2550.38	1747.93	0.622	2038.89	1267.68
A_68_P32557247	chrX:97016551-97016595	NM_001081283:165	Tmem28	INSIDE	0.907	1.859	752.17	1398.16	1.685	448.35	755.63
A_68_P32707836	chrX:138824951-138824995	NM_001033600:106	Acsl4	INSIDE	0.906	2.755	794.68	2188.96	2.495	395.71	987.47
A_68_P21105431	chr2:30679624-30679668	NM_133346:4174	Asb6	INSIDE	0.906	2.312	353.79	818.00	2.095	303.06	634.88
A_68_P21566912	chr2:118741928-118741972	NM_001045523:14600	Bahd1	INSIDE	0.906	2.900	1093.85	3172.31	2.627	900.69	2366.29
A_68_P27258522	chr10:75227236-75227280	NM_172549:-156	Cabin1	PROMOTER	0.906	2.163	7305.06	15800.65	1.959	6322.41	12388.58
A_68_P30822066	chr16:64852004-64852048	NM_178647:116	Cggbp1	INSIDE	0.906	1.861	502.75	935.83	1.686	503.16	848.20
A_68_P29086260	chr13:60703649-60703693	NM_134062:99	Dapk1	INSIDE	0.906	0.689	1900.58	1310.34	0.624	1481.97	925.31
A_68_P28737545	chr12:111517127-111517171	NM_172119:-291	Dio3	DIVERGENT_PROMOTER	0.906	0.584	2005.42	1170.28	0.529	1681.27	888.68
A_68_P24046861	chr5:122298939-122298983	NM_175474:-76	Fam109a	PROMOTER	0.906	1.564	2577.92	4032.65	1.418	2161.26	3064.60
A_68_P23317857	chr4:133042635-133042679	NM_175307:6609	Fam46b	INSIDE	0.906	2.028	886.69	1798.38	1.838	688.39	1265.27
A_68_P29976940	chr15:3929308-3929352	NM_134099:243	Fbxo4	INSIDE	0.906	1.989	508.18	1010.70	1.802	516.88	931.16
A_68_P23582143	chr5:32435937-32435982	NM_008037:-2885	Fosl2	PROMOTER	0.906	1.991	4053.18	8070.65	1.803	2564.52	4623.98
A_68_P23451688	chr5:4757569-4757613	NM_021457:626	Fzd1	INSIDE	0.906	0.703	1243.83	873.91	0.637	1152.83	734.12
A_68_P20156379	chr1:37932274-37932318	NM_001037918:3246	Lipt1	INSIDE	0.906	3.342	1954.19	6530.44	3.028	1374.07	4160.95
A_68_P31217292	chr17:48548926-48548970	NM_001110832:197	Nfya	INSIDE	0.906	0.632	3533.57	2231.54	0.572	2749.24	1573.47
A_68_P27290118	chr10:80961853-80961897	NM_010102:1008	S1pr4	INSIDE	0.906	2.200	1741.43	3831.92	1.993	1381.49	2753.88
A_68_P26885412	chr9:121671713-121671757	NM_001166644:2584	Zfp651	INSIDE	0.906	1.948	1133.07	2206.85	1.766	827.12	1460.32
A_68_P28092303	chr11:104547246-104547290	ENSMUST00000148007:248		INSIDE	0.906	2.010	534.15	1073.54	1.820	485.49	883.83
A_68_P27228311	chr10:69652022-69652071	NM_001111121:92178	Ccdc6	INSIDE	0.905	2.857	1630.69	4659.48	2.585	1336.94	3456.22
A_68_P23203727	chr4:109650158-109650202	NM_172296:-449	Dmrta2	PROMOTER	0.905	0.388	2052.51	796.11	0.351	1531.56	537.35
A_68_P24133858	chr5:139625772-139625819	NM_001081265:-381	Heatr2	PROMOTER	0.905	10.675	1522.33	16250.91	9.660	739.67	7145.52
A_68_P27804076	chr11:53113307-53113351	NM_008300:653	Hspa4	INSIDE	0.905	0.474	1240.25	587.97	0.429	1155.47	495.84
A_68_P21148580	chr2:38367238-38367282	NM_001159631:-135	Nek6	PROMOTER	0.905	2.049	513.90	1052.73	1.854	478.03	886.06
A_68_P24755177	chr6:112646572-112646616	NM_001167730:70	Rad18	INSIDE	0.905	0.676	3400.51	2297.13	0.612	2775.26	1697.42
A_68_P27045329	chr10:31328483-31328527	NM_001146349:1027	Rnf217	INSIDE	0.905	0.699	1813.12	1266.87	0.632	1643.81	1039.44
A_68_P26504535	chr9:50411810-50411854	NM_025848:122	Sdhd	INSIDE	0.905	0.618	1345.33	831.18	0.559	1101.25	615.85
A_68_P20970770	chr2:4802809-4802853	NM_175400:221	Sephs1	INSIDE	0.905	2.107	410.64	865.22	1.907	444.75	848.33
A_68_P27392327	chr10:99950250-99950294	NM_001110013:-291	Tmtc3	DIVERGENT_PROMOTER	0.905	0.714	1948.72	1392.34	0.646	1649.39	1066.13
A_68_P25589082	chr7:148661081-148661125	NM_053082:-36	Tspan4	DIVERGENT_PROMOTER	0.905	0.735	2592.32	1904.80	0.665	1966.21	1306.94
A_68_P29998080	chr15:8049104-8049148	NM_001081402:83	Wdr70	INSIDE	0.905	0.636	3185.56	2025.95	0.575	2715.84	1562.79
A_68_P29339698	chr13:114083264-114083308			Unknown	0.905	1.663	1699.17	2826.00	1.504	1343.05	2020.54
A_68_P27283430	chr10:79934572-79934616	ENSMUST00000158603:-4502		PROMOTER	0.905	1.944	3361.98	6536.15	1.760	2444.37	4303.02
A_68_P30480392	chr15:99304984-99305028	NM_029236:155	Bcdin3d	INSIDE	0.904	1.722	883.64	1521.24	1.556	645.36	1004.00
A_68_P22394779	chr3:104855704-104855748	NM_001163332:145	Cttnbp2nl	INSIDE	0.904	0.370	1552.02	574.19	0.334	1356.59	453.68

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28248077	chr12:13255581-13255625	NM_134040:378	Ddx1	INSIDE	0.904	0.703	1863.96	1309.78	0.635	1289.02	818.79
A_68_P30591036	chr16:21214742-21214786	NM_010143:9897	Ephb3	INSIDE	0.904	2.117	544.65	1153.15	1.915	489.24	936.86
A_68_P26525031	chr9:54134407-54134451	NM_177350:136	Gldn	INSIDE	0.904	1.911	491.41	938.89	1.727	483.51	835.00
A_68_P28048330	chr11:96903095-96903139	NM_026154:217	Mrpl10	INSIDE	0.904	0.607	1074.06	652.45	0.549	860.68	472.57
A_68_P31553011	chr18:23199794-23199838	NM_001161483:-2652	Nol4	PROMOTER	0.904	1.994	1599.86	3190.22	1.803	1407.92	2538.13
A_68_P31438303	chr17:90854426-90854470	NM_020252:637694	Nrxn1	INSIDE	0.904	0.424	1332.23	564.50	0.383	1057.41	405.00
A_68_P29479232	chr14:26513832-26513876	NM_134084:199	Ppif	INSIDE	0.904	0.637	1020.39	650.41	0.576	869.78	500.94
A_68_P32020395	chr19:23967551-23967595	NM_177034:134207	Apba1	INSIDE	0.903	2.464	943.55	2325.28	2.226	1008.25	2244.67
A_68_P26459693	chr9:42914668-42914712	NM_027144:-889	Arhgef12	PROMOTER	0.903	0.557	1284.33	715.07	0.503	1026.73	516.44
A_68_P23541451	chr5:23893582-23893626	NM_001002897:4357	Atg9b	INSIDE	0.903	0.607	1083.47	657.93	0.548	891.06	488.67
A_68_P30371304	chr15:80118357-80118401	NM_001044308:711	Cacna1i	INSIDE	0.903	0.574	1227.16	704.92	0.518	974.57	505.26
A_68_P31715219	chr18:53904261-53904305	NM_178686:-81	Cep120	PROMOTER	0.903	0.715	2087.69	1493.30	0.646	1624.30	1049.36
A_68_P27186923	chr10:62065160-62065204	NM_019553:-136	Ddx21	PROMOTER	0.903	0.433	1536.72	665.65	0.391	1159.76	453.82
A_68_P25495195	chr7:132695872-132695916	NM_001008700:99	Il4ra	INSIDE	0.903	1.675	2603.14	4359.57	1.513	2092.22	3164.90
A_68_P29616401	chr14:55732942-55732986	NM_177049:2808	Jph4	INSIDE	0.903	1.665	910.41	1516.24	1.504	819.24	1232.47
A_68_P27425028	chr10:106709567-106709611	NM_001033223:702	Lin7a	INSIDE	0.903	2.113	494.63	1045.37	1.908	464.65	886.69
A_68_P25574331	chr7:146022127-146022171	NM_001045483:15802	Mapk1ip1	DOWNSTREAM	0.903	1.898	2004.32	3804.27	1.713	1629.68	2792.29
A_68_P26349890	chr9:21792524-21792568	NM_023622:1351	Rgl3	INSIDE	0.903	0.568	1475.03	838.36	0.513	1197.76	614.81
A_68_P22393170	chr3:104591895-104591939	NM_007484:-35	Rhoc	PROMOTER	0.903	1.881	596.53	1122.31	1.699	537.18	912.78
A_68_P26430601	chr9:37237135-37237179	NM_001164767:3604	Robo3	INSIDE	0.903	2.151	1497.53	3220.60	1.943	1137.22	2209.24
A_68_P21101134	chr2:29922658-29922702	NM_001204875:687	Set	INSIDE	0.903	0.608	1618.39	983.76	0.549	1283.71	704.91
A_68_P27549890	chr10:129881898-129881942	NM_001103365:11030	Vmn2r86	DOWNSTREAM	0.903	3.186	366.71	1168.41	2.876	357.92	1029.36
A_68_P21113503	chr2:31993634-31993679			Unknown	0.903	2.446	257.61	630.19	2.208	237.53	524.56
A_68_P22048260	chr3:34353370-34353414			Unknown	0.903	1.891	1781.39	3368.16	1.707	1383.72	2362.60
A_68_P33005942	A_68_P33005942			Unknown	0.903	4.743	113.68	539.15	4.283	107.72	461.42
A_68_P24784500	chr6:117961807-117961851	ENSMUST00000032230:437		INSIDE	0.903	0.668	1435.10	958.74	0.603	1309.60	789.95
A_68_P31305846	chr17:66728820-66728864	NM_001114098:70248	1110012J17Rik	INSIDE	0.902	2.008	1910.28	3836.62	1.811	1495.39	2708.51
A_68_P26248108	chr8:127386840-127386884	NM_025615:67	2810004N23Rik	INSIDE	0.902	0.727	2122.54	1542.62	0.655	1554.36	1018.71
A_68_P22407413	chr3:107399619-107399663	NM_007441:1692	Alx3	INSIDE	0.902	0.538	1989.04	1069.92	0.485	1645.56	798.83
A_68_P27535079	chr10:126727356-126727401	NM_007837:-470	Ddit3	DIVERGENT_PROMOTER	0.902	2.347	2221.75	5214.23	2.117	1498.84	3173.13
A_68_P23981088	chr5:111082625-111082669	NM_027156:177	Ddx51	INSIDE	0.902	0.552	1720.43	949.02	0.498	1508.03	750.33
A_68_P22582960	chr3:140874546-140874590	NM_008811:751	Pdha2	INSIDE	0.902	2.385	1033.07	2463.77	2.150	879.31	1890.70
A_68_P26238678	chr8:125759558-125759602	NM_030176:529	Spata2L	INSIDE	0.902	0.646	1285.20	830.44	0.583	1030.59	600.50
A_68_P25094660	chr7:52968835-52968879	NM_020011:1721	Sphk2	INSIDE	0.902	3.189	1211.78	3863.88	2.877	940.44	2705.92
A_68_P30792109	chr16:58523405-58523449	NM_018784:-1	St3gal6	PROMOTER	0.902	0.701	1841.04	1290.41	0.632	1504.53	951.14
A_68_P31187138	chr17:43154011-43154055	NM_178589:529	Tnfrsf21	INSIDE	0.902	0.647	902.73	584.02	0.584	824.56	481.17
A_68_P24153574	chr5:143581988-143582032	NM_001122730:-2944	Tnrc18	PROMOTER	0.902	1.942	2678.39	5201.19	1.751	2110.42	3695.86
A_68_P20804316	chr1:169215214-169215258	NM_030724:22	Uck2	INSIDE	0.902	0.533	1248.47	665.67	0.481	1113.48	535.48
A_68_P24974110	chr7:13593210-13593254	NM_001024699:1917	Zbtb45	INSIDE	0.902	2.045	2511.70	5136.71	1.844	2214.64	4084.48
A_68_P25379198	chr7:109661711-109661755	ENSMUST00000097222:7806		DOWNSTREAM	0.902	2.439	1320.62	3221.37	2.199	1165.99	2564.30
A_68_P23637947	chr5:42235776-42235820	NM_001081422:-244	Bod1l	PROMOTER	0.901	2.309	388.61	897.37	2.080	395.00	821.58
A_68_P25582099	chr7:147256517-147256561	NM_001190386:11662	Caly	INSIDE	0.901	2.346	2170.02	5090.76	2.114	1610.82	3405.00
A_68_P30589272	chr16:20733318-20733362	NM_009893:141	Chrd	INSIDE	0.901	2.224	921.15	2048.58	2.003	723.35	1448.94
A_68_P24000793	chr5:114358500-114358544	NM_011779:193	Coro1c	INSIDE	0.901	3.678	493.88	1816.37	3.314	528.25	1750.75
A_68_P20456055	chr1:95408562-95408606	NM_145519:-96	Farp2	PROMOTER	0.901	0.592	1047.66	619.92	0.533	927.51	494.68
A_68_P23591963	chr5:34325816-34325860	NM_001033458:-284	Gm1673	PROMOTER	0.901	0.680	1493.76	1015.53	0.612	1125.13	688.85
A_68_P30490485	chr15:101062094-101062138	NM_019518:7479	Grasp	INSIDE	0.901	2.236	1736.64	3882.73	2.015	1316.52	2652.36
A_68_P26622299	chr9:71333296-71333340	NM_001164793:-553	Grinl1a	PROMOTER	0.901	2.436	960.07	2338.90	2.194	927.00	2034.27
A_68_P30547090	chr16:11254627-11254671	NR_035466:-110	Mir1945	PROMOTER	0.901	0.648	1850.35	1199.02	0.584	1587.98	927.44
A_68_P26884592	chr9:121551542-121551586	NM_011703:-269	Vipr1	DIVERGENT_PROMOTER	0.901	0.544	1221.70	664.47	0.490	1002.70	491.16
A_68_P31206541	chr17:46521167-46521211	NM_207671:474	Zfp318	INSIDE	0.901	1.709	772.27	1319.66	1.540	796.07	1226.29

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25614225	chr8:3495864-3495908	NM_080461:2749	Zfp358	INSIDE	0.901	4.545	642.47	2919.93	4.093	572.13	2341.82
A_68_P22283295	chr3:82932608-82932652	ENSMUST00000047876:538		INSIDE	0.901	1.714	736.83	1263.15	1.544	630.15	973.10
A_68_P27288864	chr10:80785360-80785404	NM_027381:1535	2510012J08Rik	INSIDE	0.900	2.937	293.82	863.01	2.644	274.55	725.94
A_68_P31731123	chr18:56732742-56732786	NM_001127338:-171	Aldh7a1	PROMOTER	0.900	0.493	1137.97	560.60	0.443	887.95	393.67
A_68_P28183243	chr11:120097692-120097736	NM_198423:3454	Bahcc1	INSIDE	0.900	0.639	2039.68	1303.20	0.575	1578.37	907.40
A_68_P26486126	chr9:47339043-47339087	NM_001025600:630	Cadm1	INSIDE	0.900	0.563	2852.15	1605.16	0.507	2135.41	1081.73
A_68_P23202005	chr4:109338819-109338863	NM_007671:-863	Cdkn2c	PROMOTER	0.900	0.545	1437.43	783.03	0.490	1076.21	527.60
A_68_P21144120	chr2:37642065-37642109	NM_001163566:10318	Crb2	INSIDE	0.900	2.021	477.45	965.13	1.819	458.74	834.29
A_68_P25098704	chr7:53632208-53632252	NM_010866:387	Myod1	INSIDE	0.900	0.679	1345.36	913.65	0.611	1097.88	670.94
A_68_P23134165	chr4:97418263-97418307	NM_001122952:169651	Nfia	INSIDE	0.900	0.661	1100.36	727.53	0.595	912.53	542.95
A_68_P21585951	chr2:122174819-122174863	NM_001013829:19814	Shf	INSIDE	0.900	2.019	691.97	1396.89	1.816	601.03	1091.52
A_68_P26983374	chr10:19570550-19570594	NM_029529:693	Slc35d3	INSIDE	0.900	1.575	1408.52	2217.98	1.418	1236.93	1753.54
A_68_P24320419	chr6:28430125-28430169	NM_019776:-201	Snd1	PROMOTER	0.900	2.586	1223.49	3163.65	2.327	1010.25	2350.64
A_68_P32109308	chr19:40587948-40587992	NM_178362:256	Sorbs1	INSIDE	0.900	0.645	1287.29	829.66	0.580	1027.77	596.23
A_68_P20914290	chr1:189431183-189431227	ENSMUST00000127489:-1465		PROMOTER	0.900	0.699	2367.05	1653.64	0.629	1842.90	1158.96
A_68_P21179669	chr2:44783090-44783134	ENSMUST00000129240:-328		PROMOTER	0.900	1.895	865.95	1641.34	1.706	885.74	1511.24
A_68_P24050675	chr5:122951393-122951437	NM_009722:820	Atp2a2	INSIDE	0.899	0.618	948.84	586.12	0.555	880.06	488.51
A_68_P32260365	chrX:11667413-11667459	NM_029510:-9757	Bcor	PROMOTER	0.899	0.565	1720.60	972.22	0.508	787.97	400.48
A_68_P31227868	chr17:50432726-50432770	NM_010021:176	Dazl	INSIDE	0.899	2.452	462.45	1134.09	2.204	444.40	979.31
A_68_P20553864	chr1:120734165-120734209	NM_001081125:216010	Gli2	INSIDE	0.899	2.520	727.31	1832.81	2.266	716.99	1625.05
A_68_P25362936	chr7:106774598-106774642	NM_001195529:993	Gm4980	INSIDE	0.899	1.972	446.92	881.38	1.773	446.42	791.68
A_68_P25031176	chr7:31140849-31140896	NM_175478:6919	Lrfn3	INSIDE	0.899	3.149	478.42	1506.49	2.832	405.84	1149.19
A_68_P31050850	chr17:12464627-12464673	NM_011948:46876	Map3k4	INSIDE	0.899	1.679	965.89	1621.77	1.509	681.93	1029.26
A_68_P25223253	chr7:79451535-79451579	NM_001024703:-75	Mctp2	PROMOTER	0.899	2.467	417.02	1028.97	2.217	456.80	1012.71
A_68_P29226006	chr13:93614678-93614722	NM_001162945:-41	Mtx3	PROMOTER	0.899	2.326	476.87	1109.03	2.091	418.70	875.50
A_68_P21843327	chr2:168578173-168578217	NM_175303:14507	Sall4	INSIDE	0.899	1.989	526.47	1047.37	1.788	448.48	801.69
A_68_P26983368	chr10:19569800-19569844	NM_029529:1443	Slc35d3	INSIDE	0.899	0.555	1517.26	841.51	0.498	1246.99	621.42
A_68_P26239285	chr8:125856857-125856901	NM_172287:266	Spire2	INSIDE	0.899	0.401	2039.35	817.12	0.360	1666.75	600.40
A_68_P30360707	chr15:78370109-78370155	NM_009218:4643	Sstr3	INSIDE	0.899	1.974	1226.45	2421.06	1.774	975.72	1731.41
A_68_P27290697	chr10:81050580-81050624	NM_019725:12326	Tle2	INSIDE	0.899	1.789	979.04	1751.51	1.607	858.15	1379.43
A_68_P24974294	chr7:13623604-13623648	NM_001168469:-7	Ube2m	PROMOTER	0.899	1.673	1311.96	2195.52	1.505	1046.81	1575.00
A_68_P21797527	chr2:160698949-160698993	NM_177263:-244	Zhx3	DIVERGENT_PROMOTER	0.899	0.696	1569.59	1093.10	0.626	1493.34	934.84
A_68_P30353821	chr15:77200742-77200786	BC100417:676		INSIDE	0.899	2.384	882.16	2102.68	2.143	739.78	1585.34
A_68_P31678552	chr18:46901420-46901464	NM_009681:-128	Ap3s1	DIVERGENT_PROMOTER	0.898	0.598	1436.08	858.15	0.537	1146.25	615.14
A_68_P27788007	chr11:50139083-50139127	NM_001110499:71	Canx	INSIDE	0.898	0.435	2047.06	890.59	0.391	1681.03	656.54
A_68_P27921607	chr11:74451400-74451447	NM_001013784:18317	E130309D14Rik	INSIDE	0.898	0.672	1060.70	713.04	0.603	922.67	556.72
A_68_P32461571	chrX:70473910-70473954	NM_007978:288	F8a	INSIDE	0.898	2.270	536.08	1216.71	2.038	401.25	817.74
A_68_P25827950	chr8:46108981-46109030	NM_001081286:73444	Fat1	INSIDE	0.898	3.184	318.98	1015.61	2.858	310.74	888.21
A_68_P25954495	chr8:73376456-73376500	NM_032397:4429	Kcnn1	INSIDE	0.898	3.380	671.05	2268.10	3.037	596.84	1812.33
A_68_P24378363	chr6:38586630-38586674	NM_001033171:587	Klrg2	INSIDE	0.898	0.651	1272.65	828.50	0.585	1154.95	675.12
A_68_P32016088	chr19:23216510-23216554	NR_035423:-7388	Mir1192	PROMOTER	0.898	0.665	1387.25	922.58	0.597	1122.97	670.34
A_68_P32697218	chrX:136595877-136595921	NM_001081668:1209	Nup62cl	INSIDE	0.898	2.127	554.82	1180.11	1.910	396.66	757.56
A_68_P30346601	chr15:76010142-76010186	NM_201394:15976	Plec	INSIDE	0.898	2.830	425.34	1203.82	2.541	338.94	861.08
A_68_P24008563	chr5:115685673-115685717	NM_026398:-165	Pop5	PROMOTER	0.898	1.617	1220.32	1972.67	1.452	1061.02	1540.15
A_68_P28186726	chr11:120645198-120645242	NM_009053:298	Rfng	INSIDE	0.898	0.553	1266.87	700.90	0.497	1152.82	573.05
A_68_P22875662	chr4:44181111-44181156	NM_175201:-723	Rnf38	PROMOTER	0.898	2.601	622.41	1618.74	2.335	610.15	1424.68
A_68_P25957633	chr8:74108592-74108640	NM_011977:15791	Slc27a1	INSIDE	0.898	2.098	924.15	1938.48	1.883	694.71	1308.17
A_68_P27629545	chr11:19920766-19920810	NM_033523:96344	Spred2	INSIDE	0.898	2.268	647.00	1467.11	2.036	553.21	1126.51
A_68_P25025683	chr7:29946879-29946923	NM_182927:6766	Spred3	INSIDE	0.898	1.910	1121.38	2141.97	1.716	872.72	1497.47
A_68_P20444768	chr1:93698701-93698745	NM_007855:669	Twist2	INSIDE	0.898	0.723	1562.40	1129.79	0.650	1247.70	810.64
A_68_P23364203	chr4:141020484-141020528	NM_009541:19919	Zbtb17	INSIDE	0.898	1.955	638.54	1248.27	1.755	599.83	1052.72

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P21937419	chr3:9452272-9452316	NM_133218:157791	Zfp704	INSIDE	0.898	2.019	399.00	805.54	1.813	393.61	713.51
A_68_P24385305	chr6:39822036-39822080			Unknown	0.898	0.620	1908.35	1183.69	0.557	1446.29	805.78
A_68_P29002651	chr13:45663653-45663697	NM_009124:396671	Atxn1	INSIDE	0.897	3.826	2945.82	11270.84	3.432	2389.25	8200.46
A_68_P31103376	chr17:25522874-25522918	NM_001163691:47832	Cacna1h	INSIDE	0.897	2.191	423.71	928.39	1.966	354.80	697.60
A_68_P30369297	chr15:79762789-79762833	NM_144811:266	Cbx7	INSIDE	0.897	1.947	2026.83	3945.98	1.747	1624.22	2837.25
A_68_P31792810	chr18:67770708-67770752	NM_001081073:30260	Cep76	DOWNSTREAM	0.897	0.570	924.59	527.08	0.511	882.98	451.34
A_68_P22291209	chr3:84283512-84283556	NM_001205355:-121	Fhdc1	PROMOTER	0.897	0.367	2113.36	776.24	0.329	1625.63	535.36
A_68_P27800934	chr11:52578718-52578762	NM_177059:533	Fstl4	INSIDE	0.897	0.684	3671.47	2510.26	0.613	2769.31	1698.85
A_68_P26156364	chr8:111864649-111864693	NR_002928:138	Gm1943	INSIDE	0.897	3.628	1239.58	4497.27	3.255	893.95	2910.05
A_68_P24428224	chr6:48547697-48547741	NM_001079901:3837	Repin1	INSIDE	0.897	2.619	338.79	887.28	2.350	315.97	742.40
A_68_P22824534	chr4:33070413-33070457	NM_027491:462	Rragd	INSIDE	0.897	2.132	656.19	1399.32	1.913	696.22	1331.73
A_68_P27807573	chr11:53794024-53794068	NM_019723:-517	Slc22a21	PROMOTER	0.897	1.627	979.41	1593.89	1.459	837.46	1222.22
A_68_P24127578	chr5:138229494-138229544	NM_001005426:489	Zcwpw1	INSIDE	0.897	6.519	1167.22	7609.32	5.846	817.42	4778.26
A_68_P32536916	chrX:91234250-91234302	ENSMUST00000118140:-118		PROMOTER	0.897	1.915	843.43	1615.10	1.717	406.50	697.91
A_68_P25833740	chr8:47085210-47085254	NM_001039562:-28	Ankrd37	PROMOTER	0.896	0.573	901.59	516.87	0.514	718.51	369.15
A_68_P30927365	chr16:85080178-85080222	NM_001198823:93752	App	INSIDE	0.896	2.908	843.05	2451.72	2.605	703.09	1831.89
A_68_P32782610	chrX:157432513-157432557	NM_001024624:79	Cdkl5	INSIDE	0.896	1.581	3556.58	5624.24	1.416	1697.33	2404.24
A_68_P31075177	chr17:17987055-17987099	NM_008215:5076	Has1	INSIDE	0.896	1.671	2408.65	4025.72	1.498	2203.82	3300.89
A_68_P23080770	chr4:86257737-86257781	NM_173400:168	Haus6	INSIDE	0.896	0.405	1715.87	695.31	0.363	1289.28	467.85
A_68_P32029538	chr19:25484679-25484723	NM_181404:173009	Kank1	INSIDE	0.896	4.044	2173.99	8790.99	3.624	1640.19	5943.97
A_68_P32140494	chr19:45857174-45857218	NM_023799:585	Mgea5	INSIDE	0.896	1.552	1486.20	2306.76	1.390	1265.56	1759.58
A_68_P20451520	chr1:94744954-94744998	NR_029559:-1978	Mir149	PROMOTER	0.896	2.155	8283.84	17848.09	1.930	5640.09	10883.24
A_68_P25949902	chr8:72635905-72635949	NM_007789:8817	Ncan	INSIDE	0.896	1.825	1815.98	3315.00	1.636	1587.47	2596.39
A_68_P30456843	chr15:95059574-95059618	NM_016743:299541	Nell2	INSIDE	0.896	2.057	763.90	1571.61	1.843	702.66	1295.33
A_68_P22695187	chr4:3865199-3865243	NM_019969:332	Plag1	INSIDE	0.896	1.656	3559.54	5893.17	1.483	2568.88	3809.52
A_68_P22204193	chr3:66025009-66025053	NM_008987:1222	Ptx3	INSIDE	0.896	2.451	1646.55	4035.73	2.197	1262.02	2772.17
A_68_P24992474	chr7:19872133-19872177	NM_001025364:-4293	Rtn2	PROMOTER	0.896	2.827	968.96	2739.17	2.533	874.12	2214.03
A_68_P28307255	chr12:28026369-28026413	NM_009234:1193	Sox11	INSIDE	0.896	1.919	1302.54	2499.73	1.719	1124.74	1933.78
A_68_P31381746	chr17:80605842-80605886	NM_001195485:781	Srsf7	INSIDE	0.896	0.611	1187.90	726.08	0.548	1110.29	607.92
A_68_P23353413	chr4:139225072-139225116	NM_031873:15642	Tas1r2	INSIDE	0.896	3.467	797.66	2765.31	3.105	678.03	2105.13
A_68_P27992698	chr11:86940439-86940483	NM_197987:-118	Trim37	PROMOTER	0.896	0.486	1740.04	846.25	0.436	1509.53	657.48
A_68_P21622817	chr2:128891746-128891790	NM_027192:86	Ttl	INSIDE	0.896	0.642	1383.93	888.00	0.575	1104.45	634.85
A_68_P21137234	chr2:35866956-35867000			Unknown	0.896	0.479	1347.83	645.43	0.429	1116.62	479.17
A_68_P20641035	chr1:137584675-137584719	ENSMUST00000112103:-14		PROMOTER	0.896	2.874	408.73	1174.71	2.575	359.50	925.58
A_68_P31175219	chr17:39982102-39982146	ENSMUST00000157647:-1946		PROMOTER	0.896	3.289	218348.60	718222.00	2.948	151257.30	445937.40
A_68_P31939675	chr19:7491423-7491467	NM_175381:-670	2700081O15Rik	PROMOTER	0.895	0.652	789.95	515.00	0.583	720.18	420.01
A_68_P31150730	chr17:33980032-33980076	NM_019421:19	Cd320	INSIDE	0.895	2.172	1440.50	3129.12	1.944	1156.43	2247.57
A_68_P24122090	chr5:137042535-137042579	NM_198602:719	Cux1	INSIDE	0.895	0.515	1632.00	839.84	0.461	1315.10	605.95
A_68_P21840413	chr2:168094194-168094238	NM_001081134:615	Kcng1	INSIDE	0.895	2.129	1437.87	3061.37	1.905	990.42	1886.70
A_68_P29330398	chr13:112545643-112545687	NM_011945:53527	Map3k1	INSIDE	0.895	2.390	1140.16	2724.47	2.139	810.08	1732.84
A_68_P25279961	chr7:90017553-90017603	NM_175366:1736	Mex3b	INSIDE	0.895	0.500	1161.42	580.62	0.448	956.32	428.03
A_68_P24591425	chr6:83051529-83051573	NM_026744:-7551	Mrpl53	PROMOTER	0.895	0.601	1376.95	827.31	0.538	1073.82	577.68
A_68_P20413388	chr1:88567300-88567344	NM_010933:-174	Nppc	PROMOTER	0.895	1.763	1139.18	2008.72	1.579	961.93	1518.56
A_68_P31256421	chr17:56613568-56613612	NM_011218:2313	Ptprs	INSIDE	0.895	0.589	1960.16	1154.00	0.527	1435.34	756.32
A_68_P23359682	chr4:140258313-140258357	NM_173867:947	Rcc2	INSIDE	0.895	0.635	1178.32	748.79	0.569	1066.09	606.26
A_68_P30605570	chr16:23927739-23927783	NM_001008230:3120	Rtp2	INSIDE	0.895	2.054	418.35	859.20	1.838	359.45	660.59
A_68_P21843350	chr2:168581447-168581491	NM_175303:11233	Sall4	INSIDE	0.895	2.566	1164.25	2987.90	2.297	943.35	2166.60
A_68_P29675223	chr14:66349464-66349508	NM_001168318:64247	Scara5	INSIDE	0.895	2.822	397.03	1120.57	2.527	312.90	790.63
A_68_P27814243	chr11:55017874-55017918	NM_153139:55	Slc36a1	INSIDE	0.895	1.717	1001.84	1720.05	1.537	900.53	1384.20
A_68_P32116952	chr19:41818141-41818185	NM_015748:184	Slit1	INSIDE	0.895	1.783	783.34	1396.69	1.596	638.32	1018.56
A_68_P31201715	chr17:45684089-45684133	NM_001013749:2516	Tmem151b	INSIDE	0.895	3.892	1793.01	6978.43	3.482	1251.09	4356.57

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P22059534	chr3:36588360-36588404	NM_019510:707	Trpc3	INSIDE	0.895	0.586	934.55	547.83	0.525	732.05	384.19
A_68_P23185611	chr4:106311721-106311765	NM_177667:16689	Ttc22	INSIDE	0.895	3.008	642.71	1932.98	2.691	546.04	1469.33
A_68_P26082676	chr8:97851882-97851927	NM_024467:3946	Zfp319	INSIDE	0.895	2.044	367.33	750.93	1.831	361.52	661.78
A_68_P25008270	chr7:25866801-25866845	NM_175477:4558	Zfp574	INSIDE	0.895	1.741	883.35	1537.77	1.558	738.85	1151.44
A_68_P24768311	chr6:114919698-114919742	ENSMUST00000164670:-499		PROMOTER	0.895	0.629	923.01	580.32	0.563	727.46	409.57
A_68_P23278549	chr4:125840190-125840234	NM_025856:-303	1700029G01Rik	PROMOTER	0.894	1.674	4006.90	6707.24	1.496	3264.99	4884.42
A_68_P23327317	chr4:134774491-134774538	NM_013885:54161	Clic4	INSIDE	0.894	3.881	1064.28	4130.46	3.471	779.07	2703.87
A_68_P21905702	chr2:180445146-180445190	NM_177852:-464	Dido1	DIVERGENT_PROMOTER	0.894	2.009	1084.89	2179.82	1.795	1063.16	1908.88
A_68_P29047198	chr13:54151095-54151139	NM_010076:-89	Drd1a	PROMOTER	0.894	0.651	1388.26	903.94	0.582	1169.17	680.59
A_68_P26658153	chr9:77955869-77955913	NM_023605:573	Fbxo9	INSIDE	0.894	0.691	2457.81	1697.89	0.617	1843.60	1138.00
A_68_P23804519	chr5:75016038-75016082	NM_001159578:57837	Lnx1	INSIDE	0.894	1.830	652.45	1194.16	1.637	495.91	811.86
A_68_P27782124	chr11:49064057-49064101	NM_001110150:25	Mgat1	INSIDE	0.894	0.674	1668.03	1123.92	0.602	1420.33	855.57
A_68_P21722730	chr2:147009969-147010013	NR_030769:172	Nkx2-2as	INSIDE	0.894	0.645	1106.53	713.17	0.576	884.23	509.32
A_68_P26017400	chr8:86496806-86496851	NM_008854:-48	Prkaca	PROMOTER	0.894	0.603	2236.05	1347.68	0.539	1833.58	987.45
A_68_P29715884	chr14:73542895-73542939	NR_033185:325	Rcbtb2	INSIDE	0.894	1.878	520.24	977.24	1.680	437.04	734.18
A_68_P28081368	chr11:102635887-102635931	NM_001110778:13156	Adam11	INSIDE	0.893	0.551	1013.64	558.08	0.492	808.55	397.64
A_68_P21781773	chr2:158054637-158054681	NM_001131021:300	D630003M21Rik	INSIDE	0.893	2.303	368.89	849.66	2.057	315.97	649.85
A_68_P26345299	chr9:20878051-20878095	NM_001039824:-114	Fdx1l	PROMOTER	0.893	0.671	1223.88	821.37	0.599	1042.72	624.58
A_68_P30363893	chr15:78858397-78858441	NM_008197:-223	H1f0	PROMOTER	0.893	1.973	784.65	1548.01	1.762	719.15	1267.09
A_68_P25466057	chr7:127039834-127039878	NM_029610:51	Lyrm1	INSIDE	0.893	0.530	2019.19	1070.06	0.473	1766.05	835.71
A_68_P30232956	chr15:55389148-55389192	NM_001168250:208	Mtbp	INSIDE	0.893	0.587	1426.30	836.89	0.524	1210.81	634.41
A_68_P31958229	chr19:11943317-11943361	NM_001011775:2366	Olfr1419	DOWNSTREAM	0.893	2.282	713.00	1627.28	2.038	571.50	1164.93
A_68_P31632687	chr18:38369690-38369734	NM_029357:-296	Pcdh1	PROMOTER	0.893	0.561	1628.03	912.99	0.501	1460.88	731.77
A_68_P24269923	chr6:17790613-17790657	NM_001083315:91419	St7	INSIDE	0.893	2.905	481.50	1398.61	2.594	490.75	1272.89
A_68_P27288943	chr10:80795596-80795640	NM_009325:4143	Tbxa2r	INSIDE	0.893	2.235	2492.34	5570.41	1.996	1690.73	3374.13
A_68_P20346777	chr1:74145308-74145352	NM_027884:25691	Tns1	INSIDE	0.893	1.733	1088.13	1885.75	1.548	960.92	1487.36
A_68_P30094310	chr15:27677668-27677712	NM_001081302:277913	Trio	INSIDE	0.893	2.331	1235.93	2881.51	2.083	969.16	2018.62
A_68_P21875502	chr2:174282709-174282753	NM_001080971:6535	Tubb1	INSIDE	0.893	2.013	1148.52	2312.36	1.798	876.83	1576.79
A_68_P29052330	chr13:55050305-55050349	NM_153131:-466	Unc5a	PROMOTER	0.893	2.652	390.21	1034.86	2.368	388.66	920.17
A_68_P26422483	chr9:35229495-35229539	ENSMUST00000154652:-1656		PROMOTER	0.893	0.616	930.36	573.49	0.550	854.23	470.02
A_68_P27933405	chr11:76486147-76486191	NM_177182:197	Bhlha9	INSIDE	0.892	1.588	1183.80	1879.78	1.416	1013.72	1435.16
A_68_P26132607	chr8:107792187-107792231	NM_015821:3661	Fbxl8	INSIDE	0.892	0.590	1532.96	904.80	0.527	1271.91	669.90
A_68_P23417739	chr4:151660365-151660409	NM_008237:5385	Hes3	INSIDE	0.892	2.008	4636.67	9310.22	1.792	3243.52	5812.43
A_68_P28748413	chr12:113416336-113416380	NM_001097621:31940	Kif26a	INSIDE	0.892	2.558	1489.18	3809.76	2.282	1364.44	3113.55
A_68_P29681980	chr14:67529185-67529229	NM_175498:-838	Pnma2	PROMOTER	0.892	0.705	1313.08	926.03	0.629	1081.10	680.19
A_68_P23326918	chr4:134708841-134708885	NM_019732:32303	Runx3	INSIDE	0.892	0.590	2478.02	1462.88	0.527	2063.71	1087.31
A_68_P24354189	chr6:34126897-34126941	NM_021435:136	Slc35b4	INSIDE	0.892	0.665	1656.19	1102.03	0.594	1227.73	728.85
A_68_P26504313	chr9:50369450-50369494	NM_025687:-99	Tex12	DIVERGENT_PROMOTER	0.892	2.725	463.21	1262.40	2.430	446.03	1083.89
A_68_P21765248	chr2:155207645-155207689	NM_178111:75	Trp53inp2	INSIDE	0.892	2.304	401.92	926.02	2.055	410.90	844.41
A_68_P27756066	chr11:44283825-44283869	NM_024475:204	Ublcp1	INSIDE	0.892	0.520	1475.52	767.30	0.464	1167.52	541.77
A_68_P27756065	chr11:44283688-44283732	NM_024475:340	Ublcp1	INSIDE	0.892	0.641	1138.10	729.61	0.572	978.87	560.05
A_68_P31841470	chr18:76305467-76305511	NM_145356:325657	Zbtb7c	INSIDE	0.892	1.724	2962.34	5106.33	1.538	2348.04	3610.50
A_68_P27282338	chr10:79768997-79769041	NM_011789:4454	Apc2	INSIDE	0.891	1.718	939.99	1615.24	1.531	807.03	1235.49
A_68_P24761303	chr6:113698666-113698710	NM_001036684:142682	Atp2b2	INSIDE	0.891	2.564	3246.56	8323.77	2.285	2163.76	4943.27
A_68_P29002652	chr13:45663747-45663791	NM_009124:396577	Atxn1	INSIDE	0.891	3.810	2675.42	10194.42	3.395	1946.25	6607.47
A_68_P30404228	chr15:85809105-85809153	NM_009886:55079	Celsr1	INSIDE	0.891	3.412	780.39	2662.54	3.039	619.98	1884.14
A_68_P21706949	chr2:144219429-144219473	NM_181417:24680	Csrp2bp	INSIDE	0.891	3.298	2238.78	7383.22	2.939	1705.62	5012.16
A_68_P23284104	chr4:126892104-126892148	NM_198618:45612	Dlgap3	INSIDE	0.891	1.552	1494.79	2319.61	1.383	1290.25	1784.79
A_68_P20941836	chr1:193960762-193960806	NR_033536:5	Gm10516	INSIDE	0.891	2.676	2122.15	5679.21	2.383	1429.62	3407.41
A_68_P28067856	chr11:100259165-100259209	NM_010593:-82	Jup	PROMOTER	0.891	0.696	1379.78	960.29	0.620	1164.11	721.74
A_68_P25285284	chr7:91030916-91030960	NM_030705:1913	Mesdc1	INSIDE	0.891	2.069	982.31	2032.07	1.844	883.45	1628.94

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31897793	chr18:86564837-86564881	NM_144946:515	Neto1	INSIDE	0.891	0.590	2052.63	1211.32	0.526	1606.27	844.86
A_68_P27614517	chr11:17059599-17059643	NM_024459:320	Ppp3r1	INSIDE	0.891	3.572	2969.67	10608.45	3.184	2643.72	8417.17
A_68_P23294937	chr4:128782610-128782654	NM_025452:-141	Tmem54	PROMOTER	0.891	1.716	4090.85	7021.22	1.529	3080.52	4709.00
A_68_P30401942	chr15:85465263-85465307			Unknown	0.891	0.643	1105.37	710.49	0.573	982.58	562.67
A_68_P30380760	chr15:81810911-81810955	NM_025503:-37	1700029P11Rik	PROMOTER	0.890	4.691	4260.78	19987.46	4.175	2898.60	12100.68
A_68_P24735712	chr6:108733427-108733471	NM_026011:396	Arl8b	INSIDE	0.890	1.975	2932.06	5790.35	1.757	2230.39	3919.63
A_68_P25591879	chr7:149136030-149136074	NM_001009929:62	Brsk2	INSIDE	0.890	0.464	1594.94	740.83	0.414	1472.64	609.10
A_68_P31113353	chr17:27083739-27083783	NM_026948:-7337	Cuta	PROMOTER	0.890	0.583	1954.15	1140.09	0.519	1695.82	880.82
A_68_P32351250	chrX:42142934-42142979	NM_001190718:382	Dcaf12l1	INSIDE	0.890	2.434	1406.27	3422.22	2.166	740.86	1605.04
A_68_P20351507	chr1:74997610-74997654	NM_010544:593	Ihh	INSIDE	0.890	0.665	1540.56	1024.81	0.592	1185.68	701.65
A_68_P30456841	chr15:95059370-95059414	NM_016743:299745	Nell2	INSIDE	0.890	2.339	404.52	946.26	2.083	371.13	773.09
A_68_P24020331	chr5:117838565-117838609	NM_028128:446	Rfc5	INSIDE	0.890	1.669	876.74	1463.34	1.485	767.04	1139.27
A_68_P27924771	chr11:75007879-75007923	NM_177708:406	Rtn4rl1	INSIDE	0.890	0.352	2486.62	874.84	0.313	2041.80	639.69
A_68_P26828802	chr9:111213792-111213836	NM_001164659:-428	Trank1	PROMOTER	0.890	1.666	1935.66	3225.03	1.483	1523.41	2259.64
A_68_P26153108	chr8:111316106-111316150	NM_007496:77585	Zfhx3	INSIDE	0.890	1.954	1169.80	2285.54	1.739	897.51	1560.72
A_68_P32288521	chrX:20002973-20003017	ENSMUST00000136093:81		INSIDE	0.890	2.401	1636.55	3928.69	2.137	885.10	1891.18
A_68_P22789805	chr4:25208818-25208862	NM_026194:128	1810074P20Rik	INSIDE	0.889	0.493	1201.30	592.31	0.439	1106.56	485.27
A_68_P28574819	chr12:81360793-81360837	NM_134156:544	Actn1	INSIDE	0.889	2.440	802.41	1957.68	2.169	843.03	1828.88
A_68_P28853793	chr13:17897267-17897311	NM_001081058:-357	Cdk13	PROMOTER	0.889	0.605	1140.77	689.66	0.537	969.01	520.64
A_68_P20613763	chr1:133026416-133026460	NM_145508:8373	Dyrk3	INSIDE	0.889	3.548	1432.28	5081.17	3.153	1217.69	3839.20
A_68_P26156365	chr8:111864724-111864768	NR_002928:62	Gm1943	INSIDE	0.889	3.269	1637.77	5353.48	2.905	1259.29	3657.66
A_68_P30404769	chr15:85889475-85889519	NM_001205353:340	Gramd4	INSIDE	0.889	3.116	2346.73	7313.48	2.771	1889.15	5235.64
A_68_P30366725	chr15:79315828-79315872	NM_008427:19821	Kcnj4	INSIDE	0.889	2.299	344.63	792.26	2.044	276.13	564.42
A_68_P23439339	chr4:154938015-154938059	NM_001159637:113	Nadk	INSIDE	0.889	1.566	1469.01	2300.80	1.393	1343.84	1871.65
A_68_P23435281	chr4:154338676-154338720	NM_172990:457	Pank4	INSIDE	0.889	0.589	1099.66	648.16	0.524	846.94	444.04
A_68_P24126059	chr5:137943930-137943974	NM_028753:-295	Pop7	PROMOTER	0.889	0.698	1459.67	1019.42	0.621	1105.83	686.23
A_68_P20172917	chr1:40738757-40738801	NM_001033289:222	Slc9a2	INSIDE	0.889	2.232	17246.89	38489.60	1.983	13377.93	26533.75
A_68_P21568535	chr2:119063252-119063296	NM_016907:179	Spint1	INSIDE	0.889	0.632	837.28	529.12	0.562	642.68	361.04
A_68_P26529575	chr9:54997611-54997655	NM_180600:457	Ube2q2	INSIDE	0.889	2.040	504.80	1029.68	1.813	467.03	846.80
A_68_P30401621	chr15:85411484-85411528	NM_001163633:-347	Wnt7b	PROMOTER	0.889	1.822	549.87	1001.87	1.619	632.13	1023.39
A_68_P26549614	chr9:58589155-58589200	NM_028598:189	2410076I21Rik	INSIDE	0.888	2.457	728.87	1791.15	2.181	717.38	1564.61
A_68_P31630976	chr18:38095246-38095290	NM_007858:-203	Diap1	PROMOTER	0.888	0.580	1141.50	662.41	0.515	988.59	509.44
A_68_P28036751	chr11:94979621-94979665	NM_010055:-1788	Dlx3	PROMOTER	0.888	2.004	725.68	1454.37	1.779	642.02	1142.29
A_68_P31156414	chr17:35042317-35042361	NM_145830:6420	Ehmt2	INSIDE	0.888	4.497	1428.50	6424.10	3.994	1083.27	4326.21
A_68_P26350220	chr9:21855814-21855858	NM_010487:631	Elavl3	INSIDE	0.888	0.451	1257.45	567.25	0.400	1010.05	404.47
A_68_P25958570	chr8:74249375-74249419	NM_028715:184	Fcho1	INSIDE	0.888	0.614	3441.64	2111.50	0.545	2579.42	1404.99
A_68_P30547079	chr16:11253448-11253492	NM_001130008:948	Gspt1	INSIDE	0.888	2.249	1059.18	2382.58	1.998	942.43	1883.18
A_68_P30347940	chr15:76210921-76210965	NM_001162489:-9518	Heatr7a	PROMOTER	0.888	0.604	1978.08	1194.86	0.536	1697.95	910.92
A_68_P28431905	chr12:52930950-52930994	NM_144788:-449	Hectd1	PROMOTER	0.888	2.789	638.70	1781.57	2.477	583.04	1444.26
A_68_P31259626	chr17:57161992-57162036	NM_010613:8916	Khsrp	INSIDE	0.888	1.776	843.68	1498.78	1.578	715.60	1129.16
A_68_P30347566	chr15:76158037-76158081	NR_028283:-95	LOC100302626	PROMOTER	0.888	0.623	2017.93	1256.67	0.553	1538.90	850.92
A_68_P32143075	chr19:46380056-46380100	NM_019408:-106	Nfkb2	PROMOTER	0.888	0.545	1261.39	687.85	0.484	1086.06	525.93
A_68_P30371156	chr15:80094548-80094592	NM_175109:166	Rps19bp1	INSIDE	0.888	0.494	2262.20	1117.65	0.439	1985.43	870.72
A_68_P23794551	chr5:73305609-73305653	NM_001113423:75	Slain2	INSIDE	0.888	0.495	1486.99	735.78	0.439	1346.56	591.65
A_68_P24118205	chr5:136333004-136333048	NM_021403:39051	Srrm3	INSIDE	0.888	2.079	4327.95	8996.79	1.845	3515.61	6487.98
A_68_P27325553	chr10:87922455-87922499	NM_011517:145	Sycp3	INSIDE	0.888	3.006	771.95	2320.57	2.670	653.58	1744.77
A_68_P26736546	chr9:94438103-94438147	NM_001033145:376	1190002N15Rik	INSIDE	0.887	1.945	419.62	816.24	1.726	405.19	699.31
A_68_P25591876	chr7:149135444-149135488	NM_029426:-189	Brsk2	PROMOTER	0.887	0.716	2210.20	1583.34	0.636	1747.49	1110.87
A_68_P24990419	chr7:19495688-19495732	NM_001033314:43	Ccdc61	INSIDE	0.887	0.481	1236.84	594.90	0.427	1035.96	442.11
A_68_P22716232	chr4:8679096-8679140	NM_001081417:61051	Chd7	INSIDE	0.887	1.567	2761.49	4327.97	1.390	2036.95	2832.29
A_68_P33015613	chr1_random:49705-49759	NM_026866:135606	Disp1	INSIDE	0.887	2.701	799.45	2159.29	2.396	656.93	1574.22

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28988894	chr13:43295868-43295912	NM_001033399:103651	Gfod1	INSIDE	0.887	1.982	525.10	1040.66	1.758	510.51	897.42
A_68_P27470614	chr10:115024633-115024677	NM_010195:182	Lgr5	INSIDE	0.887	0.578	1660.17	960.29	0.513	1335.74	685.04
A_68_P24950637	chr7:4764223-4764267	NM_133777:-302	Ube2s	PROMOTER	0.887	0.650	3030.13	1970.06	0.576	2277.73	1313.08
A_68_P25261545	chr7:86660396-86660440	ENSMUST00000150985:301		INSIDE	0.887	1.610	1105.60	1780.46	1.428	1076.53	1537.40
A_68_P27937764	chr11:77285096-77285140	NM_172945:18062	Ankrd13b	INSIDE	0.886	2.252	1376.19	3098.78	1.996	988.62	1972.84
A_68_P23299544	chr4:129665518-129665562	NM_001199696:3219	Bai2	INSIDE	0.886	0.625	2777.98	1735.37	0.554	2143.22	1186.57
A_68_P21067987	chr2:24617651-24617695	NM_001042528:895	Cacna1b	INSIDE	0.886	0.644	1720.71	1107.91	0.571	1421.25	811.02
A_68_P28155404	chr11:115665077-115665121	NM_080643:9808	Caskin2	INSIDE	0.886	2.163	2130.26	4607.16	1.917	1532.01	2936.73
A_68_P29625864	chr14:57676795-57676839	NM_016975:-34	Gja3	PROMOTER	0.886	1.641	940.77	1543.68	1.454	891.00	1295.38
A_68_P20058116	chr1:17081618-17081662	NM_020604:6330	Jph1	INSIDE	0.886	3.210	702.48	2254.85	2.843	720.91	2049.42
A_68_P21698986	chr2:142727237-142727281	NM_001081133:-58	Kif16b	PROMOTER	0.886	1.644	1231.82	2025.60	1.458	1125.94	1641.14
A_68_P25016757	chr7:28119959-28120009	NM_001113549:-1317	Ltbp4	PROMOTER	0.886	2.199	293.92	646.48	1.950	287.26	560.09
A_68_P28445669	chr12:55168877-55168921	NM_013780:819235	Npas3	INSIDE	0.886	0.696	1409.32	981.05	0.617	1159.64	715.51
A_68_P30346612	chr15:76011489-76011533	NM_201394:14630	Plec	INSIDE	0.886	2.690	867.67	2333.74	2.382	770.66	1835.71
A_68_P23194206	chr4:107694030-107694074	NM_172874:10643	Podn	INSIDE	0.886	3.121	1472.77	4597.03	2.767	1025.11	2836.50
A_68_P23982395	chr5:111308888-111308932	NM_024477:89	Ttc28	INSIDE	0.886	4.985	179.99	897.17	4.414	203.68	899.08
A_68_P25614229	chr8:3496319-3496363	NM_080461:3203	Zfp358	INSIDE	0.886	2.017	1133.62	2286.22	1.786	965.21	1723.89
A_68_P27830383	chr11:58136875-58136919	NM_178761:-48	Zfp672	DIVERGENT_PROMOTER	0.886	0.404	1305.86	527.96	0.358	1079.79	386.65
A_68_P30402119	chr15:85491531-85491575	AK083890:-4159		PROMOTER	0.886	2.426	472.99	1147.30	2.149	375.78	807.66
A_68_P31374374	chr17:79315892-79315936	NM_001177402:76	1110001A16Rik	INSIDE	0.885	1.757	2935.54	5157.45	1.556	2191.49	3409.07
A_68_P26760984	chr9:98765311-98765355	NM_028033:147	2410012M07Rik	INSIDE	0.885	2.311	9977.79	23062.86	2.047	7501.02	15352.54
A_68_P32053390	chr19:29597209-29597253	NM_001081319:459	C030046E11Rik	INSIDE	0.885	0.649	2249.76	1459.61	0.574	1757.46	1009.35
A_68_P27750784	chr11:43304478-43304526	NM_026979:16695	C1qtnf2	INSIDE	0.885	2.216	685.37	1518.99	1.961	547.19	1072.89
A_68_P32982271	chr5:134998519-134998564	NM_001039162:29763	Clip2	INSIDE	0.885	2.051	545.95	1119.78	1.816	392.01	711.91
A_68_P25090601	chr7:52262939-52262983	NM_001008422:8659	Scaf1	INSIDE	0.885	2.254	2312.44	5212.22	1.994	1685.86	3361.29
A_68_P28730244	chr12:110074293-110074337	NM_181328:-228	Slc25a29	DIVERGENT_PROMOTER	0.885	0.477	1790.65	854.77	0.423	1281.74	541.57
A_68_P25807722	chr8:41947794-41947838	NM_001044740:70	Slc7a2	INSIDE	0.885	2.787	5287.51	14737.81	2.466	4103.96	10120.58
A_68_P24604965	chr6:85382281-85382325	NM_144918:333	Smyd5	INSIDE	0.885	1.685	1943.30	3274.36	1.492	1482.54	2211.25
A_68_P25183828	chr7:72789560-72789604	NM_172310:-201	Tarsl2	PROMOTER	0.885	2.050	11629.38	23838.43	1.814	8013.07	14539.39
A_68_P31092360	chr17:23694657-23694701	NM_001033496:6515	Zfp213	INSIDE	0.885	1.838	1238.42	2275.95	1.627	962.24	1565.67
A_68_P28048036	chr11:96858742-96858786			Unknown	0.885	3.501	1930.90	6760.89	3.099	1182.97	3666.53
A_68_P20738463	chr1:157405630-157405674	NM_026683:403	Acbd6	INSIDE	0.884	0.580	1438.63	833.74	0.512	1286.86	659.21
A_68_P31383665	chr17:80942894-80942947	NM_001033443:20254	Cdkl4	INSIDE	0.884	1.995	466.18	930.16	1.764	403.77	712.27
A_68_P23332455	chr4:135728739-135728783	NM_177733:452	E2f2	INSIDE	0.884	1.985	826.98	1641.55	1.754	909.17	1594.89
A_68_P29604237	chr14:52626582-52626626	NM_001033805:-9935	G630016D24Rik	PROMOTER	0.884	2.243	517.83	1161.49	1.983	448.36	889.14
A_68_P24518613	chr6:66846160-66846204	NM_001177556:-208	Gng12	PROMOTER	0.884	1.634	2320.89	3791.60	1.444	1765.80	2550.04
A_68_P29059423	chr13:56236168-56236212	NM_001159513:721	H2afy	INSIDE	0.884	2.219	656.16	1455.91	1.961	616.69	1209.22
A_68_P25004862	chr7:25217754-25217798	NM_199013:12925	Irgc1	INSIDE	0.884	2.503	2781.22	6960.94	2.213	2083.35	4609.51
A_68_P27284037	chr10:80031748-80031792	NM_078477:8271	Klf16	INSIDE	0.884	2.100	1506.71	3164.06	1.857	1194.85	2219.18
A_68_P29842701	chr14:99698407-99698451	NM_009769:519	Klf5	INSIDE	0.884	2.429	574.82	1396.19	2.148	590.05	1267.57
A_68_P24979591	chr7:16684155-16684199	NM_025898:185	Napa	INSIDE	0.884	1.766	825.10	1457.00	1.561	741.22	1156.81
A_68_P29654921	chr14:62950975-62951019	NM_026001:55	Rnaseh2b	INSIDE	0.884	0.689	1285.98	885.54	0.609	1078.20	656.31
A_68_P20871446	chr1:181598547-181598591	NM_178653:207	Sccpdh	INSIDE	0.884	2.382	847.75	2019.24	2.105	736.66	1550.54
A_68_P23187163	chr4:106584892-106584936	NM_023672:840	Ssbp3	INSIDE	0.884	2.156	551.29	1188.82	1.906	505.26	962.94
A_68_P30385304	chr15:82729412-82729456	NR_027799:-543	Tbrg3	PROMOTER	0.884	0.586	3052.25	1789.00	0.518	2394.48	1240.03
A_68_P31215267	chr17:48111395-48111439			Unknown	0.884	2.859	671.03	1918.26	2.528	594.96	1503.78
A_68_P20530739	chr1:114313105-114313149			Unknown	0.884	0.630	2691.13	1694.34	0.557	2143.10	1192.92
A_68_P22407294	chr3:107385858-107385902			Unknown	0.884	0.645	2990.34	1927.42	0.570	2150.88	1226.01
A_68_P20977503	chr2:6050985-6051029	NM_001159657:225	5430407P10Rik	INSIDE	0.883	0.453	2161.70	979.51	0.400	1714.00	685.98
A_68_P28752032	chr12:113960100-113960144	NM_001024602:-262	AW555464	PROMOTER	0.883	0.612	1264.74	773.71	0.540	1012.69	547.17
A_68_P27891998	chr11:68715228-68715272	NR_003373:160	Gm15772	INSIDE	0.883	1.731	988.57	1711.66	1.529	904.83	1383.55

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31863473	chr18:80492422-80492466	NM_001190373:68549	Kcng2	INSIDE	0.883	2.139	537.51	1149.63	1.888	492.94	930.62
A_68_P28748273	chr12:113399710-113399754	NM_001097621:15314	Kif26a	INSIDE	0.883	2.716	962.74	2615.04	2.399	697.58	1673.63
A_68_P24171440	chr5:147840732-147840776	NM_080795:47394	Lnx2	INSIDE	0.883	2.496	2153.82	5375.62	2.203	1763.11	3884.53
A_68_P25022019	chr7:29244304-29244350	NM_001141921:7070	Lrfn1	INSIDE	0.883	1.921	859.40	1651.15	1.696	742.61	1259.68
A_68_P25343508	chr7:103358546-103358591	NM_011858:-578	Odz4	PROMOTER	0.883	2.973	4745.77	14108.42	2.626	3949.80	10372.35
A_68_P28085167	chr11:103274059-103274103	NM_183034:-102	Plekhm1	PROMOTER	0.883	2.758	598.75	1651.22	2.435	607.68	1479.59
A_68_P24949868	chr7:4610619-4610663	NM_172894:-88	Ppp6r1	PROMOTER	0.883	0.488	1643.60	801.32	0.430	1299.87	559.59
A_68_P22412277	chr3:108186677-108186721	NM_001190161:-23	Psrc1	PROMOTER	0.883	1.916	1007.11	1929.68	1.692	851.01	1439.80
A_68_P29106487	chr13:67033811-67033855	NM_008959:67	Ptdss1	INSIDE	0.883	0.563	1801.66	1014.59	0.497	1475.39	733.34
A_68_P27687432	chr11:32113340-32113384	NM_010117:8931	Rhbdf1	INSIDE	0.883	2.498	1619.09	4043.93	2.206	1199.30	2645.07
A_68_P26522398	chr9:53619438-53619482	NM_028060:119	Slc35f2	INSIDE	0.883	0.467	1630.81	761.64	0.412	1242.05	512.29
A_68_P23364321	chr4:141034275-141034319	NM_019763:60216	Spen	INSIDE	0.883	2.405	879.25	2114.58	2.123	734.20	1558.94
A_68_P29455872	chr14:22804750-22804794	NM_145459:4051	Zfp503	INSIDE	0.883	0.494	1055.14	521.10	0.436	868.70	378.86
A_68_P28724516	chr12:109154117-109154161	NM_001079883:87486	Bcl11b	INSIDE	0.882	2.757	551.62	1520.91	2.432	492.18	1196.84
A_68_P29941712	chr14:119322120-119322164	NM_025943:247	Dzip1	INSIDE	0.882	0.652	2030.30	1324.24	0.576	1648.09	948.50
A_68_P24620282	chr6:88139868-88139912	NM_008090:-8767	Gata2	PROMOTER	0.882	0.601	1261.08	758.45	0.530	1063.46	563.81
A_68_P28516080	chr12:70825874-70825918	NM_145443:-35	L2hgdh	DIVERGENT_PROMOTER	0.882	0.558	1239.16	691.65	0.493	1025.60	505.12
A_68_P27854124	chr11:62270784-62270828	NM_011308:28	Ncor1	INSIDE	0.882	1.715	2120.57	3636.39	1.512	1814.20	2743.19
A_68_P26136321	chr8:108378956-108379000	NM_021513:-24	Thap11	DIVERGENT_PROMOTER	0.882	0.608	1669.23	1014.36	0.536	1534.73	822.50
A_68_P24427164	chr6:48388295-48388339	NM_001085415:6773	Zfp467	INSIDE	0.882	1.709	1225.02	2093.33	1.507	995.08	1499.35
A_68_P25505621	chr7:134587797-134587841	NM_175163:4854	Zfp689	INSIDE	0.882	2.613	1207.11	3154.03	2.305	1017.64	2345.25
A_68_P22086836	chr3:41643672-41643716			Unknown	0.882	3.462	1857.26	6429.11	3.054	1641.30	5011.80
A_68_P23383664	chr4:145167106-145167158	ENSMUST00000117838:63		INSIDE	0.882	3.054	582.83	1779.91	2.694	430.09	1158.66
A_68_P27288891	chr10:80788278-80788322	NM_027381:4453	2510012J08Rik	INSIDE	0.881	2.577	5444.06	14031.83	2.271	4378.63	9941.86
A_68_P23542802	chr5:24083177-24083221	NM_001190443:87	Abcf2	INSIDE	0.881	0.564	1243.51	701.42	0.497	942.44	468.12
A_68_P24298740	chr6:23788658-23788702	NM_153163:620	Cadps2	INSIDE	0.881	0.559	1377.29	769.96	0.493	1170.14	576.51
A_68_P20354307	chr1:75471829-75471873	NM_001001565:4196	Chpf	INSIDE	0.881	2.373	427.64	1014.80	2.091	433.24	905.96
A_68_P21134369	chr2:35438463-35438507	NM_001114125:24507	Dab2ip	INSIDE	0.881	2.114	729.69	1542.34	1.862	671.43	1249.92
A_68_P25021008	chr7:29079932-29079976	NM_007866:6850	Dll3	INSIDE	0.881	0.673	1733.19	1165.99	0.593	1420.20	841.87
A_68_P26761431	chr9:98856538-98856582	NM_012020:535	Foxl2	INSIDE	0.881	0.643	928.63	596.97	0.566	839.59	475.53
A_68_P28087337	chr11:103672587-103672632	NM_009521:37121	Wnt3	INSIDE	0.881	1.767	842.47	1488.64	1.556	640.74	997.27
A_68_P26913056	chr10:5959839-5959883	NM_001033466:1428	Zbtb2	INSIDE	0.881	1.987	718.02	1426.92	1.750	687.92	1203.76
A_68_P29285955	chr13:104383068-104383112	BC099526:114623		INSIDE	0.881	2.201	742.43	1634.06	1.939	619.61	1201.68
A_68_P30665009	chr16:34572678-34572722	ENSMUST00000114961:918		INSIDE	0.881	0.508	1110.04	564.23	0.448	896.30	401.28
A_68_P26221248	chr8:123112748-123112792	NM_178856:205	Gins2	INSIDE	0.880	0.420	1921.46	807.71	0.370	1507.14	557.72
A_68_P27286894	chr10:80477702-80477746	NM_010319:-54	Gng7	PROMOTER	0.880	0.648	1241.59	803.96	0.570	894.68	509.65
A_68_P26847145	chr9:114842599-114842643	NM_175380:485	Gpd1l	INSIDE	0.880	0.562	987.56	554.65	0.494	807.18	398.85
A_68_P21750931	chr2:152565335-152565379	NM_010495:3347	Id1	DOWNSTREAM	0.880	0.597	1356.17	809.72	0.526	1255.72	659.90
A_68_P30343807	chr15:75577030-75577074	NM_194350:1300	Mafa	DOWNSTREAM	0.880	2.352	708.34	1666.16	2.069	642.84	1329.94
A_68_P30086028	chr15:26239162-26239206	NM_177597:358	Marchf11	INSIDE	0.880	1.952	531.23	1036.89	1.718	459.45	789.12
A_68_P22509668	chr3:127328592-127328639	NM_009718:-7447	Neurog2	PROMOTER	0.880	1.605	1673.53	2685.52	1.412	1283.43	1811.95
A_68_P24643138	chr6:92041251-92041295	NM_011630:-139	Nr2c2	PROMOTER	0.880	2.086	473.24	987.24	1.835	516.44	947.91
A_68_P26747582	chr9:96437440-96437484	NM_053268:94460	Rasa2	DOWNSTREAM	0.880	2.073	1342.99	2784.05	1.825	1210.32	2208.29
A_68_P22063905	chr3:37380234-37380278	NM_001163511:61055	Spata5	INSIDE	0.880	2.127	517.41	1100.28	1.871	461.17	862.66
A_68_P24019921	chr5:117769319-117769363	NM_001033311:66	Vsig10	INSIDE	0.880	0.630	1377.61	867.31	0.554	1042.02	577.15
A_68_P24793131	chr6:119390505-119390549	NM_009525:103839	Wnt5b	INSIDE	0.880	1.948	968.91	1887.87	1.715	832.27	1426.99
A_68_P31620633	chr18:36033456-36033500			Unknown	0.880	0.555	1099.80	610.31	0.488	909.51	443.96
A_68_P23962133	chr5:107003460-107003504	ENSMUST00000131029:252		INSIDE	0.880	2.076	767.97	1594.15	1.826	704.15	1285.79
A_68_P28608876	chr12:87585301-87585347	NM_027405:2497	1700020O03Rik	INSIDE	0.879	1.996	563.91	1125.56	1.755	455.50	799.53
A_68_P23415137	chr4:151236473-151236517	NM_001081557:-617	Camta1	PROMOTER	0.879	0.534	1227.32	655.38	0.469	987.73	463.39
A_68_P33015624	chr1_random:51004-51048	NM_026866:134312	Disp1	INSIDE	0.879	2.084	598.72	1247.50	1.832	487.48	892.85

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P21007902	chr2:11698864-11698908	NM_015792:268	Fbxo18	INSIDE	0.879	0.468	1190.76	557.58	0.412	918.09	378.05
A_68_P24025035	chr5:118619751-118619795	NM_007545:0	Hrk	INSIDE	0.879	2.156	2006.56	4326.29	1.895	1761.89	3338.29
A_68_P26270746	chr8:131209434-131209478	NM_010578:-97	Itgb1	PROMOTER	0.879	0.497	2107.81	1048.05	0.437	1682.40	735.33
A_68_P31930917	chr19:5803602-5803646	NR_002847:-953	Malat1	PROMOTER	0.879	0.512	2164.12	1107.04	0.449	1779.38	799.77
A_68_P24065430	chr5:125659058-125659102	NM_011424:504	Ncor2	INSIDE	0.879	0.637	892.22	568.14	0.560	784.37	438.91
A_68_P23184551	chr4:106136489-106136533	NM_153565:420	Pcsk9	INSIDE	0.879	0.527	1329.89	701.39	0.464	1209.62	560.90
A_68_P26843527	chr9:113966461-113966505	NM_001101510:11	Susd5	INSIDE	0.879	1.680	1375.33	2310.10	1.476	1348.70	1991.20
A_68_P31101670	chr17:25252921-25252965	NM_001163661:-30	Telo2	DIVERGENT_PROMOTER	0.879	2.479	1251.80	3103.49	2.178	937.42	2041.89
A_68_P28031427	chr11:94073436-94073480	NM_009427:691	Tob1	INSIDE	0.879	1.841	522.92	962.51	1.618	493.48	798.44
A_68_P25092433	chr7:52582778-52582822	NM_175130:6350	Trpm4	INSIDE	0.879	3.047	1093.75	3332.89	2.680	958.23	2567.65
A_68_P31403188	chr17:84585249-84585293	NM_001001806:2017	Zfp36l2	INSIDE	0.879	0.746	3473.86	2590.14	0.656	2997.06	1964.78
A_68_P22341860	chr3:94819980-94820024	NM_030074:-842	Zfp687	PROMOTER	0.879	0.596	946.71	564.18	0.524	835.88	437.77
A_68_P29502989	chr14:30791625-30791669	NM_027493:124	Actr8	INSIDE	0.878	2.037	1741.90	3547.43	1.788	1385.59	2477.26
A_68_P27226082	chr10:69284986-69285030	NM_146005:288553	Ank3	INSIDE	0.878	2.411	636.18	1533.98	2.118	503.14	1065.59
A_68_P32262595	chrX:12165037-12165081	NM_027439:174	Atp6ap2	INSIDE	0.878	2.231	2195.93	4898.77	1.959	919.05	1800.24
A_68_P28221298	chr12:8305600-8305644	NM_013527:3138	Gdf7	INSIDE	0.878	2.409	1459.90	3517.04	2.116	1270.55	2688.73
A_68_P32016033	chr19:23209323-23209367	NM_010638:-6371	Klf9	PROMOTER	0.878	1.812	5407.44	9800.32	1.591	3861.51	6143.24
A_68_P21037798	chr2:17948361-17948405	NR_028378:-493	LOC100034739	PROMOTER	0.878	0.475	1486.45	705.99	0.417	1338.60	558.44
A_68_P31127481	chr17:29484296-29484340	NM_019880:531	Mtch1	INSIDE	0.878	2.942	9126.89	26850.41	2.584	5692.52	14707.71
A_68_P24483715	chr6:58856617-58856661	NM_021432:482	Nap1l5	INSIDE	0.878	1.600	1411.86	2258.41	1.405	1079.94	1516.88
A_68_P31421200	chr17:87506806-87506850	NM_019654:-190	Socs5	PROMOTER	0.878	1.941	1005.91	1952.40	1.705	827.43	1410.48
A_68_P22385232	chr3:103083556-103083600	NM_001079830:363	Trim33	INSIDE	0.878	2.213	475.63	1052.78	1.943	457.62	889.07
A_68_P22382655	chr3:102538658-102538702	NM_027533:-12	Tspan2	PROMOTER	0.878	1.666	1465.85	2442.37	1.463	1047.61	1532.58
A_68_P26036156	chr8:90184417-90184461	NM_033327:299056	Zfp423	DOWNSTREAM	0.878	0.672	1609.80	1082.00	0.590	1253.79	739.63
A_68_P23424870	chr4:152806765-152806809	NM_001099299:50153	Ajap1	INSIDE	0.877	2.823	844.85	2385.25	2.475	778.38	1926.29
A_68_P23767825	chr5:67818729-67818773	NM_001164806:288	Bend4	INSIDE	0.877	1.872	890.42	1667.27	1.642	799.12	1312.05
A_68_P27673731	chr11:29147082-29147126	NM_025740:168	Ccdc104	INSIDE	0.877	0.607	2592.11	1573.95	0.533	2048.30	1091.15
A_68_P21822532	chr2:165058963-165059007	NM_174988:1253	Cdh22	INSIDE	0.877	0.600	2771.82	1663.64	0.526	2139.77	1126.16
A_68_P23270849	chr4:124559951-124559995	NM_177671:944	Epha10	INSIDE	0.877	0.650	1196.97	778.12	0.570	1084.26	618.41
A_68_P26156366	chr8:111864799-111864851	NR_002928:-16	Gm1943	PROMOTER	0.877	2.203	530.44	1168.49	1.932	457.17	883.10
A_68_P26804348	chr9:106549759-106549803	NM_001160353:8660	Grm2	INSIDE	0.877	2.262	1147.04	2594.88	1.983	949.81	1883.67
A_68_P28043433	chr11:96144433-96144477	NM_010461:1236	Hoxb8	INSIDE	0.877	0.594	1738.00	1031.92	0.521	1465.23	763.06
A_68_P22957168	chr4:59594155-59594199	NM_024255:-258	Hsdl2	PROMOTER	0.877	2.022	2614.58	5286.23	1.773	2108.68	3737.94
A_68_P23611442	chr5:37482587-37482631	NM_178394:40513	Jakmip1	INSIDE	0.877	2.693	235.16	633.34	2.361	203.14	479.69
A_68_P25406536	chr7:116313170-116313214	NM_057173:630	Lmo1	INSIDE	0.877	0.608	969.60	589.95	0.533	764.70	407.94
A_68_P27535213	chr10:126748669-126748713	NM_001003913:152	Mars	INSIDE	0.877	0.679	1274.04	864.85	0.596	1121.64	668.03
A_68_P20506811	chr1:108069599-108069643	NM_133821:1175	Phlpp1	INSIDE	0.877	0.503	1391.74	700.18	0.441	1156.96	510.72
A_68_P30346972	chr15:76062477-76062521	NM_001163542:-690	Plec	PROMOTER	0.877	0.506	1128.23	570.93	0.444	875.00	388.38
A_68_P30969342	chr16:92466123-92466167	NM_001081549:247	Rcan1	INSIDE	0.877	0.664	1600.56	1063.38	0.583	1306.95	761.58
A_68_P28535267	chr12:74146949-74146993	NM_009189:729	Six1	INSIDE	0.877	0.672	984.82	661.31	0.589	732.01	431.03
A_68_P25957634	chr8:74108737-74108781	NM_011977:15933	Slc27a1	INSIDE	0.877	2.589	774.69	2006.03	2.272	641.74	1458.11
A_68_P27911318	chr11:72225271-72225315	NM_177776:-77	Smtnl2	PROMOTER	0.877	0.443	2457.74	1088.17	0.388	2042.36	792.63
A_68_P22314616	chr3:88383591-88383635	NM_025448:20	Ssr2	INSIDE	0.877	0.467	1128.02	527.09	0.410	939.00	384.58
A_68_P21815997	chr2:163899961-163900005	NM_021420:69	Stk4	INSIDE	0.877	0.627	927.36	581.07	0.550	816.48	448.66
A_68_P21747903	chr2:151969066-151969110	NM_009328:-256	Tcf15	PROMOTER	0.877	0.522	1197.47	624.63	0.457	988.92	452.27
A_68_P22894265	chr4:47366582-47366626	NM_009370:428	Tgfbr1	INSIDE	0.877	1.831	1099.21	2012.41	1.606	1002.71	1610.29
A_68_P29023542	chr13:49242589-49242633	NM_029361:773	Wnk2	INSIDE	0.877	1.866	949.60	1771.74	1.637	868.31	1421.13
A_68_P27563766	chr11:5420720-5420764	NM_013842:-227	Xbp1	PROMOTER	0.877	0.475	1171.89	556.12	0.416	995.63	414.25
A_68_P25842776	chr8:48732206-48732250			Unknown	0.877	2.461	489.53	1204.91	2.157	461.34	995.28
A_68_P28183803	chr11:120166774-120166818			Unknown	0.877	0.609	2320.91	1414.24	0.534	1954.13	1043.99
A_68_P27288892	chr10:80788388-80788440	NM_027381:4567	2510012J08Rik	INSIDE	0.876	3.218	1342.72	4321.14	2.820	1074.69	3030.46

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26553627	chr9:59333545-59333589	NM_019927:615	Arih1	INSIDE	0.876	0.420	1804.53	757.95	0.368	1462.24	538.00
A_68_P25617307	chr8:4325222-4325266	NR_033527:35	Ccl25	INSIDE	0.876	0.498	1128.92	562.59	0.437	946.00	413.20
A_68_P24120337	chr5:136750787-136750831	NM_198602:292467	Cux1	INSIDE	0.876	2.919	259.86	758.47	2.556	282.14	721.23
A_68_P31150931	chr17:34048707-34048751	NM_001199733:2183	Daxx	INSIDE	0.876	2.611	597.45	1559.83	2.286	573.32	1310.69
A_68_P21569026	chr2:119148000-119148050	NM_019454:-3495	Dll4	PROMOTER	0.876	0.654	977.03	638.96	0.573	750.88	430.09
A_68_P28429305	chr12:52449483-52449527	NM_001015099:288	G2e3	INSIDE	0.876	2.516	312.43	786.10	2.205	307.14	677.14
A_68_P24451818	chr6:52590402-52590446	NM_145567:-130	Hibadh	PROMOTER	0.876	3.545	1061.80	3764.10	3.105	841.52	2613.18
A_68_P27340040	chr10:90564963-90565014	NM_027078:19205	Ikbip	INSIDE	0.876	3.832	516.65	1979.63	3.357	422.66	1418.85
A_68_P23318790	chr4:133228292-133228336	NM_001145955:248	Pigv	INSIDE	0.876	0.628	1537.22	965.66	0.550	1378.04	758.04
A_68_P29701215	chr14:70829074-70829118	NM_021308:-195	Piwil2	PROMOTER	0.876	1.668	3250.31	5422.05	1.462	2693.08	3936.18
A_68_P22405767	chr3:107145905-107145949	NM_001045807:-9719	Rbm15	PROMOTER	0.876	3.020	324.18	979.09	2.645	317.58	839.86
A_68_P30575793	chr16:17804490-17804534	NM_153790:7138	Scarf2	INSIDE	0.876	0.597	1746.76	1042.25	0.523	1495.73	781.76
A_68_P28038654	chr11:95275393-95275437	NM_025287:18	Spop	INSIDE	0.876	1.642	2808.11	4609.75	1.437	2234.70	3211.87
A_68_P27340414	chr10:90634556-90634600	NM_001080129:-251	Tmpo	PROMOTER	0.876	0.733	2305.27	1689.13	0.642	1912.46	1228.07
A_68_P29052710	chr13:55098681-55098725	NM_153131:47910	Unc5a	INSIDE	0.876	2.258	1458.83	3293.84	1.978	1203.00	2378.94
A_68_P27285197	chr10:80204884-80204928	NM_007460:50	Ap3d1	INSIDE	0.875	0.663	959.79	636.45	0.580	776.06	450.31
A_68_P26356129	chr9:23027849-23027893	NM_028472:351	Bmper	INSIDE	0.875	0.657	1299.35	853.82	0.575	1130.27	649.66
A_68_P33007789	chr4_random:128217-128261	NM_001033326:18437	Dhrsx	INSIDE	0.875	1.882	2204.84	4149.44	1.647	1811.37	2982.56
A_68_P25108777	chr7:56136031-56136075	NM_001013368:359	E2f8	INSIDE	0.875	0.607	1125.83	683.74	0.531	1032.82	548.73
A_68_P25005646	chr7:25370925-25370969	NM_023154:-1615	Ethe1	PROMOTER	0.875	2.250	5331.10	11992.35	1.969	3886.69	7654.13
A_68_P25827402	chr8:46036102-46036161	NM_001081286:570	Fat1	INSIDE	0.875	2.330	1150.14	2680.06	2.040	820.64	1674.08
A_68_P31927962	chr19:5306803-5306849	NM_001024717:8496	Gal3st3	INSIDE	0.875	2.837	379.24	1075.97	2.481	338.69	840.40
A_68_P31927965	chr19:5307061-5307105	NM_001024717:8752	Gal3st3	INSIDE	0.875	2.051	1187.86	2436.13	1.795	1079.42	1938.05
A_68_P30347069	chr15:76077165-76077209	NM_023168:-50	Grina	DIVERGENT_PROMOTER	0.875	0.737	4098.15	3022.21	0.646	3129.19	2020.11
A_68_P27995154	chr11:87431401-87431445	NM_001045527:757	Hsf5	INSIDE	0.875	2.391	1279.29	3059.40	2.091	1056.67	2209.95
A_68_P22885280	chr4:45839410-45839454	NM_018741:267	Igfbpl1	INSIDE	0.875	1.661	1465.95	2435.45	1.454	1263.17	1836.21
A_68_P20725329	chr1:155033264-155033308	NM_008485:291	Lamc2	INSIDE	0.875	0.624	971.45	606.51	0.546	824.56	450.51
A_68_P27911829	chr11:72303431-72303475	NM_153060:-46	Spns2	PROMOTER	0.875	2.874	284.38	817.41	2.516	265.35	667.65
A_68_P26234571	chr8:125135662-125135707	NM_021502:159	Trappc2l	INSIDE	0.875	0.679	1759.88	1194.45	0.594	1268.27	752.95
A_68_P24874653	chr6:136776590-136776634	NM_021714:125	Wbp11	INSIDE	0.875	0.519	2131.40	1106.10	0.454	1793.56	814.49
A_68_P30558815	chr16:13754812-13754856	AK044312:176		INSIDE	0.875	0.605	1619.73	979.75	0.529	1199.97	635.29
A_68_P21705754	chr2:143991432-143991476	ENSMUST00000099292:23572		DOWNSTREAM	0.875	0.586	1016.88	595.40	0.512	857.74	439.39
A_68_P31762240	chr18:62339500-62339544	NM_007420:91	Adrb2	INSIDE	0.874	2.929	2026.26	5934.03	2.560	1798.58	4605.07
A_68_P30404230	chr15:85809331-85809375	NM_009886:54855	Celsr1	INSIDE	0.874	2.855	1537.19	4387.99	2.496	1131.76	2825.03
A_68_P26127987	chr8:106864391-106864435	NM_024217:-81	Cmtm3	PROMOTER	0.874	4.979	12296.25	61227.81	4.354	7343.52	31972.60
A_68_P23246056	chr4:119212030-119212074	NM_172699:-240	Foxj3	DIVERGENT_PROMOTER	0.874	0.603	1433.67	863.88	0.527	1228.07	647.03
A_68_P25971957	chr8:77617610-77617654	NM_010442:116	Hmox1	INSIDE	0.874	0.641	893.64	572.73	0.560	807.91	452.65
A_68_P30650136	chr16:31933025-31933069	NM_172822:-890	Pigz	PROMOTER	0.874	0.355	1614.70	573.00	0.310	1301.58	403.71
A_68_P30489220	chr15:100870918-100870964	NM_011323:104239	Scn8a	INSIDE	0.874	6.479	1711.41	11087.85	5.661	1228.12	6952.74
A_68_P25021510	chr7:29163296-29163340	NM_011756:929	Zfp36	INSIDE	0.874	3.055	2225.08	6796.90	2.670	1755.38	4686.07
A_68_P24319372	chr6:28212314-28212358	NM_001081678:-735	Zfp800	PROMOTER	0.874	1.957	1196.51	2341.41	1.711	1061.10	1815.23
A_68_P25947616	chr8:72178703-72178747	NM_001177527:270	Zfp964	INSIDE	0.874	1.646	1082.53	1781.71	1.438	1051.95	1513.00
A_68_P31092624	chr17:23747448-23747492	NM_001033425:9648	Zscan10	INSIDE	0.874	1.828	2065.27	3775.57	1.599	1601.32	2559.97
A_68_P31157813	chr17:35272266-35272310	NM_057171:102	Bag6	INSIDE	0.873	0.617	1039.82	641.14	0.538	714.78	384.63
A_68_P32287114	chrX:19637038-19637082	NM_021715:365	Chst7	INSIDE	0.873	1.949	1259.55	2454.89	1.701	643.37	1094.32
A_68_P20825163	chr1:172815285-172815329	NM_023173:365	Dusp12	INSIDE	0.873	0.698	1268.96	885.60	0.609	1048.39	638.71
A_68_P31114356	chr17:27252698-27252742	NM_080553:58472	Itpr3	INSIDE	0.873	2.966	744.82	2209.27	2.588	511.35	1323.55
A_68_P28997653	chr13:44825548-44825592	NM_001205044:-572	Jarid2	PROMOTER	0.873	2.320	394.62	915.52	2.025	388.99	787.65
A_68_P22934428	chr4:55544566-55544610	NM_010637:759	Klf4	INSIDE	0.873	0.659	899.77	592.68	0.575	783.94	450.72
A_68_P22009790	chr3:27081996-27082040	NM_178772:93	Nceh1	INSIDE	0.873	0.389	1543.25	600.22	0.340	1256.59	426.71
A_68_P23419144	chr4:151852440-151852484	NM_153424:212	Nphp4	INSIDE	0.873	0.550	2401.43	1319.96	0.480	1842.79	884.19

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27921013	chr11:74336837-74336884	NM_001015046:66800	Rap1gap2	INSIDE	0.873	0.728	2592.51	1888.10	0.635	2117.39	1345.49
A_68_P23294684	chr4:128736191-128736235	NM_029219:698	Rnf19b	INSIDE	0.873	0.610	1738.68	1060.61	0.533	1508.23	803.54
A_68_P30953525	chr16:89885381-89885425	NM_009384:75670	Tiam1	INSIDE	0.873	2.170	379.66	823.93	1.894	358.22	678.40
A_68_P23991347	chr5:112737115-112737159	NM_009419:31410	Tpst2	INSIDE	0.873	2.471	1425.99	3522.92	2.156	1061.89	2289.65
A_68_P24084073	chr5:129106395-129106439	NR_015517:146	5930412G12Rik	INSIDE	0.872	0.640	846.04	541.27	0.558	667.89	372.70
A_68_P24925496	chr6:145814867-145814912	NM_024469:-1029	Bhlhe41	PROMOTER	0.872	0.637	1531.95	975.27	0.555	1233.23	685.00
A_68_P27839286	chr11:59653097-59653142	NM_011991:150	Cops3	INSIDE	0.872	0.543	1527.69	830.07	0.474	1156.18	547.89
A_68_P30361555	chr15:78502500-78502544	NM_183141:46021	Elfn2	INSIDE	0.872	2.885	447.59	1291.39	2.515	372.33	936.37
A_68_P31116775	chr17:27639850-27639894	NM_001013385:377	Grm4	INSIDE	0.872	1.946	1504.02	2926.97	1.697	1096.70	1861.37
A_68_P29619757	chr14:56381299-56381343	NM_020490:1056	Ltb4r2	INSIDE	0.872	0.677	1255.29	849.54	0.590	1015.33	599.05
A_68_P32181858	chr19:53404585-53404629	NM_001008543:-329	Mxi1	PROMOTER	0.872	2.460	4597.46	11311.27	2.145	3146.55	6750.54
A_68_P32143068	chr19:46379305-46379349	NM_019408:-858	Nfkb2	PROMOTER	0.872	0.497	1151.85	572.46	0.433	953.31	413.09
A_68_P20454943	chr1:95239662-95239706	NM_080850:-319	Pask	DIVERGENT_PROMOTER	0.872	0.699	2110.67	1475.09	0.609	1597.99	973.57
A_68_P27796193	chr11:51671506-51671550	NM_199299:-545	Phf15	PROMOTER	0.872	1.654	4153.28	6869.35	1.443	3366.99	4858.72
A_68_P30447284	chr15:93333655-93333701	NM_001033217:92644	Prickle1	INSIDE	0.872	2.194	1071.72	2351.23	1.914	890.92	1704.81
A_68_P24155045	chr5:143874478-143874522	NM_080561:199	Rnf216	INSIDE	0.872	1.614	1402.68	2264.03	1.408	1365.53	1923.04
A_68_P25086971	chr7:51608782-51608826	NM_001034115:43171	Shank1	INSIDE	0.872	1.675	1856.04	3109.02	1.461	1463.80	2138.35
A_68_P31349750	chr17:74396973-74397017	NM_053188:262	Srd5a2	INSIDE	0.872	0.443	1808.29	800.22	0.386	1424.46	549.98
A_68_P22889660	chr4:46626863-46626907	NM_198664:36187	Tbc1d2	INSIDE	0.872	3.262	795.20	2593.92	2.845	690.76	1965.00
A_68_P27288944	chr10:80795734-80795778	NM_009325:4281	Tbxa2r	INSIDE	0.872	2.451	3048.99	7472.80	2.137	2148.70	4591.81
A_68_P20066645	chr1:19204117-19204161	NM_001025305:2004	Tcfap2b	INSIDE	0.872	2.066	3565.75	7367.77	1.801	2815.05	5069.63
A_68_P20620974	chr1:134257507-134257551	NM_178874:30330	Tmcc2	INSIDE	0.872	5.327	1974.48	10518.96	4.646	1297.05	6026.06
A_68_P29455105	chr14:22650386-22650430	NM_011695:-374	Vdac2	PROMOTER	0.872	2.870	2625.64	7534.59	2.504	2167.00	5425.31
A_68_P25003662	chr7:24919226-24919270	NM_019941:67	Zfp235	INSIDE	0.872	0.651	1428.14	930.36	0.568	1281.49	727.82
A_68_P27268625	chr10:76978607-76978651	NM_133998:-70	1810008A18Rik	PROMOTER	0.871	0.632	870.27	550.25	0.551	736.48	405.68
A_68_P24153993	chr5:143667831-143667875	NM_007393:551	Actb	INSIDE	0.871	0.429	3209.67	1378.50	0.374	2907.59	1087.34
A_68_P21866711	chr2:172765860-172765904	NM_007557:-88	Bmp7	PROMOTER	0.871	1.565	2928.19	4583.07	1.364	2096.07	2858.44
A_68_P26445781	chr9:40686287-40686331	NM_178245:4099	Bsx	DOWNSTREAM	0.871	0.413	1713.08	706.96	0.360	1469.31	528.30
A_68_P31933967	chr19:6320701-6320745	NM_001033342:14266	Cdc42bpg	INSIDE	0.871	1.835	720.74	1322.88	1.598	573.85	917.16
A_68_P23363270	chr4:140865058-140865102	NM_010139:7926	Epha2	INSIDE	0.871	3.984	1655.48	6595.09	3.471	1201.84	4171.69
A_68_P29287623	chr13:104710322-104710366	NM_001005868:250	Erbb2ip	INSIDE	0.871	0.677	1248.07	845.51	0.590	1128.33	665.73
A_68_P20897124	chr1:186551680-186551724	NM_008250:4670	Hlx	INSIDE	0.871	0.606	1000.50	606.02	0.527	837.16	441.43
A_68_P29138729	chr13:73409301-73409345	NM_018885:11378	Irx4	DOWNSTREAM	0.871	0.585	1699.06	994.40	0.510	1628.36	829.90
A_68_P20025041	chr1:9957764-9957808	NM_145692:41415	Lrrc67	DOWNSTREAM	0.871	0.609	2970.43	1809.75	0.531	2503.54	1328.63
A_68_P30370810	chr15:80042202-80042246	NM_010795:38074	Mgat3	INSIDE	0.871	2.058	719.66	1480.88	1.791	530.71	950.66
A_68_P24053561	chr5:123479352-123479396	NM_175423:14292	Orai1	INSIDE	0.871	1.968	581.61	1144.85	1.715	445.50	764.19
A_68_P24176179	chr5:148674196-148674240	NM_025624:2015	Pomp	INSIDE	0.871	2.050	1275.08	2613.68	1.786	907.28	1620.27
A_68_P24991726	chr7:19735138-19735182	NM_026943:-26	Snrpd2	DIVERGENT_PROMOTER	0.871	0.725	3973.23	2880.75	0.632	2969.44	1876.17
A_68_P29030714	chr13:51196855-51196899	NM_146043:610	Spin1	INSIDE	0.871	0.525	1982.85	1041.34	0.457	1672.65	765.19
A_68_P27540232	chr10:127669379-127669423	NM_011589:-5721	Timeless	PROMOTER	0.871	3.062	436.90	1337.93	2.667	404.36	1078.51
A_68_P22200383	chr3:65331975-65332019	NM_178892:-372	Tiparp	PROMOTER	0.871	0.627	923.82	578.98	0.546	882.28	481.56
A_68_P24076592	chr5:127723010-127723054	NM_175432:837	Tmem132c	INSIDE	0.871	0.387	1582.26	611.72	0.337	1427.04	480.36
A_68_P23610768	chr5:37358352-37358396	NM_011716:21847	Wfs1	INSIDE	0.871	1.656	1316.95	2180.30	1.442	949.83	1370.11
A_68_P25008233	chr7:25862458-25862502	NM_175477:216	Zfp574	INSIDE	0.871	0.392	1481.03	580.40	0.341	1130.08	385.78
A_68_P25505624	chr7:134588136-134588180	NM_175163:4514	Zfp689	INSIDE	0.871	2.485	1382.72	3435.98	2.165	1050.76	2274.70
A_68_P32554229	chrX:96412142-96412186			Unknown	0.871	2.003	774.08	1550.49	1.744	446.97	779.67
A_68_P30575402	chr16:17734359-17734403			Unknown	0.871	2.173	417.98	908.32	1.893	407.78	771.86
A_68_P24015106	chr5:116894713-116894757	NR_015595:6004	2410137F16Rik	INSIDE	0.870	1.855	751.77	1394.82	1.615	588.51	950.44
A_68_P20872229	chr1:181734124-181734173	NM_026375:-2	Ahctf1	PROMOTER	0.870	0.632	969.51	612.75	0.550	722.46	397.46
A_68_P27383825	chr10:98377784-98377828	NM_026482:21	Atp2b1	INSIDE	0.870	2.508	706.86	1772.64	2.183	598.46	1306.38
A_68_P25374661	chr7:108812468-108812512	NM_009191:209	Clpb	INSIDE	0.870	0.567	1128.62	639.93	0.493	963.78	475.32

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27479308	chr10:116511163-116511209	NM_177798:74344	Frs2	INSIDE	0.870	1.872	641.53	1201.21	1.629	554.31	902.71
A_68_P25724985	chr8:26149132-26149176	NM_001081187:280	Htra4	INSIDE	0.870	2.906	777.34	2258.56	2.528	736.51	1862.15
A_68_P27987931	chr11:86070791-86070835	NM_027421:258	Ints2	INSIDE	0.870	0.667	1556.45	1037.85	0.580	1345.03	780.48
A_68_P30366728	chr15:79316188-79316232	NM_008427:19461	Kcnj4	INSIDE	0.870	2.719	1525.52	4148.39	2.366	1088.64	2575.47
A_68_P29865207	chr14:103745609-103745653	NM_207215:387	Mycbp2	INSIDE	0.870	0.620	2462.07	1527.23	0.540	2071.53	1117.82
A_68_P27897405	chr11:69647501-69647545	NM_198862:829	Nlgn2	INSIDE	0.870	1.934	703.79	1361.32	1.682	582.86	980.53
A_68_P22325408	chr3:90269752-90269796	NM_008727:14	Npr1	INSIDE	0.870	0.602	1107.03	666.74	0.524	1072.52	562.03
A_68_P27614818	chr11:17111314-17111358	NM_025443:256	Pno1	INSIDE	0.870	0.709	2298.36	1628.53	0.616	1845.26	1136.89
A_68_P24795626	chr6:119852843-119852887	NM_001166383:149	Rad52	INSIDE	0.870	0.686	1194.88	820.04	0.597	1143.92	683.17
A_68_P25091259	chr7:52379751-52379795	NM_013725:-13	Rps11	PROMOTER	0.870	0.575	1341.90	771.36	0.500	984.21	491.94
A_68_P22488493	chr3:123211082-123211126	NR_028573:-120	Snora24	PROMOTER	0.870	0.626	1027.43	642.68	0.545	877.38	477.74
A_68_P31155256	chr17:34817442-34817486	NM_031176:9985	Tnxb	INSIDE	0.870	1.717	900.21	1545.81	1.494	764.78	1142.74
A_68_P25614228	chr8:3496226-3496270	NM_080461:3111	Zfp358	INSIDE	0.870	1.935	571.83	1106.36	1.683	458.61	772.03
A_68_P32975995	chr12:18394467-18394511	ENSMUST00000080502:-72		PROMOTER	0.870	2.392	608.84	1456.18	2.081	630.39	1312.15
A_68_P28854600	chr13:18084983-18085027	NM_025904:181	1600012F09Rik	INSIDE	0.869	0.701	1274.65	894.08	0.609	1057.37	644.15
A_68_P27282332	chr10:79767774-79767818	NM_011789:3232	Apc2	INSIDE	0.869	2.388	3656.87	8733.89	2.076	2699.25	5604.91
A_68_P28046785	chr11:96650631-96650675	NM_007622:203	Cbx1	INSIDE	0.869	0.494	1413.61	698.11	0.429	1106.79	474.91
A_68_P21708093	chr2:144425785-144425829	NM_025314:118	Dtd1	INSIDE	0.869	0.681	1069.50	727.94	0.591	925.92	547.53
A_68_P31424357	chr17:88039524-88039571	NM_008532:4229	Epcam	INSIDE	0.869	2.625	372.84	978.86	2.281	387.07	883.04
A_68_P26421276	chr9:35018562-35018606	NM_172291:-74	Foxred1	DIVERGENT_PROMOTER	0.869	0.437	1548.43	676.67	0.380	1250.58	475.02
A_68_P21753005	chr2:152934198-152934242	NM_001172117:17	Hck	INSIDE	0.869	0.599	914.05	547.48	0.520	830.11	432.03
A_68_P21722291	chr2:146910728-146910772	NM_023504:331	Nkx2-4	INSIDE	0.869	2.664	751.97	2003.09	2.314	707.09	1635.90
A_68_P30542115	chr16:10411996-10412040	NM_011955:-12	Nubp1	PROMOTER	0.869	0.668	944.17	631.01	0.581	860.32	499.49
A_68_P21089695	chr2:28061711-28061755	NM_001038612:524	Olfm1	INSIDE	0.869	1.627	1541.35	2507.71	1.415	1384.94	1959.01
A_68_P21870540	chr2:173411809-173411854	NR_027957:73209	Ppp4r1l-ps	INSIDE	0.869	2.777	309.12	858.50	2.414	214.41	517.69
A_68_P31735661	chr18:57522721-57522765	NM_028447:8356	Prrc1	INSIDE	0.869	2.775	1221.69	3390.28	2.413	805.85	1944.21
A_68_P27898299	chr11:69795072-69795116	NM_018740:-357	Rai12	PROMOTER	0.869	0.483	1406.71	679.02	0.420	1215.32	509.86
A_68_P24939590	chr6:148303285-148303329	NR_003634:129	Rps4y2	INSIDE	0.869	1.918	1410.21	2704.71	1.666	1243.03	2070.60
A_68_P26569718	chr9:62129773-62129817	NM_025721:192	Spesp1	INSIDE	0.869	2.798	575.89	1611.10	2.430	502.60	1221.21
A_68_P30506930	chr16:3872290-3872334	NM_001033159:62	Zfp597	INSIDE	0.869	2.310	5535.65	12789.94	2.008	4065.17	8162.34
A_68_P26640510	chr9:74697051-74697095	ENSMUST00000160842:271		INSIDE	0.869	1.670	1508.71	2518.81	1.451	1391.82	2019.66
A_68_P20146384	chr1:36160417-36160461	NM_015818:35194	Hs6st1	INSIDE	0.868	1.963	978.06	1920.18	1.704	850.90	1449.85
A_68_P21812072	chr2:163201808-163201852	NM_021566:21879	Jph2	INSIDE	0.868	2.466	744.13	1835.07	2.140	751.71	1608.81
A_68_P21078908	chr2:26321156-26321200	NM_008714:38164	Notch1	INSIDE	0.868	1.835	1854.93	3403.59	1.592	1521.03	2421.85
A_68_P27209838	chr10:66558947-66558991	NM_001204915:768	Reep3	INSIDE	0.868	0.655	1130.56	740.18	0.569	906.29	515.27
A_68_P24085132	chr5:129288040-129288085	NM_001081388:171175	Rimbp2	INSIDE	0.868	2.478	919.33	2278.16	2.150	759.17	1632.17
A_68_P30642390	chr16:30550650-30550694	NM_172614:-8	Tmem44	PROMOTER	0.868	5.105	435.99	2225.66	4.433	505.33	2240.22
A_68_P25029338	chr7:30768885-30768929	NM_001033355:-67	Zfp568	PROMOTER	0.868	1.929	615.79	1187.88	1.674	555.88	930.78
A_68_P22061573	chr3:36962572-36962616	NM_009350:17	Adad1	INSIDE	0.867	2.272	469.16	1066.08	1.971	460.17	906.95
A_68_P27334199	chr10:89512717-89512765	NM_001128086:176487	Anks1b	INSIDE	0.867	2.633	2012.36	5298.50	2.284	1533.30	3501.44
A_68_P26569974	chr9:62191922-62191966	NM_009672:2795	Anp32a	INSIDE	0.867	1.922	1060.27	2037.41	1.666	813.61	1355.70
A_68_P25601077	chr7:150645470-150645514	NM_001161624:1463	Cdkn1c	INSIDE	0.867	2.175	346.17	752.85	1.886	327.91	618.38
A_68_P24631555	chr6:90259775-90259819	NM_027928:15383	Chst13	INSIDE	0.867	2.598	454.40	1180.42	2.252	499.07	1123.66
A_68_P26141977	chr8:109417130-109417174	NM_145412:341	Chtf8	INSIDE	0.867	1.566	4050.16	6344.42	1.357	3176.69	4312.33
A_68_P26813992	chr9:108165850-108165894	NM_010017:195	Dag1	INSIDE	0.867	4.360	4840.93	21107.51	3.782	3687.16	13944.75
A_68_P28431897	chr12:52930027-52930071	NM_144788:475	Hectd1	INSIDE	0.867	0.586	2107.41	1235.91	0.509	1887.39	959.89
A_68_P23088446	chr4:87678217-87678261	NM_027326:1073	Mllt3	INSIDE	0.867	1.911	9013.93	17224.68	1.656	5695.10	9432.97
A_68_P28621836	chr12:90498827-90498871	NM_172544:307015	Nrxn3	INSIDE	0.867	2.348	1035.06	2430.21	2.035	841.98	1713.61
A_68_P30397622	chr15:84754271-84754315	NM_016714:435	Nup50	INSIDE	0.867	0.701	1818.50	1275.42	0.608	1451.79	883.20
A_68_P27553886	chr11:3661741-3661785	NM_152818:102144	Osbp2	INSIDE	0.867	0.611	973.22	594.88	0.530	773.97	410.38
A_68_P31951137	chr19:10599680-10599724	NM_025333:-3	Sdhaf2	DIVERGENT_PROMOTER	0.867	0.595	2108.23	1255.39	0.516	1676.01	865.31

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31197209	chr17:44913929-44913973	NM_178652:-169	Supt3h	PROMOTER	0.867	0.694	1209.12	838.88	0.602	1110.31	667.90
A_68_P25264700	chr7:87226640-87226684	NM_175433:55549	Zfp710	INSIDE	0.867	5.599	2146.15	12015.37	4.854	1439.13	6985.40
A_68_P21041402	chr2:18688499-18688543	ENSMUST00000119424:7910		DOWNSTREAM	0.867	0.662	1346.87	891.74	0.574	911.08	523.20
A_68_P30280956	chr15:64144021-64144065	NM_010026:70439	Asap1	INSIDE	0.866	0.518	1540.98	798.96	0.449	1183.54	531.62
A_68_P31155037	chr17:34784214-34784258	NM_017406:112	Atf6b	INSIDE	0.866	0.636	1437.71	914.68	0.551	1213.68	668.46
A_68_P27566548	chr11:5966021-5966065	NM_001174053:-291	Camk2b	PROMOTER	0.866	0.565	1963.07	1108.52	0.489	1621.10	792.99
A_68_P24011288	chr5:116182625-116182669	NM_001080808:-1078	Ccdc64	PROMOTER	0.866	0.458	2056.27	941.30	0.396	1749.99	693.52
A_68_P32467106	chrX:71500485-71500529	NM_007927:329	Emd	INSIDE	0.866	2.166	688.32	1491.24	1.875	524.65	983.86
A_68_P23323334	chr4:134090623-134090667	NM_029759:-1977	Fam54b	PROMOTER	0.866	4.102	229.87	942.85	3.552	284.84	1011.86
A_68_P23792662	chr5:72978528-72978572	NM_001024147:239	Gm5868	INSIDE	0.866	1.574	4410.48	6944.21	1.363	3337.78	4550.13
A_68_P32040189	chr19:27397675-27397720	NM_183179:589	Kcnv2	INSIDE	0.866	2.631	288.53	759.26	2.279	222.11	506.17
A_68_P27897481	chr11:69659900-69659944	NM_023564:-196	Plscr3	PROMOTER	0.866	0.429	2485.48	1066.58	0.372	1987.56	738.94
A_68_P28671531	chr12:99927688-99927737	NM_011877:45143	Ptpn21	INSIDE	0.866	2.361	1448.94	3420.54	2.044	1165.78	2382.44
A_68_P31862860	chr18:80389507-80389558	NM_199197:7826	Rbfa	INSIDE	0.866	3.521	778.32	2740.13	3.050	657.44	2005.38
A_68_P29434939	chr14:18492981-18493025	NM_001113417:-471	Thrb	PROMOTER	0.866	2.355	1553.79	3658.48	2.039	1308.39	2667.18
A_68_P31403195	chr17:84586228-84586272	NM_001001806:1037	Zfp36l2	INSIDE	0.866	2.433	509.64	1239.84	2.107	482.28	1016.21
A_68_P32126393	chr19:43502105-43502149			Unknown	0.866	3.073	586.60	1802.37	2.662	528.52	1406.92
A_68_P31305847	chr17:66728898-66728942	NM_001114098:70170	1110012J17Rik	INSIDE	0.865	2.267	1452.35	3291.76	1.960	1052.98	2064.32
A_68_P23315717	chr4:132641057-132641101	NM_146155:73658	Ahdc1	DOWNSTREAM	0.865	0.611	1018.31	621.88	0.528	885.12	467.45
A_68_P24460753	chr6:53989704-53989748	NM_001163640:-199	Chn2	PROMOTER	0.865	0.558	1024.92	572.28	0.483	865.45	417.93
A_68_P28038132	chr11:95198164-95198208	NM_172543:-145	Fam117a	PROMOTER	0.865	0.656	891.88	585.28	0.567	769.31	436.55
A_68_P26227387	chr8:124078337-124078381	NM_133765:24348	Fbxo31	INSIDE	0.865	2.490	548.54	1366.02	2.153	472.00	1016.38
A_68_P24863967	chr6:134819942-134819986	NM_001167697:17913	Gpr19	INSIDE	0.865	3.536	676.30	2391.39	3.059	536.40	1641.09
A_68_P30363243	chr15:78758427-78758471	NM_008495:1294	Lgals1	INSIDE	0.865	0.692	1760.21	1218.25	0.599	1375.37	823.36
A_68_P25266277	chr7:87508028-87508072	NM_172903:8211	Man2a2	INSIDE	0.865	1.912	1932.47	3694.81	1.654	1330.30	2200.65
A_68_P20168276	chr1:39957440-39957484	NM_008696:-295	Map4k4	PROMOTER	0.865	2.016	752.92	1518.24	1.745	589.78	1029.15
A_68_P21731906	chr2:148558116-148558160	NM_019632:18	Napb	INSIDE	0.865	0.573	972.05	556.92	0.496	804.00	398.66
A_68_P29998112	chr15:8059193-8059237	NM_133227:-98	Nup155	PROMOTER	0.865	1.706	3614.97	6165.40	1.475	2486.84	3666.92
A_68_P27137646	chr10:52137376-52137420	NM_030250:46	Nus1	INSIDE	0.865	2.089	13326.36	27839.76	1.807	9593.03	17333.46
A_68_P27080349	chr10:39452815-39452859	NM_011264:871	Rev3l	INSIDE	0.865	0.688	2277.62	1566.19	0.594	1867.17	1110.00
A_68_P27034632	chr10:29081402-29081446	NM_001110196:824	Rnf146	INSIDE	0.865	0.631	993.92	626.90	0.545	766.87	418.15
A_68_P20233541	chr1:53841640-53841684	NM_133810:397	Stk17b	INSIDE	0.865	0.730	2383.44	1739.64	0.632	1961.17	1238.69
A_68_P23974101	chr5:109204043-109204087	NM_026109:20318	Tmed11	DOWNSTREAM	0.865	1.652	1295.03	2139.48	1.429	1013.24	1448.21
A_68_P27285909	chr10:80318182-80318226	NM_175195:185	3110056O03Rik	INSIDE	0.864	0.673	1710.84	1151.81	0.582	1581.99	919.98
A_68_P23320878	chr4:133628753-133628797	NM_001162970:4408	Aim1l	INSIDE	0.864	2.216	583.81	1293.70	1.915	433.60	830.45
A_68_P22384844	chr3:102975721-102975767	NM_026602:111	Bcas2	INSIDE	0.864	2.678	1801.70	4825.71	2.314	1251.85	2897.17
A_68_P21646235	chr2:133380368-133380412	NM_007553:1456	Bmp2	INSIDE	0.864	0.583	977.78	570.09	0.504	846.56	426.65
A_68_P28752828	chr12:114067098-114067142	NM_028023:480	Cdca4	INSIDE	0.864	0.482	1426.83	687.84	0.416	1138.69	474.11
A_68_P27091225	chr10:41529755-41529799	NM_026643:-340	Cep57l1	DIVERGENT_PROMOTER	0.864	0.600	1175.86	705.05	0.518	947.80	491.12
A_68_P28727387	chr12:109572709-109572753	NM_010010:140	Cyp46a1	INSIDE	0.864	0.563	1057.15	595.44	0.487	838.21	407.83
A_68_P27288015	chr10:80655147-80655191	NM_007828:8506	Dapk3	INSIDE	0.864	2.019	530.06	1070.21	1.744	459.21	800.82
A_68_P27010233	chr10:24431686-24431730	NM_008813:200	Enpp1	INSIDE	0.864	0.582	898.67	523.34	0.503	737.01	370.83
A_68_P23979399	chr5:110816208-110816252	NM_028596:-84	Fbrsl1	PROMOTER	0.864	0.474	2198.19	1042.00	0.409	2037.86	834.46
A_68_P25360746	chr7:106416588-106416632	NM_001043355:-245	Mtap6	PROMOTER	0.864	0.403	1499.45	603.65	0.348	1209.16	420.36
A_68_P29585968	chr14:48741266-48741310	NM_033602:745	Peli2	INSIDE	0.864	0.511	1200.44	613.88	0.442	970.72	428.93
A_68_P25957707	chr8:74119888-74119932	NM_025396:3828	Pgls	INSIDE	0.864	0.534	1028.05	548.84	0.461	842.82	388.84
A_68_P27278630	chr10:79202255-79202299	NM_172551:7050	Polrmt	INSIDE	0.864	2.175	1523.33	3313.29	1.880	1322.72	2486.57
A_68_P29094163	chr13:63665381-63665425	NM_008957:1426	Ptch1	INSIDE	0.864	3.866	2665.74	10306.10	3.342	2275.36	7604.04
A_68_P21843351	chr2:168581527-168581571	NM_175303:11153	Sall4	INSIDE	0.864	2.183	1411.67	3082.28	1.887	1177.17	2221.12
A_68_P31254021	chr17:56263845-56263889	NM_013662:9409	Sema6b	INSIDE	0.864	1.765	3571.74	6303.56	1.526	2749.03	4193.97
A_68_P29033146	chr13:51662912-51662956	NM_009167:-481	Shc3	PROMOTER	0.864	0.604	1315.45	794.00	0.521	1143.06	596.03

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P30365306	chr15:79082860-79082904	NM_020516:2296	Slc16a8	INSIDE	0.864	0.674	3452.16	2328.32	0.583	2664.63	1552.29
A_68_P25615132	chr8:3679365-3679411	NM_025701:2912	Trappc5	INSIDE	0.864	2.767	2312.31	6398.75	2.391	1616.14	3864.83
A_68_P33005881	A_68_P33005881			Unknown	0.864	5.045	224.46	1132.42	4.361	240.95	1050.77
A_68_P24059257	chr5:124539964-124540008	NM_019875:5821	Abcb9	INSIDE	0.863	2.442	1177.91	2876.12	2.107	1098.29	2313.69
A_68_P32537858	chrX:91457905-91457949	NM_012010:64	Eif2s3x	INSIDE	0.863	0.482	1417.76	682.90	0.416	677.42	281.73
A_68_P29616395	chr14:55732380-55732424	NM_177049:3370	Jph4	INSIDE	0.863	2.378	761.34	1810.68	2.053	727.62	1493.48
A_68_P32140679	chr19:45890150-45890194	NM_030716:121	Kcnip2	INSIDE	0.863	0.660	1257.68	829.55	0.569	1000.64	569.67
A_68_P28748396	chr12:113414015-113414059	NM_001097621:29618	Kif26a	INSIDE	0.863	2.982	738.34	2201.80	2.573	630.81	1622.77
A_68_P23239265	chr4:117933690-117933734	NM_011213:30290	Ptprf	INSIDE	0.863	0.676	1220.85	825.76	0.584	1055.65	616.17
A_68_P29152216	chr13:76081085-76081129	NM_028493:166	Rhobtb3	INSIDE	0.863	3.071	393.94	1209.74	2.649	372.43	986.72
A_68_P27550645	chr11:3093025-3093069	NM_030207:420	Sfi1	INSIDE	0.863	2.657	3840.67	10202.87	2.292	3585.25	8218.46
A_68_P30486391	chr15:100382046-100382090	NM_033476:310	Tcfcp2	INSIDE	0.863	0.622	839.69	522.17	0.536	645.18	346.06
A_68_P31117188	chr17:27702491-27702536	NM_001002895:159	AI413582	INSIDE	0.862	0.669	2941.84	1966.87	0.576	2225.21	1282.22
A_68_P21084957	chr2:27331585-27331629	NM_001113573:-413	Brd3	PROMOTER	0.862	0.535	1220.39	652.99	0.461	1115.33	514.51
A_68_P27263161	chr10:76086105-76086149	NM_146007:23	Col6a2	INSIDE	0.862	0.675	1095.32	739.87	0.582	956.65	557.12
A_68_P21147280	chr2:38142625-38142669	NM_146122:258	Dennd1a	INSIDE	0.862	0.600	1210.04	726.29	0.517	1055.70	546.27
A_68_P25592835	chr7:149268541-149268585	NM_008748:12627	Dusp8	INSIDE	0.862	2.225	686.48	1527.55	1.918	583.18	1118.37
A_68_P29702363	chr14:70999406-70999450	NM_194345:214	Fam160b2	INSIDE	0.862	0.582	1373.34	799.81	0.502	1073.83	538.91
A_68_P31166958	chr17:37183624-37183668	NM_019439:736	Gabbr1	INSIDE	0.862	2.582	10540.70	27217.56	2.225	8596.64	19130.09
A_68_P25954497	chr8:73376700-73376744	NM_032397:4185	Kcnn1	INSIDE	0.862	2.851	844.45	2407.94	2.457	691.33	1698.61
A_68_P25965605	chr8:75876686-75876730	NM_010687:-253	Large	PROMOTER	0.862	1.822	715.09	1302.66	1.571	605.54	951.04
A_68_P27553118	chr11:3549344-3549388	NM_001159288:-130	Morc2a	DIVERGENT_PROMOTER	0.862	0.675	1298.75	876.60	0.582	1111.55	646.43
A_68_P28535274	chr12:74147686-74147730	NM_009189:-9	Six1	PROMOTER	0.862	0.564	967.81	545.74	0.486	773.62	376.19
A_68_P29614998	chr14:55531700-55531745	NM_021551:247	Slc22a17	INSIDE	0.862	0.478	1541.79	737.13	0.412	1268.62	522.54
A_68_P27926649	chr11:75344957-75345001	NM_001199284:-217	Slc43a2	PROMOTER	0.862	0.677	1204.16	815.63	0.584	1080.83	630.75
A_68_P23974102	chr5:109204136-109204181	NM_026109:20224	Tmed11	DOWNSTREAM	0.862	2.279	1522.98	3471.45	1.964	1217.50	2390.84
A_68_P29734163	chr14:76904251-76904295	NM_009366:-44	Tsc22d1	PROMOTER	0.862	4.053	453.91	1839.76	3.494	412.43	1440.98
A_68_P25422111	chr7:119166689-119166733	NM_133758:-309	Usp47	PROMOTER	0.862	0.616	1440.36	887.33	0.531	1231.18	653.80
A_68_P23618264	chr5:38611351-38611395	NM_029162:295	Zbtb49	INSIDE	0.862	0.537	1030.61	553.08	0.463	897.33	415.34
A_68_P25505910	chr7:134655663-134655707	NR_024331:699	1700008J07Rik	INSIDE	0.861	0.603	1478.46	891.50	0.519	1091.06	566.18
A_68_P27843665	chr11:60351464-60351508	NM_172943:302	Alkbh5	INSIDE	0.861	0.585	1060.51	620.83	0.504	949.99	478.84
A_68_P32260350	chrX:11665796-11665840	NM_029510:-8139	Bcor	PROMOTER	0.861	0.664	2642.39	1754.42	0.571	1099.84	628.48
A_68_P20879817	chr1:183081001-183081045	NM_030131:-39	Cnih4	DIVERGENT_PROMOTER	0.861	0.493	1223.51	603.35	0.425	994.95	422.69
A_68_P28252839	chr12:14156651-14156695	NM_029007:2172	Fam84a	INSIDE	0.861	0.515	1109.64	571.95	0.444	864.02	383.58
A_68_P29257131	chr13:99125652-99125696	NM_008242:1475	Foxd1	INSIDE	0.861	2.196	509.92	1119.72	1.890	504.29	953.04
A_68_P26346080	chr9:21037928-21037972	NM_001110305:5826	Keap1	INSIDE	0.861	2.667	1873.44	4996.52	2.297	1432.17	3289.01
A_68_P28457817	chr12:57714096-57714140	NM_008701:153	Nkx2-9	INSIDE	0.861	0.572	2049.69	1173.40	0.493	1703.93	840.33
A_68_P21330231	chr2:73052613-73052657	NM_025942:-130	Ola1	PROMOTER	0.861	0.495	1184.56	586.20	0.426	1058.44	451.18
A_68_P31626770	chr18:37181577-37181621	NM_138663:1715	Pcdha12	INSIDE	0.861	2.661	2239.57	5959.38	2.292	1631.79	3739.29
A_68_P23524646	chr5:20692316-20692360	NM_175437:254	Pion	INSIDE	0.861	0.479	1213.94	580.90	0.412	1058.15	436.01
A_68_P24048831	chr5:122608072-122608116	NM_013636:-193	Ppp1cc	PROMOTER	0.861	2.329	2513.96	5854.58	2.005	1968.99	3948.16
A_68_P27541974	chr10:127985891-127985935	NM_018860:312	Rpl41	INSIDE	0.861	0.625	1295.97	809.64	0.538	1060.02	570.51
A_68_P31236341	chr17:51972574-51972618	NM_009122:-624	Satb1	PROMOTER	0.861	3.362	5547.79	18650.42	2.894	3728.12	10789.18
A_68_P23608244	chr5:36873039-36873083	NM_001113364:212	Tbc1d14	INSIDE	0.861	0.570	2108.24	1200.69	0.491	1502.24	736.99
A_68_P28056086	chr11:98245656-98245700	NM_011540:554	Tcap	INSIDE	0.861	2.341	853.14	1997.03	2.016	813.78	1640.91
A_68_P30499468	chr15:102567952-102567997			Unknown	0.861	3.069	665.93	2043.72	2.644	536.00	1417.14
A_68_P24059258	chr5:124540048-124540092	NM_019875:5737	Abcb9	INSIDE	0.860	2.457	1068.28	2624.29	2.114	836.79	1768.74
A_68_P31150484	chr17:33918191-33918235	NM_020581:308	Angptl4	INSIDE	0.860	2.064	494.04	1019.60	1.776	438.62	778.93
A_68_P27282339	chr10:79769158-79769202	NM_011789:4616	Apc2	INSIDE	0.860	2.443	696.68	1702.32	2.101	584.60	1228.42
A_68_P27649728	chr11:24064796-24064840	NM_001159290:84124	Bcl11a	INSIDE	0.860	3.468	1557.72	5402.52	2.982	1297.95	3869.99
A_68_P27228312	chr10:69652108-69652156	NM_001111121:92264	Ccdc6	INSIDE	0.860	2.172	1173.43	2548.98	1.868	848.88	1585.30

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25020879	chr7:29052937-29052981	NM_198425:59	Eid2	INSIDE	0.860	2.398	357.60	857.40	2.061	381.94	787.23
A_68_P30143282	chr15:37209352-37209396	NM_026496:46584	Grhl2	INSIDE	0.860	2.500	888.49	2220.80	2.150	684.71	1472.40
A_68_P24757356	chr6:113027164-113027208	NR_027010:52	Gt(ROSA)26Sor	INSIDE	0.860	0.610	1608.19	981.46	0.525	1360.97	714.57
A_68_P29071675	chr13:58230317-58230361	NM_029872:-421	Hnrnpa0	PROMOTER	0.860	0.566	1796.97	1017.54	0.487	1390.70	677.54
A_68_P25285287	chr7:91031249-91031293	NM_030705:1581	Mesdc1	INSIDE	0.860	2.020	702.60	1419.45	1.738	608.80	1057.89
A_68_P28271087	chr12:17551396-17551440	NM_013614:-260	Odc1	PROMOTER	0.860	0.499	1445.62	720.84	0.429	1132.70	485.94
A_68_P21839462	chr2:167924551-167924595	NM_021409:18069	Pard6b	INSIDE	0.860	1.955	1069.93	2091.43	1.681	912.64	1534.16
A_68_P23292757	chr4:128404849-128404893	NM_001195083:56	Phc2	INSIDE	0.860	2.914	468.62	1365.77	2.507	466.18	1168.57
A_68_P21310712	chr2:69561046-69561090	NM_001081086:-76	Ppig	PROMOTER	0.860	0.605	2280.49	1379.01	0.520	2161.66	1124.24
A_68_P28079343	chr11:102261298-102261342	NM_016759:6572	Rundc3a	INSIDE	0.860	0.655	1834.44	1201.25	0.563	1363.32	768.14
A_68_P26373636	chr9:26837227-26837271	NM_178027:431	Vps26b	INSIDE	0.860	2.361	1430.79	3378.08	2.030	1203.36	2442.82
A_68_P21844027	chr2:168719744-168719788	ENSMUST00000029064:32614		INSIDE	0.860	2.017	839.57	1693.36	1.734	641.90	1113.18
A_68_P25708988	chr8:23170683-23170727	NM_007511:-158	Atp7b	DIVERGENT_PROMOTER	0.859	0.553	1049.51	580.29	0.475	839.07	398.46
A_68_P30287853	chr15:65618917-65618962	NM_133766:337	Efr3a	INSIDE	0.859	0.626	829.51	519.19	0.537	812.52	436.69
A_68_P20058120	chr1:17082054-17082098	NM_020604:5894	Jph1	INSIDE	0.859	2.270	962.01	2184.10	1.951	918.78	1792.84
A_68_P32029539	chr19:25484768-25484818	NM_181404:173101	Kank1	INSIDE	0.859	4.443	753.30	3346.88	3.818	574.94	2195.28
A_68_P26465910	chr9:43943186-43943230	NM_023061:468	Mcam	INSIDE	0.859	2.819	10155.84	28626.69	2.421	7493.85	18142.66
A_68_P32148599	chr19:47328082-47328126	NM_001163480:24772	Neurl1a	INSIDE	0.859	1.678	1316.91	2209.16	1.440	1266.04	1823.30
A_68_P28029987	chr11:93817170-93817214	NM_001077529:-190	Nme2	PROMOTER	0.859	1.625	2610.77	4242.73	1.396	1878.02	2621.06
A_68_P26144744	chr8:109948750-109948794	NM_026277:166	Nob1	INSIDE	0.859	0.421	1470.13	619.21	0.362	1187.88	429.94
A_68_P23341302	chr4:137237494-137237538	NM_001081155:-101	Rap1gap	PROMOTER	0.859	0.566	1748.81	989.14	0.486	1551.74	753.66
A_68_P20053851	chr1:16083066-16083110	NM_011291:11426	Rpl7	DOWNSTREAM	0.859	0.658	1070.51	704.29	0.565	943.86	533.51
A_68_P32750681	chrX:149204383-149204427	NM_172441:-400	Shroom2	PROMOTER	0.859	2.098	1026.89	2154.88	1.803	516.93	931.88
A_68_P26887824	chr9:122076106-122076150	NM_001164572:49745	Snrk	INSIDE	0.859	1.931	1860.62	3593.32	1.659	1479.83	2454.32
A_68_P31809748	chr18:70631763-70631807	NM_172967:350	4930503L19Rik	INSIDE	0.858	1.613	5722.58	9227.67	1.383	4301.12	5948.33
A_68_P25030928	chr7:31099011-31099055	NM_198027:5261	Alkbh6	INSIDE	0.858	1.653	1482.99	2452.08	1.419	1240.14	1759.16
A_68_P30743455	chr16:48994040-48994084	NM_001110017:163	Dzip3	INSIDE	0.858	0.589	2142.41	1261.15	0.505	1712.68	864.69
A_68_P21338839	chr2:74529632-74529676	NM_013554:-350	Hoxd10	PROMOTER	0.858	0.420	1448.82	607.81	0.360	1203.13	432.87
A_68_P25179904	chr7:72017616-72017660	NM_023239:288	Ndnl2	INSIDE	0.858	1.856	777.85	1444.03	1.592	721.51	1148.69
A_68_P30422875	chr15:88897983-88898032	NM_001002005:7852	Panx2	INSIDE	0.858	2.181	394.11	859.70	1.871	355.02	664.41
A_68_P30346598	chr15:76009831-76009878	NM_201394:16286	Plec	INSIDE	0.858	2.468	1202.31	2967.73	2.118	769.18	1629.25
A_68_P21630923	chr2:130468446-130468490	NM_197945:71	Prosapip1	INSIDE	0.858	0.419	1380.97	579.22	0.360	1169.54	421.11
A_68_P30956060	chr16:90284235-90284280	NM_178923:413	Scaf4	INSIDE	0.858	0.356	1608.69	573.05	0.306	1406.24	429.63
A_68_P31791665	chr18:67561243-67561287	NM_026473:10880	Tubb6	INSIDE	0.858	2.172	1312.00	2849.59	1.863	932.82	1737.67
A_68_P30778638	chr16:55974440-55974484	NR_027965:268	2310061J03Rik	INSIDE	0.857	0.689	1429.28	984.82	0.590	1203.25	710.51
A_68_P27392942	chr10:100051680-100051724	NM_175128:191	4930430F08Rik	INSIDE	0.857	0.464	1322.35	613.97	0.398	1138.39	453.05
A_68_P32260338	chrX:11664552-11664596	NM_029510:-6895	Bcor	PROMOTER	0.857	4.067	589.59	2397.97	3.487	395.53	1379.31
A_68_P28153229	chr11:115255200-115255244	NM_001080929:11993	Cdr2l	INSIDE	0.857	2.854	592.12	1689.69	2.447	503.60	1232.21
A_68_P26521944	chr9:53475433-53475477	NM_001161618:158	Cul5	INSIDE	0.857	0.626	1486.86	931.41	0.537	1258.83	675.56
A_68_P24620322	chr6:88144530-88144574	NM_008090:-4105	Gata2	PROMOTER	0.857	0.551	1524.30	839.79	0.472	1206.36	569.87
A_68_P20553867	chr1:120734448-120734492	NM_001081125:215726	Gli2	INSIDE	0.857	2.089	1154.51	2411.62	1.791	937.81	1679.34
A_68_P23627553	chr5:40035844-40035888	NM_010474:4	Hs3st1	INSIDE	0.857	0.682	1595.87	1087.60	0.584	1269.92	741.66
A_68_P26020980	chr8:87186400-87186444	NM_010499:329	Ier2	INSIDE	0.857	0.680	1543.03	1049.62	0.583	1337.27	779.19
A_68_P27282832	chr10:79844574-79844618	NM_198615:5800	Mex3d	INSIDE	0.857	1.841	736.53	1356.13	1.577	590.65	931.70
A_68_P24009622	chr5:115896965-115897009	NM_008629:17293	Msi1	INSIDE	0.857	7.366	1071.52	7892.92	6.311	817.21	5157.70
A_68_P20638513	chr1:137180458-137180502	NM_001159624:181	Rnpep	INSIDE	0.857	2.543	1798.57	4574.14	2.180	1652.18	3602.14
A_68_P26044786	chr8:91566839-91566883	NM_021390:1201	Sall1	INSIDE	0.857	0.556	1461.98	812.58	0.476	1413.40	673.36
A_68_P21828030	chr2:165980793-165980837	NM_028072:342	Sulf2	INSIDE	0.857	1.862	1114.15	2074.51	1.596	929.39	1483.30
A_68_P20162423	chr1:38893157-38893201	ENSMUST00000147695:-243		PROMOTER	0.857	3.628	416.06	1509.67	3.111	484.68	1507.74
A_68_P32565630	chrX:98989988-98990032	ENSMUST00000149761:-14		PROMOTER	0.857	3.188	412.39	1314.79	2.732	225.07	614.83
A_68_P26575918	chr9:63246657-63246701	NM_027090:373	2300009A05Rik	INSIDE	0.856	0.683	1414.52	966.34	0.585	1239.80	724.90

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P30639252	chr16:30009147-30009191	NR_033631:416	4632428C04Rik	INSIDE	0.856	0.493	1521.23	749.82	0.422	1333.11	562.24
A_68_P24946542	chr7:3597193-3597237	NM_146176:344	Cnot3	INSIDE	0.856	0.544	1575.84	857.01	0.465	1320.71	614.60
A_68_P24798119	chr6:120314850-120314894	NM_145997:756	Kdm5a	INSIDE	0.856	1.785	2405.23	4292.52	1.528	1795.89	2743.81
A_68_P20823477	chr1:172519538-172519582	NM_001109985:420	Nos1ap	INSIDE	0.856	0.347	1929.22	669.04	0.297	1567.61	465.33
A_68_P31632519	chr18:38349196-38349240	NM_029357:20198	Pcdh1	DOWNSTREAM	0.856	1.946	3320.62	6461.51	1.666	2749.08	4580.35
A_68_P20053921	chr1:16095417-16095461	NM_133832:-524	Rdh10	DIVERGENT_PROMOTER	0.856	0.563	3415.37	1923.51	0.482	2715.11	1308.20
A_68_P31846733	chr18:77493478-77493522	NM_013666:68915	St8sia5	INSIDE	0.856	2.862	2168.86	6206.60	2.449	1587.05	3887.18
A_68_P23223139	chr4:114730373-114730417	NM_011527:-1737	Tal1	PROMOTER	0.856	0.612	1326.13	812.06	0.524	983.15	515.62
A_68_P21753656	chr2:153051085-153051129	NM_198617:71	Tspyl3	INSIDE	0.856	0.424	1548.04	656.72	0.363	1319.96	479.20
A_68_P23185613	chr4:106311998-106312042	NM_177667:16967	Ttc22	INSIDE	0.856	2.740	764.15	2093.66	2.344	675.82	1584.07
A_68_P26542619	chr9:57437422-57437466	NM_027895:186	Ulk3	INSIDE	0.856	3.077	416.00	1280.13	2.634	415.67	1094.84
A_68_P21076582	chr2:25994170-25994218	ENSMUST00000163836:128		INSIDE	0.856	2.011	1383.81	2782.70	1.721	919.75	1583.07
A_68_P25956923	chr8:73987625-73987669	NM_022419:-90	Abhd8	DIVERGENT_PROMOTER	0.855	0.504	1212.26	610.67	0.431	968.43	417.06
A_68_P27179425	chr10:60708665-60708712	NM_001081127:27498	Adamts14	INSIDE	0.855	2.165	1076.98	2331.96	1.851	894.61	1655.78
A_68_P31152211	chr17:34256148-34256192	NR_037970:675	Brd2	INSIDE	0.855	0.393	1509.34	592.46	0.336	1100.95	369.38
A_68_P33016565	chr7:3424475-3424519	NM_133183:-926	Cacng6	PROMOTER	0.855	0.553	1337.08	739.42	0.473	1045.67	494.68
A_68_P28313705	chr12:29237270-29237314	NM_001177964:-4090	Dcdc2c	PROMOTER	0.855	2.798	918.74	2570.65	2.392	862.57	2063.52
A_68_P31330058	chr17:71006929-71006973	NM_001128181:95864	Dlgap1	INSIDE	0.855	2.982	884.67	2638.29	2.550	682.15	1739.27
A_68_P26228890	chr8:124308660-124308704	NM_020605:54224	Jph3	INSIDE	0.855	2.364	821.48	1941.71	2.021	861.29	1740.58
A_68_P30495555	chr15:101858847-101858891	NM_010664:222	Krt18	INSIDE	0.855	1.801	1663.54	2995.82	1.539	1474.88	2269.76
A_68_P31921046	chr19:4100132-4100176	NM_008851:-467	Pitpnm1	PROMOTER	0.855	0.711	1414.35	1005.89	0.608	1175.60	714.62
A_68_P23194281	chr4:107704080-107704124	NM_172874:593	Podn	INSIDE	0.855	0.582	2366.65	1376.73	0.497	1898.04	944.02
A_68_P20348982	chr1:74552451-74552495	NM_021383:-161	Rqcd1	PROMOTER	0.855	0.737	3010.16	2218.48	0.630	2287.86	1441.16
A_68_P28038465	chr11:95246295-95246339	NM_016752:81	Slc35b1	INSIDE	0.855	0.647	1047.38	677.99	0.553	830.59	459.71
A_68_P27845266	chr11:60692244-60692288	NM_001168507:274	Tmem11	INSIDE	0.855	1.698	1575.52	2675.32	1.452	1342.62	1949.47
A_68_P29240104	chr13:96106467-96106512	NM_028106:11298	Zbed3	INSIDE	0.855	1.900	1140.12	2166.61	1.624	904.24	1468.80
A_68_P22782196	chr4:23446473-23446517	ENSMUST00000118402:-907		PROMOTER	0.855	1.642	1797.23	2951.03	1.404	1574.11	2210.24
A_68_P20844580	chr1:176767041-176767085	NM_011825:84888	Grem2	INSIDE	0.854	2.054	438.50	900.73	1.753	376.56	660.24
A_68_P22375206	chr3:101254965-101255009	NM_207205:73939	Igsf3	INSIDE	0.854	2.849	1100.20	3134.89	2.434	911.55	2218.99
A_68_P32040193	chr19:27398062-27398106	NM_183179:976	Kcnv2	INSIDE	0.854	1.829	1739.69	3181.31	1.562	1468.65	2293.79
A_68_P23658785	chr5:46247625-46247669	NM_172153:145	Lcorl	INSIDE	0.854	0.516	1728.58	891.40	0.440	1211.96	533.84
A_68_P20156381	chr1:37932438-37932488	NM_001037918:3412	Lipt1	INSIDE	0.854	3.672	252.22	926.06	3.135	263.33	825.43
A_68_P25954899	chr8:73438336-73438380	NM_173013:8486	Mtap1s	INSIDE	0.854	1.857	783.87	1455.67	1.586	694.45	1101.42
A_68_P26313299	chr9:13553619-13553663	NM_023858:16	Mtmr2	INSIDE	0.854	4.163	1367.12	5691.10	3.554	1312.84	4665.26
A_68_P26551406	chr9:58884937-58884981	NM_001042752:-710	Neo1	PROMOTER	0.854	0.640	1026.93	657.37	0.546	887.54	484.94
A_68_P28048724	chr11:96976323-96976367	NM_019507:301	Tbx21	INSIDE	0.854	0.674	1752.22	1180.27	0.575	1391.78	800.84
A_68_P27898022	chr11:69749285-69749329	NM_016875:-94	Ybx2	PROMOTER	0.854	0.546	1369.54	748.35	0.467	1164.06	543.51
A_68_P31620629	chr18:36033105-36033149			Unknown	0.854	0.714	2802.08	2001.29	0.610	2030.93	1238.93
A_68_P31215075	chr17:48073237-48073281	ENSMUST00000117186:220		INSIDE	0.854	1.880	1066.41	2004.71	1.605	799.58	1283.06
A_68_P21436189	chr2:93487479-93487523	NM_007442:4910	Alx4	INSIDE	0.853	2.497	3313.61	8274.14	2.129	2560.96	5451.94
A_68_P28195049	chr12:3427373-3427417	NM_172421:511	Asxl2	INSIDE	0.853	0.590	1462.83	863.10	0.503	1032.21	519.53
A_68_P26235080	chr8:125201697-125201741	NM_001109873:357	Cbfa2t3	INSIDE	0.853	0.579	3420.46	1978.96	0.493	2777.38	1370.29
A_68_P23898564	chr5:93634999-93635043	NM_017367:501	Ccni	INSIDE	0.853	0.572	1274.82	729.16	0.488	1232.65	601.70
A_68_P22324274	chr3:90069716-90069760	NM_201407:-717	Dennd4b	PROMOTER	0.853	2.107	919.58	1937.73	1.797	806.71	1450.05
A_68_P28598114	chr12:85749779-85749823	NM_001026214:179	Entpd5	INSIDE	0.853	0.637	2373.69	1511.16	0.543	1997.86	1085.21
A_68_P26867069	chr9:118468837-118468881	NM_018748:53423	Golga4	INSIDE	0.853	1.727	1827.39	3156.73	1.474	1381.26	2036.50
A_68_P30473865	chr15:98087521-98087565	NM_027304:196	H1fnt	INSIDE	0.853	2.591	556.21	1440.96	2.210	521.99	1153.75
A_68_P26061528	chr8:94324564-94324608	NM_008393:687	Irx3	INSIDE	0.853	0.571	1403.07	801.38	0.487	1079.53	525.94
A_68_P30423405	chr15:88970834-88970878	NM_013871:277	Mapk12	INSIDE	0.853	0.645	1357.86	875.48	0.550	1104.24	607.34
A_68_P28456273	chr12:57446579-57446623	NM_145442:281	Mbip	INSIDE	0.853	0.499	1262.00	629.64	0.426	1104.52	469.97
A_68_P31201771	chr17:45692645-45692689	NM_008690:2	Nfkbie	INSIDE	0.853	0.387	2368.21	916.67	0.330	1806.50	596.37

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P21095896	chr2:29083214-29083258	NM_133500:20324	Ntng2	INSIDE	0.853	1.906	918.60	1750.72	1.625	744.86	1210.26
A_68_P21817618	chr2:164226131-164226175	NM_009036:-2541	Rbpjl	PROMOTER	0.853	0.586	1706.75	999.85	0.499	1495.00	746.68
A_68_P29073057	chr13:58503189-58503233	NR_031761:-398	Rmi1	DIVERGENT_PROMOTER	0.853	0.536	3638.50	1949.81	0.457	2789.95	1275.95
A_68_P28957970	chr13:38085587-38085631	NM_025965:451	Ssr1	INSIDE	0.853	0.588	4399.52	2586.06	0.502	3313.17	1661.72
A_68_P28054176	chr11:97914740-97914784	NM_146028:14	Stac2	INSIDE	0.853	0.622	1609.48	1001.27	0.531	1129.05	599.38
A_68_P28176313	chr11:119036206-119036250	NM_172443:53585	Tbc1d16	INSIDE	0.853	1.661	1593.58	2647.03	1.418	1340.44	1900.26
A_68_P28974121	chr13:40818660-40818705	NM_001122948:7130	Tcfap2a	INSIDE	0.853	0.479	2078.19	995.78	0.409	1796.97	734.15
A_68_P30953391	chr16:89867896-89867940	NM_009384:93154	Tiam1	INSIDE	0.853	1.992	970.56	1933.73	1.700	719.14	1222.83
A_68_P30149668	chr15:38400702-38400746	M10062:-8338		PROMOTER	0.853	2.543	618.04	1571.97	2.171	573.36	1244.59
A_68_P25188288	chr7:73572852-73572896	NM_053080:-511	Aldh1a3	PROMOTER	0.852	0.656	950.10	622.96	0.559	774.39	432.54
A_68_P21334258	chr2:73748716-73748760	NM_175015:613	Atp5g3	INSIDE	0.852	0.477	1908.27	910.78	0.406	1500.39	609.77
A_68_P24467400	chr6:55067624-55067668	NM_009953:15320	Crhr2	INSIDE	0.852	0.358	2240.78	801.15	0.305	1837.14	559.85
A_68_P31208134	chr17:46790061-46790105	NM_025611:2796	Cul7	INSIDE	0.852	4.434	3495.97	15501.17	3.776	2347.62	8864.61
A_68_P24388783	chr6:40385658-40385702	NM_175528:452	E330009J07Rik	INSIDE	0.852	0.470	1373.65	645.17	0.400	1221.90	489.08
A_68_P21486501	chr2:103810745-103810789	NM_001142335:323	Lmo2	INSIDE	0.852	1.589	4391.84	6978.22	1.354	3518.83	4765.80
A_68_P21102112	chr2:30112106-30112150	NM_177725:18840	Lrrc8a	INSIDE	0.852	2.888	581.73	1679.83	2.460	512.01	1259.49
A_68_P25590419	chr7:148879650-148879694	NM_023566:3412	Muc2	INSIDE	0.852	1.849	847.79	1567.57	1.576	718.45	1132.19
A_68_P21722764	chr2:147013854-147013898	NM_001077632:-1738	Nkx2-2	PROMOTER	0.852	0.689	1399.54	964.39	0.587	1161.48	681.77
A_68_P26591021	chr9:65917626-65917670	NM_001025612:-110	Snx22	PROMOTER	0.852	1.814	1286.20	2333.66	1.546	1126.40	1741.43
A_68_P29433274	chr14:18005375-18005419			Unknown	0.852	1.699	1695.96	2881.32	1.448	1349.17	1953.92
A_68_P24768722	chr6:114987825-114987869	NM_026894:46	1500001M20Rik	INSIDE	0.851	2.008	836.01	1679.11	1.710	749.56	1281.84
A_68_P22062861	chr3:37211563-37211607	NM_001008502:109	Bbs12	INSIDE	0.851	0.588	1788.88	1052.48	0.501	1423.99	712.94
A_68_P26811950	chr9:107838507-107838551	NM_145621:278	Camkv	INSIDE	0.851	0.374	1986.08	742.65	0.318	1516.39	482.38
A_68_P23229430	chr4:116136663-116136707	NM_001042743:104	Mast2	INSIDE	0.851	2.859	288.28	824.32	2.432	332.93	809.85
A_68_P24623658	chr6:88674283-88674327	NM_001166249:-101	Mgll	PROMOTER	0.851	1.904	1570.90	2991.49	1.620	1364.86	2211.54
A_68_P30126798	chr15:34012651-34012695	NM_026002:199	Mtdh	INSIDE	0.851	1.997	731.60	1460.73	1.699	788.53	1339.40
A_68_P21419564	chr2:90744694-90744738	NM_026688:162	Ndufs3	INSIDE	0.851	0.685	2742.52	1877.76	0.583	2156.27	1256.89
A_68_P24466342	chr6:54894109-54894153	NM_001171007:27525	Nod1	INSIDE	0.851	3.692	294.00	1085.41	3.142	262.59	825.11
A_68_P24053560	chr5:123479219-123479263	NM_175423:14158	Orai1	INSIDE	0.851	1.820	1674.48	3047.53	1.548	1299.47	2011.75
A_68_P28451744	chr12:56521734-56521784	NM_011968:21947	Psma6	DOWNSTREAM	0.851	2.122	455.25	966.17	1.807	458.75	828.84
A_68_P30001153	chr15:8586301-8586345	NM_148938:74485	Slc1a3	INSIDE	0.851	3.821	753.82	2880.70	3.254	643.24	2092.99
A_68_P26750367	chr9:96896461-96896505	NM_145134:22292	Spsb4	INSIDE	0.851	2.744	1168.76	3207.35	2.335	1009.01	2356.47
A_68_P28466189	chr12:59313486-59313530	NM_009216:718	Sstr1	INSIDE	0.851	1.822	857.85	1562.65	1.549	820.01	1270.44
A_68_P28013352	chr11:90549070-90549114	NM_028011:-177	Tom1l1	PROMOTER	0.851	1.801	703.80	1267.67	1.532	669.21	1025.54
A_68_P30401102	chr15:85341114-85341158	ENSMUST00000079690:-105		PROMOTER	0.851	2.089	1584.15	3308.80	1.777	1179.93	2096.42
A_68_P28711045	chr12:107004711-107004755	NM_030187:60541	Ak7	INSIDE	0.850	1.886	1341.73	2530.39	1.602	1156.71	1853.46
A_68_P25656683	chr8:11634954-11634998	NR_030781:60	Ankrd10	INSIDE	0.850	0.716	2615.71	1873.79	0.609	2071.74	1261.08
A_68_P23260764	chr4:122781955-122781999	NM_007559:-431	Bmp8b	PROMOTER	0.850	0.470	1183.19	555.93	0.399	1014.81	405.06
A_68_P25021005	chr7:29079533-29079577	NM_007866:7250	Dll3	INSIDE	0.850	2.228	1079.82	2405.43	1.894	986.79	1869.02
A_68_P24870736	chr6:135994225-135994269	NM_008171:129283	Grin2b	INSIDE	0.850	2.345	945.15	2215.91	1.992	766.56	1526.93
A_68_P22375207	chr3:101255068-101255112	NM_207205:74043	Igsf3	INSIDE	0.850	2.204	915.92	2019.06	1.873	849.84	1591.81
A_68_P23598365	chr5:35448131-35448175	NM_013587:194	Lrpap1	INSIDE	0.850	0.687	1221.85	839.14	0.583	1022.85	596.75
A_68_P29446631	chr14:21212821-21212865	NM_025440:-65	Mrps16	PROMOTER	0.850	0.696	1931.82	1344.32	0.592	1717.79	1016.48
A_68_P30456844	chr15:95059724-95059769	NM_016743:299391	Nell2	INSIDE	0.850	3.069	283.24	869.21	2.608	229.68	599.04
A_68_P24602909	chr6:85026381-85026425	NR_002702:268	Npm3-ps1	INSIDE	0.850	1.705	1275.75	2174.97	1.449	1097.20	1589.41
A_68_P31632590	chr18:38357395-38357439	NM_029357:12000	Pcdh1	INSIDE	0.850	2.008	605.30	1215.59	1.707	524.54	895.22
A_68_P27830412	chr11:58144420-58144464	NM_001161338:223	Sh3bp5l	INSIDE	0.850	2.193	1761.18	3861.92	1.863	1191.87	2220.56
A_68_P22456981	chr3:117571662-117571706	NM_001190156:170	Snx7	INSIDE	0.850	0.671	1411.16	946.51	0.570	1253.01	714.41
A_68_P24912678	chr6:143782013-143782057	NM_001113559:376044	Sox5	INSIDE	0.850	2.232	1372.61	3064.02	1.898	1171.29	2223.62
A_68_P25507973	chr7:135039093-135039137	NM_178600:17	Vkorc1	INSIDE	0.850	0.722	1747.01	1261.06	0.614	1402.30	860.89
A_68_P21081716	chr2:26865601-26865645	NM_029862:137	5930434B04Rik	INSIDE	0.849	0.723	2945.24	2128.85	0.614	2187.81	1342.96

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P23562906	chr5:28793388-28793432	NR_015562:-113	9530036O11Rik	PROMOTER	0.849	0.675	1273.10	859.83	0.573	1057.69	606.54
A_68_P32710887	chrX:139401132-139401176	NM_019496:117	Ammecr1	INSIDE	0.849	1.883	935.03	1760.43	1.598	578.57	924.64
A_68_P21424190	chr2:91550470-91550514	NM_145528:241	Atg13	INSIDE	0.849	0.656	1985.80	1303.49	0.557	1465.03	816.03
A_68_P24793357	chr6:119430927-119430971	NM_133940:1263	Fbxl14	INSIDE	0.849	0.526	1048.11	551.59	0.447	758.79	339.07
A_68_P31201909	chr17:45710173-45710217	NM_008302:16	Hsp90ab1	INSIDE	0.849	0.603	1445.30	872.14	0.512	1242.38	636.56
A_68_P31929691	chr19:5609833-5609877	NR_037603:-147	Kat5	PROMOTER	0.849	0.717	3121.55	2239.32	0.609	2286.47	1392.91
A_68_P26346081	chr9:21038114-21038158	NM_001110305:5640	Keap1	INSIDE	0.849	2.108	1248.64	2632.66	1.791	1008.95	1806.74
A_68_P23809986	chr5:75970756-75970800	NM_001122733:-233	Kit	PROMOTER	0.849	0.643	870.64	559.66	0.546	702.78	383.45
A_68_P30224202	chr15:53734012-53734057	NM_177225:-43	Samd12	PROMOTER	0.849	0.555	1293.49	718.17	0.471	1027.27	484.18
A_68_P32672207	chrX:131009751-131009795	NM_028958:1257	Taf7l	INSIDE	0.849	2.137	819.26	1750.57	1.815	479.06	869.28
A_68_P26158627	chr8:112248255-112248299	NM_029468:18289	Zfp821	INSIDE	0.849	3.701	2188.25	8097.69	3.140	1624.64	5101.40
A_68_P28272752	chr12:17888520-17888564	ENSMUST00000169996:-460		PROMOTER	0.849	0.591	2038.46	1205.54	0.502	1749.75	878.76
A_68_P29390920	chr14:9498555-9498599	NM_028934:228	4930452B06Rik	INSIDE	0.848	0.548	1178.95	645.63	0.464	1027.36	476.97
A_68_P24330586	chr6:30124108-30124152	NR_038124:-2492	BB283400	DIVERGENT_PROMOTER	0.848	0.688	1193.92	821.74	0.583	1008.97	588.73
A_68_P26954143	chr10:13684496-13684540	NM_010437:-1666	Hivep2	PROMOTER	0.848	0.416	1641.40	682.86	0.353	1348.59	475.79
A_68_P26022001	chr8:87323016-87323060	NM_001081982:1201	Nfix	INSIDE	0.848	2.149	673.91	1448.31	1.824	575.31	1049.09
A_68_P20474867	chr1:99991841-99991885	NM_013626:347	Pam	INSIDE	0.848	0.461	1481.79	683.55	0.391	1186.49	464.15
A_68_P22356817	chr3:97671916-97671960	NM_177145:297	Pde4dip	INSIDE	0.848	0.534	1109.77	592.35	0.453	894.80	405.15
A_68_P26138085	chr8:108687070-108687114	NM_133792:12794	Pla2g15	INSIDE	0.848	2.057	1537.38	3162.39	1.745	1212.69	2116.21
A_68_P29701295	chr14:70843090-70843134	NM_001164082:-78	Polr3d	PROMOTER	0.848	0.649	1613.46	1047.39	0.550	1324.53	728.74
A_68_P30990392	chr16:96212465-96212509	NM_019537:24	Psmg1	INSIDE	0.848	0.543	1377.18	748.22	0.461	1174.19	540.90
A_68_P25265266	chr7:87343315-87343359	NM_013659:11610	Sema4b	INSIDE	0.848	2.530	1140.55	2885.45	2.146	1038.26	2228.13
A_68_P27325552	chr10:87922308-87922352	NM_011517:-1	Sycp3	PROMOTER	0.848	1.890	1665.99	3148.51	1.602	1243.93	1992.68
A_68_P31099002	chr17:24824527-24824571	NM_011522:2346	Syngr3	INSIDE	0.848	0.656	1709.91	1121.60	0.556	1382.87	768.81
A_68_P32021817	chr19:24205542-24205588	NM_001198985:43066	Tjp2	INSIDE	0.848	3.045	1171.94	3568.67	2.583	914.63	2362.20
A_68_P31791611	chr18:67551169-67551213	NM_026473:806	Tubb6	INSIDE	0.848	0.550	1410.19	776.03	0.467	1070.32	499.42
A_68_P24424840	chr6:47855086-47855130	NM_146175:27555	Zfp282	INSIDE	0.848	2.187	1122.42	2454.28	1.855	846.65	1570.16
A_68_P29560845	chr14:41826844-41826888	NM_027464:198	5730469M10Rik	INSIDE	0.847	0.597	1135.62	678.27	0.506	962.17	487.02
A_68_P29223870	chr13:93196035-93196079	NM_175455:133	Ankrd34b	INSIDE	0.847	0.470	1342.40	631.26	0.398	989.82	394.15
A_68_P27535286	chr10:126763506-126763550	NM_146011:2746	Arhgap9	INSIDE	0.847	0.572	960.27	549.39	0.485	820.03	397.45
A_68_P29604083	chr14:52604387-52604431	NM_001145921:-99	Arhgef40	PROMOTER	0.847	0.721	4484.95	3235.38	0.611	3772.23	2304.61
A_68_P23336930	chr4:136501732-136501776	NM_007939:10977	Epha8	INSIDE	0.847	2.119	926.27	1962.96	1.795	853.14	1531.68
A_68_P28463159	chr12:58639836-58639880	NM_008259:7250	Foxa1	DOWNSTREAM	0.847	0.552	1000.31	551.75	0.467	859.98	401.75
A_68_P25307425	chr7:96553431-96553475	NM_008055:577	Fzd4	INSIDE	0.847	0.674	1274.46	858.81	0.570	1131.08	645.27
A_68_P28977622	chr13:41454095-41454139	NM_017464:254	Nedd9	INSIDE	0.847	0.495	1344.46	665.13	0.419	1129.48	473.09
A_68_P22859776	chr4:40918121-40918165	NM_023739:167	Nfx1	INSIDE	0.847	2.781	603.07	1677.09	2.356	669.48	1577.52
A_68_P31626772	chr18:37181762-37181806	NM_138663:1901	Pcdha12	INSIDE	0.847	2.498	2044.68	5107.05	2.116	1566.88	3315.46
A_68_P22906126	chr4:49645116-49645160	NM_001163263:207	Rnf20	INSIDE	0.847	0.591	1053.45	623.07	0.501	851.05	426.20
A_68_P26817066	chr9:108756909-108756953	NM_134420:557	Slc26a6	INSIDE	0.847	1.897	611.04	1159.30	1.607	500.29	803.95
A_68_P24432385	chr6:49345373-49345417	NM_029916:-208	Stk31	PROMOTER	0.847	1.981	1375.24	2724.18	1.677	1175.56	1971.30
A_68_P29613141	chr14:55203509-55203559	NM_028890:21211	4931414P19Rik	INSIDE	0.846	2.810	961.11	2701.10	2.378	726.05	1726.61
A_68_P25608862	chr7:151924611-151924655	NM_178642:-249	Ano1	PROMOTER	0.846	0.654	1364.41	892.57	0.553	1110.48	614.54
A_68_P27793109	chr11:51103712-51103756	NM_153393:313	Col23a1	INSIDE	0.846	2.250	825.15	1856.90	1.903	710.89	1353.18
A_68_P25592942	chr7:149280795-149280840	NM_008748:372	Dusp8	INSIDE	0.846	0.498	1874.07	933.83	0.421	1519.68	640.48
A_68_P27550687	chr11:3102424-3102468	NM_023743:-139	Eif4enif1	PROMOTER	0.846	1.798	1134.89	2040.55	1.521	1129.98	1718.37
A_68_P27845442	chr11:60727111-60727155	NM_025294:162	Gm16515	INSIDE	0.846	0.498	1542.25	768.72	0.422	1393.91	587.82
A_68_P25952866	chr8:73118683-73118727	NM_023627:325	Isyna1	INSIDE	0.846	0.681	1952.76	1329.59	0.576	1583.39	912.08
A_68_P30346617	chr15:76012075-76012119	NM_201394:14044	Plec	INSIDE	0.846	2.198	868.44	1908.64	1.859	697.41	1296.78
A_68_P29619052	chr14:56262619-56262663	NM_028780:3	Tm9sf1	INSIDE	0.846	2.111	743.36	1569.51	1.786	717.39	1281.43
A_68_P26234572	chr8:125135779-125135823	NM_021502:275	Trappc2l	INSIDE	0.846	0.582	1061.95	617.98	0.492	841.89	414.51
A_68_P21910753	chr2:181194478-181194522	NM_028125:-369	Zbtb46	PROMOTER	0.846	3.523	296.02	1042.86	2.981	273.26	814.63

						Sham group			TiO$_2$-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P22200393	chr3:65333036-65333080	NR_027955:278	4931440P22Rik	INSIDE	0.845	7.501	2998.69	22493.29	6.336	2445.82	15495.75
A_68_P28752183	chr12:113976936-113976980	NM_001024602:16574	AW555464	INSIDE	0.845	2.502	1254.50	3138.79	2.115	923.51	1953.46
A_68_P31092909	chr17:23803781-23803825	NM_153784:6313	Ccdc64b	INSIDE	0.845	2.321	983.42	2282.87	1.961	689.77	1352.74
A_68_P24980345	chr7:16803427-16803471	NM_027883:3933	Dhx34	INSIDE	0.845	2.059	1223.24	2518.49	1.741	1039.51	1809.45
A_68_P26779718	chr9:102255865-102255909	NM_001168296:1137	Ephb1	INSIDE	0.845	0.598	876.13	523.58	0.505	718.66	362.76
A_68_P30365867	chr15:79177744-79177788	NM_010755:-341	Maff	PROMOTER	0.845	0.472	1357.58	640.12	0.399	1002.50	399.61
A_68_P22788125	chr4:24825516-24825560	NM_026742:309	Ndufaf4	INSIDE	0.845	1.624	2329.14	3781.68	1.372	2006.99	2754.22
A_68_P30447285	chr15:93333764-93333813	NM_001033217:92534	Prickle1	INSIDE	0.845	2.747	1239.55	3404.62	2.322	996.51	2313.83
A_68_P30955584	chr16:90220772-90220816	NM_011434:-192	Sod1	PROMOTER	0.845	0.708	1796.50	1272.14	0.598	1342.95	803.56
A_68_P22889892	chr4:46663146-46663190	NM_198664:-97	Tbc1d2	PROMOTER	0.845	0.622	1510.32	939.35	0.526	1227.64	645.16
A_68_P28974008	chr13:40804611-40804655	NM_001122948:21180	Tcfap2a	DOWNSTREAM	0.845	1.641	3567.68	5854.06	1.387	2770.82	3843.59
A_68_P21568844	chr2:119119741-119119785	NM_172269:5285	Vps18	INSIDE	0.845	3.629	393.78	1428.90	3.065	413.21	1266.63
A_68_P24127580	chr5:138229716-138229763	NM_001005426:710	Zcwpw1	INSIDE	0.845	2.819	328.05	924.88	2.381	247.13	588.52
A_68_P22775540	chr4:21858745-21858789	NM_175234:294	6230409E13Rik	INSIDE	0.844	0.433	1644.96	711.75	0.365	1239.34	452.61
A_68_P30284264	chr15:64753856-64753901	NM_009623:-20	Adcy8	PROMOTER	0.844	0.629	2752.57	1731.47	0.531	1994.22	1058.58
A_68_P25393095	chr7:112729883-112729927	NM_009685:145	Apbb1	INSIDE	0.844	0.627	3486.44	2186.44	0.529	2863.81	1515.12
A_68_P28080439	chr11:102467320-102467364	NM_020510:1598	Fzd2	INSIDE	0.844	0.467	1313.42	613.52	0.394	977.12	385.31
A_68_P28154358	chr11:115465110-115465154	NM_173048:88	Gga3	INSIDE	0.844	0.704	3247.71	2287.12	0.594	2693.78	1601.01
A_68_P30723335	chr16:44746085-44746129	NM_001159329:370	Gtpbp8	INSIDE	0.844	0.633	1488.96	942.66	0.534	1223.51	653.74
A_68_P31154614	chr17:34724452-34724496	NM_010929:23235	Notch4	INSIDE	0.844	1.809	740.81	1339.76	1.526	749.62	1143.69
A_68_P28058442	chr11:98635216-98635261	NM_145434:1318	Nr1d1	INSIDE	0.844	0.418	1698.78	710.58	0.353	1410.94	498.39
A_68_P29141938	chr13:73901290-73901334	NM_011390:168	Slc12a7	INSIDE	0.844	0.362	1681.38	609.15	0.306	1346.79	412.02
A_68_P23974100	chr5:109203943-109203987	NM_026109:20418	Tmed11	DOWNSTREAM	0.844	3.253	1606.18	5224.30	2.746	1268.02	3482.08
A_68_P23537865	chr5:23181176-23181220	ENSMUST00000157734:-999		PROMOTER	0.844	0.594	2044.09	1214.40	0.501	1691.12	847.96
A_68_P23293014	chr4:128444607-128444651	NM_001009819:8127	A3galt2	INSIDE	0.843	2.123	937.50	1989.94	1.789	732.16	1309.88
A_68_P23410308	chr4:150502691-150502741	NM_001081557:733161	Camta1	INSIDE	0.843	3.548	243.31	863.24	2.992	284.83	852.21
A_68_P25827948	chr8:46108836-46108887	NM_001081286:73300	Fat1	INSIDE	0.843	1.960	612.52	1200.55	1.653	485.15	801.77
A_68_P28925106	chr13:31899841-31899885	NM_008592:1348	Foxc1	INSIDE	0.843	2.497	8538.70	21323.20	2.106	7056.43	14862.57
A_68_P27540023	chr10:127631990-127632034	NM_001033264:322	Gls2	INSIDE	0.843	0.610	2468.36	1505.85	0.514	2010.81	1033.63
A_68_P23057188	chr4:82152852-82152896	NM_001113209:-1662	Nfib	PROMOTER	0.843	0.708	3677.72	2604.44	0.597	3020.24	1803.18
A_68_P26469101	chr9:44516750-44516794	NM_153537:26505	Phldb1	INSIDE	0.843	2.202	5956.48	13116.50	1.857	4222.49	7841.62
A_68_P30941180	chr16:87699079-87699123	NM_007520:-98	Bach1	PROMOTER	0.842	0.698	1390.25	969.99	0.588	1170.73	687.99
A_68_P23339477	chr4:136913646-136913690	NM_009861:-16	Cdc42	PROMOTER	0.842	0.614	1579.56	969.48	0.517	1370.41	708.21
A_68_P28752835	chr12:114067766-114067810	NM_028023:-188	Cdca4	PROMOTER	0.842	0.310	2017.10	624.48	0.261	1681.75	438.22
A_68_P28170157	chr11:118109191-118109235	NM_001112699:694	Cyth1	INSIDE	0.842	0.470	2414.59	1133.78	0.395	1843.68	728.50
A_68_P25015865	chr7:27951492-27951536	NM_053208:307	Egln2	INSIDE	0.842	0.722	2223.61	1606.29	0.609	1773.09	1078.93
A_68_P25828057	chr8:46122480-46122524	NM_001081286:86941	Fat1	INSIDE	0.842	2.290	1495.56	3424.15	1.927	1163.48	2241.65
A_68_P24009123	chr5:115791151-115791195	NM_029645:-2	Gatc	DIVERGENT_PROMOTER	0.842	0.443	1174.32	520.54	0.373	950.29	354.82
A_68_P27790975	chr11:50673295-50673343	NM_173372:9132	Grm6	INSIDE	0.842	2.803	2362.89	6623.81	2.361	1723.20	4068.20
A_68_P25022015	chr7:29243791-29243835	NM_001141921:6556	Lrfn1	INSIDE	0.842	2.349	901.80	2118.36	1.978	696.70	1378.32
A_68_P22659607	chr3:153568738-153568782	NM_031870:342	Msh4	INSIDE	0.842	2.678	1040.93	2787.60	2.255	853.02	1923.64
A_68_P26789125	chr9:103905125-103905169	NM_172460:273	Nphp3	INSIDE	0.842	0.620	2069.66	1282.76	0.522	1503.92	784.49
A_68_P29773664	chr14:84847873-84847917	NM_001013753:4525	Pcdh17	INSIDE	0.842	0.609	1262.16	768.49	0.513	954.01	489.04
A_68_P30423730	chr15:89010897-89010941	NM_001159521:-6638	Plxnb2	PROMOTER	0.842	2.007	1075.11	2158.17	1.690	771.87	1304.10
A_68_P27899678	chr11:70053293-70053337	NM_173742:40	Rnasek	INSIDE	0.842	0.548	1113.42	610.43	0.461	1061.30	489.73
A_68_P28554952	chr12:77707425-77707469	NM_013675:104088	Spnb1	INSIDE	0.842	3.208	1040.29	3336.90	2.702	880.95	2380.71
A_68_P27355933	chr10:93296604-93296648	NM_183199:2327	Usp44	INSIDE	0.842	0.495	2735.13	1352.72	0.417	2373.21	988.57
A_68_P29478597	chr14:26427163-26427207	NM_183208:148514	Zmiz1	INSIDE	0.842	2.052	639.13	1311.76	1.729	636.65	1100.50
A_68_P20878145	chr1:182780796-182780840	NM_145943:-463	BC031781	PROMOTER	0.841	0.417	1415.75	590.85	0.351	1148.27	402.97
A_68_P30589271	chr16:20732979-20733023	NM_009893:-199	Chrd	DIVERGENT_PROMOTER	0.841	0.572	1229.58	703.86	0.481	1050.85	505.84
A_68_P23309920	chr4:131604337-131604381	NM_001128606:635	Epb4.1	INSIDE	0.841	0.384	1988.56	764.59	0.323	1544.96	499.28

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27542235	chr10:128027332-128027376	NM_010153:-797	Erbb3	PROMOTER	0.841	0.622	954.63	593.98	0.523	833.52	436.03
A_68_P23979254	chr5:110792817-110792861	NM_028596:23308	Fbrsl1	INSIDE	0.841	2.338	709.52	1658.95	1.966	628.71	1236.14
A_68_P28044104	chr11:96227502-96227546	NM_008266:453	Hoxb1	INSIDE	0.841	0.745	3022.97	2252.46	0.626	2255.98	1413.11
A_68_P24051800	chr5:123157735-123157779	NM_011026:191	P2rx4	INSIDE	0.841	0.484	1104.25	534.23	0.407	1003.83	408.21
A_68_P24820336	chr6:125330635-125330679	NM_198604:-134	Plekhg6	PROMOTER	0.841	0.637	1638.21	1043.27	0.535	1210.62	648.09
A_68_P25361265	chr7:106497731-106497775	NM_001111043:3997	Serpinh1	INSIDE	0.841	2.368	338.34	801.29	1.992	337.33	671.87
A_68_P31142305	chr17:31991956-31992000	NM_010831:759	Sik1	INSIDE	0.841	0.560	1794.67	1005.78	0.471	1359.62	640.97
A_68_P22149791	chr3:54590206-54590250	NM_019483:30725	Smad9	INSIDE	0.841	2.986	592.83	1770.20	2.513	464.02	1165.92
A_68_P21900705	chr2:179710112-179710156	NM_001081092:1217	Taf4a	INSIDE	0.841	0.612	1104.19	676.22	0.515	1024.62	527.83
A_68_P32143398	chr19:46423369-46423413	NM_029186:-7979	Tmem180	PROMOTER	0.841	0.681	1202.77	819.04	0.573	1066.21	610.71
A_68_P31092445	chr17:23713641-23713685	NM_011747:22792	Zfp13	INSIDE	0.841	2.003	3237.70	6483.62	1.683	2222.09	3740.30
A_68_P23577043	chr5:31502922-31502966	NM_001177901:1471	Zfp513	INSIDE	0.841	1.794	2833.42	5084.28	1.510	2127.60	3211.95
A_68_P21075529	chr2:25838219-25838263	NM_001115076:562	Camsap1	INSIDE	0.840	0.349	2459.48	857.50	0.293	1757.85	514.98
A_68_P31259561	chr17:57151014-57151058	NM_133801:-325	Gtf2f1	PROMOTER	0.840	0.596	890.11	530.47	0.501	710.78	355.84
A_68_P21061711	chr2:23011327-23011371	NM_025979:196	Mastl	INSIDE	0.840	0.541	2425.39	1312.03	0.455	1981.07	900.55
A_68_P23029299	chr4:76096333-76096377	NM_011211:143849	Ptprd	INSIDE	0.840	1.835	2360.85	4331.46	1.542	1943.50	2996.46
A_68_P32222444	chr19:60019679-60019723	NM_001164367:-143	Rab11fip2	PROMOTER	0.840	0.696	2582.40	1796.74	0.584	1964.00	1147.72
A_68_P32785478	chrX:158155051-158155095	NM_198409:-412	Rai2	PROMOTER	0.840	1.904	3649.39	6949.06	1.600	1784.25	2854.18
A_68_P23344732	chr4:137806580-137806624	NM_001099631:277	Sh2d5	INSIDE	0.840	0.645	1589.00	1024.64	0.542	1208.23	654.45
A_68_P30094471	chr15:27703578-27703623	NM_001081302:252003	Trio	INSIDE	0.840	1.858	1192.90	2216.32	1.561	943.03	1471.60
A_68_P29520332	chr14:33670216-33670260	NM_178791:297	E130203B14Rik	INSIDE	0.839	0.711	1730.52	1230.86	0.597	1390.75	830.25
A_68_P20294249	chr1:64782318-64782364	NM_001042659:1984	Fzd5	INSIDE	0.839	5.371	1979.74	10632.29	4.503	1388.87	6254.72
A_68_P24828616	chr6:126689917-126689961	NM_013568:754	Kcna6	INSIDE	0.839	0.557	1358.83	757.31	0.468	1052.09	492.13
A_68_P23981083	chr5:111082064-111082108	NM_153570:315	Noc4l	INSIDE	0.839	0.479	1293.22	619.38	0.402	1024.15	411.38
A_68_P28538088	chr12:74646850-74646894	NM_178715:510	Tmem30b	INSIDE	0.839	0.725	1678.50	1217.50	0.609	1581.41	962.87
A_68_P30094308	chr15:27677507-27677551	NM_001081302:278075	Trio	INSIDE	0.839	3.245	2551.20	8278.08	2.724	1764.09	4804.83
A_68_P29246777	chr13:97312887-97312931	NM_001164222:219	Col4a3bp	INSIDE	0.838	0.504	2272.10	1144.97	0.422	1892.11	798.92
A_68_P25436573	chr7:121706377-121706421	NM_177382:88	Cyp2r1	INSIDE	0.838	2.920	922.45	2693.46	2.448	781.30	1912.52
A_68_P28067418	chr11:100181178-100181222	NM_011508:-109	Eif1	PROMOTER	0.838	0.437	2243.97	979.77	0.366	1773.19	648.95
A_68_P20562790	chr1:122503715-122503759	NM_010133:4673	En1	INSIDE	0.838	0.610	941.65	574.80	0.511	755.26	386.30
A_68_P23317854	chr4:133042232-133042276	NM_175307:6207	Fam46b	INSIDE	0.838	2.113	1133.72	2395.88	1.771	862.68	1527.71
A_68_P25361474	chr7:106529779-106529823	NM_201352:-258	Gdpd5	PROMOTER	0.838	0.368	2189.56	804.77	0.308	1655.63	509.86
A_68_P23080771	chr4:86257888-86257932	NM_173400:16	Haus6	INSIDE	0.838	0.600	2512.77	1507.68	0.503	2060.10	1035.95
A_68_P20457528	chr1:95700326-95700370	NM_025454:-193	Ing5	DIVERGENT_PROMOTER	0.838	0.531	2125.75	1127.76	0.445	1702.19	756.96
A_68_P24385096	chr6:39760909-39760954	NM_001010930:4	Mrps33	INSIDE	0.838	0.666	1232.22	820.19	0.558	995.78	555.31
A_68_P21873559	chr2:173946554-173946598	NM_213733:10725	Npepl1	INSIDE	0.838	2.223	1230.40	2735.09	1.862	956.97	1782.12
A_68_P27896914	chr11:69572502-69572546	NM_009089:-799	Polr2a	PROMOTER	0.838	0.448	1435.65	643.67	0.376	1141.82	428.92
A_68_P23437243	chr4:154597315-154597359	NM_011385:-692	Ski	PROMOTER	0.838	0.488	1637.15	799.35	0.409	1335.08	546.54
A_68_P32203281	chr19:56900903-56900947	NM_001002241:-4277	Tdrd1	PROMOTER	0.838	3.575	1541.92	5511.63	2.994	1335.27	3998.16
A_68_P25182465	chr7:72515444-72515488	NM_001163574:664	Tjp1	INSIDE	0.838	0.451	1199.80	541.71	0.378	1127.36	426.68
A_68_P26924748	chr10:8238264-8238308	NM_177387:337	Ust	INSIDE	0.838	0.628	1818.21	1141.89	0.526	1446.51	761.02
A_68_P24127577	chr5:138229403-138229447	NM_001005426:395	Zcwpw1	INSIDE	0.838	4.658	4961.26	23107.48	3.903	3308.65	12912.46
A_68_P20433092	chr1:91838560-91838604	AK081208:9752		DOWNSTREAM	0.838	0.615	1137.59	699.34	0.515	913.29	470.42
A_68_P29964256	chr14:123312237-123312281	NM_145466:129	A2ld1	INSIDE	0.837	0.580	1247.69	724.09	0.486	1032.87	501.90
A_68_P26749714	chr9:96789401-96789445	NM_153420:419	Acpl2	INSIDE	0.837	1.598	11400.84	18215.34	1.337	7753.75	10365.61
A_68_P27937765	chr11:77285191-77285236	NM_172945:17967	Ankrd13b	INSIDE	0.837	2.437	986.70	2404.69	2.039	746.09	1521.07
A_68_P30379098	chr15:81524468-81524512	NM_001164320:3227	Chadl	INSIDE	0.837	1.903	931.17	1772.17	1.593	849.19	1353.18
A_68_P25539016	chr7:140315036-140315089	NM_009980:104	Ctbp2	INSIDE	0.837	6.739	8489.67	57208.31	5.643	5766.75	32541.26
A_68_P24157331	chr5:144383673-144383717	NM_011182:379	Cyth3	INSIDE	0.837	0.619	2940.81	1820.75	0.518	2421.05	1254.35
A_68_P22046078	chr3:33980177-33980221	NM_001026211:50	Dnajc19	INSIDE	0.837	2.294	1818.87	4171.60	1.919	1822.02	3496.11
A_68_P26022687	chr8:87447829-87447873	NM_019945:13402	Mast1	INSIDE	0.837	3.366	2594.52	8733.19	2.819	2070.38	5835.84

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25360755	chr7:106417510-106417554	NM_001043355:677	Mtap6	INSIDE	0.837	0.628	1611.00	1012.14	0.526	1275.96	670.76
A_68_P25503619	chr7:134164872-134164916	NM_001102563:-169	Prrt2	PROMOTER	0.837	0.674	1980.82	1334.45	0.564	1623.20	914.93
A_68_P30470421	chr15:97535782-97535826	NM_028003:449	Rpap3	INSIDE	0.837	0.532	2592.71	1379.78	0.445	2129.83	948.57
A_68_P23929477	chr5:100845100-100845144	NM_026969:131	Sec31a	INSIDE	0.837	0.639	4753.27	3036.33	0.535	3834.12	2051.00
A_68_P31421198	chr17:87506616-87506660	NM_019654:-380	Socs5	PROMOTER	0.837	0.623	2025.63	1262.46	0.522	1551.06	808.92
A_68_P26752039	chr9:97266104-97266148	NM_030219:4251	Trim42	INSIDE	0.837	1.713	1266.56	2169.73	1.435	936.30	1343.28
A_68_P29064231	chr13:56989096-56989140	NM_012035:7831	Trpc7	INSIDE	0.837	2.003	1397.94	2800.23	1.677	1109.71	1861.38
A_68_P24019922	chr5:117769425-117769469	NM_001033311:172	Vsig10	INSIDE	0.837	0.555	1269.90	704.89	0.465	1017.03	472.71
A_68_P22611705	chr3:145601523-145601567	NM_025555:549	2410004B18Rik	INSIDE	0.836	2.090	1694.76	3542.55	1.748	1502.16	2625.09
A_68_P20433237	chr1:91865288-91865332	NM_139152:45842	Asb18	INSIDE	0.836	0.614	910.98	559.70	0.514	932.09	478.75
A_68_P21633703	chr2:131005234-131005278	NM_007682:492	Cenpb	INSIDE	0.836	0.697	1407.97	981.77	0.583	1260.68	734.53
A_68_P30978140	chr16:93884209-93884253	NM_028083:85	Chaf1b	INSIDE	0.836	0.602	1468.67	884.33	0.503	1235.04	621.58
A_68_P23618838	chr5:38710862-38710906	NM_013503:137	Drd5	INSIDE	0.836	0.703	2326.95	1635.08	0.587	1805.55	1060.21
A_68_P27278710	chr10:79217823-79217867	NM_023304:-19	Fgf22	DIVERGENT_PROMOTER	0.836	0.643	1437.69	924.45	0.537	1366.73	734.30
A_68_P27093479	chr10:41916731-41916775	NM_019740:79796	Foxo3	INSIDE	0.836	2.428	504.00	1223.79	2.029	451.40	915.92
A_68_P24005877	chr5:115199469-115199513	NM_001077360:24010	Git2	INSIDE	0.836	2.405	404.42	972.47	2.010	359.96	723.56
A_68_P26954156	chr10:13685876-13685920	NM_010437:-286	Hivep2	PROMOTER	0.836	1.896	3028.80	5742.48	1.585	2118.13	3357.01
A_68_P25022018	chr7:29244235-29244279	NM_001141921:7000	Lrfn1	INSIDE	0.836	2.015	853.81	1720.63	1.685	740.35	1247.82
A_68_P25087548	chr7:51717376-51717420	NM_198250:19542	Lrrc4b	INSIDE	0.836	2.820	1178.24	3322.97	2.359	879.94	2075.36
A_68_P26021274	chr8:87229387-87229431	NM_008535:4053	Lyl1	DOWNSTREAM	0.836	2.345	9842.90	23077.43	1.960	7106.69	13926.16
A_68_P24064309	chr5:125507455-125507499	NM_011424:152108	Ncor2	INSIDE	0.836	2.509	502.10	1259.66	2.097	396.57	831.62
A_68_P26261060	chr8:129588304-129588348	NM_001122850:371	Pard3	INSIDE	0.836	0.632	1077.90	681.60	0.529	900.13	475.94
A_68_P29145568	chr13:74454823-74454867	NM_011051:-70	Pdcd6	PROMOTER	0.836	0.723	3217.51	2326.04	0.605	2497.81	1510.14
A_68_P23292758	chr4:128405111-128405155	NM_001195083:318	Phc2	INSIDE	0.836	2.392	394.41	943.34	2.001	383.35	766.92
A_68_P30346557	chr15:76004653-76004697	NM_201394:21466	Plec	INSIDE	0.836	2.787	381.91	1064.37	2.330	394.28	918.64
A_68_P26349532	chr9:21722448-21722492	NM_031874:95	Rab3d	INSIDE	0.836	0.634	3431.03	2173.89	0.530	2699.16	1429.24
A_68_P28086207	chr11:103510830-103510874	NM_001033212:30	Rprml	INSIDE	0.836	0.424	1471.23	623.98	0.354	1185.66	420.20
A_68_P29599193	chr14:51551001-51551045	NM_001033271:-498	Tmem55b	PROMOTER	0.836	0.498	1214.84	604.75	0.416	999.90	416.29
A_68_P30887977	chr16:77014158-77014202	NM_013918:-133	Usp25	PROMOTER	0.836	2.016	658.76	1328.19	1.685	731.21	1231.86
A_68_P28058999	chr11:98725426-98725472	NM_197940:537	Wipf2	INSIDE	0.836	4.318	4205.98	18161.31	3.611	2774.09	10018.33
A_68_P24155682	chr5:144015330-144015374	NM_017467:16349	Zfp316	INSIDE	0.836	2.049	1156.56	2370.00	1.714	932.25	1597.53
A_68_P30084545	chr15:25914824-25914868	NM_144523:726	Zfp622	INSIDE	0.836	2.153	1354.77	2917.03	1.800	967.60	1741.30
A_68_P31922425	chr19:4305540-4305585	NM_130863:393	Adrbk1	INSIDE	0.835	0.684	2844.94	1947.04	0.572	2418.39	1382.82
A_68_P31097729	chr17:24642452-24642496	NM_027937:16747	Caskin1	INSIDE	0.835	2.324	907.65	2109.59	1.942	720.26	1398.49
A_68_P25026494	chr7:30092897-30092941	NM_013874:3895	Dpf1	INSIDE	0.835	0.674	1321.46	890.83	0.563	1020.19	574.53
A_68_P28204869	chr12:5216958-5217002	NM_001164493:165508	Klhl29	INSIDE	0.835	2.049	1012.42	2074.75	1.710	830.51	1420.58
A_68_P24947884	chr7:4089157-4089201	NM_172736:521	Leng8	INSIDE	0.835	0.497	1320.42	655.99	0.415	1177.59	488.29
A_68_P27285756	chr10:80297241-80297285	NM_001013758:9522	Lingo3	INSIDE	0.835	2.009	1234.22	2480.15	1.678	904.42	1517.45
A_68_P21722816	chr2:147019569-147019613	NM_001077632:-7452	Nkx2-2	PROMOTER	0.835	0.307	1700.90	521.85	0.256	1333.91	341.63
A_68_P23807627	chr5:75549167-75549211	NM_001083316:-3002	Pdgfra	PROMOTER	0.835	0.478	1569.50	750.41	0.399	1201.05	479.50
A_68_P32117862	chr19:41986317-41986361	NM_023418:-22	Pgam1	PROMOTER	0.835	0.712	1393.00	991.48	0.594	1161.05	689.95
A_68_P22880596	chr4:45024872-45024916	NM_001163283:390	Zbtb5	INSIDE	0.835	0.718	2651.71	1902.85	0.599	2149.08	1287.38
A_68_P23577057	chr5:31504483-31504527	NM_001177901:-89	Zfp513	PROMOTER	0.835	0.674	1362.30	918.19	0.563	1091.28	613.92
A_68_P23593508	chr5:34631202-34631246	NM_001015039:-251	Zfyve28	PROMOTER	0.835	0.568	1207.31	685.78	0.474	1209.81	573.74
A_68_P27283449	chr10:79938176-79938220	ENSMUST00000158603:-898		PROMOTER	0.835	0.532	1044.95	556.06	0.444	896.94	398.50
A_68_P30339170	chr15:74551517-74551561	NM_198607:-125	4930572J05Rik	PROMOTER	0.834	0.701	1296.07	908.61	0.585	1094.67	639.91
A_68_P20774314	chr1:163806929-163806973	NM_172645:-158	AI848100	PROMOTER	0.834	0.536	2342.79	1255.42	0.447	1860.48	831.85
A_68_P28032141	chr11:94189750-94189794	NM_146024:458	Ankrd40	INSIDE	0.834	0.435	1618.14	704.48	0.363	1384.50	502.81
A_68_P21310282	chr2:69485168-69485213	NM_028284:-121	Bbs5	PROMOTER	0.834	0.679	1071.59	727.56	0.566	924.54	523.36
A_68_P32128060	chr19:43764426-43764470	NM_053103:270	Entpd7	INSIDE	0.834	0.652	1718.37	1120.87	0.544	1306.44	710.99
A_68_P21115868	chr2:32391385-32391429	NM_153560:528	Fam102a	INSIDE	0.834	0.524	1876.38	983.65	0.437	1506.60	658.52

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P32408601	chrX:56388072-56388116	NM_010200:-481	Fgf13	PROMOTER	0.834	2.220	1596.46	3544.25	1.852	781.17	1446.65
A_68_P28813934	chr13:8995156-8995200	NM_027000:80	Gtpbp4	INSIDE	0.834	0.639	1998.13	1277.53	0.533	1558.88	831.46
A_68_P25656260	chr8:11561678-11561724	NM_011919:5635	Ing1	INSIDE	0.834	3.371	1852.46	6245.36	2.811	1241.89	3491.15
A_68_P25048199	chr7:35988939-35988987	NM_001024707:11402	Lrp3	INSIDE	0.834	2.822	582.63	1644.04	2.354	479.44	1128.41
A_68_P31601523	chr18:32323206-32323251	NM_011946:486	Map3k2	INSIDE	0.834	0.580	1139.82	661.35	0.484	988.27	478.47
A_68_P21906901	chr2:180627963-180628007	NR_029538:-760	Mir124a-3	PROMOTER	0.834	0.665	2614.41	1738.89	0.554	2404.10	1332.97
A_68_P30458577	chr15:95358659-95358703	NM_016743:457	Nell2	INSIDE	0.834	0.534	1125.38	600.62	0.445	975.99	434.60
A_68_P28445680	chr12:55170082-55170135	NM_013780:820445	Npas3	INSIDE	0.834	2.025	708.40	1434.71	1.689	510.88	863.10
A_68_P25169316	chr7:69609111-69609155	NM_013788:264	Peg12	INSIDE	0.834	2.337	808.77	1890.06	1.948	810.55	1579.08
A_68_P26727062	chr9:92436930-92436974	NM_001142916:-108	Plod2	PROMOTER	0.834	0.691	3076.45	2124.97	0.576	2330.63	1343.10
A_68_P24338425	chr6:31500974-31501020	NM_013723:12941	Podxl	INSIDE	0.834	2.208	1141.38	2519.77	1.841	863.76	1590.25
A_68_P23374911	chr4:142984150-142984195	NM_031377:-171	Pramel1	PROMOTER	0.834	4.724	1115.23	5268.06	3.939	731.23	2880.57
A_68_P22957026	chr4:59561660-59561704	NM_144904:554	Rod1	INSIDE	0.834	0.736	6136.42	4515.15	0.614	5484.20	3365.31
A_68_P21707833	chr2:144381436-144381490	NM_019787:-550	Sec23b	DIVERGENT_PROMOTER	0.834	2.599	1620.28	4211.75	2.168	1298.09	2814.63
A_68_P30686668	chr16:38562990-38563034	NM_001205287:86	Tmem39a	INSIDE	0.834	0.684	1580.42	1081.37	0.571	1204.71	687.37
A_68_P27688945	chr11:32355498-32355542	NM_173784:149	Ubtd2	INSIDE	0.834	0.532	1344.48	714.93	0.444	1245.06	552.47
A_68_P24424842	chr6:47855282-47855326	NM_146175:27751	Zfp282	INSIDE	0.834	1.802	1940.99	3496.80	1.503	1511.45	2271.30
A_68_P32260340	chrX:11664828-11664872	NM_029510:-7171	Bcor	PROMOTER	0.833	0.631	1291.29	814.87	0.526	631.69	331.98
A_68_P23336494	chr4:136436600-136436644	NM_009777:5470	C1qb	INSIDE	0.833	2.628	607.59	1596.83	2.189	476.49	1042.82
A_68_P26816890	chr9:108734418-108734462	NM_080437:5790	Celsr3	INSIDE	0.833	0.690	4015.26	2771.34	0.575	3004.32	1727.62
A_68_P21833673	chr2:166930335-166930379	NM_008420:83943	Kcnb1	INSIDE	0.833	1.977	647.33	1279.47	1.646	518.74	853.82
A_68_P27880945	chr11:66908117-66908162	NM_001099635:16338	Myh3	INSIDE	0.833	4.082	390.66	1594.61	3.400	391.80	1332.29
A_68_P22774362	chr4:21612942-21612986	NM_001080771:146	Prdm13	INSIDE	0.833	0.713	1941.38	1384.16	0.594	1542.59	916.34
A_68_P21579354	chr2:120997006-120997050	NM_153387:87	Tubgcp4	INSIDE	0.833	0.616	944.64	581.57	0.513	822.10	421.44
A_68_P25785791	chr8:37521054-37521098	ENSMUST00000036363:-134		PROMOTER	0.833	0.637	1849.46	1178.02	0.531	1435.16	761.44
A_68_P32565626	chrX:98989424-98989468	ENSMUST00000151231:-548		DIVERGENT_PROMOTER	0.833	2.477	663.21	1643.11	2.063	318.25	656.50
A_68_P30337609	chr15:74348773-74348817	NM_174991:2169	Bai1	INSIDE	0.832	0.491	2356.87	1158.04	0.409	1852.55	757.31
A_68_P30198096	chr15:48621384-48621428	NM_001081391:2129	Csmd3	INSIDE	0.832	0.638	842.60	537.26	0.530	679.96	360.50
A_68_P26804377	chr9:106553386-106553432	NM_001160353:5032	Grm2	INSIDE	0.832	3.006	499.89	1502.52	2.501	437.36	1093.76
A_68_P31050851	chr17:12464717-12464771	NM_011948:46782	Map3k4	INSIDE	0.832	2.888	460.37	1329.55	2.404	363.23	873.21
A_68_P21490976	chr2:104656612-104656656	NM_001123327:219	Qser1	INSIDE	0.832	0.514	1934.05	993.54	0.427	1560.73	667.13
A_68_P26630974	chr9:72892721-72892765	NM_023635:71	Rab27a	INSIDE	0.832	0.576	1410.63	813.13	0.479	1177.57	564.61
A_68_P22900935	chr4:48597734-48597778	NM_021436:-308	Tmeff1	PROMOTER	0.832	0.656	1416.20	929.54	0.546	1108.38	605.63
A_68_P22313147	chr3:88137223-88137267	NM_024246:1111	Tmem79	INSIDE	0.832	4.222	647.69	2734.50	3.514	466.87	1640.82
A_68_P24005309	chr5:115108492-115108536	NM_022017:-84	Trpv4	PROMOTER	0.832	0.610	1417.60	864.84	0.507	1298.06	658.75
A_68_P30422258	chr15:88785483-88785529	NM_172818:-658	Ttll8	PROMOTER	0.832	1.941	1723.59	3345.69	1.615	1330.56	2148.45
A_68_P23586715	chr5:33361518-33361562	NM_011738:76	Ywhah	INSIDE	0.832	2.596	527.49	1369.50	2.159	559.05	1207.22
A_68_P30718917	chr16:43980124-43980168	NM_001007460:-983	Zdhhc23	PROMOTER	0.832	1.942	519.96	1009.58	1.615	512.95	828.65
A_68_P25372489	chr7:108450404-108450448	NM_001111111:176	Atg16l2	INSIDE	0.831	0.620	965.64	598.30	0.515	848.32	436.64
A_68_P23281850	chr4:126430722-126430766	NM_001035525:-54	AU040320	DIVERGENT_PROMOTER	0.831	0.619	1124.53	695.96	0.514	950.16	488.38
A_68_P21617368	chr2:127952024-127952068	NM_009754:273	Bcl2l11	INSIDE	0.831	0.368	1812.74	667.93	0.306	1235.62	378.27
A_68_P20975269	chr2:5636008-5636052	NM_177343:-320	Camk1d	PROMOTER	0.831	0.525	1297.47	681.07	0.436	1026.33	447.84
A_68_P24010912	chr5:116112718-116112762	NM_001080808:68828	Ccdc64	INSIDE	0.831	2.357	423.45	998.19	1.958	382.60	749.20
A_68_P26554288	chr9:59450755-59450799	NM_175235:24633	Celf6	INSIDE	0.831	2.229	495.55	1104.70	1.852	404.11	748.57
A_68_P25654578	chr8:11312336-11312380	NM_009931:468	Col4a1	INSIDE	0.831	0.619	1687.39	1044.18	0.514	1278.63	657.79
A_68_P21603039	chr2:125331555-125331599	NM_007993:598	Fbn1	INSIDE	0.831	0.613	863.59	529.22	0.509	710.15	361.66
A_68_P22649285	chr3:151874067-151874111	NM_057172:667	Fubp1	INSIDE	0.831	0.499	1870.83	934.26	0.415	1419.14	589.27
A_68_P29083952	chr13:60278886-60278930	NM_008086:-12	Gas1	PROMOTER	0.831	0.706	2005.48	1415.34	0.587	1776.31	1042.19
A_68_P25361481	chr7:106530607-106530651	NM_201352:570	Gdpd5	INSIDE	0.831	0.682	1666.57	1137.33	0.567	1276.94	723.83
A_68_P25010079	chr7:26165188-26165232	NM_001039507:9915	Lipe	INSIDE	0.831	2.240	1581.31	3542.75	1.862	1160.07	2160.43
A_68_P31142265	chr17:31986788-31986832	NM_010831:5927	Sik1	INSIDE	0.831	2.537	649.81	1648.84	2.108	413.00	870.65

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31155202	chr17:34809736-34809780	NM_031176:2279	Tnxb	INSIDE	0.831	2.419	1549.30	3748.11	2.010	1240.71	2493.58
A_68_P28813402	chr13:8870285-8870334	NM_172445:-21	Wdr37	PROMOTER	0.831	0.630	928.03	584.44	0.523	713.09	373.02
A_68_P24020116	chr5:117807608-117807652	NM_021539:317	Wsb2	INSIDE	0.831	1.928	703.28	1356.16	1.603	673.01	1078.99
A_68_P30132825	chr15:35256447-35256491	BC048602:1822		INSIDE	0.831	2.556	477.12	1219.30	2.123	492.32	1045.20
A_68_P27571288	chr11:6963967-6964011	NM_009622:497	Adcy1	INSIDE	0.830	0.588	1061.37	623.97	0.488	813.31	396.69
A_68_P29578141	chr14:47380448-47380492	NM_028222:255	Cdkn3	INSIDE	0.830	0.425	1282.64	545.50	0.353	1117.93	394.69
A_68_P31493067	chr18:11054984-11055028	NM_010258:2499	Gata6	INSIDE	0.830	0.508	2117.02	1076.38	0.422	1700.34	717.60
A_68_P29071678	chr13:58230674-58230718	NM_029872:-779	Hnrnpa0	PROMOTER	0.830	0.499	1944.86	970.58	0.414	1396.62	578.44
A_68_P25503741	chr7:134185905-134185949	NM_145588:8	Kif22	INSIDE	0.830	0.594	1063.83	631.90	0.493	874.09	430.69
A_68_P23615666	chr5:38208748-38208792	NM_010835:7054	Msx1	DOWNSTREAM	0.830	0.539	987.77	532.82	0.448	782.37	350.19
A_68_P25394030	chr7:112884773-112884817	NM_025897:304	Rrp8	INSIDE	0.830	0.655	1826.48	1196.84	0.544	1597.32	868.74
A_68_P21116392	chr2:32467870-32467914	NM_001025310:5412	St6galnac6	INSIDE	0.830	2.381	1443.90	3437.73	1.977	1054.61	2085.19
A_68_P20261296	chr1:59030751-59030795	NM_172656:358	Stradb	INSIDE	0.830	0.315	1861.15	586.90	0.262	1580.32	413.76
A_68_P31106587	chr17:25970332-25970376	NM_019719:-48	Stub1	PROMOTER	0.830	0.494	1456.73	719.43	0.410	1026.08	420.59
A_68_P32700068	chrX:137134513-137134557	NM_001077364:527	Tsc22d3	INSIDE	0.830	3.434	10152.40	34866.77	2.849	4142.57	11802.72
A_68_P27926121	chr11:75259177-75259221	NM_138950:9021	Wdr81	INSIDE	0.830	2.860	1817.91	5199.44	2.374	1406.09	3337.43
A_68_P31166726	chr17:37139890-37139935	NR_033137:-698	Zfp57	PROMOTER	0.830	1.750	5450.29	9538.82	1.453	3978.80	5782.52
A_68_P23226518	chr4:115570734-115570778	ENSMUST00000165938:7486		INSIDE	0.830	0.426	1678.02	715.16	0.354	1251.63	442.56
A_68_P32121151	chr19:42507010-42507054	NM_145123:-759	Crtac1	PROMOTER	0.829	0.681	3644.99	2481.41	0.564	2969.64	1675.25
A_68_P23185129	chr4:106233508-106233552	NM_053272:-112	Dhcr24	PROMOTER	0.829	0.595	3823.78	2274.70	0.493	3141.11	1548.55
A_68_P31329271	chr17:70865401-70865445	NM_001128180:-6027	Dlgap1	PROMOTER	0.829	2.840	1784.23	5067.56	2.354	1370.05	3225.01
A_68_P23335295	chr4:136249748-136249792	NM_010142:142080	Ephb2	INSIDE	0.829	2.350	1439.96	3383.47	1.947	1171.93	2281.98
A_68_P21874768	chr2:174156475-174156519	NM_001077510:907	Gnas	INSIDE	0.829	0.627	5082.01	3183.94	0.519	3811.55	1979.83
A_68_P24990866	chr7:19590929-19590973	NM_178757:1537	Irf2bp1	INSIDE	0.829	1.912	1160.99	2219.45	1.584	944.37	1496.27
A_68_P28834525	chr13:13683099-13683143	NM_010748:445	Lyst	INSIDE	0.829	0.402	1498.25	602.83	0.333	1166.06	388.73
A_68_P23229427	chr4:116136423-116136467	NM_001042743:344	Mast2	INSIDE	0.829	2.254	754.76	1701.02	1.869	729.97	1364.56
A_68_P25972609	chr8:77736900-77736944	NM_029182:-920	Rasd2	PROMOTER	0.829	0.607	1270.00	770.72	0.503	961.34	483.77
A_68_P27278808	chr10:79230093-79230137	NR_027505:-428	Rnf126	DIVERGENT_PROMOTER	0.829	0.486	1948.86	947.35	0.403	1529.51	616.10
A_68_P30386712	chr15:82952941-82952985	NM_029101:269	Rrp7a	INSIDE	0.829	0.613	1122.46	687.69	0.508	996.88	506.45
A_68_P28070585	chr11:100721516-100721560	NM_001164062:-259	Stat5a	PROMOTER	0.829	2.175	624.83	1359.20	1.803	594.69	1072.06
A_68_P27356009	chr10:93308576-93308623	NM_183199:14300	Usp44	INSIDE	0.829	3.633	412.48	1498.74	3.011	411.78	1239.98
A_68_P22164434	chr3:57379528-57379572	NM_133784:248	Wwtr1	INSIDE	0.829	0.675	1800.26	1215.36	0.560	1482.64	830.15
A_68_P29703314	chr14:71166767-71166811	NM_023045:-353	Xpo7	DIVERGENT_PROMOTER	0.829	0.661	958.15	633.03	0.547	847.36	463.88
A_68_P22118944	chr3:49186715-49186759			Unknown	0.829	1.930	1943.15	3750.65	1.600	1557.72	2492.21
A_68_P23818499	chr5:77286360-77286404	NM_001163793:16759	C530008M17Rik	INSIDE	0.828	3.015	2264.38	6827.67	2.497	1496.12	3735.72
A_68_P25083571	chr7:50930445-50930489	NM_145582:3066	Ctu1	INSIDE	0.828	4.649	898.16	4175.55	3.851	810.04	3119.69
A_68_P23600267	chr5:35740761-35740805	NM_010445:9017	Hmx1	DOWNSTREAM	0.828	0.341	1603.41	546.62	0.282	1197.28	338.08
A_68_P21901454	chr2:179838474-179838518	NM_133849:431	Hrh3	INSIDE	0.828	0.445	1345.15	599.01	0.369	1118.61	412.45
A_68_P21842272	chr2:168396475-168396519	NM_001136073:19195	Nfatc2	INSIDE	0.828	2.861	3159.20	9037.90	2.370	2507.05	5940.78
A_68_P23354399	chr4:139377567-139377611	NM_011039:11295	Pax7	INSIDE	0.828	0.559	2494.24	1394.72	0.463	1864.31	863.28
A_68_P25091450	chr7:52409544-52409588	NM_029406:-201	Pih1d1	PROMOTER	0.828	0.673	2825.45	1900.65	0.557	1866.22	1038.85
A_68_P21750311	chr2:152460303-152460347	NM_009047:7581	Rem1	INSIDE	0.828	2.574	1374.88	3538.98	2.132	1225.80	2613.35
A_68_P25228921	chr7:80554435-80554479	NM_177740:34051	Rgma	INSIDE	0.828	2.280	3245.69	7399.53	1.887	2781.12	5247.67
A_68_P26023615	chr8:87604389-87604433	NM_026399:235	Wdr83	INSIDE	0.828	0.683	4115.69	2810.43	0.565	3139.07	1774.40
A_68_P25035565	chr7:31993563-31993607	AK141529:209		INSIDE	0.828	0.637	1246.25	794.30	0.528	946.47	499.71
A_68_P31933117	chr19:6184699-6184743	NM_001165919:311	1700123I01Rik	INSIDE	0.827	3.716	168.06	624.46	3.074	175.43	539.28
A_68_P24994777	chr7:20282272-20282316	NM_009696:2221	Apoe	INSIDE	0.827	2.187	732.38	1601.67	1.809	577.31	1044.13
A_68_P24004990	chr5:115060897-115060941	NM_001004180:42659	BC057022	INSIDE	0.827	3.137	1875.72	5883.63	2.594	1205.40	3127.09
A_68_P23361907	chr4:140616661-140616705	NM_001145958:-222	Crocc	PROMOTER	0.827	0.633	1836.39	1162.23	0.524	1280.16	670.39
A_68_P28737553	chr12:111517859-111517903	NM_172119:441	Dio3	INSIDE	0.827	0.619	1284.72	795.49	0.512	1198.90	614.15
A_68_P29695818	chr14:69955482-69955526	NM_026174:297	Entpd4	INSIDE	0.827	2.253	1246.07	2807.53	1.864	1090.53	2032.43

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25828171	chr8:46136649-46136693	NM_001081286:101109	Fat1	INSIDE	0.827	2.372	1211.51	2873.83	1.962	938.46	1841.67
A_68_P25198318	chr7:75309835-75309879	NM_010513:212714	Igf1r	INSIDE	0.827	1.939	1005.87	1950.49	1.603	788.23	1263.68
A_68_P31114983	chr17:27340878-27340922	NM_146075:483	Lemd2	INSIDE	0.827	2.006	435.26	873.08	1.659	468.01	776.30
A_68_P25087545	chr7:51717003-51717047	NM_198250:19168	Lrrc4b	INSIDE	0.827	1.875	852.69	1598.54	1.551	705.59	1094.11
A_68_P31731072	chr18:56722122-56722166	NM_001162989:-78	Phax	DIVERGENT_PROMOTER	0.827	0.637	960.63	611.67	0.527	757.38	398.86
A_68_P31862861	chr18:80389593-80389637	NM_199197:7744	Rbfa	INSIDE	0.827	4.134	769.33	3180.71	3.417	628.46	2147.64
A_68_P30489327	chr15:100883994-100884038	NM_011323:117315	Scn8a	DOWNSTREAM	0.827	3.412	296.51	1011.57	2.823	316.48	893.44
A_68_P31020946	chr17:6079495-6079539	NM_001111017:223	Serac1	INSIDE	0.827	0.486	2595.49	1260.14	0.402	1922.38	771.91
A_68_P26766660	chr9:99776718-99776762	NM_011440:-151	Sox14	PROMOTER	0.827	0.504	1302.44	656.74	0.417	1120.07	467.29
A_68_P21116281	chr2:32449587-32449631	NM_001025311:-5620	St6galnac6	PROMOTER	0.827	2.726	831.09	2265.55	2.254	734.49	1655.57
A_68_P21092315	chr2:28496957-28497001	NM_022887:216	Tsc1	INSIDE	0.827	0.711	1778.38	1264.33	0.588	1489.84	875.79
A_68_P31369876	chr17:78600703-78600747	NM_015800:1137	Crim1	INSIDE	0.826	0.464	1964.46	911.11	0.383	1599.80	612.63
A_68_P20831360	chr1:174102609-174102653	NM_153555:24485	Dcaf8	INSIDE	0.826	3.441	625.86	2153.52	2.843	584.37	1661.30
A_68_P21423682	chr2:91470084-91470128	NM_010168:6465	F2	INSIDE	0.826	2.118	1072.42	2271.42	1.750	907.85	1589.14
A_68_P30422458	chr15:88813404-88813448	NM_031260:3	Mov10l1	INSIDE	0.826	2.012	530.31	1066.91	1.663	468.51	778.93
A_68_P25590418	chr7:148879577-148879621	NM_023566:3338	Muc2	INSIDE	0.826	2.473	552.39	1365.86	2.043	482.22	985.28
A_68_P26500012	chr9:49605941-49605986	NM_001081445:1211	Ncam1	INSIDE	0.826	0.625	1049.40	655.37	0.516	791.02	407.81
A_68_P22680847	chr3:157230503-157230547	NM_011196:669	Ptger3	INSIDE	0.826	0.665	882.49	586.46	0.549	792.51	434.77
A_68_P26578200	chr9:63605412-63605456	NM_016769:367	Smad3	INSIDE	0.826	0.660	1333.86	880.00	0.545	1038.51	566.23
A_68_P27466126	chr10:114237761-114237805	NM_146241:644	Trhde	INSIDE	0.826	0.710	1484.59	1053.78	0.586	1252.40	734.49
A_68_P20976551	chr2:5872361-5872405	NM_001081132:-132	Upf2	DIVERGENT_PROMOTER	0.826	0.650	1793.21	1165.60	0.537	1449.56	778.71
A_68_P24183689	chr5:149996098-149996142	NM_001013378:-15	Uspl1	DIVERGENT_PROMOTER	0.826	2.792	1030.66	2877.36	2.307	884.23	2039.95
A_68_P29493853	chr14:29318903-29318947	NM_009524:266	Wnt5a	INSIDE	0.826	0.426	1634.94	695.92	0.352	1287.60	452.89
A_68_P26082681	chr8:97852582-97852626	NM_024467:3246	Zfp319	INSIDE	0.826	2.356	782.59	1843.73	1.946	696.37	1355.32
A_68_P27360774	chr10:94151095-94151139	NR_015524:242	4932415G12Rik	INSIDE	0.825	0.435	1890.30	822.10	0.359	1557.69	559.20
A_68_P25190568	chr7:73985326-73985370	NM_001033877:728	Adamts17	INSIDE	0.825	0.498	1256.99	625.60	0.410	1037.68	425.89
A_68_P32031151	chr19:25746889-25746933	NM_145831:10	Dmrt2	INSIDE	0.825	0.578	1111.70	642.01	0.477	987.56	470.65
A_68_P29055899	chr13:55672091-55672135	NM_001162881:-776	Fam193b	PROMOTER	0.825	0.659	1536.79	1012.90	0.544	1209.16	657.76
A_68_P22293157	chr3:84618617-84618661	NM_001177773:-860	Fbxw7	PROMOTER	0.825	0.577	2719.81	1569.79	0.476	2222.88	1058.36
A_68_P23284716	chr4:127003696-127003740	NM_008126:2651	Gjb3	INSIDE	0.825	2.684	1032.52	2771.60	2.215	749.37	1659.52
A_68_P26810120	chr9:107537483-107537527	NM_008138:169	Gnai2	INSIDE	0.825	0.555	1934.99	1074.55	0.458	1354.21	620.09
A_68_P24828013	chr6:126594315-126594359	NM_010595:1483	Kcna1	INSIDE	0.825	0.576	1828.48	1052.30	0.475	1493.19	708.83
A_68_P27285757	chr10:80297352-80297396	NM_001013758:9410	Lingo3	INSIDE	0.825	2.337	2153.52	5031.72	1.928	1702.08	3281.85
A_68_P21102113	chr2:30112262-30112306	NM_177725:18996	Lrrc8a	INSIDE	0.825	2.907	325.56	946.34	2.399	305.88	733.87
A_68_P27279616	chr10:79366039-79366083	NM_001163276:5623	Med16	INSIDE	0.825	2.505	360.85	904.08	2.067	316.30	653.91
A_68_P26772682	chr9:100977752-100977796	NM_001100451:-676	Msl2	PROMOTER	0.825	0.609	1313.71	799.86	0.503	1100.47	553.09
A_68_P31713139	chr18:53577609-53577653	NM_008908:31	Ppic	INSIDE	0.825	0.599	2574.71	1541.72	0.494	1990.09	983.50
A_68_P21570878	chr2:119501345-119501389	NM_030112:563	Rtf1	INSIDE	0.825	1.723	4381.10	7549.94	1.422	2766.83	3935.70
A_68_P20149053	chr1:36614863-36614907	NM_001126047:342	Sema4c	INSIDE	0.825	0.490	1520.79	745.05	0.404	1301.49	525.89
A_68_P30478335	chr15:98957305-98957349	NM_139140:51	Spats2	INSIDE	0.825	2.452	10006.92	24536.77	2.023	6962.91	14088.64
A_68_P21796151	chr2:160472451-160472495	NM_009408:840	Top1	INSIDE	0.825	0.630	2043.12	1286.59	0.519	1645.45	854.70
A_68_P21839205	chr2:167875907-167875952			Unknown	0.825	0.475	1308.14	620.73	0.392	1032.08	404.19
A_68_P32565210	chrX:98893741-98893785	ENSMUST00000073812:-6573		PROMOTER	0.825	2.088	2308.74	4820.56	1.723	921.05	1587.24
A_68_P20644618	chr1:138112553-138112597	NM_028872:18267	5730559C18Rik	INSIDE	0.824	2.071	1224.34	2535.64	1.707	915.21	1562.68
A_68_P29413817	chr14:13655575-13655619	NM_001042617:-3	Cadps	PROMOTER	0.824	0.510	1177.83	600.28	0.420	950.08	398.87
A_68_P26249222	chr8:127578659-127578703	NM_174853:586	Disc1	INSIDE	0.824	0.608	1147.09	696.94	0.501	893.51	447.57
A_68_P23657735	chr5:46030561-46030605	NM_021416:158	Fam184b	INSIDE	0.824	0.579	1054.80	610.36	0.477	953.44	454.37
A_68_P27094069	chr10:41994845-41994889	NM_019740:1682	Foxo3	INSIDE	0.824	2.125	850.24	1806.96	1.752	803.46	1407.56
A_68_P30513463	chr16:5049834-5049878	NM_001079814:147	Glyr1	INSIDE	0.824	0.461	1626.13	750.08	0.380	1318.55	501.02
A_68_P23955547	chr5:105909960-105910004	NM_001033550:65189	Lrrc8b	INSIDE	0.824	4.012	552.75	2217.53	3.304	495.14	1636.15
A_68_P29269914	chr13:101514118-101514163	NM_001190264:474	Mrps36	INSIDE	0.824	2.606	1497.82	3902.64	2.146	1267.24	2719.56

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31110191	chr17:26569160-26569204	NM_001081656:17273	Neurl1b	INSIDE	0.824	2.006	615.25	1234.15	1.652	503.45	831.70
A_68_P31626273	chr18:37107754-37107798	NM_007766:-4566	Pcdha4	PROMOTER	0.824	1.786	1202.16	2146.84	1.472	981.29	1444.06
A_68_P24589127	chr6:82602908-82602952	NM_025882:-71	Pole4	PROMOTER	0.824	2.655	619.96	1646.11	2.187	533.87	1167.68
A_68_P26714889	chr9:89803449-89803494	NM_001039655:-1141	Rasgrf1	PROMOTER	0.824	1.831	817.48	1497.06	1.508	692.04	1043.75
A_68_P24992475	chr7:19872268-19872312	NM_001025364:-4157	Rtn2	PROMOTER	0.824	2.230	771.60	1720.57	1.837	764.72	1404.83
A_68_P26823387	chr9:110283734-110283778	NM_001001144:47960	Scap	INSIDE	0.824	1.906	876.48	1670.65	1.571	733.14	1151.43
A_68_P28314928	chr12:29435138-29435182	NM_001161410:99	Ttc15	INSIDE	0.824	0.508	1511.76	767.98	0.419	1279.59	535.52
A_68_P21533268	chr2:113057184-113057228	ENSMUST00000099579:-3		PROMOTER	0.824	3.295	172.06	566.94	2.714	202.89	550.70
A_68_P31933968	chr19:6320770-6320814	NM_001033342:14336	Cdc42bpg	INSIDE	0.823	1.891	826.44	1562.76	1.557	652.08	1015.16
A_68_P27997873	chr11:87916729-87916773	NM_198013:4103	Cuedc1	INSIDE	0.823	1.930	778.48	1502.72	1.588	695.98	1105.09
A_68_P20639341	chr1:137326555-137326604	NM_153774:489	Ipo9	INSIDE	0.823	2.473	4257.68	10528.41	2.036	2811.02	5722.20
A_68_P30346593	chr15:76009282-76009326	NM_201394:16836	Plec	INSIDE	0.823	3.693	324.22	1197.19	3.039	299.88	911.30
A_68_P30577647	chr16:18128056-18128100	NM_022982:280	Rtn4r	INSIDE	0.823	0.666	2499.02	1663.55	0.548	2189.30	1198.97
A_68_P24763847	chr6:114081056-114081100	NM_172890:-156	Slc6a11	PROMOTER	0.823	0.692	1395.60	965.66	0.569	1263.33	719.06
A_68_P29117521	chr13:69878252-69878296	NM_001145162:501	Ube2ql1	INSIDE	0.823	0.683	1804.11	1233.10	0.563	1467.36	825.74
A_68_P27177057	chr10:60293808-60293852	NM_029770:499	Unc5b	INSIDE	0.823	0.577	1068.23	615.91	0.474	881.75	418.29
A_68_P26744826	chr9:95855075-95855119	NM_011916:-82	Xrn1	PROMOTER	0.823	0.631	2724.72	1719.43	0.520	2035.75	1057.74
A_68_P26082678	chr8:97852139-97852183	NM_024467:3690	Zfp319	INSIDE	0.823	2.659	504.27	1340.89	2.188	450.26	985.17
A_68_P21839460	chr2:167924365-167924409	NM_021409:17883	Pard6b	INSIDE	0.822	2.357	1429.97	3370.88	1.938	1197.95	2321.38
A_68_P21839461	chr2:167924453-167924497	NM_021409:17971	Pard6b	INSIDE	0.822	2.900	1784.44	5175.47	2.384	1438.31	3429.20
A_68_P27431037	chr10:107769728-107769772	NM_054056:506	Pawr	INSIDE	0.822	0.559	1056.42	590.89	0.460	964.80	443.47
A_68_P31626317	chr18:37114129-37114173	NM_009959:-5943	Pcdha5	PROMOTER	0.822	3.480	2306.08	8024.77	2.859	1562.60	4467.33
A_68_P26237922	chr8:125626652-125626696	NR_028128:-283	Snord68	PROMOTER	0.822	0.472	1328.56	626.66	0.388	1156.25	448.36
A_68_P28520551	chr12:71553926-71553970	NM_028339:-192	Tmx1	PROMOTER	0.822	0.504	1094.21	551.81	0.414	802.27	332.41
A_68_P29438119	chr14:19159713-19159757	NM_009455:4624	Ube2e1	INSIDE	0.822	0.712	1979.15	1409.66	0.586	1744.52	1021.48
A_68_P26139676	chr8:108939349-108939393	NM_011764:132	Zfp90	INSIDE	0.822	0.634	1158.61	734.07	0.521	875.79	456.12
A_68_P31256676	chr17:56651744-56651788	NM_011483:140	Znrf4	INSIDE	0.822	1.878	691.37	1298.27	1.544	611.57	944.01
A_68_P31175212	A_68_P31175212			Unknown	0.822	5.231	929.87	4864.38	4.302	668.87	2877.32
A_68_P26276226	chr9:4260571-4260615			Unknown	0.822	2.186	1243.11	2718.05	1.798	1022.85	1838.69
A_68_P24830750	chr6:127059445-127059489	NM_177003:104	9630033F20Rik	INSIDE	0.821	0.573	1803.02	1034.02	0.471	1466.12	690.02
A_68_P31637167	chr18:39152800-39152844	NM_175164:24	Arhgap26	INSIDE	0.821	0.361	1667.86	601.65	0.296	1398.74	414.48
A_68_P32111333	chr19:40906458-40906502	NM_172839:712	Ccnj	INSIDE	0.821	2.290	632.98	1449.54	1.879	544.68	1023.72
A_68_P24994309	chr7:20189517-20189561	NM_016680:279	Clasrp	INSIDE	0.821	0.701	1272.87	892.06	0.576	1052.60	605.80
A_68_P31540304	chr18:20716579-20716623	NM_007883:-16	Dsg2	PROMOTER	0.821	0.619	1397.11	865.46	0.509	1097.69	558.26
A_68_P20613817	chr1:133034698-133034742	NM_145508:91	Dyrk3	INSIDE	0.821	2.595	366.79	951.96	2.131	319.06	679.81
A_68_P25827834	chr8:46095559-46095614	NM_001081286:60025	Fat1	INSIDE	0.821	2.238	538.62	1205.17	1.838	477.07	876.83
A_68_P21102110	chr2:30111958-30112002	NM_177725:18692	Lrrc8a	INSIDE	0.821	2.215	1155.02	2558.82	1.818	968.74	1761.40
A_68_P32140496	chr19:45857387-45857431	NM_023799:373	Mgea5	INSIDE	0.821	0.534	1036.11	553.01	0.438	857.47	375.52
A_68_P27349650	chr10:92185045-92185089	NM_008682:97	Nedd1	INSIDE	0.821	0.539	1124.68	606.41	0.443	949.17	420.24
A_68_P23244925	chr4:118992833-118992877	NM_028677:274	Ppih	INSIDE	0.821	0.577	1732.38	999.65	0.473	1247.07	590.49
A_68_P25091649	chr7:52437106-52437150	NM_053256:764	Pth2	INSIDE	0.821	0.435	1245.67	541.48	0.357	920.81	328.58
A_68_P28707013	chr12:106270418-106270462	NR_028576:-881	Scarna13	PROMOTER	0.821	0.590	1257.06	741.17	0.484	1078.69	521.88
A_68_P30360709	chr15:78370273-78370318	NM_009218:4480	Sstr3	INSIDE	0.821	2.353	729.54	1716.49	1.932	607.47	1173.52
A_68_P30176272	chr15:43308622-43308666	NM_025736:-130	Ttc35	PROMOTER	0.821	0.455	1580.20	719.45	0.374	1384.05	517.59
A_68_P24302938	chr6:24615029-24615073	NM_028459:-55	Wasl	PROMOTER	0.821	0.581	1880.17	1092.74	0.477	1700.76	811.20
A_68_P24427166	chr6:48388473-48388517	NM_001085415:6595	Zfp467	INSIDE	0.821	1.941	2733.78	5305.90	1.593	2381.77	3793.85
A_68_P31022094	chr17:6256953-6256997	ENSMUST00000121576:3072		DOWNSTREAM	0.821	0.676	1249.79	845.23	0.555	1161.31	644.54
A_68_P27975823	chr11:83993524-83993568	ENSMUST00000137500:172		INSIDE	0.821	2.059	1399.52	2881.46	1.690	1258.28	2126.38
A_68_P27843672	chr11:60352207-60352251	NM_172943:1044	Alkbh5	INSIDE	0.820	0.555	1121.80	622.61	0.455	915.91	416.92
A_68_P30484703	chr15:100058755-100058799	NM_007497:487	Atf1	INSIDE	0.820	3.124	198.88	621.25	2.562	280.55	718.84
A_68_P31925372	chr19:4839600-4839644	NM_207268:257	Ccdc87	INSIDE	0.820	1.835	1270.30	2330.91	1.504	1092.45	1643.53

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25230684	chr7:80885602-80885646	NM_001162532:432	Fam174b	INSIDE	0.820	0.463	1806.77	836.71	0.380	1562.77	593.59
A_68_P24476403	chr6:56654673-56654717	NM_025520:-1	Lsm5	PROMOTER	0.820	0.489	1126.32	550.58	0.401	939.16	376.62
A_68_P31632607	chr18:38359003-38359047	NM_029357:10392	Pcdh1	INSIDE	0.820	2.188	531.96	1163.87	1.793	427.51	766.54
A_68_P22165656	chr3:57651792-57651836	NM_019410:-135	Pfn2	PROMOTER	0.820	0.365	2647.45	967.06	0.300	2277.47	682.23
A_68_P32075619	chr19:33466689-33466733	NM_001146342:75	Rnls	INSIDE	0.820	1.736	1218.37	2114.60	1.424	1076.53	1532.83
A_68_P30363495	chr15:78798496-78798540	NM_001039155:20365	Triobp	INSIDE	0.820	2.378	2642.41	6284.61	1.951	1781.52	3475.56
A_68_P21433076	chr2:93028001-93028045	NM_001025246:282	Trp53i11	INSIDE	0.820	0.691	1250.08	863.62	0.566	1004.82	568.94
A_68_P22168177	chr3:58220956-58221000	NM_001081229:1368	Tsc22d2	INSIDE	0.820	3.239	347.65	1126.19	2.656	322.18	855.65
A_68_P22970879	chr4:63156617-63156661	NM_001008791:347	Whrn	INSIDE	0.820	0.640	2340.97	1497.08	0.524	1908.12	1000.19
A_68_P30425031	chr15:89240528-89240572	NM_001162882:144	1700007E06Rik	INSIDE	0.819	2.012	1442.96	2902.61	1.648	1171.78	1931.10
A_68_P23262656	chr4:123088950-123088994	NM_001167918:182	D830031N03Rik	INSIDE	0.819	0.665	1689.79	1124.17	0.545	1278.35	696.94
A_68_P31099849	chr17:24986693-24986737	NM_023480:533	Fahd1	INSIDE	0.819	2.067	986.71	2039.36	1.693	933.85	1580.62
A_68_P28176853	chr11:119129394-119129438	NM_008064:95	Gaa	INSIDE	0.819	2.064	959.63	1980.90	1.690	902.90	1525.92
A_68_P24116582	chr5:135964932-135964981	NM_146001:56036	Hip1	INSIDE	0.819	0.526	1066.04	560.53	0.431	913.01	393.11
A_68_P25528906	chr7:138686742-138686786	NM_008257:288	Hmx3	INSIDE	0.819	0.654	1224.61	800.79	0.535	965.53	516.87
A_68_P30501057	chr15:102796954-102796998	NM_010462:-250	Hoxc10	PROMOTER	0.819	0.536	1918.77	1029.28	0.439	1366.28	600.03
A_68_P25095291	chr7:53074739-53074783	NM_145963:5357	Kcnj14	INSIDE	0.819	1.992	1523.38	3035.18	1.632	1425.05	2325.57
A_68_P30939711	chr16:87432394-87432438	NM_001081068:435	Ltn1	INSIDE	0.819	0.647	2196.34	1420.48	0.530	1700.69	901.16
A_68_P27279591	chr10:79362212-79362259	NM_001163276:9448	Med16	INSIDE	0.819	2.057	1609.00	3309.68	1.684	1268.24	2136.25
A_68_P26134882	chr8:108138235-108138279	NR_035492:-1109	Mir1966	PROMOTER	0.819	0.488	1178.97	575.24	0.400	1187.37	474.76
A_68_P30423620	chr15:88997813-88997857	NM_001159521:6446	Plxnb2	INSIDE	0.819	2.109	1309.57	2761.50	1.727	1019.90	1761.59
A_68_P23232474	chr4:116782205-116782250	NM_008958:13267	Ptch2	INSIDE	0.819	2.659	1172.81	3118.36	2.177	1016.94	2213.91
A_68_P21780566	chr2:157854552-157854596	NM_027434:45	Rprd1b	INSIDE	0.819	0.701	2164.36	1516.83	0.574	1758.62	1009.21
A_68_P27936385	chr11:77029455-77029499	NM_177710:-450	Ssh2	PROMOTER	0.819	0.579	942.93	545.51	0.474	828.32	392.25
A_68_P28636740	chr12:93017016-93017060	NM_175367:7838	Ston2	INSIDE	0.819	1.887	950.99	1794.46	1.545	801.41	1237.95
A_68_P22059538	chr3:36588855-36588899	NM_019510:213	Trpc3	INSIDE	0.819	2.044	634.93	1297.53	1.673	644.18	1077.85
A_68_P25158146	chr7:66484168-66484212	NM_001033962:69	Ube3a	INSIDE	0.819	0.620	917.26	569.06	0.508	732.20	372.02
A_68_P22413522	chr3:108394356-108394400	NM_181400:183	Wdr47	INSIDE	0.819	0.643	1740.14	1119.49	0.527	1466.23	772.95
A_68_P31206536	chr17:46520399-46520443	NM_207671:-294	Zfp318	PROMOTER	0.819	0.488	1579.77	770.62	0.399	1296.77	517.93
A_68_P29961930	chr14:122873605-122873656	NM_009574:-975	Zic2	DIVERGENT_PROMOTER	0.819	3.206	673.75	2159.84	2.625	608.70	1598.08
A_68_P29033260	chr13:51690350-51690394			Unknown	0.819	1.635	5981.68	9779.46	1.339	4571.47	6120.90
A_68_P27556423	chr11:4118542-4118586	NM_028022:311	Gatsl3	INSIDE	0.818	0.698	1597.53	1114.46	0.571	1371.65	783.19
A_68_P28156584	chr11:115836130-115836174	NM_001005608:114	Itgb4	INSIDE	0.818	0.534	1004.05	536.00	0.437	949.08	414.30
A_68_P28201374	chr12:4599811-4599855	NM_001198969:19	Itsn2	INSIDE	0.818	2.360	334.47	789.23	1.930	330.09	637.23
A_68_P25394536	chr7:112959464-112959508	NM_025301:115	Mrpl17	INSIDE	0.818	0.585	2305.70	1349.82	0.479	2005.00	960.49
A_68_P21626036	chr2:129513877-129513921	NM_018863:1706	Pdyn	INSIDE	0.818	2.371	2654.47	6293.01	1.939	2296.96	4454.06
A_68_P20053920	chr1:16095231-16095275	NM_133832:-710	Rdh10	DIVERGENT_PROMOTER	0.818	0.636	1131.41	720.10	0.521	1088.96	567.19
A_68_P31412096	chr17:86084881-86084925	NM_011380:2692	Six2	INSIDE	0.818	0.497	2138.77	1062.09	0.406	1611.16	654.61
A_68_P27287002	chr10:80494365-80494409	NM_134135:2271	Slc39a3	INSIDE	0.818	2.052	1457.52	2990.17	1.678	1184.88	1987.84
A_68_P25235045	chr7:81649413-81649459	NM_001038643:50230	Slco3a1	INSIDE	0.818	2.350	1180.55	2774.81	1.923	974.02	1873.02
A_68_P26887820	chr9:122075655-122075699	NM_001164572:49293	Snrk	INSIDE	0.818	2.374	1952.23	4634.09	1.941	1548.11	3005.53
A_68_P20634935	chr1:136606036-136606080	NM_009307:62801	Syt2	INSIDE	0.818	1.950	1240.39	2419.25	1.596	1068.73	1705.42
A_68_P27845267	chr11:60692365-60692409	NM_001168507:154	Tmem11	INSIDE	0.818	0.674	2204.68	1486.27	0.551	1582.59	872.54
A_68_P28166382	chr11:117515746-117515790	NM_198022:166	Tnrc6c	INSIDE	0.818	0.371	1624.49	603.19	0.304	1321.58	401.33
A_68_P28682593	chr12:101758834-101758878	NM_001033213:176	Ttc7b	INSIDE	0.818	2.244	406.96	913.39	1.836	375.78	690.06
A_68_P28553604	chr12:77472031-77472075	NM_178744:800	Zbtb1	INSIDE	0.818	0.610	1110.22	677.17	0.499	856.60	427.17
A_68_P23276158	chr4:125407005-125407049			Unknown	0.818	0.537	1203.46	646.39	0.440	877.39	385.62
A_68_P21044870	chr2:19352656-19352700	ENSMUST00000137714:932		INSIDE	0.818	0.601	926.12	556.47	0.491	741.25	364.11
A_68_P33007149	chr9_random:50218-50262	NR_015516:-3168	4930526I15Rik	PROMOTER	0.817	2.443	1058.05	2584.36	1.995	894.99	1785.63
A_68_P26158887	chr8:112303066-112303110	NM_009677:549	Ap1g1	INSIDE	0.817	0.559	1196.11	668.81	0.457	1001.38	457.42
A_68_P28739139	chr12:111829705-111829749	NR_033340:143	B930059L03Rik	INSIDE	0.817	0.583	1336.19	778.83	0.476	1143.54	544.61

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28731497	chr12:110271448-110271492	NM_001163175:34957	Begain	INSIDE	0.817	1.885	733.91	1383.42	1.539	657.93	1012.77
A_68_P26790785	chr9:104164746-104164790	NM_001163026:492	Dnajc13	INSIDE	0.817	2.167	4265.32	9244.58	1.772	2836.12	5024.55
A_68_P21102298	chr2:30141644-30141688	NM_177648:208	Dolk	INSIDE	0.817	0.636	2141.72	1361.40	0.520	1725.59	896.54
A_68_P28152425	chr11:115127972-115128017	NM_010350:563	Grin2c	INSIDE	0.817	0.457	1288.04	588.57	0.373	943.08	351.96
A_68_P27924587	chr11:74982348-74982392	NM_001098203:-716	Hic1	PROMOTER	0.817	0.597	1009.92	603.14	0.488	856.57	417.84
A_68_P32385148	chrX:50341666-50341710	NM_013556:434	Hprt	INSIDE	0.817	2.559	5237.74	13405.70	2.091	2399.18	5016.67
A_68_P23439342	chr4:154938332-154938376	NM_001159637:431	Nadk	INSIDE	0.817	0.634	1284.15	813.54	0.518	1043.34	540.32
A_68_P22593186	chr3:142544706-142544750	NM_178654:240	Pkn2	INSIDE	0.817	0.583	1830.48	1067.98	0.476	1757.69	837.39
A_68_P29622736	chr14:57021701-57021745	NM_001033043:189	Rnf17	INSIDE	0.817	2.942	1239.93	3647.56	2.404	1047.13	2517.04
A_68_P27930796	chr11:76057294-76057338	NM_183263:79	Rnmtl1	INSIDE	0.817	0.617	1852.30	1143.59	0.505	1575.54	794.92
A_68_P27165506	chr10:58276067-58276111	NM_172788:-18	Sh3rf3	PROMOTER	0.817	1.841	824.17	1517.40	1.504	715.88	1076.56
A_68_P23694281	chr5:52759674-52759718	NM_011435:4654	Sod3	INSIDE	0.817	1.875	961.50	1803.16	1.533	917.69	1406.91
A_68_P31620710	chr18:36047752-36047796			Unknown	0.817	0.511	1310.63	670.35	0.418	1007.16	420.77
A_68_P27883393	chr11:67269391-67269435	ENSMUST00000136796:187		INSIDE	0.817	0.663	980.52	649.69	0.541	823.51	445.54
A_68_P20161229	chr1:38683722-38683766	NM_010678:38056	Aff3	INSIDE	0.816	0.674	1546.99	1042.07	0.550	1079.51	593.43
A_68_P29874397	chr14:105339298-105339349	NR_015593:300960	D130009I18Rik	INSIDE	0.816	3.268	733.13	2395.75	2.665	634.00	1689.91
A_68_P20613761	chr1:133026181-133026240	NM_145508:8601	Dyrk3	INSIDE	0.816	2.252	493.92	1112.10	1.837	379.24	696.70
A_68_P24005876	chr5:115199309-115199353	NM_001077360:24170	Git2	INSIDE	0.816	2.281	705.22	1608.36	1.860	661.50	1230.49
A_68_P28842029	chr13:15555847-15555891	NM_008130:313	Gli3	INSIDE	0.816	0.686	2773.12	1901.88	0.560	2305.85	1290.95
A_68_P23440310	chr4:155113949-155113993	NM_001101506:5058	Gm5151	INSIDE	0.816	2.069	681.27	1409.27	1.688	565.33	954.02
A_68_P24142210	chr5:141082443-141082487	NM_008494:-830	Lfng	PROMOTER	0.816	0.571	1190.66	680.29	0.466	1075.69	501.24
A_68_P27533638	chr10:126478027-126478071	NM_001205036:402	LOC100504608	INSIDE	0.816	1.882	7658.51	14413.93	1.535	6041.52	9274.65
A_68_P28748042	chr12:113369264-113369308	NR_029590:196	Mir203	DOWNSTREAM	0.816	0.621	1882.93	1169.30	0.507	1428.37	724.12
A_68_P25948616	chr8:72426603-72426647	NM_023312:-167	Ndufa13	PROMOTER	0.816	0.457	1212.76	554.46	0.373	993.68	370.60
A_68_P20625766	chr1:135027721-135027765	NM_133819:0	Ppp1r15b	INSIDE	0.816	0.686	2217.65	1520.60	0.560	1704.29	953.82
A_68_P22558739	chr3:136333126-136333170	NM_008913:-585	Ppp3ca	PROMOTER	0.816	0.601	1122.77	675.18	0.490	923.32	452.80
A_68_P23062649	chr4:83132368-83132412	NM_133948:-96	Psip1	PROMOTER	0.816	3.822	235.05	898.34	3.119	213.73	666.56
A_68_P31213957	chr17:47873861-47873905	NM_001161722:-103	Tcfeb	PROMOTER	0.816	0.597	1517.99	906.23	0.487	1172.66	571.23
A_68_P24639210	chr6:91423696-91423740	NM_028766:-26	Tmem43	DIVERGENT_PROMOTER	0.816	2.461	865.57	2130.10	2.009	832.68	1672.96
A_68_P25360662	chr7:106397588-106397632			Unknown	0.816	0.585	1185.61	693.53	0.477	1034.68	493.70
A_68_P22353013	chr3:96963291-96963335	NM_019800:613	Acp6	INSIDE	0.815	0.625	879.85	550.21	0.510	877.09	447.16
A_68_P26716245	chr9:90058242-90058286	NM_001003911:449	Adamts7	INSIDE	0.815	0.473	1391.93	657.90	0.385	1010.83	389.51
A_68_P23595356	chr5:34959356-34959400	NM_001024458:43016	Add1	INSIDE	0.815	3.868	868.95	3361.03	3.151	680.04	2142.87
A_68_P32573855	chrX:100810329-100810376	NR_028381:8741	B230206F22Rik	INSIDE	0.815	3.401	1140.83	3880.36	2.772	420.52	1165.76
A_68_P27281215	chr10:79601896-79601940	NM_001195268:-1786	Dos	PROMOTER	0.815	0.661	1621.12	1071.53	0.539	1301.01	700.94
A_68_P23363148	chr4:140847464-140847508	NM_010139:-9668	Epha2	PROMOTER	0.815	0.549	1673.33	918.79	0.448	1347.67	603.12
A_68_P27643872	chr11:22908277-22908321	NM_028672:-5088	Fam161a	PROMOTER	0.815	0.486	1360.31	661.32	0.396	1195.90	473.90
A_68_P26224355	chr8:123608416-123608460	NM_010426:65	Foxf1a	INSIDE	0.815	0.521	1842.14	958.97	0.424	1456.71	618.14
A_68_P30490488	chr15:101062388-101062432	NM_019518:7773	Grasp	INSIDE	0.815	1.892	1188.77	2249.15	1.542	972.73	1499.73
A_68_P30369638	chr15:79832223-79832267	NM_011057:12994	Pdgfb	INSIDE	0.815	1.843	811.88	1496.15	1.503	693.77	1042.45
A_68_P26798484	chr9:105547053-105547097	NM_001081309:1750	Pik3r4	INSIDE	0.815	3.839	2090.85	8026.68	3.127	1384.47	4329.72
A_68_P27550647	chr11:3093206-3093251	NM_030207:238	Sfi1	INSIDE	0.815	2.804	1648.32	4621.38	2.284	1615.38	3690.08
A_68_P26710369	chr9:88377894-88377938	NM_019796:-681	Syncrip	PROMOTER	0.815	0.664	1064.23	707.14	0.541	963.89	521.67
A_68_P24153533	chr5:143577184-143577235	NM_001122730:1857	Tnrc18	INSIDE	0.815	0.585	1026.14	600.34	0.477	834.57	397.82
A_68_P29613383	chr14:55251294-55251338	NM_199470:8885	Cdh24	INSIDE	0.814	2.114	1357.84	2870.73	1.720	1065.71	1833.45
A_68_P28944867	chr13:35832810-35832854	NM_001123386:-438	Cdyl	PROMOTER	0.814	0.548	1368.65	749.76	0.446	1152.88	514.25
A_68_P25186369	chr7:73254042-73254086	NM_001081163:-336	Chsy1	PROMOTER	0.814	0.614	1764.17	1082.99	0.500	1452.78	726.19
A_68_P30347860	chr15:76199569-76199613	NM_021555:263	Fam203a	INSIDE	0.814	0.558	1106.35	617.43	0.455	990.92	450.40
A_68_P32048649	chr19:28752873-28752917	NM_175459:1673	Glis3	INSIDE	0.814	0.326	2026.39	659.66	0.265	1703.27	451.43
A_68_P25953597	chr8:73240870-73240914	NM_001195253:-1549	Gm3336	PROMOTER	0.814	2.263	659.54	1492.52	1.841	553.77	1019.58
A_68_P22403735	chr3:106839334-106839378	NM_008418:277	Kcna3	INSIDE	0.814	0.547	1240.57	678.25	0.445	1076.81	478.93

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P24009624	chr5:115897187-115897231	NM_008629:17515	Msi1	INSIDE	0.814	2.107	610.25	1285.56	1.715	532.72	913.78
A_68_P31958296	chr19:11952929-11952973	NM_001011775:-7246	Olfr1419	PROMOTER	0.814	1.766	1185.98	2094.63	1.437	1045.12	1501.60
A_68_P25184946	chr7:73007817-73007861	NM_011048:817	Pcsk6	INSIDE	0.814	0.651	1019.07	663.41	0.530	805.73	427.21
A_68_P22582961	chr3:140874616-140874660	NM_008811:681	Pdha2	INSIDE	0.814	2.864	320.89	919.05	2.330	268.50	625.69
A_68_P32050333	chr19:29038408-29038452	NM_028922:21	Ppapdc2	INSIDE	0.814	3.000	263.02	789.02	2.442	278.31	679.70
A_68_P24424177	chr6:47601567-47601611	NR_002841:3505	Rn4.5s	DOWNSTREAM	0.814	2.124	4121.65	8753.93	1.730	4008.40	6933.13
A_68_P21704892	chr2:143836307-143836351	NM_024281:671	Rrbp1	INSIDE	0.814	0.560	1748.77	980.02	0.456	1488.05	678.45
A_68_P20585376	chr1:127456998-127457042	NM_028787:-572	Slc35f5	PROMOTER	0.814	0.412	1423.14	586.16	0.335	1051.52	352.38
A_68_P27533591	chr10:126467810-126467854	NM_025537:38	Tsfm	INSIDE	0.814	0.564	1271.47	716.50	0.459	1173.58	538.27
A_68_P22964917	chr4:62180863-62180907	NM_008525:213	Alad	INSIDE	0.813	0.600	2901.92	1741.03	0.487	2160.01	1052.99
A_68_P22058855	chr3:36470553-36470597	NM_009828:344	Ccna2	INSIDE	0.813	0.708	3464.00	2453.85	0.576	2706.78	1558.18
A_68_P26126979	chr8:106666779-106666826	NM_009868:41278	Cdh5	INSIDE	0.813	2.638	1011.63	2668.97	2.145	796.31	1708.27
A_68_P25677292	chr8:14894723-14894769	NM_012000:6211	Cln8	INSIDE	0.813	2.853	2042.33	5827.35	2.320	1312.90	3046.01
A_68_P28728196	chr12:109701593-109701638	NM_001043335:40590	Eml1	INSIDE	0.813	1.862	972.80	1811.73	1.515	717.48	1086.99
A_68_P30590963	chr16:21204850-21204894	NM_010143:5	Ephb3	INSIDE	0.813	0.508	1602.97	815.02	0.413	1312.40	542.27
A_68_P23973158	chr5:109058614-109058658	NM_153569:122	Gak	INSIDE	0.813	0.684	1092.64	747.73	0.557	1003.40	558.40
A_68_P25890523	chr8:59800718-59800762	NM_010402:961	Hand2	INSIDE	0.813	0.408	1284.15	524.48	0.332	1197.46	397.67
A_68_P20556979	chr1:121319156-121319200	NM_008381:-353	Inhbb	PROMOTER	0.813	0.631	1367.48	862.75	0.513	1105.20	566.60
A_68_P21840412	chr2:168094076-168094120	NM_001081134:733	Kcng1	INSIDE	0.813	1.742	5555.72	9677.14	1.416	3828.65	5420.34
A_68_P30347565	chr15:76157913-76157957	NR_028283:29	LOC100302626	INSIDE	0.813	0.514	1117.03	574.35	0.418	1000.07	417.92
A_68_P30496845	chr15:102078472-102078518	NM_001042727:-1711	Rarg	PROMOTER	0.813	3.102	991.33	3074.68	2.521	710.20	1790.41
A_68_P22336401	chr3:93248647-93248691	NM_001163098:2417	Tchh	INSIDE	0.813	0.599	1005.50	601.88	0.487	864.68	420.73
A_68_P27938059	chr11:77326725-77326769	NM_001024920:29	Trp53i13	INSIDE	0.813	0.600	3461.57	2076.97	0.488	2818.63	1374.55
A_68_P30284260	chr15:64753424-64753468	NM_009623:412	Adcy8	INSIDE	0.812	0.697	1410.75	983.76	0.566	1163.75	658.75
A_68_P31097726	chr17:24642065-24642109	NM_027937:16359	Caskin1	INSIDE	0.812	2.040	583.48	1190.42	1.656	527.38	873.16
A_68_P25843136	chr8:48798707-48798751	NM_172407:557	Cdkn2aip	INSIDE	0.812	0.544	2411.10	1311.01	0.441	2199.38	970.91
A_68_P31227867	chr17:50432626-50432673	NM_010021:275	Dazl	INSIDE	0.812	2.909	568.37	1653.12	2.362	506.03	1195.01
A_68_P28575260	chr12:81440954-81440998	NM_177267:96612	Dcaf5	INSIDE	0.812	2.048	1092.65	2237.67	1.662	829.56	1378.81
A_68_P21071850	chr2:25251471-25251515	NM_009849:99	Entpd2	INSIDE	0.812	0.652	867.39	565.96	0.530	705.75	373.91
A_68_P28080237	chr11:102417265-102417309	NM_001159492:186	Gpatch8	INSIDE	0.812	0.572	2756.72	1575.75	0.464	2120.03	984.37
A_68_P21339416	chr2:74601588-74601632	NM_010467:574	Hoxd1	INSIDE	0.812	0.673	1600.51	1076.60	0.546	1355.64	740.02
A_68_P28513153	chr12:70269731-70269775	NM_001081406:-48	Lrr1	DIVERGENT_PROMOTER	0.812	0.572	1318.55	754.63	0.465	1203.59	559.49
A_68_P21611761	chr2:126959499-126959543	NM_144818:170	Ncaph	INSIDE	0.812	0.705	5180.30	3651.13	0.572	4208.28	2408.93
A_68_P31629837	chr18:37913139-37913183	NM_033594:-2266	Pcdhga11	PROMOTER	0.812	2.617	728.16	1905.64	2.126	675.81	1436.54
A_68_P31791666	chr18:67561362-67561406	NM_026473:11000	Tubb6	INSIDE	0.812	2.212	3043.21	6732.90	1.797	2265.52	4070.50
A_68_P31925605	chr19:4878917-4878961	NM_001168517:249	Zdhhc24	INSIDE	0.812	0.592	1247.69	738.68	0.481	1055.31	507.11
A_68_P27288259	chr10:80702644-80702688	NM_001034895:6759	Zfr2	INSIDE	0.812	2.633	4258.66	11212.50	2.137	2772.79	5926.03
A_68_P26226906	chr8:123992825-123992870	ENSMUST00000127664:1558107		INSIDE	0.812	3.315	694.24	2301.22	2.691	577.83	1555.21
A_68_P27288889	chr10:80788110-80788154	NM_027381:4285	2510012J08Rik	INSIDE	0.811	2.487	601.11	1495.22	2.017	619.03	1248.71
A_68_P23225791	chr4:115457470-115457514	NM_181040:-97	Atpaf1	DIVERGENT_PROMOTER	0.811	0.683	2251.82	1538.51	0.554	2050.75	1136.43
A_68_P24098214	chr5:131915626-131915670	NM_177047:1102565	Auts2	INSIDE	0.811	2.899	1738.09	5038.31	2.352	1297.96	3052.40
A_68_P20411440	chr1:88199681-88199725	NM_145222:-93	B3gnt7	PROMOTER	0.811	0.532	1730.14	920.77	0.432	1343.21	579.70
A_68_P24786762	chr6:118369695-118369739	NM_194339:-281	Bms1	PROMOTER	0.811	0.604	1349.03	814.57	0.490	1079.91	529.11
A_68_P25589535	chr7:148725503-148725549	NM_001142681:230	Chid1	INSIDE	0.811	2.360	4701.82	11095.67	1.913	2997.19	5732.99
A_68_P25535522	chr7:139788929-139788973	NM_009123:2370	Nkx1-2	INSIDE	0.811	0.572	3907.31	2233.34	0.464	2929.32	1358.17
A_68_P30346542	chr15:76002933-76002977	NM_201394:23186	Plec	INSIDE	0.811	2.170	733.48	1591.59	1.761	615.47	1083.55
A_68_P30452811	chr15:94353830-94353874	NM_172437:20086	Pus7l	INSIDE	0.811	2.108	1546.64	3260.33	1.710	1242.22	2124.78
A_68_P30956055	chr16:90283789-90283833	NM_178923:860	Scaf4	INSIDE	0.811	0.581	884.84	514.31	0.472	708.61	334.13
A_68_P21608667	chr2:126379090-126379134	NM_011978:353	Slc27a2	INSIDE	0.811	0.600	1535.14	921.32	0.487	1263.87	615.42
A_68_P25235044	chr7:81649285-81649329	NM_001038643:50360	Slco3a1	INSIDE	0.811	1.982	1126.41	2232.41	1.608	832.74	1339.17
A_68_P22149841	chr3:54598287-54598331	NM_019483:38805	Smad9	INSIDE	0.811	1.923	1313.74	2526.80	1.561	1017.77	1588.24

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P24950521	chr7:4740854-4740898	NM_029384:286	2210411K11Rik	INSIDE	0.810	0.577	1193.00	688.53	0.467	996.58	465.66
A_68_P23542072	chr5:23980190-23980234	NM_139153:22218	Agap3	INSIDE	0.810	4.612	750.67	3461.75	3.734	915.35	3417.66
A_68_P23284201	chr4:126910870-126910914	NM_198618:64378	Dlgap3	INSIDE	0.810	1.937	908.30	1759.09	1.569	820.33	1287.45
A_68_P28577472	chr12:81859091-81859135	NM_001008423:2590	Gm1568	INSIDE	0.810	2.558	351.66	899.57	2.072	340.88	706.38
A_68_P26810384	chr9:107579026-107579070	NM_008140:2875	Gnat1	INSIDE	0.810	0.445	1947.30	866.57	0.360	1585.56	571.34
A_68_P24053125	chr5:123402247-123402291	NM_001005866:36274	Kdm2b	INSIDE	0.810	0.555	4107.41	2279.22	0.449	3196.83	1436.81
A_68_P27282555	chr10:79798362-79798406	NM_001204931:5495	Reep6	INSIDE	0.810	2.095	4137.15	8665.67	1.697	2927.22	4967.30
A_68_P26574117	chr9:62994383-62994430	NM_172446:381	Skor1	INSIDE	0.810	2.713	1677.17	4549.51	2.196	1085.81	2384.39
A_68_P28161639	chr11:116713577-116713621	NM_011358:810	Srsf2	INSIDE	0.810	0.474	2300.98	1090.07	0.384	1985.14	761.65
A_68_P20354641	chr1:75518362-75518406	NM_027886:281	Stk11ip	INSIDE	0.810	0.606	1089.98	660.13	0.491	788.50	387.02
A_68_P25049871	chr7:36322745-36322789	NM_028034:-3	Tdrd12	PROMOTER	0.810	1.992	1300.41	2590.69	1.614	1091.78	1762.30
A_68_P30388745	chr15:83319976-83320026	NM_178869:21337	Ttll1	INSIDE	0.810	2.811	1330.42	3740.39	2.279	1131.76	2578.78
A_68_P31383664	chr17:80942827-80942871	NM_001033443:20326	Cdkl4	INSIDE	0.809	2.206	1142.41	2519.93	1.784	955.18	1703.97
A_68_P29737947	chr14:77557522-77557566	NM_172813:922	Enox1	INSIDE	0.809	0.712	1395.87	994.14	0.576	1278.96	736.49
A_68_P28888883	chr13:24853418-24853464	NM_020567:366	Gmnn	INSIDE	0.809	0.634	2224.43	1410.30	0.513	1910.56	979.58
A_68_P24126247	chr5:137972597-137972641	NM_010312:1839	Gnb2	INSIDE	0.809	3.013	550.47	1658.82	2.439	497.87	1214.36
A_68_P23417688	chr4:151654062-151654106	NM_178406:5614	Gpr153	INSIDE	0.809	2.096	941.50	1973.12	1.696	821.65	1393.84
A_68_P30332045	chr15:73526210-73526254	NM_173365:11703	Gpr20	INSIDE	0.809	2.081	2135.78	4445.23	1.684	1830.62	3082.41
A_68_P28981522	chr13:42144875-42144919	NM_007772:-2493	Hivep1	PROMOTER	0.809	0.605	1930.04	1166.98	0.489	1747.64	855.27
A_68_P31201908	chr17:45710098-45710142	NM_008302:90	Hsp90ab1	INSIDE	0.809	0.591	970.15	573.25	0.478	858.97	410.81
A_68_P25088124	chr7:51807600-51807645	NM_009473:1671	Nr1h2	INSIDE	0.809	4.922	600.89	2957.48	3.979	452.34	1800.08
A_68_P29696768	chr14:70107233-70107277	NM_001146012:133	R3hcc1	INSIDE	0.809	0.710	1472.39	1045.47	0.575	1138.80	654.40
A_68_P26056688	chr8:93593942-93593986	NM_011250:-28	Rbl2	PROMOTER	0.809	1.871	812.42	1520.34	1.515	733.28	1110.58
A_68_P21420491	chr2:90910449-90910493	NM_026721:-92	Slc39a13	PROMOTER	0.809	0.671	2480.34	1664.54	0.543	1879.04	1020.27
A_68_P23232777	chr4:116828074-116828118	NR_028524:-917	Snord38a	PROMOTER	0.809	0.550	1107.02	609.04	0.445	817.91	364.09
A_68_P27365035	chr10:94879052-94879097	NM_001168655:-228	Socs2	PROMOTER	0.809	0.670	1244.63	834.35	0.542	902.89	489.81
A_68_P30686670	chr16:38563148-38563193	NM_001205287:244	Tmem39a	INSIDE	0.809	1.679	3066.36	5148.75	1.358	2307.75	3134.03
A_68_P22973923	chr4:63678590-63678634	NM_011607:29437	Tnc	INSIDE	0.809	1.926	1120.63	2158.22	1.558	905.01	1409.93
A_68_P27780099	chr11:48630768-48630812	NM_145377:103	Trim41	INSIDE	0.809	0.672	2087.89	1403.35	0.544	1867.33	1014.97
A_68_P21739505	chr2:150326509-150326553	ENSMUST00000121441:51		INSIDE	0.809	2.567	846.89	2174.05	2.078	711.46	1478.43
A_68_P22037671	chr3:32264236-32264280	NR_027966:-152	4930429B21Rik	PROMOTER	0.808	0.541	1487.56	805.02	0.437	1197.62	523.63
A_68_P21578340	chr2:120834005-120834049	NM_010761:-117	Ccndbp1	PROMOTER	0.808	1.658	7464.74	12373.25	1.339	5258.71	7041.94
A_68_P25092032	chr7:52496418-52496462	NM_007645:-2231	Cd37	PROMOTER	0.808	0.602	2903.59	1748.21	0.486	2335.67	1135.76
A_68_P31350934	chr17:74715375-74715419	NM_001146224:155	Dpy30	INSIDE	0.808	0.592	2319.89	1372.37	0.478	1777.73	850.02
A_68_P32213508	chr19:58528871-58528915	NM_010279:64	Gfra1	INSIDE	0.808	0.639	3066.61	1958.19	0.516	2452.03	1265.29
A_68_P30588158	chr16:20548336-20548380	NR_030670:271	Gm15760	INSIDE	0.808	0.616	3285.40	2023.21	0.498	2497.22	1242.59
A_68_P24687696	chr6:99642117-99642161	NM_008158:-534	Gpr27	PROMOTER	0.808	0.588	1450.95	853.32	0.475	1147.20	544.90
A_68_P23592056	chr5:34343661-34343705	NM_001001985:5050	Nat8l	INSIDE	0.808	1.815	1118.74	2030.72	1.467	871.62	1278.37
A_68_P21777847	chr2:157385700-157385749	NM_010923:-121	Nnat	PROMOTER	0.808	3.784	1602.45	6063.34	3.057	1071.00	3273.94
A_68_P29729991	chr14:76186878-76186922	NM_026232:-56	Slc25a30	PROMOTER	0.808	0.713	1605.06	1144.88	0.576	1283.88	740.06
A_68_P22313145	chr3:88136905-88136949	NM_024246:1429	Tmem79	INSIDE	0.808	3.041	2536.21	7712.57	2.458	1856.71	4563.79
A_68_P22766411	chr4:19636348-19636392	NM_177327:-230	Wwp1	PROMOTER	0.808	2.410	754.58	1818.32	1.946	650.30	1265.80
A_68_P21752665	chr2:152880537-152880585	NM_001011732:22973	Xkr7	INSIDE	0.808	2.442	605.32	1478.50	1.972	481.40	949.50
A_68_P25029849	chr7:30875328-30875372	NM_152814:179	Zfp566	INSIDE	0.808	0.733	2322.73	1701.88	0.592	1857.12	1099.79
A_68_P20770259	chr1:163072817-163072861	NM_028664:-4	Ankrd45	PROMOTER	0.807	0.430	1277.94	549.52	0.347	1132.28	393.11
A_68_P28752185	chr12:113977133-113977177	NM_001024602:16770	AW555464	INSIDE	0.807	1.928	2103.28	4055.69	1.556	1676.72	2608.87
A_68_P26554291	chr9:59451119-59451163	NM_175235:24997	Celf6	INSIDE	0.807	2.773	616.50	1709.23	2.238	565.95	1266.63
A_68_P25784086	chr8:37209993-37210038	NM_172911:52134	D8Ertd82e	INSIDE	0.807	4.372	2118.31	9260.84	3.530	1446.93	5107.13
A_68_P28196937	chr12:3808024-3808068	NM_007872:1067	Dnmt3a	INSIDE	0.807	0.678	3921.10	2658.32	0.547	2921.65	1597.77
A_68_P28748140	chr12:113383889-113383933	NM_001097621:-508	Kif26a	PROMOTER	0.807	0.661	3053.67	2018.82	0.534	1990.56	1062.45
A_68_P25266279	chr7:87508205-87508253	NM_172903:8033	Man2a2	INSIDE	0.807	2.538	807.97	2050.61	2.049	691.90	1417.75

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26783897	chr9:103014037-103014081	NM_173781:-345	Rab6b	PROMOTER	0.807	0.610	1300.75	794.03	0.493	1142.38	563.00
A_68_P31868118	chr18:81184539-81184583	NM_178280:-1243	Sall3	PROMOTER	0.807	0.607	2104.16	1276.96	0.489	1642.39	803.94
A_68_P25090670	chr7:52271335-52271379	NM_001008422:263	Scaf1	INSIDE	0.807	0.534	1326.50	707.70	0.431	986.17	424.57
A_68_P29638534	chr14:60059619-60059663	NM_001081024:74	Setdb2	INSIDE	0.807	0.614	1508.96	927.01	0.496	1304.70	646.66
A_68_P24009788	chr5:115932764-115932808	NM_001167691:1520	Sirt4	INSIDE	0.807	1.876	879.69	1650.20	1.513	717.65	1086.15
A_68_P28104292	chr11:106781905-106781949	NM_025481:103	Smurf2	INSIDE	0.807	2.268	492.89	1118.10	1.830	521.61	954.67
A_68_P23364326	chr4:141034893-141034937	NM_019763:59598	Spen	INSIDE	0.807	2.252	972.21	2189.69	1.817	819.20	1488.62
A_68_P32565191	chrX:98891432-98891476	ENSMUST00000073812:-4265		PROMOTER	0.807	2.583	1519.39	3925.27	2.084	681.01	1419.40
A_68_P28724512	chr12:109153627-109153678	NM_001079883:87972	Bcl11b	INSIDE	0.806	1.804	936.23	1689.15	1.453	817.97	1188.83
A_68_P26476240	chr9:45636562-45636606	NM_001081373:137	Cep164	INSIDE	0.806	0.512	1534.30	784.85	0.412	1037.93	427.74
A_68_P28833517	chr13:13485882-13485926	NM_031999:-13	Gpr137b	PROMOTER	0.806	0.407	1871.33	761.26	0.328	1767.45	579.64
A_68_P22082265	chr3:40754710-40754754	NM_001040399:180	Larp1b	INSIDE	0.806	0.506	2757.34	1394.25	0.408	2328.59	949.05
A_68_P23912411	chr5:97821152-97821196	NM_001033191:175	Naa11	INSIDE	0.806	2.737	1392.02	3809.31	2.204	1113.38	2454.21
A_68_P31112754	chr17:26981531-26981575	NM_008700:-3042	Nkx2-5	PROMOTER	0.806	0.664	986.58	654.64	0.535	872.69	466.99
A_68_P23435279	chr4:154338485-154338529	NM_172990:265	Pank4	INSIDE	0.806	0.748	7008.13	5239.65	0.603	5440.38	3279.40
A_68_P26345841	chr9:20986277-20986321	NM_183408:16141	Pde4a	INSIDE	0.806	0.658	1422.49	935.62	0.530	1183.91	627.84
A_68_P27287758	chr10:80616510-80616554	NM_021501:13933	Pias4	DOWNSTREAM	0.806	2.582	2208.29	5700.80	2.082	1656.90	3449.48
A_68_P31375199	chr17:79451854-79451898	NM_027455:631	Qpct	INSIDE	0.806	0.455	1506.96	684.94	0.366	1250.21	457.93
A_68_P30716740	chr16:43618606-43618656	NM_019778:371234	Zbtb20	INSIDE	0.806	3.225	291.63	940.66	2.600	266.26	692.40
A_68_P28098904	chr11:105850208-105850252	NM_009598:13709	Ace	INSIDE	0.805	2.153	1263.70	2720.57	1.733	937.11	1623.73
A_68_P27852923	chr11:62062610-62062654	NM_007413:147	Adora2b	INSIDE	0.805	0.680	1194.85	812.29	0.548	971.26	531.79
A_68_P25956773	chr8:73929899-73929944	NM_172756:11	Ankle1	INSIDE	0.805	0.690	1234.54	851.54	0.555	1100.45	610.69
A_68_P23915892	chr5:98460062-98460106	NM_133738:-103	Antxr2	PROMOTER	0.805	1.791	1316.54	2357.53	1.441	1113.46	1604.39
A_68_P28182254	chr11:119947830-119947874	NM_009734:289	Azi1	INSIDE	0.805	2.067	564.97	1167.68	1.663	491.91	818.08
A_68_P31097725	chr17:24641975-24642019	NM_027937:16269	Caskin1	INSIDE	0.805	2.003	1071.97	2147.36	1.612	943.99	1521.65
A_68_P23600188	chr5:35731369-35731413	NM_010445:-375	Hmx1	PROMOTER	0.805	0.681	1611.39	1096.57	0.548	1326.77	726.76
A_68_P20799110	chr1:168168534-168168578	NM_175296:319	Mael	INSIDE	0.805	2.481	1173.42	2911.52	1.997	1091.83	2179.88
A_68_P28178598	chr11:119410881-119410925	NM_008730:-1768	Nptx1	PROMOTER	0.805	0.516	1321.71	681.65	0.415	1150.04	477.39
A_68_P26261061	chr8:129588412-129588456	NM_001122850:479	Pard3	INSIDE	0.805	0.558	2135.35	1191.25	0.449	1819.34	817.11
A_68_P28048198	chr11:96883375-96883419	NM_031183:8514	Sp6	INSIDE	0.805	0.392	1929.87	756.05	0.315	1585.22	500.04
A_68_P24542637	chr6:72566597-72566641	NM_009444:124	Tgoln2	INSIDE	0.805	0.612	1873.19	1145.82	0.493	1377.41	678.67
A_68_P25505622	chr7:134587895-134587939	NM_175163:4756	Zfp689	INSIDE	0.805	3.294	622.58	2050.66	2.651	573.90	1521.20
A_68_P25735802	chr8:28088218-28088262	NM_001101502:433	Zfp703	INSIDE	0.805	0.429	1964.14	843.05	0.345	1512.03	522.12
A_68_P20793719	chr1:167212029-167212073			Unknown	0.805	0.565	1190.41	672.34	0.455	1014.34	461.10
A_68_P24944592	chr6:149302140-149302189	ENSMUST00000121073:184		INSIDE	0.805	2.213	1004.73	2223.04	1.781	804.25	1432.35
A_68_P30561772	chr16:14361819-14361863	NM_008576:188	Abcc1	INSIDE	0.804	0.550	1946.56	1071.20	0.442	1706.87	754.74
A_68_P28156898	chr11:115885554-115885598	NM_008211:242	H3f3b	INSIDE	0.804	0.724	1613.93	1168.55	0.582	1318.44	767.42
A_68_P23230436	chr4:116358568-116358616	NM_011034:389	Prdx1	INSIDE	0.804	0.681	1367.06	930.87	0.547	1220.62	668.25
A_68_P22889711	chr4:46633603-46633647	NM_198664:29447	Tbc1d2	INSIDE	0.804	2.316	449.16	1040.13	1.861	395.57	736.13
A_68_P25065179	chr7:38846240-38846284	AK181724:13916		INSIDE	0.804	0.557	1065.15	593.41	0.448	924.23	414.05
A_68_P32208747	chr19:57776636-57776680	NM_181415:91135	Atrnl1	INSIDE	0.803	2.043	727.90	1486.81	1.640	624.45	1024.28
A_68_P27480858	chr10:116813406-116813450	NM_001013391:601	Cpsf6	INSIDE	0.803	0.569	1725.07	982.14	0.457	1486.65	680.06
A_68_P21812643	chr2:163298309-163298353	NM_173397:35	Fitm2	INSIDE	0.803	0.685	1866.65	1279.19	0.550	1588.40	873.90
A_68_P29134818	chr13:72768061-72768105	NM_010574:1657	Irx2	INSIDE	0.803	0.589	1517.45	893.05	0.473	1213.97	573.69
A_68_P29603744	chr14:52533018-52533062	NM_001145959:123	Ndrg2	INSIDE	0.803	0.400	3052.52	1221.08	0.321	2452.61	787.53
A_68_P24432388	chr6:49345736-49345780	NM_029916:156	Stk31	INSIDE	0.803	2.409	1547.34	3727.08	1.935	1231.38	2383.00
A_68_P21900704	chr2:179710019-179710063	NM_001081092:1311	Taf4a	INSIDE	0.803	0.565	1031.24	582.59	0.453	975.21	442.22
A_68_P25805593	chr8:41509486-41509530	NM_178395:340	Zdhhc2	INSIDE	0.803	0.559	1042.91	583.03	0.449	878.56	394.41
A_68_P25009107	chr7:26010932-26010976	NM_175436:4485	Zfp526	INSIDE	0.803	1.813	1490.63	2703.15	1.456	1281.94	1865.92
A_68_P31256673	chr17:56651469-56651513	NM_011483:416	Znrf4	INSIDE	0.803	2.633	274.25	722.14	2.115	266.74	564.04
A_68_P21061278	chr2:22923647-22923691	NM_001102436:-52	Acbd5	PROMOTER	0.802	0.700	1291.24	904.21	0.561	1115.71	626.20

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P24004992	chr5:115061116-115061160	NM_001004180:42879	BC057022	INSIDE	0.802	1.940	2152.69	4175.61	1.557	1573.41	2449.08
A_68_P25592831	chr7:149268090-149268134	NM_008748:13077	Dusp8	INSIDE	0.802	2.104	548.87	1154.99	1.688	489.26	826.00
A_68_P25827836	chr8:46095713-46095772	NM_001081286:60181	Fat1	INSIDE	0.802	2.370	1018.95	2414.46	1.899	840.91	1597.24
A_68_P29625865	chr14:57676961-57677005	NM_016975:-200	Gja3	PROMOTER	0.802	0.446	1531.27	683.57	0.358	1320.60	472.86
A_68_P30332048	chr15:73526555-73526599	NM_173365:11359	Gpr20	INSIDE	0.802	4.275	1332.35	5695.48	3.429	1108.44	3801.11
A_68_P23303539	chr4:130505898-130505942	NM_010769:5621	Matn1	INSIDE	0.802	2.215	724.86	1605.38	1.776	677.90	1203.81
A_68_P26709443	chr9:88222649-88222693	NM_011851:224	Nt5e	INSIDE	0.802	0.716	1439.48	1031.13	0.574	1168.88	671.31
A_68_P22356138	chr3:97555598-97555642	NM_178080:16317	Pde4dip	INSIDE	0.802	2.165	1110.03	2403.35	1.736	926.49	1608.66
A_68_P31162033	chr17:36116300-36116344	NR_028516:-354	Prr3	PROMOTER	0.802	0.451	1637.29	738.71	0.362	1350.99	488.73
A_68_P24759853	chr6:113445166-113445210	NM_172487:6624	Prrt3	INSIDE	0.802	2.014	1921.37	3869.54	1.614	1581.80	2553.77
A_68_P28323157	chr12:30687355-30687399	NM_181395:64476	Pxdn	INSIDE	0.802	2.150	2239.03	4814.49	1.724	1524.63	2628.58
A_68_P32148714	chr19:47341896-47341940	NM_001164717:196983	Sh3pxd2a	INSIDE	0.802	1.983	626.77	1242.83	1.590	546.83	869.74
A_68_P24657049	chr6:94450199-94450243	NM_026255:-87	Slc25a26	PROMOTER	0.802	0.594	893.98	531.23	0.477	680.67	324.54
A_68_P27316751	chr10:86371555-86371599	NM_138673:99111	Stab2	INSIDE	0.802	1.908	1859.11	3547.63	1.530	1402.97	2146.85
A_68_P22861754	chr4:41296077-41296121	NM_023305:70	Ubap1	INSIDE	0.802	1.747	8809.50	15393.21	1.401	5994.99	8397.22
A_68_P28086886	chr11:103610912-103610956	NM_011719:201	Wnt9b	INSIDE	0.802	0.642	1356.92	870.77	0.515	1210.23	622.73
A_68_P23081884	chr4:86520053-86520097	NM_139306:-243	Acer2	PROMOTER	0.801	0.494	1545.04	763.28	0.396	1353.81	535.88
A_68_P28155402	chr11:115664810-115664854	NM_080643:10074	Caskin2	INSIDE	0.801	2.989	927.92	2773.96	2.394	694.21	1662.27
A_68_P21116979	chr2:32563681-32563725	NM_130860:4602	Cdk9	INSIDE	0.801	2.454	2222.70	5455.10	1.965	1690.11	3320.59
A_68_P25601076	chr7:150645402-150645446	NM_001161624:1531	Cdkn1c	INSIDE	0.801	2.480	1016.55	2520.58	1.986	967.73	1922.34
A_68_P32130474	chr19:44181784-44181828	NM_001162410:161	Chuk	INSIDE	0.801	0.575	2933.43	1686.37	0.460	2560.95	1178.71
A_68_P24125354	chr5:137799067-137799111	NM_001159571:7752	Ephb4	INSIDE	0.801	2.995	748.92	2242.75	2.398	717.83	1721.42
A_68_P28920311	chr13:31066026-31066075	NM_025588:-134	Exoc2	PROMOTER	0.801	2.692	430.81	1159.91	2.156	322.02	694.18
A_68_P25656210	chr8:11555759-11555803	NM_011919:-285	Ing1	DIVERGENT_PROMOTER	0.801	1.811	9106.75	16493.52	1.451	6002.05	8707.05
A_68_P22774361	chr4:21612852-21612896	NM_001080771:236	Prdm13	INSIDE	0.801	0.551	2543.57	1402.01	0.442	1902.06	840.26
A_68_P21875637	chr2:174298721-174298768	NM_025531:-302	Slmo2	PROMOTER	0.801	0.662	948.97	627.81	0.530	762.81	404.12
A_68_P23523161	chr5:20388465-20388509	NM_177601:216	Tmem60	INSIDE	0.801	0.674	1080.29	728.52	0.540	985.78	532.29
A_68_P26023616	chr8:87604506-87604561	NM_026399:112	Wdr83	INSIDE	0.801	0.592	1223.97	724.61	0.474	902.38	428.08
A_68_P23321772	chr4:133801543-133801587	NM_024215:-58	Zfp593	PROMOTER	0.801	0.448	1154.06	516.79	0.359	951.16	341.14
A_68_P26863464	chr9:117781580-117781624	ENSMUST00000126482:-659		PROMOTER	0.801	0.388	2552.18	989.34	0.311	2022.79	628.23
A_68_P23281043	chr4:126287319-126287363	NM_001013755:243	5730409E04Rik	INSIDE	0.800	0.449	1199.13	538.90	0.360	967.05	347.80
A_68_P32141576	chr19:46072976-46073020	NM_198296:-20	9130011E15Rik	DIVERGENT_PROMOTER	0.800	0.609	3376.13	2054.99	0.487	2826.37	1375.73
A_68_P23345846	chr4:138011165-138011209	NM_025451:124	Camk2n1	INSIDE	0.800	0.505	1565.13	789.91	0.404	1282.71	517.92
A_68_P32054107	chr19:29722618-29722662	NM_001081213:270	Ermp1	INSIDE	0.800	0.604	1081.17	653.45	0.483	990.71	478.77
A_68_P23193225	chr4:107526982-107527026	NM_001080926:52141	Lrp8	INSIDE	0.800	1.877	1005.88	1887.81	1.502	799.35	1200.73
A_68_P25042628	chr7:34981548-34981592	NM_026549:96	Pdcd2l	INSIDE	0.800	0.666	3019.70	2010.26	0.533	2596.07	1383.19
A_68_P32185221	chr19:53977782-53977826	NM_001168491:-36	Pdcd4	PROMOTER	0.800	0.571	1108.59	633.12	0.457	934.92	427.19
A_68_P26798485	chr9:105547166-105547210	NM_001081309:1864	Pik3r4	INSIDE	0.800	3.331	3043.64	10137.93	2.663	1964.40	5231.43
A_68_P31755045	chr18:61173853-61173897	NM_201353:-21	Slc6a7	PROMOTER	0.800	2.380	655.52	1560.29	1.905	526.23	1002.56
A_68_P30642386	chr16:30550244-30550288	NM_172614:398	Tmem44	INSIDE	0.800	0.612	1917.84	1173.52	0.490	1469.65	719.63
A_68_P30363683	chr15:78823581-78823625	NM_001024716:10117	Triobp	INSIDE	0.800	2.145	737.46	1581.73	1.716	588.14	1008.97
A_68_P28190094	chr11:121215805-121215849	NM_025793:-65	Wdr45l	PROMOTER	0.800	0.567	2079.26	1179.20	0.454	1720.77	780.82
A_68_P25239813	chr7:82600787-82600831	NM_029332:389	Akap13	INSIDE	0.799	0.578	2179.06	1259.32	0.462	1855.18	856.43
A_68_P32145201	chr19:46728817-46728861	NM_001177813:30948	D19Wsu162e	INSIDE	0.799	3.560	941.53	3351.46	2.845	742.71	2113.26
A_68_P20938880	chr1:193399417-193399461	NM_029766:-25	Dtl	DIVERGENT_PROMOTER	0.799	0.499	1957.77	977.07	0.399	1552.75	619.51
A_68_P28577475	chr12:81859600-81859644	NM_001008423:2080	Gm1568	INSIDE	0.799	2.465	600.90	1480.99	1.968	613.31	1207.12
A_68_P29681797	chr14:67487667-67487711	NM_001034881:2	Gm5464	INSIDE	0.799	5.802	194.74	1129.84	4.634	253.50	1174.66
A_68_P21536547	chr2:113598045-113598089	NM_011824:739	Grem1	INSIDE	0.799	0.657	1153.40	758.19	0.525	991.86	520.93
A_68_P24062056	chr5:125029108-125029152	NM_181410:-26	Gtf2h3	DIVERGENT_PROMOTER	0.799	2.135	644.98	1376.86	1.706	541.57	923.70
A_68_P23600185	chr5:35731082-35731126	NM_010445:-661	Hmx1	PROMOTER	0.799	0.681	1746.98	1189.53	0.544	1283.69	698.71
A_68_P31201903	chr17:45709434-45709478	NM_008302:754	Hsp90ab1	INSIDE	0.799	0.687	1111.52	763.76	0.549	993.22	545.45

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P32466327	chrX:71330719-71330763	NM_010788:192	Mecp2	INSIDE	0.799	1.683	8983.52	15118.27	1.345	3774.63	5078.48
A_68_P28052175	chr11:97560549-97560593	NM_001163307:128	Pcgf2	INSIDE	0.799	2.687	378.29	1016.44	2.147	255.46	548.52
A_68_P26166524	chr8:113618170-113618214	NM_198308:-452	Pdpr	PROMOTER	0.799	0.647	1087.26	703.33	0.517	755.27	390.35
A_68_P21310713	chr2:69561124-69561168	NM_001081086:2	Ppig	INSIDE	0.799	0.689	1808.45	1246.09	0.551	1541.64	849.08
A_68_P26702532	chr9:86910466-86910510	NM_001037907:117	Ripply2	INSIDE	0.799	0.513	5800.32	2976.61	0.410	5046.40	2068.96
A_68_P21796148	chr2:160471963-160472007	NM_009408:352	Top1	INSIDE	0.799	0.456	1977.87	902.59	0.365	1698.63	619.55
A_68_P24630038	chr6:89785494-89785538	NM_053221:10015	Vmn1r42	DOWNSTREAM	0.799	5.436	1341.77	7293.64	4.345	1087.16	4724.09
A_68_P30386395	chr15:82887268-82887312	AK139602:181917		INSIDE	0.799	0.679	1274.74	865.51	0.543	1096.49	594.89
A_68_P20262086	chr1:59177080-59177125	NM_001033449:-162	Als2cr4	PROMOTER	0.798	0.620	2541.24	1575.66	0.495	2065.36	1022.11
A_68_P26402548	chr9:31720871-31720915	NM_013800:-22	Barx2	PROMOTER	0.798	0.653	1290.75	843.30	0.521	1026.58	535.12
A_68_P23767828	chr5:67819201-67819245	NM_001164806:-184	Bend4	PROMOTER	0.798	0.612	1430.84	875.71	0.488	1459.17	712.60
A_68_P31201121	chr17:45570773-45570817	NM_152810:-138	Cdc5l	PROMOTER	0.798	1.746	4553.17	7950.95	1.394	3570.96	4977.73
A_68_P20613815	chr1:133034491-133034535	NM_145508:299	Dyrk3	INSIDE	0.798	0.388	1903.91	737.79	0.309	1538.30	475.86
A_68_P23279079	chr4:125933821-125933865	NM_001145970:-279	Mtap7d1	DIVERGENT_PROMOTER	0.798	0.681	1148.67	781.68	0.543	968.11	525.62
A_68_P25981541	chr8:79709878-79709922	NM_001083906:283494	Nr3c2	INSIDE	0.798	2.496	1077.38	2689.56	1.991	864.39	1721.08
A_68_P25065936	chr7:39006581-39006625	NM_024413:6411	Plekhf1	INSIDE	0.798	2.635	2722.24	7171.96	2.102	2196.77	4618.03
A_68_P29042000	chr13:53214301-53214345	NM_013846:167156	Ror2	INSIDE	0.798	1.893	963.91	1825.06	1.510	729.40	1101.72
A_68_P26133226	chr8:107873426-107873470	NM_001081332:1291	Slc9a5	INSIDE	0.798	0.685	1043.02	714.22	0.547	837.35	457.77
A_68_P25445803	chr7:123175462-123175506	NM_001025560:-923	Sox6	PROMOTER	0.798	0.629	1124.99	707.92	0.502	1006.17	505.51
A_68_P27629549	chr11:19921210-19921254	NM_033523:96788	Spred2	INSIDE	0.798	1.751	1621.89	2839.58	1.397	1347.94	1883.09
A_68_P28871499	chr13:21272176-21272220	NM_009054:371	Trim27	INSIDE	0.798	2.924	426.51	1247.26	2.334	489.79	1143.02
A_68_P31204668	chr17:46168904-46168948	NM_001110266:-6814	Vegfa	PROMOTER	0.798	0.551	2313.40	1274.51	0.440	1706.61	750.23
A_68_P29102506	chr13:65358717-65358761	ENSMUST00000099425:-2108		PROMOTER	0.798	2.456	665.42	1634.22	1.961	629.23	1233.73
A_68_P26807153	chr9:107133795-107133839	NM_153413:424	Dock3	INSIDE	0.797	0.582	1231.47	716.20	0.464	1086.53	503.91
A_68_P22318570	chr3:89125764-89125808	NM_010108:1015	Efna3	INSIDE	0.797	2.052	20287.54	41635.05	1.636	14433.25	23617.11
A_68_P20969130	chr2:4524621-4524665	NM_001177844:43843	Frmd4a	INSIDE	0.797	2.848	835.02	2378.06	2.270	738.84	1677.31
A_68_P31116318	chr17:27571972-27572016	NM_001013385:68255	Grm4	INSIDE	0.797	2.700	2479.07	6694.18	2.153	1852.75	3988.77
A_68_P25494602	chr7:132588659-132588703	NM_029842:547	Jmjd5	INSIDE	0.797	0.701	1806.94	1266.91	0.559	1361.71	761.25
A_68_P30480086	chr15:99256305-99256349	NM_001001884:31853	Nckap5l	INSIDE	0.797	2.717	980.19	2662.97	2.166	799.74	1732.11
A_68_P32326386	chrX:35474728-35474772	NM_001185002:734	Rhox13	INSIDE	0.797	2.716	566.46	1538.67	2.165	271.12	586.98
A_68_P31003192	chr17:3114390-3114434	NM_134123:-559	Scaf8	PROMOTER	0.797	0.591	2644.18	1562.64	0.471	2228.16	1049.01
A_68_P22185876	chr3:61962735-61962779			Unknown	0.797	4.051	1323.34	5360.40	3.227	1239.79	4000.71
A_68_P25262394	chr7:86805544-86805588	NM_029835:485	5730590G19Rik	INSIDE	0.796	0.337	1510.27	508.32	0.268	1334.12	357.21
A_68_P23205991	chr4:110070245-110070289	NM_001048189:-129	Agbl4	PROMOTER	0.796	10.775	953.54	10274.64	8.573	815.62	6992.58
A_68_P30579475	chr16:18398299-18398343	NM_033474:49954	Arvcf	INSIDE	0.796	1.852	1251.60	2317.39	1.474	994.31	1465.14
A_68_P31423369	chr17:87845478-87845522	NM_007589:775	Calm2	INSIDE	0.796	2.222	360.58	801.38	1.768	403.73	713.97
A_68_P23202004	chr4:109338719-109338763	NM_007671:-763	Cdkn2c	PROMOTER	0.796	0.522	1423.08	742.48	0.415	1145.94	475.68
A_68_P23284202	chr4:126910975-126911019	NM_198618:64482	Dlgap3	INSIDE	0.796	1.910	1835.76	3505.62	1.520	1524.51	2316.91
A_68_P23203753	chr4:109652919-109652963	NM_172296:2311	Dmrta2	INSIDE	0.796	0.598	1113.65	666.16	0.476	971.34	462.25
A_68_P30641169	chr16:30309242-30309286	NM_008148:1601	Gp5	INSIDE	0.796	0.683	1115.88	762.56	0.544	1105.36	600.98
A_68_P32152321	chr19:47929609-47929653	NM_010362:152	Gsto1	INSIDE	0.796	0.547	1185.96	648.15	0.435	973.70	423.48
A_68_P29485181	chr14:27928181-27928226	NM_134437:76017	Il17rd	DOWNSTREAM	0.796	0.597	1185.03	707.41	0.475	1063.32	505.54
A_68_P21816598	chr2:163994001-163994045	NM_008435:2827	Kcns1	INSIDE	0.796	0.504	1052.16	529.83	0.401	841.30	337.16
A_68_P30359964	chr15:78267418-78267462	NM_001081367:8383	Kctd17	INSIDE	0.796	1.953	8458.99	16521.82	1.555	5692.08	8852.67
A_68_P26346111	chr9:21043277-21043321	NM_001110305:478	Keap1	INSIDE	0.796	2.041	549.63	1122.04	1.625	556.77	904.85
A_68_P27282830	chr10:79844326-79844370	NM_198615:6048	Mex3d	INSIDE	0.796	3.507	3056.13	10718.42	2.792	2223.38	6207.88
A_68_P27282472	chr10:79786332-79786376	NM_008793:5864	Pcsk4	INSIDE	0.796	0.724	3463.79	2508.81	0.576	2649.31	1527.29
A_68_P20681325	chr1:145851425-145851469	NM_009061:-167	Rgs2	PROMOTER	0.796	0.688	1239.00	852.32	0.548	1023.20	560.37
A_68_P24008785	chr5:115722817-115722861	NM_016698:66	Rnf10	INSIDE	0.796	1.891	855.83	1618.00	1.504	692.45	1041.78
A_68_P28683727	chr12:101963505-101963549	NM_153587:-288	Rps6ka5	PROMOTER	0.796	0.501	1697.03	849.39	0.398	1454.97	579.78
A_68_P31411763	chr17:86021219-86021263	NM_011381:1067	Six3	INSIDE	0.796	0.523	1300.12	680.15	0.417	1118.43	465.95

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28708613	chr12:106575627-106575671	ENSMUST00000138649:446		INSIDE	0.796	0.737	3065.22	2259.34	0.587	2148.30	1260.30
A_68_P23392563	chr4:147504999-147505043	NM_027426:-213	2610109H07Rik	DIVERGENT_PROMOTER	0.795	1.898	1119.45	2124.81	1.509	1062.99	1603.94
A_68_P27289154	chr10:80827741-80827785	NM_001014836:803	4930404N11Rik	INSIDE	0.795	0.636	1596.04	1015.24	0.506	1240.29	627.06
A_68_P25656688	chr8:11635549-11635593	NR_030781:-534	Ankrd10	PROMOTER	0.795	0.617	1129.90	697.66	0.491	1027.37	504.46
A_68_P23770432	chr5:68238811-68238855	NM_001038999:-162	Atp8a1	PROMOTER	0.795	0.421	2562.61	1079.58	0.335	1867.00	625.57
A_68_P24631556	chr6:90259867-90259911	NM_027928:15291	Chst13	INSIDE	0.795	2.233	747.00	1668.32	1.775	590.45	1047.93
A_68_P24780086	chr6:117119255-117119299	NM_021704:724	Cxcl12	INSIDE	0.795	0.650	1017.40	661.01	0.516	775.09	400.31
A_68_P26274325	chr9:3532341-3532385	NM_001033322:9	Gucy1a2	INSIDE	0.795	0.412	3746.97	1544.94	0.328	2853.81	935.09
A_68_P30991213	chr16:96349447-96349491	NM_008251:-136	Hmgn1	PROMOTER	0.795	0.579	3884.42	2247.93	0.460	3347.10	1540.61
A_68_P28784064	chr12:120476208-120476252	NM_177290:519	Itgb8	INSIDE	0.795	0.549	1275.00	699.72	0.436	1048.21	457.44
A_68_P20058167	chr1:17088173-17088217	NM_020604:-224	Jph1	PROMOTER	0.795	0.453	1399.94	634.59	0.360	1148.82	414.01
A_68_P23303540	chr4:130506009-130506056	NM_010769:5733	Matn1	INSIDE	0.795	2.635	781.43	2059.33	2.096	665.69	1395.03
A_68_P24152140	chr5:143005995-143006039	NM_019943:14	Papolb	INSIDE	0.795	2.355	982.80	2314.36	1.873	879.56	1647.52
A_68_P24609842	chr6:86338816-86338860	NM_025823:8306	Pcyox1	INSIDE	0.795	3.382	1443.73	4882.72	2.687	1095.70	2944.20
A_68_P27911822	chr11:72302639-72302683	NM_153060:746	Spns2	INSIDE	0.795	0.639	2023.29	1293.55	0.508	1566.35	795.77
A_68_P31093837	chr17:23956103-23956154	NM_175229:15975	Srrm2	INSIDE	0.795	2.644	476.53	1259.81	2.102	378.38	795.31
A_68_P20346376	chr1:74083629-74083673	NM_027884:87371	Tns1	INSIDE	0.795	0.690	1437.73	992.17	0.549	1212.12	664.97
A_68_P33005896	A_68_P33005896			Unknown	0.795	3.378	223.35	754.56	2.685	198.56	533.14
A_68_P30364603	chr15:78971259-78971303	NM_138581:401	1700088E04Rik	INSIDE	0.794	0.518	1044.62	540.70	0.411	835.86	343.32
A_68_P31144956	chr17:32457857-32457902	NM_019774:219	Akap8	INSIDE	0.794	0.527	1405.83	741.14	0.419	1103.77	462.30
A_68_P23410171	chr4:150482915-150482959	NM_001081557:752941	Camta1	INSIDE	0.794	2.028	594.78	1206.29	1.610	573.96	923.95
A_68_P23205807	chr4:110024246-110024290	NM_001163397:248	Elavl4	INSIDE	0.794	0.577	1060.55	611.88	0.458	881.15	403.47
A_68_P26828613	chr9:111174392-111174436	NM_175266:66	Epm2aip1	INSIDE	0.794	0.588	1199.42	705.57	0.467	1029.65	480.81
A_68_P31382678	chr17:80772747-80772791	NR_028385:114	Gm10190	INSIDE	0.794	2.048	678.83	1389.99	1.626	645.52	1049.33
A_68_P30332047	chr15:73526357-73526401	NM_173365:11557	Gpr20	INSIDE	0.794	3.669	5254.41	19277.74	2.913	3668.75	10685.37
A_68_P31116319	chr17:27572063-27572107	NM_001013385:68165	Grm4	INSIDE	0.794	1.951	1667.99	3253.90	1.548	1167.90	1808.19
A_68_P31849646	chr18:78006372-78006416	NM_146089:125	Haus1	INSIDE	0.794	0.550	1895.70	1042.42	0.436	1607.94	701.63
A_68_P32135961	chr19:45100549-45100593	NM_001130526:7946	Lzts2	INSIDE	0.794	2.257	1283.96	2897.43	1.791	1021.10	1828.80
A_68_P22312504	chr3:88018933-88018977	NR_037276:-138	Mir3093	PROMOTER	0.794	0.553	1277.46	706.36	0.439	1009.13	442.94
A_68_P25979817	chr8:79425933-79425977	NM_001083906:-452	Nr3c2	DIVERGENT_PROMOTER	0.794	0.666	950.33	633.19	0.529	737.22	390.13
A_68_P30346597	chr15:76009753-76009797	NM_201394:16366	Plec	INSIDE	0.794	2.036	835.40	1700.92	1.616	651.84	1053.21
A_68_P26476665	chr9:45714864-45714908	NM_178709:74	Rnf214	INSIDE	0.794	0.303	2121.81	642.80	0.240	1499.34	360.53
A_68_P23993057	chr5:113006567-113006611	NM_019982:-383	Sez6l	PROMOTER	0.794	0.475	1214.56	576.44	0.377	918.12	345.94
A_68_P25954772	chr8:73416640-73416684	NM_053248:-6	Slc5a5	PROMOTER	0.794	0.677	1330.86	901.21	0.538	1074.17	577.90
A_68_P29645531	chr14:61253807-61253851	NM_001033272:263	Spata13	INSIDE	0.794	0.710	2260.45	1604.20	0.564	1912.91	1078.36
A_68_P22321610	chr3:89577295-89577339	NM_027315:-214	Ube2q1	DIVERGENT_PROMOTER	0.794	0.559	1747.18	976.55	0.444	1467.44	650.99
A_68_P32977627	A_68_P32977627			Unknown	0.794	3.117	379.87	1183.90	2.473	265.55	656.77
A_68_P27263122	chr10:76077175-76077220	NM_146007:8952	Col6a2	INSIDE	0.793	2.678	1143.96	3063.33	2.123	834.94	1772.23
A_68_P25539010	chr7:140314266-140314310	NM_009980:878	Ctbp2	INSIDE	0.793	0.364	1853.86	675.08	0.289	1450.57	418.95
A_68_P24600272	chr6:84534727-84534771	NM_175475:9056	Cyp26b1	INSIDE	0.793	0.624	1409.22	879.80	0.495	1184.35	586.09
A_68_P21489530	chr2:104334257-104334301	NM_001145824:368	Hipk3	INSIDE	0.793	0.705	3121.46	2199.53	0.559	2319.50	1296.18
A_68_P25474218	chr7:128644164-128644208	NM_001081327:108377	Hs3st2	INSIDE	0.793	1.925	1093.34	2104.96	1.527	762.61	1164.55
A_68_P23971132	chr5:108741872-108741916	NM_001081234:-49	Pigg	PROMOTER	0.793	0.639	1191.92	761.88	0.507	899.34	456.02
A_68_P31106621	chr17:25974180-25974224	NM_144816:-130	Rhbdl1	PROMOTER	0.793	0.696	2187.16	1521.95	0.552	1768.71	975.91
A_68_P27985860	chr11:85699977-85700021	NM_011536:-3566	Tbx4	PROMOTER	0.793	0.624	863.08	538.16	0.495	689.49	341.04
A_68_P30596852	chr16:22265731-22265775	NM_009186:250	Tra2b	INSIDE	0.793	0.714	1921.62	1372.20	0.566	1550.19	877.31
A_68_P28813406	chr13:8870643-8870687	NM_172445:-376	Wdr37	PROMOTER	0.793	0.625	1133.03	707.63	0.495	862.26	426.85
A_68_P26158628	chr8:112248320-112248367	NM_029468:18356	Zfp821	INSIDE	0.793	3.930	860.67	3382.67	3.116	688.30	2144.48
A_68_P27933039	chr11:76414995-76415040	ENSMUST00000136893:197		INSIDE	0.793	2.961	265.10	785.01	2.348	240.70	565.18
A_68_P24605101	chr6:85402012-85402056	NR_028081:-70	1700040I03Rik	PROMOTER	0.792	0.580	968.47	562.01	0.459	840.88	386.30
A_68_P20858583	chr1:179188004-179188048	NM_011785:-9128	Akt3	PROMOTER	0.792	0.405	1341.82	543.79	0.321	1219.65	391.34

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P23418304	chr4:151737452-151737496	NM_001081376:24715	Chd5	INSIDE	0.792	2.085	926.93	1932.40	1.651	667.66	1102.28
A_68_P20354315	chr1:75472667-75472712	NM_001001565:3357	Chpf	INSIDE	0.792	3.588	777.09	2788.22	2.843	626.69	1781.89
A_68_P26538931	chr9:56712893-56712937	NM_139001:4	Cspg4	INSIDE	0.792	0.446	1808.57	807.23	0.354	1312.23	463.95
A_68_P23342967	chr4:137514113-137514157	NM_199307:95983	Ece1	INSIDE	0.792	2.825	1300.11	3672.81	2.237	957.14	2141.12
A_68_P25278636	chr7:89796890-89796934	NM_177894:126	Fam154b	INSIDE	0.792	0.508	1195.75	607.22	0.402	871.66	350.63
A_68_P25507080	chr7:134895891-134895935	NM_172748:5624	Fbxl19	INSIDE	0.792	1.967	2795.93	5498.53	1.558	2221.01	3460.87
A_68_P32127028	chr19:43598925-43598969	NM_010324:149	Got1	INSIDE	0.792	0.554	1466.38	811.66	0.439	1218.46	534.30
A_68_P29187682	chr13:83884651-83884695	NR_029545:6254	Mir9-2	DOWNSTREAM	0.792	2.460	679.05	1670.33	1.947	657.41	1280.03
A_68_P26164571	chr8:113262720-113262764	NM_198625:17359	Mtss1l	INSIDE	0.792	2.028	959.92	1947.04	1.606	789.18	1267.44
A_68_P25094159	chr7:52887970-52888014	NM_028544:5086	Rasip1	INSIDE	0.792	2.842	277.30	788.16	2.252	299.84	675.24
A_68_P25398385	chr7:114353404-114353448	NM_029660:468	Rbmxl2	INSIDE	0.792	1.810	887.32	1605.61	1.433	879.29	1259.86
A_68_P28033655	chr11:94410319-94410363	NM_001013381:181	Rsad1	INSIDE	0.792	0.587	1387.97	815.09	0.465	1161.65	540.60
A_68_P25959795	chr8:74659320-74659364	NM_001001491:152	Tpm4	INSIDE	0.792	0.644	1410.60	908.00	0.510	1082.34	552.04
A_68_P21538595	chr2:114027026-114027070	NM_175466:120	Zfp770	INSIDE	0.792	0.533	2007.10	1069.73	0.422	1470.72	620.75
A_68_P21710713	chr2:144994120-144994164	ENSMUST00000153249:488		INSIDE	0.792	0.591	1023.36	605.18	0.468	917.92	429.82
A_68_P24098212	chr5:131915457-131915501	NM_177047:1102735	Auts2	INSIDE	0.791	2.045	1315.98	2691.60	1.618	1063.18	1719.72
A_68_P28356773	chr12:36883113-36883157	NM_025840:278	Bzw2	INSIDE	0.791	0.629	1086.66	683.52	0.497	992.86	493.68
A_68_P30588036	chr16:20531197-20531241	NM_007889:14082	Dvl3	INSIDE	0.791	2.107	1027.71	2165.25	1.666	856.30	1426.49
A_68_P24673423	chr6:97437832-97437876	NM_145148:129797	Frmd4b	INSIDE	0.791	0.680	1301.11	884.71	0.538	1185.88	637.55
A_68_P27137438	chr10:52101546-52101590	NM_001199272:362	Gopc	INSIDE	0.791	0.530	1080.03	572.02	0.419	923.77	387.10
A_68_P23955548	chr5:105910054-105910098	NM_001033550:65283	Lrrc8b	INSIDE	0.791	2.457	916.13	2251.13	1.945	723.96	1407.89
A_68_P25954898	chr8:73438225-73438269	NM_173013:8374	Mtap1s	INSIDE	0.791	1.970	756.75	1490.61	1.558	632.31	985.10
A_68_P30356221	chr15:77671902-77671946	NM_022410:621	Myh9	INSIDE	0.791	0.430	1553.78	668.10	0.340	1287.05	437.78
A_68_P28614435	chr12:88488792-88488836	NM_153415:38	Pomt2	INSIDE	0.791	0.677	1172.39	793.41	0.535	926.12	495.69
A_68_P23281396	chr4:126355179-126355223	NM_011970:314	Psmb2	INSIDE	0.791	0.607	1124.22	681.91	0.480	962.02	461.52
A_68_P29716892	chr14:73725013-73725057	NM_009029:564	Rb1	INSIDE	0.791	0.652	832.61	542.45	0.515	721.34	371.84
A_68_P28730242	chr12:110074008-110074052	NM_181328:56	Slc25a29	INSIDE	0.791	0.512	1280.31	655.94	0.405	1136.94	460.91
A_68_P26239401	chr8:125877966-125878010	NM_172287:21376	Spire2	INSIDE	0.791	3.222	1162.72	3746.67	2.550	913.94	2330.27
A_68_P31655792	chr18:42671854-42671899	NM_001039474:736	Tcerg1	INSIDE	0.791	0.360	1569.99	565.91	0.285	1191.52	339.63
A_68_P27290698	chr10:81050747-81050791	NM_019725:12492	Tle2	INSIDE	0.791	1.858	1519.75	2823.53	1.470	1246.50	1832.78
A_68_P26037059	chr8:90304768-90304819	NM_033327:178701	Zfp423	INSIDE	0.791	2.850	807.87	2302.24	2.255	601.27	1355.90
A_68_P22942709	chr4:57002896-57002940	NM_001142965:345	6430704M03Rik	INSIDE	0.790	0.617	1460.89	901.20	0.487	1195.78	582.74
A_68_P30434242	chr15:91029845-91029889	NM_011994:-7628	Abcd2	PROMOTER	0.790	2.489	1613.79	4017.53	1.967	1266.43	2491.19
A_68_P24761383	chr6:113708921-113708965	NM_001036684:132428	Atp2b2	INSIDE	0.790	2.435	693.73	1688.99	1.924	554.09	1066.02
A_68_P27677358	chr11:29924538-29924582	NM_146016:1473	Eml6	INSIDE	0.790	0.667	1639.53	1093.25	0.527	1278.20	673.67
A_68_P22058735	chr3:36451526-36451570	NM_019393:21	Exosc9	INSIDE	0.790	0.617	997.54	615.09	0.487	820.44	399.84
A_68_P23404235	chr4:149461799-149461843	NM_177366:209	Gpr157	INSIDE	0.790	0.657	3643.79	2393.97	0.519	2725.60	1414.51
A_68_P28069613	chr11:100569782-100569828	NM_001038010:3977	Kat2a	INSIDE	0.790	5.559	775.22	4309.77	4.392	627.80	2757.55
A_68_P20023666	chr1:9690703-9690747	NM_008651:-434	Mybl1	PROMOTER	0.790	0.524	3346.48	1752.69	0.414	3102.25	1284.09
A_68_P30346023	chr15:75922119-75922163	NM_144847:-1697	Nrbp2	PROMOTER	0.790	0.705	1829.34	1289.71	0.557	1466.43	817.24
A_68_P21888791	chr2:177877035-177877079	NM_028806:419	Phactr3	INSIDE	0.790	0.420	2300.94	967.19	0.332	1857.84	616.67
A_68_P26554814	chr9:59528143-59528187	NM_011099:23750	Pkm2	DOWNSTREAM	0.790	0.632	1250.01	789.45	0.499	921.89	459.76
A_68_P26429009	chr9:36953011-36953055	NM_001029838:1819	Pknox2	INSIDE	0.790	0.706	1508.41	1065.30	0.558	1284.52	716.81
A_68_P26477010	chr9:45763375-45763419	NM_172257:-64	Sidt2	PROMOTER	0.790	0.572	891.47	509.66	0.452	799.21	360.94
A_68_P29097414	chr13:64253902-64253946	NM_175494:583	Zfp367	INSIDE	0.790	1.997	650.41	1299.11	1.578	661.52	1044.01
A_68_P30345226	chr15:75805450-75805494	NM_001081065:5858	Zfp707	INSIDE	0.790	2.397	2579.78	6182.57	1.892	1825.64	3454.93
A_68_P20443148	chr1:93437540-93437584	NM_023046:-94	Asb1	PROMOTER	0.789	0.655	871.23	570.53	0.517	703.02	363.33
A_68_P21073894	chr2:25562637-25562681	NM_023326:260	Bmyc	INSIDE	0.789	0.470	1640.08	770.07	0.371	1461.61	541.58
A_68_P30135995	chr15:35867423-35867467	NM_053071:557	Cox6c	INSIDE	0.789	0.464	2393.16	1109.45	0.366	2147.25	784.98
A_68_P24758531	chr6:113232209-113232253	NM_170673:-70	Cpne9	PROMOTER	0.789	0.619	1004.33	621.87	0.489	797.67	389.88
A_68_P23317855	chr4:133042356-133042402	NM_175307:6331	Fam46b	INSIDE	0.789	1.913	1472.11	2815.59	1.509	1133.38	1710.07

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P21576347	chr2:120454717-120454761	NM_025475:19567	Haus2	DOWNSTREAM	0.789	2.642	2677.27	7073.22	2.085	2001.75	4174.41
A_68_P31156848	chr17:35114489-35114533	NM_013558:4863	Hspa1l	INSIDE	0.789	1.920	803.94	1543.33	1.514	724.85	1097.51
A_68_P21834170	chr2:167013596-167013640	NM_008420:681	Kcnb1	INSIDE	0.789	3.617	2033.38	7354.66	2.852	1488.81	4246.35
A_68_P31117526	chr17:27760252-27760296	NM_019837:123	Nudt3	INSIDE	0.789	0.683	1380.78	942.97	0.539	1295.70	698.51
A_68_P21909035	chr2:180922349-180922393	NM_025598:323	Ppdpf	INSIDE	0.789	0.688	1682.40	1158.08	0.543	1473.69	800.30
A_68_P31415738	chr17:86657395-86657443	NM_011104:90294	Prkce	INSIDE	0.789	3.234	783.34	2533.10	2.551	531.58	1356.00
A_68_P23313960	chr4:132324400-132324444	NM_011284:148	Rpa2	INSIDE	0.789	1.754	5586.66	9799.81	1.384	4250.62	5882.97
A_68_P28957528	chr13:38022622-38022667	NM_001177869:41905	Rreb1	INSIDE	0.789	2.709	1096.74	2971.03	2.137	843.17	1801.78
A_68_P30348904	chr15:76353697-76353741	NM_130893:-1159	Scrt1	PROMOTER	0.789	0.638	1553.60	991.47	0.504	1207.32	608.05
A_68_P27934858	chr11:76759228-76759272	NM_178645:93	Blmh	INSIDE	0.788	0.470	1111.37	522.06	0.370	944.39	349.45
A_68_P27980568	chr11:84771399-84771443	NM_007607:165	Car4	INSIDE	0.788	0.592	1038.07	614.29	0.467	870.02	405.90
A_68_P23321455	chr4:133742851-133742895	NM_144527:128	Ccdc21	INSIDE	0.788	0.438	3592.35	1573.61	0.345	2581.22	890.61
A_68_P21715593	chr2:145760272-145760316	NM_025820:142	Crnkl1	INSIDE	0.788	0.650	838.52	545.14	0.512	713.61	365.44
A_68_P24620370	chr6:88149892-88149936	NM_008090:1257	Gata2	INSIDE	0.788	0.517	1237.67	640.47	0.408	983.22	401.08
A_68_P23329299	chr4:135126083-135126127	NM_001013756:3431	Grhl3	INSIDE	0.788	0.455	1543.51	702.24	0.359	1260.49	452.16
A_68_P31317443	chr17:68623323-68623367	NM_177278:208	L3mbtl4	INSIDE	0.788	0.522	1924.87	1004.77	0.411	1540.18	633.73
A_68_P25269267	chr7:88049772-88049816	NM_026523:163	Nmb	INSIDE	0.788	0.668	916.30	611.98	0.526	693.99	365.35
A_68_P25096455	chr7:53289295-53289339	NM_153057:251	Nomo1	INSIDE	0.788	0.561	1743.90	977.57	0.442	1286.58	568.68
A_68_P31442550	chr17:91488113-91488157	NM_020252:4008	Nrxn1	INSIDE	0.788	2.731	1459.43	3985.64	2.152	1145.37	2464.51
A_68_P21565426	chr2:118503248-118503292	NM_001145854:289	Pak6	INSIDE	0.788	0.523	2039.39	1066.82	0.412	1637.26	675.04
A_68_P24933416	chr6:147212616-147212660	NM_008970:-31	Pthlh	PROMOTER	0.788	0.599	1023.17	613.39	0.473	892.46	421.82
A_68_P26540099	chr9:56924722-56924766	NM_001110350:562	Sin3a	INSIDE	0.788	0.550	1674.60	920.86	0.433	1265.53	548.47
A_68_P21440995	chr2:94246447-94246491	NM_183106:378	Ttc17	INSIDE	0.788	0.672	1305.52	876.73	0.529	1175.59	622.09
A_68_P23984451	chr5:111652451-111652495	NM_024477:343651	Ttc28	INSIDE	0.788	2.366	650.78	1539.93	1.864	570.04	1062.46
A_68_P26154344	chr8:111480628-111480672	NM_007496:242107	Zfhx3	INSIDE	0.788	3.113	8966.03	27910.81	2.453	6223.44	15264.81
A_68_P26335719	chr9:17902437-17902481			Unknown	0.788	2.073	908.93	1884.09	1.634	774.15	1265.04
A_68_P26595466	chr9:66682276-66682320	NM_026674:215	Aph1c	INSIDE	0.787	0.499	1417.17	706.66	0.392	1076.92	422.69
A_68_P21109232	chr2:31315774-31315818	NM_007494:-9993	Ass1	PROMOTER	0.787	0.604	905.63	547.20	0.475	781.03	371.34
A_68_P23818506	chr5:77287203-77287247	NM_001163793:17601	C530008M17Rik	INSIDE	0.787	2.830	1138.95	3223.46	2.229	843.00	1878.70
A_68_P27643752	chr11:22891041-22891085	NM_009837:470	Cct4	INSIDE	0.787	1.990	1152.09	2292.21	1.565	887.39	1389.17
A_68_P23973400	chr5:109089732-109089776	NM_199011:34	Dgkq	INSIDE	0.787	0.708	1557.49	1102.01	0.557	1314.02	731.50
A_68_P33015626	chr1_random:51169-51219	NM_026866:134144	Disp1	INSIDE	0.787	2.366	924.83	2187.80	1.862	779.59	1451.60
A_68_P26431143	chr9:37338011-37338055	NM_027102:2359	Esam	INSIDE	0.787	0.452	1385.70	626.46	0.356	1237.98	440.35
A_68_P25641013	chr8:9207908-9207952	NM_173446:563093	Fam155a	INSIDE	0.787	1.962	1645.18	3228.57	1.545	1218.05	1881.97
A_68_P21073090	chr2:25433092-25433136	NM_001005424:2505	Gm996	INSIDE	0.787	0.665	977.20	650.04	0.524	809.10	423.68
A_68_P28043962	chr11:96207315-96207359	NM_010458:2254	Hoxb3	INSIDE	0.787	0.611	3005.71	1835.01	0.480	2386.44	1145.97
A_68_P21833675	chr2:166930471-166930515	NM_008420:83807	Kcnb1	INSIDE	0.787	3.179	2570.88	8173.89	2.504	2075.55	5196.67
A_68_P25279953	chr7:90016571-90016615	NM_175366:750	Mex3b	INSIDE	0.787	0.572	1006.50	575.24	0.450	847.80	381.21
A_68_P29094230	chr13:63673702-63673746	NM_008957:-6896	Ptch1	PROMOTER	0.787	0.528	1078.78	569.35	0.415	851.06	353.30
A_68_P24992503	chr7:19878546-19878590	NM_001025364:2121	Rtn2	INSIDE	0.787	1.907	1070.52	2041.20	1.502	792.46	1189.88
A_68_P22151536	chr3:54916119-54916163	NM_001144987:53	Spg20	INSIDE	0.787	0.611	1275.02	778.62	0.481	1182.67	568.67
A_68_P20708501	chr1:152240022-152240066	NM_133780:77	Tpr	INSIDE	0.787	0.698	1664.96	1162.22	0.549	1367.92	751.41
A_68_P24162462	chr5:145528953-145528997	NM_001081362:-686	Trrap	DIVERGENT_PROMOTER	0.787	0.548	1260.57	690.69	0.431	1131.86	488.21
A_68_P22321613	chr3:89577798-89577842	NM_027315:290	Ube2q1	INSIDE	0.787	2.050	619.19	1269.03	1.613	530.83	856.41
A_68_P31259847	chr17:57201924-57201968	NM_177638:247	Crb3	INSIDE	0.786	0.474	1823.65	863.88	0.372	1980.49	737.02
A_68_P25083575	chr7:50930997-50931041	NM_145582:3618	Ctu1	INSIDE	0.786	2.155	607.06	1307.94	1.694	510.47	864.92
A_68_P30387020	chr15:83002487-83002532	NM_029787:129	Cyb5r3	INSIDE	0.786	0.674	963.18	649.22	0.530	875.50	463.99
A_68_P28067609	chr11:100216864-100216908	NM_010404:569	Hap1	INSIDE	0.786	0.704	1896.72	1335.55	0.553	1513.43	837.62
A_68_P28071795	chr11:100940981-100941025	NM_010475:1278	Hsd17b1	INSIDE	0.786	2.495	405.84	1012.56	1.961	338.52	663.73
A_68_P29615710	chr14:55633787-55633831	NM_026890:-482	Ngdn	PROMOTER	0.786	0.695	1628.30	1131.71	0.546	1263.05	689.66
A_68_P23118557	chr4:94269595-94269639	NM_172695:322	Plaa	INSIDE	0.786	0.484	1427.52	690.46	0.380	1186.84	451.20

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28958210	chr13:38129314-38129358	NM_024242:479	Riok1	INSIDE	0.786	0.471	1316.71	619.71	0.370	1022.77	378.17
A_68_P26542153	chr9:57352112-57352156	NM_133982:226	Rpp25	INSIDE	0.786	0.452	2150.27	972.86	0.356	1731.46	615.65
A_68_P21597423	chr2:124435474-124435518	NM_172537:-535	Sema6d	PROMOTER	0.786	0.631	1709.03	1078.93	0.496	1407.64	698.35
A_68_P21820791	chr2:164793332-164793376	NM_020333:-133	Slc12a5	PROMOTER	0.786	0.305	1936.61	590.40	0.240	1698.09	407.05
A_68_P28094594	chr11:105026351-105026396	ENSMUST00000118770:1561		INSIDE	0.786	3.683	2301.27	8475.40	2.896	1631.93	4726.09
A_68_P28353676	chr12:36219581-36219625	NM_013464:59	Ahr	INSIDE	0.785	0.686	1265.01	867.82	0.539	1008.86	543.38
A_68_P22186535	chr3:62143067-62143111	NM_001081295:390	Arhgef26	INSIDE	0.785	0.680	1014.99	690.23	0.534	891.54	475.73
A_68_P29020698	chr13:48761248-48761292	NM_007526:2866	Barx1	INSIDE	0.785	0.536	1175.24	630.03	0.421	970.69	408.71
A_68_P24397200	chr6:42215074-42215118	NM_007610:59	Casp2	INSIDE	0.785	2.617	3449.54	9029.06	2.056	2443.25	5022.20
A_68_P27677369	chr11:29925854-29925898	NM_146016:157	Eml6	INSIDE	0.785	0.255	2570.45	655.84	0.200	2238.13	448.55
A_68_P25289618	chr7:91754406-91754450	NM_010176:24	Fah	INSIDE	0.785	2.492	11138.49	27761.34	1.957	7746.14	15162.73
A_68_P24046888	chr5:122302574-122302618	NM_175474:3560	Fam109a	INSIDE	0.785	1.892	921.33	1743.44	1.485	755.11	1120.99
A_68_P25951053	chr8:72839794-72839838	NM_001163282:143	Gdf1	INSIDE	0.785	0.622	859.29	534.52	0.488	716.81	350.03
A_68_P30473863	chr15:98087348-98087392	NM_027304:368	H1fnt	INSIDE	0.785	2.290	757.85	1735.62	1.798	648.21	1165.37
A_68_P28567643	chr12:80190635-80190679	NM_029988:1	Pigh	INSIDE	0.785	0.533	1316.70	701.67	0.418	1164.44	486.83
A_68_P20852903	chr1:178204921-178204965	NM_176916:501	Pld5	INSIDE	0.785	0.599	1459.78	874.96	0.471	1177.74	554.22
A_68_P28946214	chr13:36061069-36061113	NM_029628:1316	Ppp1r3g	INSIDE	0.785	2.438	538.32	1312.50	1.914	467.54	894.87
A_68_P27924764	chr11:75007008-75007052	NM_177708:-464	Rtn4rl1	DIVERGENT_PROMOTER	0.785	0.553	5084.91	2810.76	0.434	3777.54	1638.58
A_68_P25512303	chr7:135888587-135888631	NM_001029982:225	Sec23ip	INSIDE	0.785	0.703	1214.88	854.60	0.552	996.46	549.92
A_68_P21635426	chr2:131346286-131346330	NM_001177833:28711	Smox	INSIDE	0.785	2.231	515.87	1150.70	1.752	543.24	951.72
A_68_P32092159	chr19:36908711-36908755	NM_001163635:11	Tnks2	INSIDE	0.785	2.479	690.28	1711.35	1.945	643.41	1251.44
A_68_P21710706	chr2:144993149-144993193	ENSMUST00000110007:-319		PROMOTER	0.785	0.731	2122.66	1552.53	0.574	1645.08	944.26
A_68_P22289848	chr3:84063239-84063283	ENSMUST00000147901:31		INSIDE	0.785	0.487	5121.18	2492.89	0.382	4179.99	1596.63
A_68_P22061571	chr3:36962331-36962381	NM_009350:-221	Adad1	PROMOTER	0.784	3.972	915.55	3636.40	3.115	712.04	2217.72
A_68_P28680130	chr12:101369148-101369192	NM_183155:28693	BC002230	INSIDE	0.784	1.912	1364.53	2609.26	1.500	1186.17	1779.01
A_68_P31125953	chr17:29235369-29235414	NM_007669:4675	Cdkn1a	INSIDE	0.784	2.063	962.51	1985.83	1.618	807.60	1307.07
A_68_P28051747	chr11:97491171-97491215	NM_175332:-162	E130012A19Rik	PROMOTER	0.784	1.987	5633.44	11196.28	1.559	4539.81	7075.96
A_68_P21903063	chr2:180068623-180068667	NM_008093:740	Gata5	INSIDE	0.784	0.435	1414.92	615.09	0.341	1302.30	443.91
A_68_P27794865	chr11:51419667-51419711	NM_001048061:695	Hnrnpab	INSIDE	0.784	0.646	2508.22	1619.65	0.506	2054.21	1039.81
A_68_P30477337	chr15:98748179-98748223	NM_029098:329	Lmbr1l	INSIDE	0.784	0.518	1305.31	675.76	0.406	1167.71	474.18
A_68_P24012822	chr5:116474390-116474434	NM_031869:25	Prkab1	INSIDE	0.784	0.574	1454.25	834.91	0.450	1227.45	552.31
A_68_P20796002	chr1:167637880-167637924	NM_001038846:323	Rcsd1	INSIDE	0.784	0.498	1441.05	716.99	0.390	1139.18	444.23
A_68_P22871555	chr4:43429277-43429321	NM_199057:9853	Rusc2	INSIDE	0.784	2.019	745.96	1505.77	1.582	627.14	992.43
A_68_P32021815	chr19:24205388-24205432	NM_001198985:43220	Tjp2	INSIDE	0.784	2.008	1023.81	2055.52	1.574	917.83	1444.56
A_68_P24819776	chr6:125235862-125235906	NM_009446:176	Tuba3a	INSIDE	0.784	2.101	514.93	1081.71	1.646	486.31	800.69
A_68_P21084617	chr2:27281328-27281372	NM_009500:995	Vav2	INSIDE	0.784	0.550	3355.40	1845.98	0.431	2589.20	1116.20
A_68_P20940739	chr1:193731090-193731134	NR_030669:294	1700034H15Rik	INSIDE	0.783	0.581	1422.83	826.96	0.455	1174.09	534.49
A_68_P28046786	chr11:96650730-96650774	NM_007622:303	Cbx1	INSIDE	0.783	0.466	1151.24	536.75	0.365	1002.65	365.83
A_68_P24631549	chr6:90258988-90259041	NM_027928:16165	Chst13	INSIDE	0.783	3.001	427.30	1282.39	2.350	400.98	942.15
A_68_P27542104	chr10:128007271-128007315	NM_010153:19265	Erbb3	INSIDE	0.783	2.066	640.76	1323.81	1.617	571.31	923.99
A_68_P31254846	chr17:56395500-56395544	NM_010192:-693	Fem1a	PROMOTER	0.783	0.539	1959.17	1056.46	0.422	1599.44	675.58
A_68_P32141594	chr19:46078185-46078229	NM_176785:239	Hps6	INSIDE	0.783	0.534	2211.08	1180.66	0.418	1894.19	791.78
A_68_P28600850	chr12:86217424-86217472	NM_013589:-3	Ltbp2	PROMOTER	0.783	0.626	2039.80	1276.61	0.490	1500.51	734.97
A_68_P22659608	chr3:153568818-153568862	NM_031870:262	Msh4	INSIDE	0.783	2.121	750.09	1591.03	1.662	601.54	999.65
A_68_P30382865	chr15:82169342-82169386	NM_008669:-108	Naga	DIVERGENT_PROMOTER	0.783	0.666	1125.97	749.40	0.521	897.36	467.44
A_68_P28058390	chr11:98629362-98629406	NM_145434:7172	Nr1d1	INSIDE	0.783	2.381	783.05	1864.75	1.865	670.07	1249.75
A_68_P32150070	chr19:47538439-47538483	NM_001164717:441	Sh3pxd2a	INSIDE	0.783	0.638	987.71	630.13	0.499	787.84	393.42
A_68_P23590342	chr5:34000582-34000626	NM_026698:-123	Tmem129	DIVERGENT_PROMOTER	0.783	0.613	1964.20	1203.99	0.480	1477.52	708.81
A_68_P25019106	chr7:28623585-28623629	NM_011762:4	Zfp59	INSIDE	0.783	0.396	1377.99	545.36	0.310	1279.23	396.64
A_68_P31305848	chr17:66729002-66729046	NM_001114098:70066	1110012J17Rik	INSIDE	0.782	2.677	1782.37	4770.63	2.094	1323.99	2771.88
A_68_P28724511	chr12:109153539-109153583	NM_001079883:88064	Bcl11b	INSIDE	0.782	2.289	1559.74	3570.42	1.789	1379.55	2468.13

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P23585862	chr5:33196731-33196775	NM_194340:127	C330019G07Rik	INSIDE	0.782	0.666	1934.47	1287.93	0.521	1521.05	792.17
A_68_P28153128	chr11:115235533-115235577	NM_175454:-6521	C630004H02Rik	DIVERGENT_PROMOTER	0.782	0.528	1203.70	635.07	0.412	935.18	385.61
A_68_P30349019	chr15:76371485-76371529	NM_029643:2134	Gpr172b	INSIDE	0.782	2.493	754.89	1882.08	1.950	582.33	1135.58
A_68_P24946692	chr7:3616894-3616938	NM_027203:526	Leng1	INSIDE	0.782	0.559	1788.56	1000.04	0.437	1412.88	618.10
A_68_P21794500	chr2:160193311-160193355	NM_010658:-531	Mafb	PROMOTER	0.782	1.907	2362.42	4504.88	1.491	1754.92	2616.16
A_68_P24466341	chr6:54894000-54894044	NM_001171007:27633	Nod1	INSIDE	0.782	1.904	1744.26	3320.52	1.488	1572.63	2340.39
A_68_P21151182	chr2:38781242-38781286	NM_010264:717	Nr6a1	INSIDE	0.782	0.726	2374.23	1724.83	0.568	1754.60	997.23
A_68_P30486485	chr15:100408605-100408649	NM_010127:8170	Pou6f1	INSIDE	0.782	1.994	1593.14	3175.96	1.559	1200.83	1871.96
A_68_P30496913	chr15:102087851-102087895	NM_011244:42	Rarg	INSIDE	0.782	1.783	3944.03	7033.80	1.395	2742.69	3826.34
A_68_P30964219	chr16:91660394-91660440	NM_019973:12348	Son	INSIDE	0.782	3.432	1042.31	3577.32	2.686	853.13	2291.10
A_68_P27466133	chr10:114238616-114238660	NM_146241:-212	Trhde	PROMOTER	0.782	0.596	941.03	560.93	0.466	781.50	364.06
A_68_P21291249	chr2:66094636-66094680	NM_001047604:16	Ttc21b	INSIDE	0.782	0.637	1031.76	656.96	0.498	869.67	432.79
A_68_P27287711	chr10:80610869-80610913	NM_010731:11875	Zbtb7a	INSIDE	0.782	2.419	1566.59	3788.83	1.892	1281.89	2425.37
A_68_P31841472	chr18:76305759-76305803	NM_145356:325949	Zbtb7c	INSIDE	0.782	2.521	835.85	2106.82	1.971	699.89	1379.69
A_68_P26986177	chr10:20032526-20032570	NM_001025392:274	Bclaf1	INSIDE	0.781	0.409	1805.45	737.70	0.319	1390.79	443.53
A_68_P27261502	chr10:75808270-75808314	NM_001081419:-285	Dip2a	PROMOTER	0.781	0.466	3866.54	1800.83	0.364	3086.53	1122.30
A_68_P20457518	chr1:95698322-95698366	NM_001105667:167	Dtymk	INSIDE	0.781	0.518	1641.47	850.00	0.405	1474.50	596.67
A_68_P23195766	chr4:108055710-108055754	NM_001099303:222	Fam159a	INSIDE	0.781	7.982	848.23	6770.59	6.234	623.66	3887.73
A_68_P25095386	chr7:53088149-53088193	NM_008172:33881	Grin2d	INSIDE	0.781	0.514	1116.60	573.74	0.401	952.37	382.22
A_68_P21840389	chr2:168088474-168088518	NM_001081134:6335	Kcng1	INSIDE	0.781	2.746	938.43	2577.35	2.145	816.10	1750.41
A_68_P28290822	chr12:25335897-25335941	NM_178357:-317	Klf11	PROMOTER	0.781	0.631	1591.57	1004.94	0.493	1120.23	552.48
A_68_P21127262	chr2:34226792-34226836	NM_016768:742	Pbx3	INSIDE	0.781	0.485	1418.91	688.00	0.379	1110.36	420.31
A_68_P22101769	chr3:45184575-45184623	NM_011043:2279	Pcdh10	INSIDE	0.781	0.637	1018.86	649.44	0.498	771.74	384.01
A_68_P26554635	chr9:59505156-59505202	NM_011099:764	Pkm2	INSIDE	0.781	0.531	1200.23	637.60	0.415	969.73	402.31
A_68_P25065938	chr7:39006759-39006803	NM_024413:6233	Plekhf1	INSIDE	0.781	1.843	2384.98	4394.92	1.439	1767.42	2543.09
A_68_P24325038	chr6:29128989-29129033	NM_001101443:574	Prrt4	INSIDE	0.781	1.769	1692.34	2993.39	1.382	1582.91	2187.01
A_68_P26512820	chr9:51856174-51856218	NM_001104617:151	Rdx	INSIDE	0.781	1.987	828.26	1645.64	1.553	759.13	1178.57
A_68_P22829977	chr4:34136995-34137039	NM_026293:26	Spaca1	INSIDE	0.781	2.203	633.70	1395.97	1.720	591.26	1016.72
A_68_P23364324	chr4:141034644-141034688	NM_019763:59846	Spen	INSIDE	0.781	2.419	736.44	1781.70	1.889	523.94	989.64
A_68_P30446395	chr15:93167839-93167883	NM_024189:-494	Yaf2	PROMOTER	0.781	0.681	1281.39	872.48	0.532	1089.59	579.39
A_68_P21824617	chr2:165389151-165389195			Unknown	0.781	4.009	1154.64	4629.23	3.133	1031.55	3232.00
A_68_P32473672	chrX:73212006-73212050	ENSMUST00000121090:-7721		PROMOTER	0.781	2.416	1892.68	4571.93	1.886	808.29	1524.18
A_68_P29193440	chr13:85328880-85328924	NM_023243:-179	Ccnh	PROMOTER	0.780	0.584	1161.85	679.06	0.456	1044.99	476.58
A_68_P27894485	chr11:69160283-69160327	NM_146019:22624	Chd3	INSIDE	0.780	1.837	1228.24	2255.95	1.433	948.15	1358.91
A_68_P32121142	chr19:42506084-42506128	NM_145123:167	Crtac1	INSIDE	0.780	0.704	2008.61	1414.15	0.549	1624.29	891.87
A_68_P28067417	chr11:100180968-100181012	NM_011508:-319	Eif1	PROMOTER	0.780	0.656	2339.70	1535.09	0.512	1762.17	901.65
A_68_P28038135	chr11:95198498-95198542	NM_172543:189	Fam117a	INSIDE	0.780	0.632	870.25	550.06	0.493	720.26	354.93
A_68_P23323336	chr4:134090794-134090838	NM_029759:-2149	Fam54b	PROMOTER	0.780	2.851	305.64	871.32	2.224	316.25	703.32
A_68_P29034753	chr13:51942852-51942896	NM_011817:831	Gadd45g	INSIDE	0.780	1.842	5899.19	10863.54	1.436	3976.36	5708.13
A_68_P25091031	chr7:52332036-52332080	NM_001163684:14260	Nosip	INSIDE	0.780	2.328	1045.18	2433.59	1.817	855.32	1554.05
A_68_P26343621	chr9:20531598-20531642	NM_173777:1038	Olfm2	INSIDE	0.780	0.528	2618.29	1381.49	0.412	2132.64	877.73
A_68_P23072594	chr4:84851732-84851776	NM_019535:395	Sh3gl2	INSIDE	0.780	0.704	1943.66	1368.42	0.549	1495.45	821.72
A_68_P24991409	chr7:19680854-19680898	NM_011383:984	Six5	INSIDE	0.780	0.563	1147.41	645.73	0.439	804.67	353.31
A_68_P30964221	chr16:91660638-91660682	NM_019973:12592	Son	INSIDE	0.780	1.920	4922.17	9453.00	1.499	3814.02	5716.52
A_68_P23938669	chr5:102498892-102498936	NM_172882:26	Wdfy3	INSIDE	0.780	0.714	4522.09	3227.59	0.556	3414.30	1899.95
A_68_P31206429	chr17:46464876-46464920	NM_145140:-2183	Abcc10	PROMOTER	0.779	0.569	1201.95	683.78	0.443	1051.80	466.06
A_68_P32097030	chr19:37765358-37765402	NM_001105201:5211	Cyp26c1	INSIDE	0.779	0.684	993.01	679.09	0.533	913.93	487.10
A_68_P23200236	chr4:108953010-108953054	NM_007943:153	Eps15	INSIDE	0.779	0.545	1886.16	1028.08	0.425	1765.29	749.74
A_68_P24142209	chr5:141082297-141082341	NM_008494:-976	Lfng	PROMOTER	0.779	0.711	1613.01	1146.07	0.554	1196.20	662.37
A_68_P30363604	chr15:78813243-78813287	NM_001024716:-221	Triobp	PROMOTER	0.779	0.569	2914.40	1656.97	0.443	2324.51	1029.02
A_68_P26158626	chr8:112248068-112248112	NM_029468:18103	Zfp821	INSIDE	0.779	3.186	613.30	1954.22	2.482	519.80	1290.40

						Sham group			TiO$_2$-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25503174	chr7:134093374-134093418	NM_001039645:-301	Asphd1	DIVERGENT_PROMOTER	0.778	0.631	918.96	580.05	0.491	760.01	373.37
A_68_P25588373	chr7:148547408-148547453	NR_033532:3579	B230206H07Rik	INSIDE	0.778	3.297	7334.63	24181.37	2.565	5321.88	13652.11
A_68_P24055344	chr5:123821115-123821164	NM_029850:26683	Bcl7a	INSIDE	0.778	2.589	737.73	1910.30	2.014	583.53	1175.27
A_68_P24141810	chr5:141000020-141000064	NM_021528:18480	Chst12	INSIDE	0.778	2.668	1186.21	3165.11	2.077	829.81	1723.60
A_68_P24780082	chr6:117118689-117118733	NM_021704:158	Cxcl12	INSIDE	0.778	2.510	2476.86	6217.17	1.953	2128.04	4157.09
A_68_P24138666	chr5:140449442-140449486	NM_175522:65568	Elfn1	INSIDE	0.778	2.680	2740.33	7343.56	2.085	2005.87	4182.15
A_68_P20826006	chr1:172995780-172995824	NM_010188:-6268	Fcgr3	PROMOTER	0.778	0.498	12537.63	6247.46	0.387	11319.62	4386.23
A_68_P21839458	chr2:167924133-167924177	NM_021409:17651	Pard6b	INSIDE	0.778	2.322	1320.69	3066.84	1.807	1066.94	1928.10
A_68_P28322711	chr12:30623110-30623154	NM_181395:232	Pxdn	INSIDE	0.778	0.655	1363.19	892.93	0.509	971.61	495.01
A_68_P30473042	chr15:97923469-97923513	NM_144851:346	Senp1	INSIDE	0.778	0.544	1256.94	683.70	0.423	1090.05	461.25
A_68_P27925674	chr11:75161948-75161992	NM_001102611:36	Smyd4	INSIDE	0.778	0.572	1535.09	877.86	0.445	1536.92	684.07
A_68_P21912035	chr2:181415320-181415364	NM_009326:328	Tcea2	INSIDE	0.778	0.496	1561.28	774.43	0.386	1298.25	501.03
A_68_P26593994	chr9:66440646-66440690	NM_144937:119	Usp3	INSIDE	0.778	0.698	2173.75	1518.14	0.543	1871.76	1017.02
A_68_P27835783	chr11:59063276-59063320	NM_009522:40955	Wnt3a	INSIDE	0.778	1.932	1275.63	2464.85	1.504	1031.52	1551.44
A_68_P21823503	chr2:165205763-165205807	NM_178411:7975	Zfp334	INSIDE	0.778	2.035	1403.61	2856.41	1.583	1165.51	1845.06
A_68_P30503431	chr15:103144557-103144601	NM_013866:25939	Zfp385a	INSIDE	0.778	3.860	3916.57	15118.68	3.003	2644.28	7940.23
A_68_P24761385	chr6:113709127-113709171	NM_001036684:132222	Atp2b2	INSIDE	0.777	2.268	1125.08	2551.91	1.763	843.89	1487.64
A_68_P24592899	chr6:83299323-83299367	NM_175277:-133	Bola3	PROMOTER	0.777	0.621	3564.21	2212.91	0.483	2767.34	1335.64
A_68_P21746890	chr2:151796229-151796275	NM_028666:3458	Fam110a	INSIDE	0.777	3.289	1145.03	3765.55	2.554	890.25	2273.85
A_68_P30501064	chr15:102797841-102797885	NM_010462:636	Hoxc10	INSIDE	0.777	0.609	874.41	532.78	0.474	685.89	324.84
A_68_P27995155	chr11:87431487-87431532	NM_001045527:844	Hsf5	INSIDE	0.777	2.936	509.38	1495.57	2.282	447.63	1021.28
A_68_P20058161	chr1:17087384-17087428	NM_020604:564	Jph1	INSIDE	0.777	0.707	3488.58	2467.38	0.550	2849.06	1565.92
A_68_P27279589	chr10:79361980-79362024	NM_001163276:9681	Med16	INSIDE	0.777	2.355	1612.47	3798.15	1.831	1125.48	2060.28
A_68_P21630442	chr2:130389408-130389452	NM_207207:-62	Mrps26	PROMOTER	0.777	0.387	1693.66	654.78	0.300	1394.13	418.69
A_68_P21777850	chr2:157385964-157386008	NM_010923:141	Nnat	INSIDE	0.777	1.835	1359.03	2493.85	1.426	1122.42	1600.09
A_68_P28602643	chr12:86518346-86518390	NM_008827:-133	Pgf	PROMOTER	0.777	0.665	1308.87	870.25	0.516	1039.14	536.54
A_68_P30423563	chr15:88991030-88991074	NM_001159521:13228	Plxnb2	INSIDE	0.777	2.890	1668.28	4820.98	2.245	1161.47	2607.35
A_68_P32552601	chrX:96133272-96133316	NM_207633:175	Yipf6	INSIDE	0.777	2.641	952.87	2516.81	2.052	695.58	1427.36
A_68_P31147863	chr17:33103125-33103169	NM_153063:371	Zfp472	INSIDE	0.777	0.625	1452.03	906.83	0.485	1159.33	562.81
A_68_P25581871	chr7:147222691-147222735	NM_027201:423	Zfp511	INSIDE	0.777	0.482	1602.93	772.10	0.374	1236.24	462.95
A_68_P31120935	chr17:28314314-28314358	NM_172617:-26	Zfp523	PROMOTER	0.777	0.442	1182.87	522.27	0.343	933.57	320.37
A_68_P24979387	chr7:16647658-16647714	NM_001099277:-9604	Zfp541	PROMOTER	0.777	2.337	493.57	1153.48	1.815	428.33	777.42
A_68_P20049940	chr1:15276455-15276499			Unknown	0.777	0.523	1157.85	605.96	0.407	900.62	366.40
A_68_P24686647	chr6:99471695-99471739	ENSMUST00000155466:145075		INSIDE	0.777	0.626	2444.00	1529.68	0.486	1928.83	937.96
A_68_P28593717	chr12:84962112-84962165	ENSMUST00000166167:979		DOWNSTREAM	0.777	2.565	509.59	1307.33	1.994	430.76	858.97
A_68_P27835482	chr11:59022044-59022088	NM_024210:204	2310033P09Rik	INSIDE	0.776	0.700	1867.78	1307.43	0.543	1297.05	704.67
A_68_P21823609	chr2:165221660-165221704	NM_029021:4212	4833422F24Rik	INSIDE	0.776	3.252	549.32	1786.63	2.524	463.42	1169.71
A_68_P30579428	chr16:18393075-18393119	NM_033474:44730	Arvcf	INSIDE	0.776	0.468	1668.29	780.70	0.363	1204.09	437.39
A_68_P26893781	chr9:123125176-123125220	NM_133974:-42	Cdcp1	PROMOTER	0.776	0.636	1437.40	914.66	0.494	1297.98	640.99
A_68_P24226573	chr6:8459493-8459537	NM_133236:-81	Glcci1	PROMOTER	0.776	1.901	889.13	1689.90	1.474	753.60	1111.03
A_68_P27278521	chr10:79187599-79187649	NM_008226:8246	Hcn2	INSIDE	0.776	4.094	1348.72	5522.02	3.177	964.08	3062.63
A_68_P22403734	chr3:106839172-106839216	NM_008418:115	Kcna3	INSIDE	0.776	0.690	6383.92	4403.92	0.536	4855.12	2599.99
A_68_P24332082	chr6:30409887-30409931	NM_029742:58000	Klhdc10	DOWNSTREAM	0.776	0.594	948.30	563.42	0.461	877.16	404.30
A_68_P26824823	chr9:110532457-110532506	NM_183276:24184	Nbeal2	INSIDE	0.776	2.630	838.91	2206.37	2.042	600.73	1226.46
A_68_P27178540	chr10:60552155-60552199	NM_025273:86	Pcbd1	INSIDE	0.776	0.620	1152.13	714.89	0.482	910.57	438.54
A_68_P22246603	chr3:75360626-75360670	NM_019745:73	Pdcd10	INSIDE	0.776	0.445	2028.13	902.53	0.345	1698.10	586.28
A_68_P26293556	chr9:8901995-8902039	NM_008829:2184	Pgr	INSIDE	0.776	0.661	1160.63	766.92	0.513	971.24	498.11
A_68_P29336876	chr13:113590895-113590939	NM_008247:-83	Ppap2a	PROMOTER	0.776	0.571	1362.37	777.70	0.443	1075.18	476.16
A_68_P29527054	chr14:34768675-34768719	NM_015745:1489	Rbp3	INSIDE	0.776	2.712	979.13	2655.67	2.105	773.06	1627.67
A_68_P28314235	chr12:29320659-29320703	NM_011300:138	Rps7	INSIDE	0.776	0.593	991.30	587.82	0.460	871.72	401.35
A_68_P21604776	chr2:125608207-125608251	NM_177608:378	Secisbp2l	INSIDE	0.776	0.533	2043.88	1090.11	0.414	1676.32	694.18

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P20183364	chr1:42548598-42548642			Unknown	0.776	0.521	1325.55	691.12	0.405	1035.42	419.13
A_68_P22345155	chr3:95491890-95491934	NM_144899:-131	Adamtsl4	PROMOTER	0.775	0.353	1756.99	619.55	0.273	1438.39	393.11
A_68_P24098219	chr5:131916213-131916257	NM_177047:1101979	Auts2	INSIDE	0.775	2.145	709.65	1521.95	1.662	537.73	893.56
A_68_P20969129	chr2:4524543-4524587	NM_001177844:43765	Frmd4a	INSIDE	0.775	2.134	2111.23	4505.34	1.655	1714.55	2837.26
A_68_P26525029	chr9:54134177-54134221	NM_177350:-94	Gldn	PROMOTER	0.775	0.632	1463.07	924.00	0.490	1216.94	595.71
A_68_P23232472	chr4:116781942-116781986	NM_008958:13004	Ptch2	INSIDE	0.775	2.038	1530.24	3118.02	1.578	1105.21	1744.46
A_68_P30452812	chr15:94353918-94353962	NM_172437:19998	Pus7l	INSIDE	0.775	1.859	1106.16	2056.70	1.441	1040.12	1499.26
A_68_P29696766	chr14:70107048-70107092	NM_001146012:317	R3hcc1	INSIDE	0.775	0.546	1414.98	772.18	0.423	1132.39	478.80
A_68_P27687431	chr11:32113256-32113300	NM_010117:9015	Rhbdf1	INSIDE	0.775	2.035	1584.90	3225.38	1.577	1110.81	1751.67
A_68_P30486392	chr15:100382126-100382170	NM_033476:230	Tcfcp2	INSIDE	0.775	2.558	527.61	1349.81	1.983	498.01	987.74
A_68_P20228142	chr1:52687609-52687653	NM_001142647:82	Tmem194b	INSIDE	0.775	1.937	1478.25	2864.03	1.501	1256.95	1886.79
A_68_P21047274	chr2:19831411-19831455	ENSMUST00000114610:26		INSIDE	0.775	3.881	776.08	3011.69	3.009	736.92	2217.17
A_68_P21483984	chr2:103406229-103406273	NM_178890:-216	Abtb2	PROMOTER	0.774	2.335	3815.88	8909.27	1.807	2729.21	4932.48
A_68_P32717147	chrX:140752774-140752818	NM_026247:288	Alg13	INSIDE	0.774	2.344	2565.95	6015.59	1.815	1194.47	2167.85
A_68_P27981858	chr11:85048078-85048122	NM_025825:522	Appbp2	INSIDE	0.774	0.709	1823.86	1293.84	0.549	1634.10	897.50
A_68_P20827005	chr1:173200387-173200431	NM_020579:-50	B4galt3	PROMOTER	0.774	0.683	2297.04	1569.37	0.529	1977.43	1045.68
A_68_P26040515	chr8:90886224-90886268	NM_012047:-156	Brd7	PROMOTER	0.774	0.616	954.52	588.29	0.477	863.55	412.14
A_68_P21821920	chr2:164967484-164967528	NM_174988:92731	Cdh22	INSIDE	0.774	2.159	1888.25	4077.01	1.670	1566.23	2616.21
A_68_P30588850	chr16:20672735-20672779	NM_001005331:-65	Eif4g1	PROMOTER	0.774	0.614	3143.73	1929.12	0.475	2315.81	1099.28
A_68_P28159316	chr11:116295859-116295905	NR_003376:356	Gm7367	INSIDE	0.774	2.170	679.96	1475.62	1.679	488.43	820.01
A_68_P20058118	chr1:17081821-17081865	NM_020604:6128	Jph1	INSIDE	0.774	2.694	984.90	2653.32	2.084	936.74	1952.03
A_68_P27288385	chr10:80720479-80720523	NM_010768:211	Matk	INSIDE	0.774	1.935	1296.17	2508.55	1.498	1108.52	1660.34
A_68_P21421546	chr2:91096010-91096054	NM_030880:-937	Pacsin3	PROMOTER	0.774	0.579	1001.85	579.90	0.448	830.74	372.13
A_68_P25737020	chr8:28284902-28284946	NM_001080813:194	Rab11fip1	INSIDE	0.774	0.488	1860.42	907.96	0.378	1573.62	594.48
A_68_P27550649	chr11:3093369-3093413	NM_030207:76	Sfi1	INSIDE	0.774	2.220	10782.01	23938.27	1.718	9874.11	16966.01
A_68_P26238683	chr8:125760064-125760108	NM_030176:23	Spata2L	INSIDE	0.774	0.672	966.76	650.05	0.520	817.06	425.07
A_68_P31093748	chr17:23944200-23944249	NM_175229:4071	Srrm2	INSIDE	0.774	2.790	1281.96	3577.15	2.159	962.97	2078.86
A_68_P24160100	chr5:144984626-144984670	NM_027410:-201	Tecpr1	PROMOTER	0.774	0.662	1099.98	728.14	0.512	893.09	457.50
A_68_P31953349	chr19:10944024-10944068	NM_133804:223	Tmem132a	INSIDE	0.774	0.690	1155.52	797.37	0.534	899.40	480.08
A_68_P28261145	chr12:15823651-15823695	NM_144551:-81	Trib2	PROMOTER	0.774	0.391	1834.82	717.18	0.303	1360.12	411.64
A_68_P26650022	chr9:76415008-76415052	AK049628:-108		PROMOTER	0.774	0.461	1791.24	826.16	0.357	1519.29	542.48
A_68_P28143200	chr11:113510983-113511027	NM_013581:162	Cog1	INSIDE	0.773	0.618	1413.70	873.68	0.478	1112.47	531.53
A_68_P20885894	chr1:184212723-184212767	NM_007853:146	Degs1	INSIDE	0.773	0.425	1432.03	608.02	0.328	1205.36	395.42
A_68_P32030717	chr19:25684634-25684678	NM_177360:-370	Dmrt3	PROMOTER	0.773	0.692	3422.82	2368.75	0.535	2759.62	1476.10
A_68_P20960553	chr2:3036013-3036057	NM_001081161:375	Fam171a1	INSIDE	0.773	2.379	478.45	1138.37	1.840	500.51	920.95
A_68_P22291220	chr3:84284795-84284843	NM_001033301:-457	Fhdc1	PROMOTER	0.773	0.655	4622.63	3027.50	0.506	3305.09	1672.38
A_68_P23440270	chr4:155108999-155109043	NM_001101506:108	Gm5151	INSIDE	0.773	0.732	6159.66	4506.77	0.566	5267.62	2979.89
A_68_P28069615	chr11:100569978-100570022	NM_001038010:3781	Kat2a	INSIDE	0.773	2.398	700.21	1679.16	1.853	573.39	1062.57
A_68_P28004886	chr11:89160716-89160763	NM_008711:3134	Nog	DOWNSTREAM	0.773	0.601	1425.98	856.34	0.464	1040.92	483.25
A_68_P23543335	chr5:24191462-24191506	NM_016736:-148	Nub1	PROMOTER	0.773	1.811	16627.77	30117.09	1.400	11157.24	15615.51
A_68_P31626612	chr18:37159632-37159676	NM_009961:-5319	Pcdha10	PROMOTER	0.773	2.024	655.47	1326.61	1.565	582.46	911.37
A_68_P31097498	chr17:24607655-24607699	NM_025954:259	Pgp	INSIDE	0.773	0.645	2839.44	1831.97	0.499	2135.98	1065.33
A_68_P25361263	chr7:106497545-106497589	NM_001111043:4183	Serpinh1	INSIDE	0.773	2.119	637.11	1350.03	1.637	517.37	847.13
A_68_P21265073	chr2:61431374-61431418	NM_001164071:243	Tank	INSIDE	0.773	0.530	1112.51	589.97	0.410	934.52	383.28
A_68_P27288945	chr10:80795851-80795895	NM_009325:4397	Tbxa2r	INSIDE	0.773	1.962	1294.98	2541.30	1.517	899.70	1365.25
A_68_P31372684	chr17:79024264-79024308	NM_001197028:116884	Vit	INSIDE	0.773	2.399	840.61	2016.36	1.853	680.50	1261.23
A_68_P21823445	chr2:165194080-165194124	NM_001005425:-6483	Zfp663	PROMOTER	0.773	0.640	1233.60	789.76	0.495	1279.03	632.92
A_68_P32975885	A_68_P32975885			Unknown	0.773	2.417	907.64	2193.77	1.869	892.15	1667.12
A_68_P21485723	chr2:103659521-103659569	ENSMUST00000167989:89		INSIDE	0.773	3.473	271.76	943.80	2.685	270.47	726.28
A_68_P25417173	chr7:118266112-118266156	NR_015573:55	1700012D14Rik	INSIDE	0.772	0.401	1841.94	738.96	0.310	1651.38	511.63
A_68_P20416260	chr1:89083300-89083344	NM_027084:3255	1700027L20Rik	INSIDE	0.772	0.575	1199.85	689.35	0.443	920.52	408.12

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26570105	chr9:62211596-62211640	NM_009672:22469	Anp32a	INSIDE	0.772	2.230	2353.23	5247.76	1.721	1958.11	3370.80
A_68_P25828114	chr8:46129885-46129933	NM_001081286:94347	Fat1	INSIDE	0.772	2.476	621.67	1539.38	1.913	467.87	894.95
A_68_P27815757	chr11:55283721-55283765	NM_013716:489	G3bp1	INSIDE	0.772	0.525	1999.91	1049.37	0.405	1678.10	680.19
A_68_P26528147	chr9:54711749-54711793	NM_022655:209	Ireb2	INSIDE	0.772	0.632	1304.60	825.06	0.488	1243.94	607.03
A_68_P21005388	chr2:11211825-11211873	NM_008859:117840	Prkcq	INSIDE	0.772	2.341	327.68	766.96	1.806	339.73	613.62
A_68_P24994420	chr7:20214602-20214646	NM_009046:163	Relb	INSIDE	0.772	2.587	944.34	2442.58	1.996	765.50	1527.99
A_68_P26809840	chr9:107501144-107501188	NM_009153:6567	Sema3b	INSIDE	0.772	2.108	775.25	1633.87	1.626	662.38	1077.18
A_68_P24389050	chr6:40421239-40421283	NM_028358:-153	Ssbp1	PROMOTER	0.772	0.553	1940.06	1073.00	0.427	1562.07	667.29
A_68_P28635991	chr12:92886270-92886322	NM_175367:138580	Ston2	INSIDE	0.772	2.309	1073.99	2479.91	1.784	805.18	1436.17
A_68_P21081133	chr2:26771936-26771980	NM_013678:18	Surf2	INSIDE	0.772	0.615	990.00	608.80	0.475	722.16	342.79
A_68_P22059399	chr3:36570106-36570152	NM_019510:18961	Trpc3	INSIDE	0.772	2.259	512.11	1156.89	1.745	416.46	726.51
A_68_P31479226	chr18:7869155-7869199	NM_001146298:-18	Wac	PROMOTER	0.772	0.658	4327.51	2848.19	0.508	3410.77	1732.16
A_68_P26290459	chr9:8004389-8004433	NM_001171147:186	Yap1	INSIDE	0.772	0.437	2781.46	1216.72	0.338	2340.05	790.53
A_68_P25614628	A_68_P25614628			Unknown	0.772	0.712	2137.43	1521.80	0.550	1716.36	943.59
A_68_P31215872	chr17:48232748-48232792	NM_026625:6189	1700067P10Rik	DOWNSTREAM	0.771	0.693	1383.81	959.19	0.535	1204.51	644.02
A_68_P26742257	chr9:95412328-95412372	NM_001114977:65	2610101N10Rik	INSIDE	0.771	0.679	1255.94	852.85	0.523	997.16	521.90
A_68_P29622468	chr14:56983893-56983937	NM_138652:10	Atp12a	INSIDE	0.771	0.716	1359.98	973.58	0.552	1063.97	586.94
A_68_P27649722	chr11:24064060-24064104	NM_001159290:83388	Bcl11a	INSIDE	0.771	5.780	171.08	988.79	4.458	189.93	846.63
A_68_P26822033	chr9:110019921-110019966	NM_133347:-1857	Dhx30	PROMOTER	0.771	0.349	2441.22	852.03	0.269	2058.80	553.77
A_68_P26137131	chr8:108503327-108503371	NM_027960:-29	Dpep3	PROMOTER	0.771	2.001	1106.15	2213.68	1.542	818.90	1263.10
A_68_P21621792	chr2:128689765-128689810	NM_024237:120	Fbln7	INSIDE	0.771	0.606	2112.05	1280.47	0.467	1702.98	795.53
A_68_P26244127	chr8:126755799-126755843	NM_139272:527	Galnt2	INSIDE	0.771	0.577	1435.22	828.57	0.445	1152.19	512.98
A_68_P27286893	chr10:80477575-80477619	NM_010319:74	Gng7	INSIDE	0.771	0.554	2094.59	1159.80	0.427	1585.66	676.78
A_68_P30339719	chr15:74630243-74630287	NM_029627:134	Ly6k	INSIDE	0.771	2.036	836.02	1702.06	1.569	709.31	1112.74
A_68_P26132669	chr8:107800240-107800284	NM_030152:-84	Nol3	PROMOTER	0.771	0.722	9262.70	6688.81	0.557	6935.79	3860.77
A_68_P30961703	chr16:91227699-91227743	NM_016967:1926	Olig2	INSIDE	0.771	0.659	2946.46	1941.98	0.508	2430.37	1234.62
A_68_P27447375	chr10:110602439-110602483	NM_001003717:603	Osbpl8	INSIDE	0.771	0.618	1319.94	815.71	0.476	1118.32	532.64
A_68_P31784090	chr18:66094724-66094768	NM_013833:3997	Rax	INSIDE	0.771	0.666	946.65	630.04	0.513	761.69	390.92
A_68_P30970963	chr16:92699012-92699056	NM_001111023:-1461	Runx1	PROMOTER	0.771	0.690	1215.85	839.36	0.532	1061.96	565.16
A_68_P21747684	chr2:151931743-151931787	NM_029688:299	Srxn1	INSIDE	0.771	0.630	1137.14	716.83	0.486	889.12	432.39
A_68_P27288893	chr10:80788499-80788543	NM_027381:4673	2510012J08Rik	INSIDE	0.770	2.472	2173.21	5372.07	1.903	1703.88	3242.56
A_68_P24183687	chr5:149995851-149995895	NR_015478:-233	5730422E09Rik	DIVERGENT_PROMOTER	0.770	0.561	2749.52	1542.27	0.432	2193.22	946.99
A_68_P23392318	chr4:147462079-147462123	NM_009642:73	Agtrap	INSIDE	0.770	0.527	1888.24	995.65	0.406	1412.79	573.28
A_68_P23315556	chr4:132617579-132617623	NM_146155:50180	Ahdc1	INSIDE	0.770	1.869	3316.30	6197.67	1.438	2456.72	3533.18
A_68_P28724528	chr12:109155568-109155612	NM_001079883:86034	Bcl11b	INSIDE	0.770	2.346	1360.95	3192.76	1.806	1024.30	1849.70
A_68_P25090363	chr7:52225872-52225916	NM_153679:4250	Cpt1c	INSIDE	0.770	0.452	1237.98	559.66	0.348	908.26	316.11
A_68_P21566328	chr2:118639932-118639976	NM_026412:216	D2Ertd750e	INSIDE	0.770	2.983	2047.40	6107.29	2.298	1444.98	3320.23
A_68_P23335296	chr4:136249920-136249964	NM_010142:141908	Ephb2	INSIDE	0.770	2.293	934.48	2142.35	1.765	694.62	1226.03
A_68_P30555521	chr16:13110069-13110113	NM_015769:262	Ercc4	INSIDE	0.770	0.648	979.07	634.92	0.499	894.86	446.83
A_68_P20644880	chr1:138157179-138157223	NM_001101516:250	Gpr25	INSIDE	0.770	2.434	353.49	860.44	1.875	401.57	752.86
A_68_P28069614	chr11:100569881-100569928	NM_001038010:3877	Kat2a	INSIDE	0.770	3.024	1053.28	3185.52	2.329	843.67	1965.28
A_68_P31614609	chr18:34936465-34936509	NM_001081256:-175	Kdm3b	PROMOTER	0.770	0.608	1077.18	654.42	0.468	954.43	446.76
A_68_P21077002	chr2:26057533-26057577	NM_001039653:4522	Lhx3	INSIDE	0.770	0.469	1373.34	644.02	0.361	1059.91	382.71
A_68_P32559513	chrX:97624742-97624791	NM_001163191:415	Otud6a	INSIDE	0.770	2.174	2184.05	4749.01	1.674	869.01	1454.69
A_68_P22518662	chr3:128907576-128907620	NM_001042502:-9256	Pitx2	PROMOTER	0.770	0.660	1920.85	1268.31	0.508	1180.50	599.85
A_68_P26460307	chr9:43013586-43013630	NM_011139:230	Pou2f3	INSIDE	0.770	1.883	5303.84	9986.21	1.450	4048.38	5869.73
A_68_P23577159	chr5:31522755-31522799	NM_008014:142	Ppm1g	INSIDE	0.770	0.682	1373.02	936.28	0.525	1192.18	626.06
A_68_P25089821	chr7:52124278-52124322	NM_133949:858	Ptov1	INSIDE	0.770	0.365	2074.63	757.77	0.281	1519.32	427.16
A_68_P26567742	chr9:61762149-61762193	NM_018853:147	Rplp1	INSIDE	0.770	0.398	1364.55	543.23	0.307	1115.65	342.08
A_68_P32796351	chrX:160514199-160514243	NM_009173:-239	Siah1b	PROMOTER	0.770	2.222	949.12	2109.03	1.711	543.82	930.55
A_68_P21483992	chr2:103407094-103407138	NM_178890:650	Abtb2	INSIDE	0.769	0.563	1542.60	868.45	0.433	1403.51	607.37

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P24983044	chr7:17323761-17323805	NM_198613:-10	Ap2s1	PROMOTER	0.769	0.644	1033.25	665.85	0.496	881.90	437.17
A_68_P23609441	chr5:37139453-37139497	NM_133724:444	Cno	INSIDE	0.769	0.395	1479.41	583.77	0.304	1150.30	349.14
A_68_P26693200	chr9:85221504-85221548	NM_001160379:-769	Fam46a	PROMOTER	0.769	2.914	8360.81	24361.72	2.241	7304.92	16373.35
A_68_P28493840	chr12:66176906-66176950	NM_178912:336	Fancm	INSIDE	0.769	0.664	2725.87	1808.67	0.510	2130.09	1086.30
A_68_P21874396	chr2:174110775-174110819	NM_019690:976	Gnas	INSIDE	0.769	2.354	678.20	1596.61	1.810	589.03	1066.23
A_68_P26258435	chr8:129118517-129118561	NM_001164598:-1202	Irf2bp2	PROMOTER	0.769	0.617	926.03	571.27	0.474	791.98	375.75
A_68_P30370807	chr15:80041905-80041949	NM_010795:37776	Mgat3	INSIDE	0.769	2.870	1061.77	3046.93	2.207	887.51	1959.11
A_68_P25952998	chr8:73135664-73135708	NM_133772:-3473	Ssbp4	DIVERGENT_PROMOTER	0.769	0.677	3248.76	2199.83	0.521	2484.21	1293.48
A_68_P23801063	chr5:74464594-74464638	NM_177561:-180	Usp46	PROMOTER	0.769	0.508	2113.07	1073.24	0.390	1796.84	701.53
A_68_P22346431	chr3:95734111-95734155	NM_023210:953	Anp32e	INSIDE	0.768	2.087	512.85	1070.34	1.603	518.42	831.09
A_68_P23225794	chr4:115457937-115457981	NM_181040:369	Atpaf1	INSIDE	0.768	0.648	2391.22	1550.41	0.498	2164.24	1077.12
A_68_P27364531	chr10:94786138-94786182	NM_009950:571	Cradd	INSIDE	0.768	0.425	1921.34	817.30	0.327	1562.66	510.28
A_68_P21752117	chr2:152777180-152777224	NM_145744:-61	Dusp15	PROMOTER	0.768	0.617	882.69	544.59	0.474	786.72	372.94
A_68_P24138654	chr5:140448211-140448259	NM_175522:64338	Elfn1	INSIDE	0.768	3.080	1711.95	5272.60	2.365	1176.69	2782.46
A_68_P24602879	chr6:85019299-85019343	NM_177077:187	Exoc6b	INSIDE	0.768	0.271	2582.46	700.88	0.208	2186.10	455.63
A_68_P24131505	chr5:139231244-139231288	NM_030565:232	Fam20c	INSIDE	0.768	0.638	2771.19	1767.10	0.490	2143.05	1049.51
A_68_P27924560	chr11:74979095-74979139	NM_001098203:2538	Hic1	INSIDE	0.768	2.478	330.28	818.30	1.903	320.22	609.53
A_68_P25652440	chr8:11007123-11007167	NM_001081212:1286	Irs2	INSIDE	0.768	0.705	1468.72	1034.89	0.541	1260.35	682.35
A_68_P31542492	chr18:21160633-21160677	NM_019706:813	Rnf138	INSIDE	0.768	0.631	1700.39	1073.00	0.484	1390.12	673.43
A_68_P21571541	chr2:119613237-119613281	NM_001163701:15	Rpap1	INSIDE	0.768	0.676	1296.47	875.94	0.519	1233.67	640.21
A_68_P31560666	chr18:24688433-24688477	NM_144861:251	Rprd1a	INSIDE	0.768	0.651	2299.37	1497.49	0.500	1946.09	973.11
A_68_P25269238	chr7:88046152-88046196	NM_028026:-19	Wdr73	PROMOTER	0.768	2.616	577.31	1510.45	2.009	562.66	1130.53
A_68_P23364088	chr4:141001073-141001117	NM_009541:507	Zbtb17	INSIDE	0.768	0.677	4324.19	2928.76	0.520	3152.01	1640.33
A_68_P25008264	chr7:25866238-25866282	NM_175477:3996	Zfp574	INSIDE	0.768	1.983	1945.85	3859.23	1.524	1353.49	2062.64
A_68_P24319368	chr6:28211888-28211932	NM_001081678:-309	Zfp800	PROMOTER	0.768	0.519	1383.68	718.79	0.399	1144.22	456.51
A_68_P28737720	chr12:111558182-111558226	AK200124:417643		INSIDE	0.768	2.424	951.56	2306.20	1.862	719.80	1340.14
A_68_P26372146	chr9:26541704-26541748	ENSMUST00000067362:291		INSIDE	0.768	0.598	3139.58	1877.13	0.459	2422.97	1112.40
A_68_P21586516	chr2:122293842-122293886	NR_027919:-331	Bambi-ps1	PROMOTER	0.767	0.627	1333.20	835.76	0.481	1135.11	545.52
A_68_P26169911	chr8:114255931-114255975	NM_001198839:84	Bcar1	INSIDE	0.767	0.667	3069.19	2046.85	0.511	2633.68	1346.90
A_68_P31329273	chr17:70865582-70865626	NM_001128180:-5845	Dlgap1	PROMOTER	0.767	1.945	1430.47	2782.88	1.492	1195.82	1783.95
A_68_P25005397	chr7:25318691-25318735	NM_153134:3046	Irgq	INSIDE	0.767	2.133	1211.77	2585.08	1.636	1056.05	1727.97
A_68_P31150843	chr17:34027445-34027489	NM_001195298:112	Kifc1	INSIDE	0.767	2.028	3364.24	6822.25	1.555	2681.67	4169.08
A_68_P24993843	chr7:20118011-20118055	NM_199149:29715	Lrrc68	INSIDE	0.767	3.796	1228.05	4662.05	2.911	895.78	2607.70
A_68_P31097947	chr17:24670396-24670440	NM_177375:274	Rab26	INSIDE	0.767	0.502	1256.80	630.31	0.385	971.17	373.76
A_68_P23538328	chr5:23293397-23293441	NM_177323:-143	Rint1	DIVERGENT_PROMOTER	0.767	0.503	1294.18	651.22	0.386	994.11	383.43
A_68_P31253059	chr17:56110248-56110292	NM_001159523:366	Shd	INSIDE	0.767	2.140	4792.95	10254.57	1.641	3232.11	5303.67
A_68_P30979272	chr16:94079709-94079753	NM_011377:-5774	Sim2	PROMOTER	0.767	0.615	903.11	555.02	0.471	762.45	359.44
A_68_P32081999	chr19:34821540-34821584	NM_172838:39	Slc16a12	INSIDE	0.767	0.616	1035.43	637.47	0.472	848.91	400.65
A_68_P24382791	chr6:39327608-39327652	NM_028123:76	Slc37a3	INSIDE	0.767	0.519	6979.47	3624.66	0.398	5674.71	2261.20
A_68_P25025682	chr7:29946707-29946751	NM_182927:6938	Spred3	INSIDE	0.767	1.983	1774.60	3519.28	1.521	1525.13	2319.32
A_68_P24118746	chr5:136438629-136438673	NM_001160366:11696	Srcrb4d	INSIDE	0.767	0.688	2526.33	1737.74	0.528	1940.74	1024.27
A_68_P30344887	chr15:75740593-75740637	NM_178646:450	Tigd5	INSIDE	0.767	0.542	2743.28	1486.21	0.416	2190.79	910.63
A_68_P23321804	chr4:133805561-133805605	NM_024215:-4076	Zfp593	PROMOTER	0.767	2.804	2813.16	7889.49	2.150	2007.59	4317.04
A_68_P30474024	chr15:98126375-98126419	NM_173769:118	Zfp641	INSIDE	0.767	0.723	4153.37	3004.28	0.555	3182.34	1765.33
A_68_P20252948	chr1:57463462-57463506	NM_001037742:34	1110034B05Rik	INSIDE	0.766	0.624	930.72	580.56	0.478	803.96	384.12
A_68_P25933299	chr8:69010150-69010194	NM_025465:234	1810029B16Rik	INSIDE	0.766	0.547	2901.53	1587.36	0.419	2516.68	1054.93
A_68_P23441288	chr4:155266214-155266258	NM_207223:253	Acap3	INSIDE	0.766	0.533	1720.39	916.58	0.408	1420.28	579.80
A_68_P27383820	chr10:98377065-98377109	NM_026482:-699	Atp2b1	PROMOTER	0.766	0.426	6502.00	2769.40	0.326	5300.06	1728.55
A_68_P26845894	chr9:114598017-114598061	NM_146229:90	Dync1li1	INSIDE	0.766	0.551	1037.15	571.07	0.422	853.13	359.98
A_68_P31106389	chr17:25946375-25946419	NM_001164225:367	Fbxl16	INSIDE	0.766	0.557	2696.33	1502.72	0.427	2122.95	906.28
A_68_P29936842	chr14:118536259-118536304	NM_021434:-67	Gpr180	DIVERGENT_PROMOTER	0.766	0.680	2275.92	1548.55	0.521	1888.15	984.02

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P23297928	chr4:129349890-129349934	NM_008468:99	Kpna6	INSIDE	0.766	0.681	2570.42	1751.59	0.522	2251.63	1176.00
A_68_P25101644	chr7:54100954-54100998	NM_010699:-197	Ldha	PROMOTER	0.766	0.472	1332.26	629.45	0.362	1119.19	405.16
A_68_P25370887	chr7:108147267-108147311	NM_008773:13217	P2ry2	INSIDE	0.766	3.358	2343.59	7869.08	2.573	1716.51	4416.98
A_68_P30650847	chr16:32079473-32079517	NM_177326:-135	Pak2	PROMOTER	0.766	0.477	1850.96	882.74	0.365	1478.55	539.81
A_68_P24019803	chr5:117737771-117737817	NM_018858:-221	Pebp1	PROMOTER	0.766	0.575	1503.95	865.38	0.441	1224.01	539.38
A_68_P21820156	chr2:164682452-164682496	NM_011125:734	Pltp	INSIDE	0.766	0.700	1415.20	991.33	0.536	1268.86	680.47
A_68_P28159867	chr11:116395295-116395339	NM_011451:-737	Sphk1	PROMOTER	0.766	0.657	1987.19	1305.45	0.503	1514.77	762.29
A_68_P31104080	chr17:25611583-25611627	NM_027951:3070	Tekt4	INSIDE	0.766	0.542	1277.44	692.21	0.415	994.75	412.73
A_68_P20937461	chr1:193149904-193149948	NM_025864:83	Tmem206	INSIDE	0.766	0.535	1125.56	601.64	0.410	813.09	333.09
A_68_P22492341	chr3:124024087-124024131	NM_146140:154	Tram1l1	INSIDE	0.766	0.620	1694.40	1051.20	0.475	1428.82	679.33
A_68_P29733552	chr14:76816020-76816064	NM_207652:415	Tsc22d1	INSIDE	0.766	0.706	1932.11	1364.63	0.541	1362.98	737.09
A_68_P26814404	chr9:108249925-108249969	NM_011678:-215	Usp4	PROMOTER	0.766	0.541	1001.14	541.59	0.414	806.21	333.92
A_68_P23315908	chr4:132686610-132686654	NM_153423:85	Wasf2	INSIDE	0.766	0.626	920.67	575.94	0.479	737.06	353.08
A_68_P31939561	chr19:7457740-7457784	NM_001033139:-246	AI846148	PROMOTER	0.765	0.685	1251.28	856.70	0.524	1009.24	528.34
A_68_P21099934	chr2:29724540-29724584	NM_207298:-451	Cercam	PROMOTER	0.765	0.524	1004.51	526.06	0.400	925.08	370.45
A_68_P31928605	chr19:5424975-5425019	NM_024176:-80	Drap1	DIVERGENT_PROMOTER	0.765	0.656	4645.32	3046.63	0.502	3353.67	1682.55
A_68_P21708095	chr2:144425963-144426007	NM_025314:296	Dtd1	INSIDE	0.765	2.011	1212.96	2439.50	1.538	1057.67	1627.17
A_68_P30181641	chr15:44451230-44451274	NM_019480:66	Ebag9	INSIDE	0.765	0.405	1411.51	572.15	0.310	1185.78	367.54
A_68_P26224700	chr8:123652354-123652398	NM_008024:792	Foxl1	INSIDE	0.765	0.704	5086.60	3581.77	0.539	3994.16	2152.08
A_68_P23355530	chr4:139590457-139590501	NM_198610:212248	Igsf21	INSIDE	0.765	2.302	2079.85	4786.88	1.761	1429.59	2518.09
A_68_P29701860	chr14:70930843-70930887	NM_145219:237	Lgi3	INSIDE	0.765	0.703	2673.73	1879.37	0.538	2162.86	1163.34
A_68_P21840230	chr2:168056944-168056988	NM_001160330:845	Mocs3	INSIDE	0.765	2.649	349.56	926.11	2.027	351.71	712.94
A_68_P24444199	chr6:51383406-51383450	NM_010903:760	Nfe2l3	INSIDE	0.765	0.687	1242.62	853.45	0.525	1004.84	528.00
A_68_P27710218	chr11:35860780-35860826	NM_011856:896943	Odz2	INSIDE	0.765	3.841	2336.65	8974.07	2.940	1591.99	4680.31
A_68_P24933418	chr6:147212829-147212873	NM_008970:-243	Pthlh	PROMOTER	0.765	0.626	1132.86	709.52	0.479	946.50	453.66
A_68_P23072596	chr4:84851915-84851959	NM_019535:577	Sh3gl2	INSIDE	0.765	0.462	1398.26	645.76	0.353	1179.41	416.76
A_68_P32775568	chrX:156065624-156065668	NM_001135727:307	Sh3kbp1	INSIDE	0.765	2.224	1301.14	2893.48	1.700	716.85	1218.88
A_68_P27798798	chr11:52174210-52174254	NM_011694:-384	Vdac1	PROMOTER	0.765	0.595	1287.93	766.54	0.455	1011.04	460.24
A_68_P21570236	chr2:119373458-119373502	NM_019769:38	1500003O03Rik	INSIDE	0.764	0.722	1519.00	1096.16	0.551	1228.78	677.12
A_68_P25089688	chr7:52108003-52108047	NM_026270:3428	Akt1s1	INSIDE	0.764	2.277	3686.71	8392.84	1.739	2459.79	4277.36
A_68_P28741420	chr12:112215750-112215794	NM_175207:1459	Ankrd9	INSIDE	0.764	2.803	1253.44	3513.93	2.141	914.41	1957.34
A_68_P30588543	chr16:20622319-20622363	NM_028420:-989	Camk2n2	DIVERGENT_PROMOTER	0.764	0.548	976.33	535.01	0.419	787.99	329.80
A_68_P28160635	chr11:116515087-116515131	NM_030206:519	Cygb	INSIDE	0.764	0.609	5401.70	3291.76	0.466	4420.00	2058.74
A_68_P20910366	chr1:188792121-188792165	NM_033077:848	D1Pas1	INSIDE	0.764	2.574	1599.88	4118.67	1.966	1274.12	2505.30
A_68_P29134802	chr13:72765932-72765976	NR_030701:58	D430050G20	INSIDE	0.764	0.739	2690.45	1988.52	0.565	2203.54	1244.29
A_68_P23270863	chr4:124562706-124562750	NM_177671:3700	Epha10	INSIDE	0.764	2.537	365.01	926.04	1.939	353.49	685.35
A_68_P21423681	chr2:91470003-91470047	NM_010168:6547	F2	INSIDE	0.764	2.440	608.47	1484.93	1.864	571.41	1065.30
A_68_P27093480	chr10:41916896-41916940	NM_019740:79630	Foxo3	INSIDE	0.764	3.580	862.48	3087.46	2.734	780.90	2134.82
A_68_P21579980	chr2:121115168-121115212	NM_032393:-147	Mtap1a	PROMOTER	0.764	0.576	1461.29	841.75	0.440	1152.96	507.33
A_68_P29508107	chr14:31639042-31639086	NM_028839:285	Tmem110	INSIDE	0.764	0.412	1366.65	563.22	0.315	1115.45	351.07
A_68_P30752013	chr16:50529490-50529534	ENSMUST00000150937:898		INSIDE	0.764	0.572	982.09	562.18	0.437	919.28	401.79
A_68_P25326412	chr7:99889756-99889800	NR_015510:191	4632427E13Rik	INSIDE	0.763	0.431	1559.67	671.99	0.329	1252.89	412.05
A_68_P31065261	chr17:15512852-15512896	NM_007865:-87	Dll1	PROMOTER	0.763	0.674	1315.71	886.30	0.514	1070.25	549.94
A_68_P25589002	chr7:148650716-148650760	NM_001025103:3746	Efcab4a	INSIDE	0.763	0.608	1624.47	988.02	0.464	1329.00	616.44
A_68_P28470863	chr12:60320797-60320841	NM_001033156:-348	Fbxo33	PROMOTER	0.763	0.497	1678.33	834.83	0.379	1514.29	574.62
A_68_P30021002	chr15:12251634-12251678	NM_025673:406	Golph3	INSIDE	0.763	0.535	1375.95	736.03	0.408	1211.56	494.41
A_68_P25008201	chr7:25857783-25857827	NM_008168:-416	Grik5	DIVERGENT_PROMOTER	0.763	2.094	4509.78	9442.99	1.597	3633.91	5804.25
A_68_P21833672	chr2:166930250-166930294	NM_008420:84027	Kcnb1	INSIDE	0.763	2.219	1628.42	3613.84	1.694	1250.17	2117.88
A_68_P30359899	chr15:78259252-78259296	NM_001081367:217	Kctd17	INSIDE	0.763	0.600	949.92	569.58	0.457	800.16	365.83
A_68_P22373053	chr3:100881249-100881294	NM_011197:32818	Ptgfrn	INSIDE	0.763	2.893	550.00	1591.21	2.207	527.56	1164.53
A_68_P31932820	chr19:6117874-6117918	NM_133678:690	Sac3d1	INSIDE	0.763	0.665	2805.28	1865.06	0.508	2301.12	1167.91

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P29064232	chr13:56989171-56989218	NM_012035:7755	Trpc7	INSIDE	0.763	3.081	1555.88	4793.48	2.351	1063.15	2499.68
A_68_P30401623	chr15:85411668-85411712	NM_001163633:-531	Wnt7b	PROMOTER	0.763	0.593	1445.48	857.11	0.453	1153.69	522.08
A_68_P33007659	A_68_P33007659			Unknown	0.763	2.815	620.93	1747.64	2.146	790.16	1696.07
A_68_P21570454	chr2:119420252-119420296	NR_015473:243	1700020I14Rik	INSIDE	0.762	0.647	1949.28	1260.75	0.493	1604.19	790.35
A_68_P27418180	chr10:105278284-105278328	NM_207522:130	BC067068	INSIDE	0.762	0.630	1019.55	642.11	0.480	896.88	430.14
A_68_P21905662	chr2:180436767-180436811	NM_175551:17	Dido1	INSIDE	0.762	0.502	2224.30	1117.71	0.383	1748.83	669.52
A_68_P25564247	chr7:144390078-144390122	NM_001113414:116028	Ebf3	INSIDE	0.762	1.959	1326.67	2599.11	1.492	929.22	1386.69
A_68_P32559512	chrX:97624640-97624684	NM_001163191:311	Otud6a	INSIDE	0.762	2.983	2745.97	8192.31	2.275	1206.88	2745.35
A_68_P30346631	chr15:76013891-76013935	NM_201394:12228	Plec	INSIDE	0.762	2.227	1356.03	3020.39	1.696	973.86	1651.83
A_68_P25092683	chr7:52622134-52622178	NM_029741:233	Ppfia3	INSIDE	0.762	0.527	1604.44	844.96	0.402	1302.75	523.11
A_68_P30784944	chr16:57231378-57231422	NM_026254:179	Tbc1d23	INSIDE	0.762	0.593	1285.10	761.67	0.451	1116.27	503.99
A_68_P29141048	chr13:73764517-73764561	NM_009354:90	Tert	INSIDE	0.762	1.976	1416.85	2799.94	1.506	1132.52	1705.53
A_68_P26153174	chr8:111324296-111324340	NM_007496:85775	Zfhx3	INSIDE	0.762	2.224	1277.97	2841.65	1.695	1120.40	1899.19
A_68_P24596104	chr6:83864539-83864583	NM_001166371:214	Zfml	INSIDE	0.762	0.661	1927.71	1274.75	0.504	1771.44	892.51
A_68_P30778639	chr16:55974658-55974702	NR_027965:50	2310061J03Rik	INSIDE	0.761	0.565	1035.08	584.69	0.430	926.21	398.07
A_68_P21425383	chr2:91764069-91764117	NM_007699:1747	Chrm4	INSIDE	0.761	0.424	1259.33	533.58	0.322	967.01	311.65
A_68_P26240290	chr8:126039221-126039265	NM_001170976:113	Dbndd1	INSIDE	0.761	0.307	1854.06	569.93	0.234	1644.65	384.81
A_68_P22629195	chr3:148480715-148480769	NM_001081298:136857	Lphn2	INSIDE	0.761	2.286	556.61	1272.58	1.739	453.96	789.55
A_68_P27143269	chr10:53349507-53349551	NM_027830:717	Mcm9	INSIDE	0.761	0.424	1247.69	529.54	0.323	1148.74	371.04
A_68_P25090597	chr7:52262575-52262619	NM_001008422:9023	Scaf1	INSIDE	0.761	1.887	1426.94	2692.57	1.436	1086.58	1560.29
A_68_P21820817	chr2:164796549-164796593	NM_020333:3083	Slc12a5	INSIDE	0.761	0.639	1607.03	1027.43	0.487	1250.90	608.67
A_68_P21774859	chr2:156866427-156866471	NM_001164663:38553	9830001H06Rik	INSIDE	0.760	2.153	2109.78	4542.63	1.636	1679.61	2748.12
A_68_P30927368	chr16:85080443-85080487	NM_001198823:93488	App	INSIDE	0.760	4.274	8974.78	38354.18	3.248	6222.87	20211.52
A_68_P31936767	chr19:7008564-7008608	NM_008431:419	Kcnk4	INSIDE	0.760	0.464	1384.89	641.91	0.352	1110.58	391.47
A_68_P31472610	chr18:6240800-6240844	NM_008448:700	Kif5b	INSIDE	0.760	0.507	1732.27	878.34	0.385	1390.87	535.99
A_68_P21906907	chr2:180628640-180628684	NR_029538:-82	Mir124a-3	PROMOTER	0.760	0.589	2740.62	1613.61	0.447	2579.08	1153.62
A_68_P25261461	chr7:86649744-86649788	NR_029818:-383	Mir9-3	PROMOTER	0.760	0.675	2707.75	1828.91	0.513	2006.82	1029.79
A_68_P21368925	chr2:79297045-79297089	NM_010894:-273	Neurod1	PROMOTER	0.760	0.581	1692.17	982.36	0.441	1204.27	531.04
A_68_P31412095	chr17:86084743-86084787	NM_011380:2830	Six2	INSIDE	0.760	0.543	1389.85	755.32	0.413	1115.68	460.60
A_68_P25508611	chr7:135153487-135153531	NM_001079932:5617	Trim72	INSIDE	0.760	3.323	1416.09	4705.66	2.524	1148.62	2899.58
A_68_P27550009	chr10:129907495-129907539	NM_001103366:26919	Vmn2r87	DOWNSTREAM	0.760	0.634	1197.02	758.96	0.482	1020.47	492.01
A_68_P26038239	chr8:90467780-90467824	NM_033327:15692	Zfp423	INSIDE	0.760	0.647	1397.64	904.92	0.492	1151.65	566.68
A_68_P20141346	chr1:34987069-34987113			Unknown	0.760	1.891	1648.35	3117.82	1.438	1392.47	2002.71
A_68_P29613385	chr14:55251451-55251495	NM_199470:8729	Cdh24	INSIDE	0.759	2.608	1494.81	3898.76	1.980	1253.70	2482.55
A_68_P23229781	chr4:116229645-116229689	NM_029868:-665	Gpbp1l1	DIVERGENT_PROMOTER	0.759	0.603	1409.91	850.32	0.458	1098.76	502.84
A_68_P21978658	chr3:20054786-20054830	NM_013755:187	Gyg	INSIDE	0.759	2.439	618.07	1507.64	1.851	605.46	1120.50
A_68_P20296825	chr1:65225492-65225536	NM_010497:202	Idh1	INSIDE	0.759	0.505	1519.66	767.93	0.384	1313.12	503.72
A_68_P28596608	chr12:85489337-85489381	NM_027438:81	Pnma1	INSIDE	0.759	0.737	2839.95	2093.83	0.559	2171.61	1214.88
A_68_P27278631	chr10:79202347-79202393	NM_172551:6956	Polrmt	INSIDE	0.759	2.068	895.96	1852.57	1.569	698.73	1096.52
A_68_P31932823	chr19:6118207-6118251	NM_133678:358	Sac3d1	INSIDE	0.759	2.699	904.96	2442.85	2.048	856.42	1754.36
A_68_P31236175	chr17:51951926-51951970	NM_001163630:-569	Satb1	PROMOTER	0.759	0.674	1664.32	1122.45	0.512	1312.62	671.70
A_68_P20455841	chr1:95375481-95375525	NM_001159717:-67	Septin2	DIVERGENT_PROMOTER	0.759	0.398	1663.92	661.52	0.302	1383.89	417.50
A_68_P32109940	chr19:40686579-40686623	NM_026260:105	Tctn3	INSIDE	0.759	4.481	1221.25	5472.18	3.399	1266.94	4306.96
A_68_P25032376	chr7:31371948-31371992	NM_029274:1775	Wbp7	INSIDE	0.759	2.098	814.25	1708.65	1.593	662.89	1056.20
A_68_P30490574	chr15:101076776-101076820			Unknown	0.759	0.481	1391.82	669.76	0.365	1043.46	380.88
A_68_P27271358	chr10:77441308-77441352	NM_026431:-64	1810043G02Rik	DIVERGENT_PROMOTER	0.758	1.961	1246.24	2443.34	1.487	1153.05	1714.29
A_68_P25585260	chr7:148041975-148042019	NM_018742:286	Bet1l	INSIDE	0.758	0.488	1542.26	753.09	0.370	1092.19	404.26
A_68_P21564013	chr2:118256823-118256868	NM_001177806:41998	Eif2ak4	INSIDE	0.758	2.785	1532.47	4268.20	2.110	1267.99	2675.63
A_68_P32227241	chr19:60865885-60865929	NM_010123:690	Eif3a	INSIDE	0.758	0.678	960.48	651.26	0.514	819.74	421.14
A_68_P24928967	chr6:146450896-146450940	NM_010586:-484	Itpr2	PROMOTER	0.758	0.356	1794.69	638.29	0.270	1589.18	428.59
A_68_P32136319	chr19:45151445-45151489	NM_178929:838	Kazald1	INSIDE	0.758	0.469	1280.83	600.24	0.355	1073.67	381.52

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26216539	chr8:122394248-122394292	NM_146219:8066	Klhl36	INSIDE	0.758	2.590	433.49	1122.73	1.963	403.03	790.94
A_68_P20156378	chr1:37932157-37932205	NM_001037918:3130	Lipt1	INSIDE	0.758	2.314	1086.00	2512.84	1.753	870.77	1526.44
A_68_P25905384	chr8:63111913-63111957	NM_027756:278	Mfap3l	INSIDE	0.758	0.718	2065.69	1482.91	0.544	1624.78	884.54
A_68_P21742299	chr2:150834816-150834860	NM_207204:296	Ninl	INSIDE	0.758	0.673	1031.21	694.51	0.511	931.31	475.46
A_68_P23540260	chr5:23670805-23670849	NM_153092:46	Nupl2	INSIDE	0.758	0.682	1158.84	790.44	0.517	979.55	506.17
A_68_P31207757	chr17:46728534-46728578	NM_175168:37897	Ptk7	INSIDE	0.758	2.805	1181.71	3314.18	2.127	970.73	2064.31
A_68_P28054016	chr11:97888717-97888766	NM_009078:504	Rpl19	INSIDE	0.758	0.557	1297.13	722.96	0.422	847.78	358.09
A_68_P25735818	chr8:28090001-28090046	NM_001101502:2216	Zfp703	INSIDE	0.758	0.716	1362.21	975.21	0.543	1212.30	658.17
A_68_P26181049	chr8:116372565-116372609	NM_172466:153	Adamts18	INSIDE	0.757	0.570	1293.42	737.73	0.432	1091.80	471.19
A_68_P21105433	chr2:30679802-30679847	NM_133346:3996	Asb6	INSIDE	0.757	2.705	2329.11	6299.81	2.047	1769.42	3621.35
A_68_P21760472	chr2:154262476-154262520	NM_009823:279	Cbfa2t2	INSIDE	0.757	0.674	2507.16	1689.71	0.510	2109.18	1075.58
A_68_P25950969	chr8:72826268-72826312	NM_001024922:61	Ddx49	INSIDE	0.757	0.670	1826.64	1223.43	0.507	1590.87	806.81
A_68_P25737430	chr8:28371048-28371092	NM_007918:272	Eif4ebp1	INSIDE	0.757	0.626	1433.30	897.06	0.474	1305.78	618.34
A_68_P21477092	chr2:102291506-102291550	NM_010218:421	Fjx1	INSIDE	0.757	2.283	509.09	1162.05	1.729	542.88	938.61
A_68_P23246060	chr4:119212433-119212477	NM_172699:162	Foxj3	INSIDE	0.757	0.625	1072.63	670.57	0.473	947.00	448.19
A_68_P27286725	chr10:80448582-80448626	NM_001038655:15506	Gng7	INSIDE	0.757	0.661	1736.38	1148.38	0.501	1473.60	737.76
A_68_P30485949	chr15:100299584-100299628	NM_134093:142	Letmd1	INSIDE	0.757	0.604	1297.60	784.07	0.458	1052.01	481.33
A_68_P27536275	chr10:126950036-126950080	NM_001098789:-1936	Ndufa4l2	PROMOTER	0.757	0.639	1063.39	679.54	0.484	908.51	439.54
A_68_P28057357	chr11:98448589-98448634	NM_025661:-52	Ormdl3	PROMOTER	0.757	0.348	1863.58	648.73	0.263	1600.82	421.77
A_68_P23323176	chr4:134063064-134063108	NM_027995:10194	Paqr7	INSIDE	0.757	2.679	815.00	2183.22	2.028	747.79	1516.59
A_68_P32131423	chr19:44358700-44358744	NM_009128:-9443	Scd2	PROMOTER	0.757	0.541	1566.89	847.32	0.409	1128.78	462.02
A_68_P24130913	chr5:139060841-139060885	NM_001044747:109	Zfp68	INSIDE	0.757	0.516	1986.28	1025.87	0.391	1559.51	610.06
A_68_P27776268	chr11:47802068-47802112	ENSMUST00000128558:381		INSIDE	0.757	0.641	1684.77	1080.17	0.485	1435.01	696.51
A_68_P23171814	chr4:104040511-104040555	NM_177259:357	Dab1	INSIDE	0.756	0.571	968.88	552.89	0.432	760.52	328.23
A_68_P31330905	chr17:71167433-71167477	NM_001128180:296005	Dlgap1	INSIDE	0.756	2.089	658.75	1375.98	1.578	553.61	873.86
A_68_P26350080	chr9:21823071-21823117	NM_010487:33373	Elavl3	INSIDE	0.756	2.159	777.11	1677.74	1.633	600.90	981.12
A_68_P23979394	chr5:110815716-110815760	NM_028596:408	Fbrsl1	INSIDE	0.756	0.738	3010.58	2222.21	0.558	2223.41	1239.94
A_68_P23145552	chr4:99323494-99323538	NM_010425:527	Foxd3	INSIDE	0.756	0.505	1295.31	654.10	0.382	1097.70	419.09
A_68_P24112564	chr5:134789737-134789781	NM_001080746:858	Gtf2i	INSIDE	0.756	0.620	1754.63	1087.85	0.468	1589.47	744.53
A_68_P27845572	chr11:60745829-60745873	NM_008928:292	Map2k3	INSIDE	0.756	0.680	1126.32	766.36	0.515	966.93	497.51
A_68_P31849791	chr18:78033691-78033735	NM_013831:424	Pstpip2	INSIDE	0.756	1.932	5337.41	10313.82	1.461	3912.21	5715.55
A_68_P30497429	chr15:102186223-102186267	NM_153416:-5054	Aaas	PROMOTER	0.755	0.663	3145.72	2086.45	0.501	2468.30	1235.46
A_68_P24540596	chr6:72185582-72185630	NM_153778:-35	Atoh8	PROMOTER	0.755	0.590	867.71	512.14	0.446	620.60	276.64
A_68_P27649724	chr11:24064291-24064335	NM_001159290:83618	Bcl11a	INSIDE	0.755	2.343	442.71	1037.30	1.769	402.21	711.51
A_68_P27954533	chr11:80289924-80289969	NM_009871:-601	Cdk5r1	PROMOTER	0.755	0.507	1243.18	629.77	0.382	1007.76	385.32
A_68_P25083582	chr7:50931965-50932009	NM_145582:4586	Ctu1	INSIDE	0.755	2.110	1462.65	3085.89	1.594	1172.14	1868.01
A_68_P31677781	chr18:46757255-46757299	NM_010120:-81	Eif1a	DIVERGENT_PROMOTER	0.755	0.546	3993.45	2181.56	0.412	3065.18	1263.66
A_68_P22314312	chr3:88336667-88336711	NM_001029890:372	Mex3a	INSIDE	0.755	0.570	1102.56	628.68	0.431	851.84	366.92
A_68_P24191783	chr5:151396465-151396509	NM_133898:614	N4bp2l1	INSIDE	0.755	0.592	1243.16	735.99	0.447	1194.64	534.27
A_68_P23527254	chr5:21181777-21181821	NM_178728:25365	Napepld	INSIDE	0.755	3.177	3711.00	11788.84	2.400	2694.81	6467.31
A_68_P24591291	chr6:83027998-83028042	NM_197992:-363	Pcgf1	DIVERGENT_PROMOTER	0.755	0.599	1584.73	949.18	0.452	1261.37	570.48
A_68_P24210894	chr6:5446053-5446097	NM_013743:204	Pdk4	INSIDE	0.755	3.414	601.61	2053.74	2.578	569.99	1469.50
A_68_P24117607	chr5:136209485-136209529	NM_008898:44423	Por	INSIDE	0.755	2.489	3128.33	7787.77	1.880	2219.74	4172.64
A_68_P20874687	chr1:182185972-182186016	NM_011183:-9913	Psen2	PROMOTER	0.755	0.652	4521.26	2947.48	0.492	3393.94	1670.69
A_68_P24622637	chr6:88468937-88468981	NM_016906:-164	Sec61a1	PROMOTER	0.755	0.733	2086.15	1529.15	0.553	1699.53	940.58
A_68_P20901343	chr1:187279029-187279073	NM_001033286:324	Slc30a10	INSIDE	0.755	0.721	1790.47	1290.22	0.544	1479.37	804.76
A_68_P27286217	chr10:80363400-80363444	NM_013895:292	Timm13	INSIDE	0.755	0.630	2361.90	1487.33	0.476	1899.19	903.21
A_68_P31982710	chr19:16948092-16948136	NM_008023:206	Foxb2	INSIDE	0.754	0.581	1627.07	944.66	0.438	1381.12	604.28
A_68_P27271930	chr10:77531936-77531980	NM_015790:-154	Icosl	PROMOTER	0.754	0.704	1541.96	1084.89	0.531	1266.54	672.13
A_68_P28582489	chr12:82833007-82833051	NM_001174107:49129	Map3k9	INSIDE	0.754	3.261	915.98	2987.43	2.458	766.66	1884.66
A_68_P25962046	chr8:75071784-75071828	NM_027485:403	Med26	INSIDE	0.754	0.638	1361.31	868.19	0.481	1182.74	568.46

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28051870	chr11:97521455-97521499	NM_139311:-3249	Mllt6	PROMOTER	0.754	0.721	2780.63	2005.72	0.544	1984.94	1079.84
A_68_P31097571	chr17:24615950-24615994	NM_019988:51	Mlst8	INSIDE	0.754	0.632	1702.66	1075.33	0.476	1247.26	593.98
A_68_P29592280	chr14:49792675-49792719	NM_001081430:795	Naa30	INSIDE	0.754	0.542	1319.94	715.06	0.408	1188.63	485.30
A_68_P20937887	chr1:193221193-193221237	NM_144880:-294	Ppp2r5a	PROMOTER	0.754	0.735	4797.09	3527.03	0.555	3232.62	1792.69
A_68_P30595532	chr16:22009791-22009835	NM_029457:256	Senp2	INSIDE	0.754	2.209	909.67	2009.73	1.666	866.73	1444.15
A_68_P20720491	chr1:154233746-154233790	NM_025677:44	Tsen15	INSIDE	0.754	0.671	1296.27	870.40	0.506	1211.01	613.06
A_68_P24954141	chr7:6084325-6084369	NM_001013012:23227	Zfp787	INSIDE	0.754	2.601	572.12	1487.91	1.962	568.35	1115.10
A_68_P26663733	chr9:79190276-79190323			Unknown	0.754	2.407	728.53	1753.93	1.816	584.46	1061.15
A_68_P28073804	chr11:101286517-101286561	NM_026865:109	1700113I22Rik	INSIDE	0.753	0.526	1924.87	1012.70	0.396	1625.19	643.76
A_68_P26055366	chr8:93352604-93352648	NM_177224:-107	Chd9	PROMOTER	0.753	0.569	1158.12	659.34	0.429	1119.20	479.78
A_68_P31208133	chr17:46789942-46789986	NM_025611:2678	Cul7	INSIDE	0.753	2.865	3707.29	10622.66	2.157	2555.40	5511.77
A_68_P26247505	chr8:127275218-127275262	NM_001081120:469	Fam89a	INSIDE	0.753	2.104	709.52	1492.61	1.584	673.57	1067.04
A_68_P29717291	chr14:73785051-73785095	NM_008410:6	Itm2b	INSIDE	0.753	0.679	1181.56	801.90	0.511	1101.28	562.78
A_68_P28745984	chr12:113012732-113012779	NM_008450:15696	Klc1	INSIDE	0.753	2.645	854.57	2260.20	1.992	698.98	1392.71
A_68_P21628851	chr2:130099810-130099854	NM_024193:-315	Nop56	PROMOTER	0.753	0.589	1529.59	901.16	0.444	1210.99	537.31
A_68_P21395952	chr2:84877451-84877495	NM_001136081:-135	Ssrp1	PROMOTER	0.753	0.596	1794.59	1069.29	0.449	1444.64	648.39
A_68_P28055913	chr11:98219858-98219902	NM_021547:183	Stard3	INSIDE	0.753	0.716	2720.50	1948.43	0.539	2111.90	1138.81
A_68_P22889664	chr4:46627300-46627344	NM_198664:35749	Tbc1d2	INSIDE	0.753	2.081	557.89	1161.08	1.567	563.03	882.42
A_68_P25182468	chr7:72515865-72515909	NM_001163574:244	Tjp1	INSIDE	0.753	0.586	1586.09	929.94	0.442	1289.18	569.52
A_68_P31304162	chr17:66425686-66425730	NM_001025572:678	Ankrd12	INSIDE	0.752	0.397	2334.54	926.33	0.299	1889.54	564.05
A_68_P24791291	chr6:119058809-119058853	NM_001159533:-623	Cacna1c	PROMOTER	0.752	0.692	2040.00	1410.94	0.520	1732.21	901.24
A_68_P26971595	chr10:17442918-17442962	NM_010828:-93	Cited2	PROMOTER	0.752	0.576	938.19	540.81	0.433	818.80	354.79
A_68_P21580440	chr2:121180697-121180741	NM_009897:-3658	Ckmt1	DIVERGENT_PROMOTER	0.752	6.892	4393.71	30282.69	5.184	2731.70	14160.44
A_68_P23609442	chr5:37139552-37139596	NM_133724:344	Cno	INSIDE	0.752	0.492	1658.57	815.97	0.370	1460.05	540.27
A_68_P33015623	chr1_random:50870-50914	NM_026866:134446	Disp1	INSIDE	0.752	3.859	1595.54	6157.32	2.904	1232.47	3578.90
A_68_P28177057	chr11:119160971-119161015	NM_138669:365	Eif4a3	INSIDE	0.752	0.390	1541.60	600.45	0.293	1295.08	379.40
A_68_P32219571	chr19:59533895-59533939	NM_010132:737	Emx2	INSIDE	0.752	0.563	1134.53	638.74	0.424	950.58	402.58
A_68_P30956557	chr16:90387057-90387101	NM_015755:437	Hunk	INSIDE	0.752	0.529	1991.11	1054.18	0.398	1469.10	584.63
A_68_P25091032	chr7:52332198-52332242	NM_001163684:14422	Nosip	INSIDE	0.752	2.002	1318.48	2639.36	1.506	904.93	1362.80
A_68_P27611243	chr11:16407800-16407844	NM_001109971:665	Sec61g	INSIDE	0.752	0.652	1432.70	933.91	0.490	1144.58	561.39
A_68_P23897742	chr5:93522042-93522086	NM_001009818:-418	Septin11	PROMOTER	0.752	0.717	1741.64	1249.06	0.540	1356.56	732.01
A_68_P29614992	chr14:55530977-55531021	NM_021551:971	Slc22a17	INSIDE	0.752	0.620	1021.78	633.54	0.466	843.41	393.24
A_68_P24979889	chr7:16726009-16726053	NM_148946:10382	Slc8a2	INSIDE	0.752	2.400	4234.24	10163.72	1.806	3078.32	5559.76
A_68_P26736540	chr9:94437557-94437601	NM_001033145:922	1190002N15Rik	INSIDE	0.751	0.547	1626.04	888.99	0.410	1220.65	500.90
A_68_P27282403	chr10:79777962-79778006	NM_011789:13420	Apc2	INSIDE	0.751	2.485	490.80	1219.72	1.867	439.35	820.19
A_68_P21906146	chr2:180511719-180511763	NM_080641:-135	Bhlhe23	PROMOTER	0.751	0.632	1411.97	892.71	0.475	1177.13	559.12
A_68_P27171639	chr10:59414574-59414618	NM_029083:-78	Ddit4	PROMOTER	0.751	0.433	2092.76	906.95	0.325	1767.82	575.18
A_68_P27930669	chr11:76030890-76030934	NM_177367:162	Gemin4	INSIDE	0.751	0.576	910.93	524.30	0.432	839.85	362.98
A_68_P25496224	chr7:132851162-132851206	NM_207239:18	Gtf3c1	INSIDE	0.751	0.609	1123.97	684.17	0.457	982.70	449.00
A_68_P29330352	chr13:112539067-112539121	NM_011945:60097	Map3k1	INSIDE	0.751	4.470	442.35	1977.27	3.356	346.72	1163.63
A_68_P27259065	chr10:75322775-75322819	NM_010798:199	Mif	INSIDE	0.751	0.556	1341.18	745.86	0.418	1150.90	480.66
A_68_P29368029	chr13:119175953-119175997	NM_021556:85	Mrps30	INSIDE	0.751	0.641	1004.96	643.91	0.481	879.71	423.40
A_68_P27940747	chr11:77796871-77796915	NM_174852:575	Phf12	INSIDE	0.751	0.648	897.70	581.29	0.486	772.41	375.55
A_68_P30364608	chr15:78971835-78971879	NM_027231:60	Polr2f	INSIDE	0.751	0.699	1185.84	829.23	0.525	972.15	510.85
A_68_P21116391	chr2:32467758-32467803	NM_001025310:5300	St6galnac6	INSIDE	0.751	1.937	1672.81	3239.78	1.454	1182.19	1718.33
A_68_P30960422	chr16:91011625-91011669	NM_001164483:-93	Synj1	PROMOTER	0.751	0.626	977.14	611.95	0.471	754.40	354.98
A_68_P22144349	chr3:53667639-53667683	NM_026435:69	Ufm1	INSIDE	0.751	0.512	3239.67	1657.93	0.384	2500.67	961.49
A_68_P24087712	chr5:129731705-129731749			Unknown	0.751	1.961	1658.56	3252.40	1.473	1286.91	1895.39
A_68_P27473553	chr10:115550386-115550437	NM_001161855:562	4933416C03Rik	INSIDE	0.750	3.151	737.92	2325.49	2.364	646.11	1527.30
A_68_P21061192	chr2:22895312-22895356	NM_001077190:426	Abi1	INSIDE	0.750	0.536	1825.15	978.84	0.402	1397.45	562.12
A_68_P27334200	chr10:89512839-89512884	NM_001128086:176608	Anks1b	INSIDE	0.750	2.019	1687.64	3406.94	1.513	1290.95	1953.63

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P24098213	chr5:131915558-131915602	NM_177047:1102633	Auts2	INSIDE	0.750	2.228	1972.61	4394.55	1.670	1390.00	2321.41
A_68_P33015612	chr1_random:49603-49647	NM_026866:135714	Disp1	INSIDE	0.750	2.479	1203.91	2984.80	1.859	1021.81	1899.87
A_68_P25020502	chr7:28955130-28955174	NM_007991:386	Fbl	INSIDE	0.750	0.657	2086.21	1371.33	0.493	1500.51	740.20
A_68_P25021326	chr7:29135937-29135981	NR_028129:-600	LOC100302567	PROMOTER	0.750	0.704	1843.72	1297.36	0.528	1495.25	789.25
A_68_P28744813	chr12:112812529-112812573	NM_021516:-170	Mark3	PROMOTER	0.750	0.446	1177.91	524.85	0.334	974.47	325.59
A_68_P31258177	chr17:56896595-56896639	NM_008738:337	Nrtn	INSIDE	0.750	0.545	3023.00	1646.40	0.409	2590.97	1058.68
A_68_P25370884	chr7:108146949-108146996	NM_008773:13533	P2ry2	INSIDE	0.750	2.333	1304.45	3043.77	1.751	957.93	1677.20
A_68_P22313387	chr3:88169930-88169974	NM_198410:1442	Paqr6	INSIDE	0.750	1.968	2552.37	5021.94	1.476	1726.13	2547.70
A_68_P26350662	chr9:21961189-21961233	NM_001082532:-79	Pigyl	PROMOTER	0.750	0.662	1722.82	1139.74	0.496	1384.66	687.40
A_68_P20937880	chr1:193219969-193220013	NM_144880:930	Ppp2r5a	INSIDE	0.750	0.705	3049.39	2150.18	0.529	2310.78	1221.66
A_68_P21006980	chr2:11524509-11524553	NM_152824:296	Rbm17	INSIDE	0.750	0.597	1178.71	703.93	0.448	1072.30	480.38
A_68_P31093845	chr17:23957117-23957161	NM_175229:16985	Srrm2	INSIDE	0.750	3.152	605.41	1908.04	2.365	464.21	1097.79
A_68_P27579286	chr11:8564350-8564394	NM_001083587:166	Tns3	INSIDE	0.750	0.601	1095.69	658.29	0.451	932.85	420.27
A_68_P25589083	chr7:148661175-148661219	NM_053082:58	Tspan4	INSIDE	0.750	0.540	2771.04	1495.93	0.405	2237.84	906.18
A_68_P26335720	chr9:17902560-17902604			Unknown	0.750	1.957	959.13	1877.38	1.467	804.56	1180.66
A_68_P28532686	chr12:73637244-73637288	NM_026327:-77	1810048J11Rik	PROMOTER	0.749	0.704	1631.30	1147.95	0.527	1232.10	649.34
A_68_P23019856	chr4:73897951-73897995	NM_144787:190	Kdm4c	INSIDE	0.749	0.531	1555.39	825.86	0.397	1346.46	535.15
A_68_P24159376	chr5:144861468-144861512	NM_001081109:186	Lmtk2	INSIDE	0.749	0.611	1453.21	887.21	0.457	1219.88	557.86
A_68_P24993270	chr7:20014656-20014700	NM_172279:29165	Mark4	INSIDE	0.749	4.542	4624.11	21004.36	3.403	3072.09	10453.33
A_68_P23429537	chr4:153545094-153545138	NM_001162977:295	Megf6	INSIDE	0.749	0.537	1432.78	769.90	0.403	1090.70	439.24
A_68_P25578896	chr7:146768160-146768204	NR_027857:514	Nkx6-2	INSIDE	0.749	0.600	880.27	527.83	0.449	800.52	359.69
A_68_P23401741	chr4:149029526-149029570	NM_001164052:7877	Pik3cd	INSIDE	0.749	2.242	1693.63	3797.84	1.679	1212.25	2035.00
A_68_P25239156	chr7:82453635-82453679	NM_001109753:-384	Sv2b	PROMOTER	0.749	0.630	1083.00	682.11	0.472	815.96	385.07
A_68_P25399113	chr7:114514015-114514059	NM_021889:-267	Syt9	PROMOTER	0.749	2.842	822.03	2335.96	2.130	756.97	1612.02
A_68_P30133049	chr15:35300992-35301036	NM_177151:-286	Vps13b	PROMOTER	0.749	0.638	1851.27	1180.39	0.478	1585.07	757.08
A_68_P21425962	chr2:91848767-91848819	NM_011957:15535	Creb3l1	INSIDE	0.748	0.613	1134.88	696.16	0.459	924.58	424.30
A_68_P26224616	chr8:123641972-123642016	NM_013519:1924	Foxc2	INSIDE	0.748	0.452	2059.33	930.75	0.338	1502.21	508.14
A_68_P23451690	chr5:4757789-4757833	NM_021457:406	Fzd1	INSIDE	0.748	0.615	1147.11	705.82	0.460	1101.05	506.77
A_68_P29626124	chr14:57723397-57723441	NM_008125:121	Gjb2	INSIDE	0.748	0.424	1340.57	568.86	0.317	1178.80	374.04
A_68_P23438939	chr4:154865343-154865387	NM_001160016:-105	Gnb1	PROMOTER	0.748	0.373	1696.09	632.47	0.279	1477.08	412.14
A_68_P26458702	chr9:42753013-42753057	NM_175481:-580	Grik4	PROMOTER	0.748	0.643	1128.46	725.18	0.480	959.40	460.92
A_68_P28043961	chr11:96207239-96207283	NM_010458:2178	Hoxb3	INSIDE	0.748	0.588	1999.34	1175.51	0.440	1528.78	672.33
A_68_P24804132	chr6:121363263-121363307	NM_001033354:60412	Iqsec3	INSIDE	0.748	2.426	1272.67	3088.05	1.816	1111.19	2017.95
A_68_P21901578	chr2:179854064-179854108	NM_144500:16	Osbpl2	INSIDE	0.748	0.741	5590.34	4140.89	0.554	4519.93	2504.22
A_68_P25184943	chr7:73007475-73007519	NM_011048:475	Pcsk6	INSIDE	0.748	0.465	1906.94	887.49	0.348	1627.15	566.42
A_68_P31405197	chr17:84911642-84911686	NM_177606:430	Plekhh2	INSIDE	0.748	0.549	1423.60	781.66	0.411	1182.80	485.68
A_68_P27954013	chr11:80196733-80196777	NM_001130169:-26	Zfp207	DIVERGENT_PROMOTER	0.748	0.602	1654.08	996.38	0.450	1408.10	634.05
A_68_P21079937	chr2:26459672-26459716	NM_026212:36	Agpat2	INSIDE	0.747	2.206	12143.17	26784.43	1.648	8004.23	13189.17
A_68_P22407401	chr3:107398395-107398439	NM_007441:468	Alx3	INSIDE	0.747	0.441	1273.71	562.26	0.330	1113.66	367.35
A_68_P27968098	chr11:82577707-82577751	NM_009839:62	Cct6b	INSIDE	0.747	0.572	1245.05	711.70	0.427	1114.39	475.64
A_68_P22412528	chr3:108217361-108217405	NM_001004177:1030	Celsr2	INSIDE	0.747	2.251	1216.99	2739.76	1.681	914.50	1537.70
A_68_P23331195	chr4:135472662-135472706	NM_009924:21366	Cnr2	INSIDE	0.747	1.927	1631.80	3144.12	1.439	1254.78	1805.74
A_68_P24226570	chr6:8459130-8459177	NM_133236:-442	Glcci1	PROMOTER	0.747	0.715	1468.06	1050.04	0.534	1099.51	587.09
A_68_P29302881	chr13:107811807-107811851	NM_001145779:366	Kif2a	INSIDE	0.747	0.571	2198.80	1255.71	0.427	1683.25	718.27
A_68_P25360742	chr7:106416261-106416305	NM_001043355:-573	Mtap6	PROMOTER	0.747	0.572	1035.22	591.88	0.427	869.05	371.18
A_68_P27843265	chr11:60290482-60290526	NM_001103171:7664	Myo15	INSIDE	0.747	2.556	492.55	1259.08	1.909	485.20	926.12
A_68_P22325403	chr3:90269219-90269263	NM_008727:548	Npr1	INSIDE	0.747	0.626	3898.33	2441.08	0.468	3367.22	1575.46
A_68_P31106680	chr17:25981271-25981315	NM_145999:504	Rhot2	INSIDE	0.747	0.702	3811.97	2677.90	0.525	2639.14	1384.61
A_68_P27765281	chr11:45793634-45793678	NM_173384:-155	Sox30	PROMOTER	0.747	2.362	3370.35	7960.35	1.764	2693.06	4749.86
A_68_P26421199	chr9:35007341-35007385	NM_001177847:128	Tirap	INSIDE	0.747	0.659	4380.39	2884.65	0.492	3286.97	1617.87
A_68_P29428730	chr14:17197854-17197898	NM_009409:157	Top2b	INSIDE	0.747	0.631	2044.92	1290.26	0.472	1654.95	780.52

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P20157015	chr1:38054294-38054338	NM_172054:-263	Txndc9	DIVERGENT_PROMOTER	0.747	0.598	1344.44	804.56	0.447	1056.21	472.41
A_68_P27287692	chr10:80607786-80607830	NM_010731:8793	Zbtb7a	INSIDE	0.747	2.402	526.12	1263.92	1.794	473.68	849.93
A_68_P28068578	chr11:100388533-100388577	NM_001199296:760	Acly	INSIDE	0.746	0.718	1680.34	1206.42	0.535	1421.73	761.01
A_68_P22408057	chr3:107499480-107499524	NM_145542:-36	Ahcyl1	PROMOTER	0.746	0.549	2462.37	1350.98	0.409	1857.23	760.37
A_68_P30480359	chr15:99300814-99300863	NM_029236:4323	Bcdin3d	INSIDE	0.746	2.810	548.82	1542.28	2.096	469.74	984.78
A_68_P31097727	chr17:24642185-24642229	NM_027937:16479	Caskin1	INSIDE	0.746	2.946	3532.54	10408.17	2.199	2560.17	5629.98
A_68_P26078517	chr8:97125206-97125250	NM_028221:398	Fam192a	INSIDE	0.746	0.664	1194.97	793.17	0.495	1048.98	519.52
A_68_P24642399	chr6:91928996-91929040	NM_172731:-8085	Fgd5	PROMOTER	0.746	0.589	1297.09	764.52	0.440	1194.84	525.67
A_68_P27827736	chr11:57641574-57641618	NM_008213:4053	Hand1	DOWNSTREAM	0.746	0.664	1261.49	838.09	0.496	1112.21	551.12
A_68_P21527758	chr2:112079571-112079615	NM_207206:-405	Lpcat4	PROMOTER	0.746	0.616	1010.11	622.49	0.460	911.13	419.00
A_68_P21769695	chr2:155970095-155970139	NM_025946:37	Romo1	INSIDE	0.746	0.541	1864.94	1009.46	0.404	1528.17	617.15
A_68_P27215509	chr10:67504533-67504577	NM_001081346:62209	Rtkn2	INSIDE	0.746	2.901	595.15	1726.72	2.163	588.10	1272.18
A_68_P21843312	chr2:168575835-168575879	NM_175303:16845	Sall4	INSIDE	0.746	2.066	1456.62	3008.75	1.540	1172.05	1805.02
A_68_P21783958	chr2:158440228-158440272	NM_009508:3757	Slc32a1	INSIDE	0.746	0.533	1516.90	808.27	0.397	1137.18	451.99
A_68_P25957305	chr8:74049435-74049479	NM_198095:11880	Bst2	DOWNSTREAM	0.745	0.640	894.81	572.44	0.477	851.22	405.93
A_68_P30588037	chr16:20531290-20531334	NM_007889:14176	Dvl3	INSIDE	0.745	1.826	3827.58	6990.44	1.360	2865.64	3898.17
A_68_P27289051	chr10:80812913-80812957	NM_001163165:237	Hmg20b	INSIDE	0.745	0.528	1367.59	722.49	0.393	1080.30	425.00
A_68_P28621834	chr12:90498622-90498666	NM_172544:306811	Nrxn3	INSIDE	0.745	3.199	393.77	1259.55	2.384	393.09	937.22
A_68_P25956547	chr8:73895356-73895400	NM_029865:182	Ocel1	INSIDE	0.745	0.695	1196.11	830.72	0.518	958.25	496.10
A_68_P32218817	chr19:59419763-59419807	NM_001033222:486	Pdzd8	INSIDE	0.745	0.707	2121.45	1499.65	0.527	1619.88	853.00
A_68_P27833777	chr11:58775607-58775651	NM_031172:-1654	Trim17	PROMOTER	0.745	1.997	1144.68	2285.94	1.488	847.69	1261.26
A_68_P32217660	chr19:59241128-59241172	NM_009501:3369	Vax1	INSIDE	0.745	0.658	1012.97	667.01	0.491	906.79	444.97
A_68_P30401336	chr15:85374246-85374290	NM_001163634:34232	Wnt7b	INSIDE	0.745	2.100	690.67	1450.41	1.565	647.26	1012.84
A_68_P26885413	chr9:121671857-121671901	NM_001166644:2728	Zfp651	INSIDE	0.745	2.120	927.84	1966.69	1.579	767.15	1211.40
A_68_P28939819	chr13:34744472-34744516	NM_025831:56	1300014I06Rik	INSIDE	0.744	0.435	1409.06	613.62	0.324	1269.42	411.06
A_68_P20936232	chr1:192921750-192921794	NM_030060:-520	Batf3	PROMOTER	0.744	0.643	1837.44	1181.13	0.478	1601.35	765.35
A_68_P23262159	chr4:123019941-123019985	NM_007558:84	Bmp8a	INSIDE	0.744	0.705	1845.18	1300.66	0.524	1518.93	796.23
A_68_P26591858	chr9:66068690-66068734	NM_010019:62680	Dapk2	INSIDE	0.744	3.005	4345.16	13055.44	2.236	3347.90	7485.03
A_68_P24138653	chr5:140448112-140448156	NM_175522:64238	Elfn1	INSIDE	0.744	2.249	2270.52	5106.73	1.674	1746.68	2923.46
A_68_P25099052	chr7:53682950-53683004	NM_001112739:31110	Kcnc1	INSIDE	0.744	2.520	609.40	1535.94	1.876	465.96	874.18
A_68_P23409061	chr4:150288454-150288498	NM_020569:-4446	Park7	DIVERGENT_PROMOTER	0.744	0.503	1317.03	663.04	0.375	1122.42	420.62
A_68_P27565177	chr11:5737772-5737817	NM_017401:225	Polm	INSIDE	0.744	0.699	1513.09	1058.30	0.521	1186.56	617.70
A_68_P22317133	chr3:88894786-88894830	NM_001083808:-855	Rusc1	PROMOTER	0.744	0.630	1839.01	1159.05	0.469	1607.42	753.95
A_68_P21137058	chr2:35834687-35834731	NM_028921:436	Ttll11	INSIDE	0.744	0.317	1912.53	606.12	0.236	1624.80	383.27
A_68_P21040932	chr2:18616488-18616532	NM_001001334:-4138	BC061194	PROMOTER	0.743	0.656	1568.20	1028.56	0.488	1255.34	612.01
A_68_P28454004	chr12:56962132-56962176	NM_001037756:24802	Brms1l	INSIDE	0.743	3.004	1076.31	3233.01	2.230	847.73	1890.80
A_68_P26813048	chr9:108008754-108008798	NM_007567:83938	Bsn	INSIDE	0.743	2.107	1412.61	2976.51	1.566	1101.26	1724.08
A_68_P31605182	chr18:33098803-33098847	NM_009793:130	Camk4	INSIDE	0.743	0.683	1968.68	1344.77	0.508	1730.29	878.40
A_68_P33015611	chr1_random:49523-49567	NM_026866:135794	Disp1	INSIDE	0.743	3.353	590.76	1980.80	2.492	484.38	1207.01
A_68_P30180492	chr15:44258965-44259009	NM_175009:-670	Eny2	PROMOTER	0.743	0.517	1223.99	632.46	0.384	1018.16	390.97
A_68_P20455837	chr1:95375021-95375065	NM_133808:343	Hdlbp	INSIDE	0.743	0.388	2499.77	970.23	0.288	2038.42	587.76
A_68_P29071671	chr13:58229883-58229927	NM_029872:13	Hnrnpa0	INSIDE	0.743	0.552	1149.66	634.29	0.410	1060.04	434.56
A_68_P31863635	chr18:80519494-80519538	NM_001190373:41477	Kcng2	INSIDE	0.743	2.913	368.20	1072.74	2.165	331.57	717.89
A_68_P20864306	chr1:180459903-180459947	NM_001161665:669	Kif26b	INSIDE	0.743	0.606	1363.58	825.89	0.450	1029.62	463.58
A_68_P25951934	chr8:72976066-72976110	NM_001122830:24754	Klhl26	INSIDE	0.743	3.302	501.01	1654.25	2.454	518.10	1271.45
A_68_P29977212	chr15:3976767-3976811	NM_024188:361	Oxct1	INSIDE	0.743	0.655	826.36	541.07	0.486	744.84	362.34
A_68_P24059430	chr5:124573768-124573812	NM_011256:92637	Pitpnm2	INSIDE	0.743	2.267	739.80	1676.94	1.684	625.56	1053.61
A_68_P22549107	chr3:134492132-134492176	NM_021382:184	Tacr3	INSIDE	0.743	0.651	813.01	529.14	0.484	668.73	323.51
A_68_P21936418	chr3:9251625-9251669	NM_177660:1080	Zbtb10	INSIDE	0.743	0.524	4449.27	2333.04	0.389	3450.01	1343.30
A_68_P21825959	chr2:165622131-165622175	NM_027230:88036	Zmynd8	INSIDE	0.743	2.291	11741.14	26900.75	1.703	9261.99	15769.84
A_68_P31661524	chr18:43597803-43597847	ENSMUST00000121805:116		INSIDE	0.743	0.615	1079.61	664.34	0.457	914.23	417.86

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P24047008	chr5:122319680-122319724	NM_007804:178132	Cux2	INSIDE	0.742	2.362	645.46	1524.79	1.753	489.91	858.88
A_68_P31097237	chr17:24563905-24563949	NM_010023:299	Eci1	INSIDE	0.742	0.566	1163.00	658.71	0.420	956.23	401.93
A_68_P31418978	chr17:87152455-87152501	NM_010137:-725	Epas1	PROMOTER	0.742	0.582	2128.48	1238.06	0.431	1658.53	715.49
A_68_P23313223	chr4:132194907-132194951	NM_210071:-32	Eya3	PROMOTER	0.742	0.561	1026.66	576.02	0.416	961.09	399.93
A_68_P28998902	chr13:44998214-44998258	NM_001205043:171597	Jarid2	INSIDE	0.742	2.532	1481.69	3751.16	1.877	1224.38	2298.64
A_68_P23513988	chr5:18732289-18732333	NM_001170746:-553	Magi2	PROMOTER	0.742	0.454	1769.41	803.66	0.337	1425.13	480.16
A_68_P22218637	chr3:68810132-68810176	NR_029529:-3539	Mir15b	PROMOTER	0.742	0.359	1820.11	652.92	0.266	1449.84	385.87
A_68_P28055697	chr11:98189678-98189722	NM_010895:1259	Neurod2	INSIDE	0.742	0.683	4121.95	2814.81	0.507	3439.85	1742.75
A_68_P26706397	chr9:87624704-87624748	NM_023814:1369	Tbx18	INSIDE	0.742	0.647	2561.53	1656.42	0.480	2249.90	1079.08
A_68_P22336424	chr3:93251272-93251316	NM_001163098:5043	Tchh	INSIDE	0.742	0.638	1957.48	1249.51	0.474	1487.27	704.32
A_68_P22818476	chr4:32024578-32024622	AK142691:4357		DOWNSTREAM	0.742	0.623	903.10	562.88	0.463	716.22	331.41
A_68_P26057105	chr8:93657970-93658014	NM_010241:1403	Aktip	INSIDE	0.741	0.613	1315.24	805.92	0.454	1058.45	480.67
A_68_P20998751	chr2:10001887-10001931	NM_001112738:229	Atp5c1	INSIDE	0.741	0.498	1896.87	944.31	0.369	1415.27	522.23
A_68_P32567808	chrX:99447383-99447427	NM_007709:-296	Cited1	PROMOTER	0.741	2.379	1949.08	4636.43	1.763	1218.88	2148.76
A_68_P26344762	chr9:20757074-20757118	NM_001199433:-29	Dnmt1	PROMOTER	0.741	0.450	1820.89	818.95	0.333	1502.97	500.79
A_68_P20969133	chr2:4524944-4524988	NM_001177844:44167	Frmd4a	INSIDE	0.741	2.056	968.19	1990.36	1.522	745.27	1134.57
A_68_P27973305	chr11:83567284-83567328	NM_145432:168	Heatr6	INSIDE	0.741	0.710	1341.40	952.54	0.526	1100.61	579.17
A_68_P31672404	chr18:45719853-45719897	NM_080465:67	Kcnn2	INSIDE	0.741	0.520	1294.22	673.22	0.386	1100.13	424.20
A_68_P30251032	chr15:58765375-58765419	NM_023172:32	Ndufb9	INSIDE	0.741	2.234	715.81	1598.87	1.656	675.94	1119.14
A_68_P29051304	chr13:54867489-54867533	NM_033610:291	Sncb	INSIDE	0.741	0.553	2006.16	1110.27	0.410	1489.44	610.62
A_68_P31055435	chr17:13109226-13109270	NM_013686:-82	Tcp1	DIVERGENT_PROMOTER	0.741	0.592	1368.37	809.96	0.438	996.98	437.15
A_68_P30094306	chr15:27677312-27677364	NM_001081302:278265	Trio	INSIDE	0.741	4.333	1320.19	5720.37	3.211	1064.20	3417.62
A_68_P23937432	chr5:102311610-102311654	NM_172882:187308	Wdfy3	INSIDE	0.741	2.294	1048.54	2405.02	1.699	859.83	1460.45
A_68_P23167117	chr4:103292545-103292589	ENSMUST00000106827:297		INSIDE	0.741	2.289	548.36	1254.94	1.695	503.90	853.98
A_68_P30394509	chr15:84237243-84237293	NM_001163145:40259	1810041L15Rik	INSIDE	0.740	2.659	6179.66	16431.01	1.968	3919.49	7715.36
A_68_P26016334	chr8:86264880-86264924	NM_001163029:308	Cd97	INSIDE	0.740	0.589	1079.89	636.09	0.436	909.81	396.58
A_68_P27186921	chr10:62064974-62065018	NM_019553:50	Ddx21	INSIDE	0.740	0.619	907.52	561.93	0.458	723.64	331.63
A_68_P21177699	chr2:44412715-44412759	NM_172662:304406	Gtdc1	DOWNSTREAM	0.740	0.553	1450.86	802.51	0.410	1194.08	489.05
A_68_P26809757	chr9:107490272-107490316	NM_025903:246	Ifrd2	INSIDE	0.740	0.613	1771.52	1085.73	0.454	1486.18	674.03
A_68_P24054545	chr5:123678394-123678438	NM_026000:218	Psmd9	INSIDE	0.740	0.486	2118.47	1029.52	0.360	1661.37	597.57
A_68_P31622955	chr18:36441203-36441247	NM_008989:409	Pura	INSIDE	0.740	0.708	2664.09	1885.18	0.524	2195.46	1149.44
A_68_P31097160	chr17:24551864-24551908	NM_001080127:267	Rnps1	INSIDE	0.740	0.603	1159.01	698.68	0.446	929.97	414.68
A_68_P24973143	chr7:13404105-13404149	NM_026046:83	Zfp329	INSIDE	0.740	0.577	1442.37	832.68	0.427	1140.39	487.21
A_68_P20858943	chr1:179253140-179253187			Unknown	0.740	3.127	318.70	996.42	2.312	277.21	641.02
A_68_P22832216	chr4:34663543-34663589	NM_027041:13889	1700003M02Rik	INSIDE	0.739	3.398	192.55	654.32	2.511	203.16	510.22
A_68_P26888896	chr9:122260961-122261005	NM_026179:249	Abhd5	INSIDE	0.739	0.456	1488.24	679.33	0.338	1372.71	463.35
A_68_P27765616	chr11:45869574-45869618	NM_009616:108	Adam19	INSIDE	0.739	0.727	2472.74	1798.80	0.537	2026.60	1089.05
A_68_P26216375	chr8:122364400-122364444	NM_028071:57	Cotl1	INSIDE	0.739	0.408	1493.83	609.12	0.301	1152.02	346.98
A_68_P26137128	chr8:108503069-108503114	NM_027960:228	Dpep3	INSIDE	0.739	5.178	1554.18	8047.69	3.824	1140.70	4362.13
A_68_P31424360	chr17:88039882-88039941	NM_008532:4593	Epcam	INSIDE	0.739	2.389	525.69	1255.78	1.765	428.88	757.03
A_68_P28575794	chr12:81564131-81564176	NM_133798:72	Exd2	INSIDE	0.739	0.672	1316.22	883.89	0.497	1057.30	525.02
A_68_P26138083	chr8:108686810-108686868	NM_133792:12540	Pla2g15	INSIDE	0.739	2.084	918.97	1915.36	1.539	760.89	1171.37
A_68_P21776096	chr2:157104650-157104694	NM_019642:-161	Rpn2	PROMOTER	0.739	0.567	979.45	555.53	0.419	882.95	369.88
A_68_P29619288	chr14:56300374-56300418	NM_145705:258	Tinf2	INSIDE	0.739	0.501	1407.61	705.31	0.370	1161.83	429.98
A_68_P30255516	chr15:59480386-59480430	NM_144549:200	Trib1	INSIDE	0.739	0.619	948.94	587.33	0.458	765.05	350.13
A_68_P21365112	chr2:78708612-78708656	NM_009454:-569	Ube2e3	PROMOTER	0.739	0.439	1259.62	552.74	0.324	1016.54	329.72
A_68_P23227081	chr4:115652001-115652045	ENSMUST00000125761:38258		INSIDE	0.739	0.484	1630.75	788.77	0.358	1269.13	453.86
A_68_P31791927	chr18:67608929-67608973	NM_027130:-160	Afg3l2	PROMOTER	0.738	2.584	13481.67	34840.73	1.908	9870.08	18827.93
A_68_P26166332	chr8:113580916-113580960	NM_028274:700	Exosc6	INSIDE	0.738	0.641	1639.80	1051.41	0.473	1384.10	655.34
A_68_P26693191	chr9:85220481-85220525	NM_001160378:229	Fam46a	INSIDE	0.738	0.636	3853.51	2451.08	0.469	3093.79	1452.25
A_68_P21428050	chr2:92210966-92211010	NM_001166633:205	Gyltl1b	INSIDE	0.738	0.448	1441.07	645.51	0.330	1136.68	375.60

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28099141	chr11:105882018-105882062	NM_001037712:12524	Kcnh6	INSIDE	0.738	0.508	1155.24	586.36	0.374	947.35	354.62
A_68_P23429536	chr4:153544927-153544971	NM_001162977:127	Megf6	INSIDE	0.738	0.568	1305.64	741.69	0.419	968.78	405.92
A_68_P31462885	chr18:4375737-4375781	NM_026157:169	Mtpap	INSIDE	0.738	0.465	1320.44	614.40	0.343	957.27	328.76
A_68_P32134813	chr19:44910513-44910557	NM_011037:78651	Pax2	INSIDE	0.738	0.546	2166.19	1182.22	0.403	1551.03	625.13
A_68_P21871011	chr2:173485139-173485183	NR_027957:-120	Ppp4r1l-ps	DIVERGENT_PROMOTER	0.738	0.456	1292.56	589.14	0.336	1010.01	339.76
A_68_P25090919	chr7:52308886-52308930	NM_175022:-657	Prr12	PROMOTER	0.738	0.712	1500.33	1068.45	0.525	1365.97	717.80
A_68_P24158012	chr5:144493603-144493647	NM_029749:-475	Usp42	PROMOTER	0.738	0.486	1476.50	717.45	0.359	1173.47	420.71
A_68_P24022912	chr5:118292434-118292478	ENSMUST00000111935:262		INSIDE	0.738	0.352	1606.41	564.68	0.259	1220.54	316.54
A_68_P27282383	chr10:79775753-79775797	NM_011789:11210	Apc2	INSIDE	0.737	2.678	259.71	695.46	1.974	287.81	568.09
A_68_P25429180	chr7:120350610-120350654	NM_007489:-346	Arntl	PROMOTER	0.737	0.496	1556.30	771.77	0.365	1030.62	376.43
A_68_P28743347	chr12:112556990-112557038	NM_183016:58915	Cdc42bpb	INSIDE	0.737	2.555	441.16	1127.10	1.884	376.49	709.36
A_68_P23317811	chr4:133036049-133036093	NM_175307:23	Fam46b	INSIDE	0.737	0.407	2133.25	868.72	0.300	1726.30	517.90
A_68_P24589802	chr6:82723996-82724040	NM_013820:430	Hk2	INSIDE	0.737	0.559	1600.55	894.17	0.412	1221.32	503.06
A_68_P25196741	chr7:75095612-75095656	NM_010513:-1508	Igf1r	PROMOTER	0.737	0.537	1439.37	773.28	0.396	1137.59	450.35
A_68_P24990857	chr7:19589831-19589875	NM_178757:439	Irf2bp1	INSIDE	0.737	0.594	2734.43	1623.11	0.437	2033.12	889.32
A_68_P22165657	chr3:57651863-57651907	NM_019410:-205	Pfn2	PROMOTER	0.737	0.700	1700.02	1189.86	0.516	1578.85	814.11
A_68_P30346541	chr15:76002795-76002839	NM_201394:23324	Plec	INSIDE	0.737	2.366	736.04	1741.78	1.745	642.26	1120.79
A_68_P28739965	chr12:111975801-111975845	NM_027149:-336	Wdr20a	PROMOTER	0.737	0.496	1415.72	701.77	0.365	1129.44	412.52
A_68_P24951589	chr7:4969379-4969423	NM_025324:2291	Zfp524	INSIDE	0.737	1.873	2204.66	4128.25	1.380	1639.57	2263.03
A_68_P22202957	chr3:65778426-65778470	AK133062:4613		DOWNSTREAM	0.737	0.612	1689.50	1034.26	0.451	1335.44	602.26
A_68_P20641033	chr1:137584481-137584525	ENSMUST00000112103:180		INSIDE	0.737	0.648	1065.98	691.20	0.478	914.77	437.39
A_68_P23442481	chr4:155484106-155484150	NM_145557:22	9430015G10Rik	INSIDE	0.736	0.657	1798.94	1182.66	0.484	1648.04	797.92
A_68_P30931283	chr16:85803597-85803643	NM_009621:-260	Adamts1	PROMOTER	0.736	0.415	1574.19	652.51	0.305	1255.45	382.98
A_68_P24605770	chr6:85537797-85537841	NM_145223:294	Alms1	INSIDE	0.736	0.584	1180.21	688.87	0.430	915.29	393.38
A_68_P23103737	chr4:91038861-91038905	NM_010486:-136	Elavl2	PROMOTER	0.736	0.705	1320.87	931.77	0.519	1234.22	640.71
A_68_P25828112	chr8:46129668-46129713	NM_001081286:94129	Fat1	INSIDE	0.736	2.199	1693.45	3723.43	1.617	1211.44	1959.17
A_68_P27924569	chr11:74980234-74980278	NM_001098203:1398	Hic1	INSIDE	0.736	0.512	1334.77	683.39	0.377	1210.30	455.82
A_68_P23355139	chr4:139521507-139521551	NM_173427:2413	Klhdc7a	INSIDE	0.736	2.704	1205.03	3258.92	1.990	957.09	1904.15
A_68_P21122758	chr2:33496074-33496118	NM_010725:-65	Lmx1b	PROMOTER	0.736	0.606	1331.28	806.58	0.446	1035.90	461.67
A_68_P23842571	chr5:82223744-82223788	NM_198702:773149	Lphn3	INSIDE	0.736	2.809	2070.38	5814.88	2.066	1458.92	3014.37
A_68_P28177561	chr11:119251986-119252030	NR_035453:223	Mir1932	DOWNSTREAM	0.736	0.637	881.70	561.33	0.469	757.45	354.94
A_68_P27449072	chr10:110910120-110910164	NM_015781:-105	Nap1l1	PROMOTER	0.736	0.428	1530.79	654.53	0.315	1218.52	383.70
A_68_P22920588	chr4:53024879-53024923	NM_025623:105	Nipsnap3b	INSIDE	0.736	0.650	1103.11	717.03	0.479	797.21	381.64
A_68_P21101092	chr2:29917364-29917408	NM_023871:-129	Set	PROMOTER	0.736	0.529	2496.37	1320.15	0.389	1917.42	746.57
A_68_P23819149	chr5:77403640-77403684	NM_025691:-63	Srp72	PROMOTER	0.736	0.527	1566.95	826.32	0.388	1287.43	499.44
A_68_P22869409	chr4:43013406-43013450	NM_009503:-49	Vcp	PROMOTER	0.736	0.633	2142.68	1356.37	0.466	1602.18	746.04
A_68_P28712493	chr12:107248661-107248705	NM_001029843:210	Vrk1	INSIDE	0.736	0.729	1701.18	1240.16	0.536	1260.60	676.07
A_68_P32326562	chrX:35534336-35534380	NM_001079513:-8611	Zbtb33	PROMOTER	0.736	2.048	2849.40	5834.73	1.507	1293.01	1948.22
A_68_P24973142	chr7:13403941-13403985	NM_026046:247	Zfp329	INSIDE	0.736	0.660	2398.56	1583.41	0.486	1930.04	938.28
A_68_P20141347	chr1:34987195-34987239			Unknown	0.736	2.619	1381.48	3617.66	1.926	1228.56	2366.42
A_68_P21037980	chr2:17969325-17969369	NM_028317:730	2810030E01Rik	INSIDE	0.735	0.702	1521.11	1068.52	0.517	1323.68	683.79
A_68_P33007148	chr9_random:50071-50115	NR_015516:-3316	4930526I15Rik	PROMOTER	0.735	2.607	653.18	1702.71	1.917	553.65	1061.22
A_68_P24330600	chr6:30125802-30125846	NR_038124:-798	BB283400	DIVERGENT_PROMOTER	0.735	0.637	1000.05	637.37	0.468	815.40	381.80
A_68_P25047600	chr7:35903087-35903131	NM_007678:-1203	Cebpa	PROMOTER	0.735	0.600	1750.07	1050.28	0.441	1435.10	633.00
A_68_P23343151	chr4:137549520-137549564	NM_172703:158	Eif4g3	INSIDE	0.735	0.500	2430.91	1214.73	0.367	2002.04	735.73
A_68_P31099381	chr17:24889759-24889803	NM_001012402:-167	Hs3st6	PROMOTER	0.735	0.561	1429.04	802.30	0.412	1135.73	468.40
A_68_P26416478	chr9:34296474-34296518	NM_001190913:181	Kirrel3	INSIDE	0.735	0.671	992.40	666.19	0.493	896.32	442.24
A_68_P23260019	chr4:122638179-122638223	NM_029662:231	Mfsd2a	INSIDE	0.735	0.631	1691.29	1067.63	0.464	1483.90	688.89
A_68_P27710217	chr11:35860615-35860667	NM_011856:897105	Odz2	INSIDE	0.735	2.196	634.02	1392.52	1.615	520.40	840.34
A_68_P31936611	chr19:6984134-6984178	NM_012021:-21	Prdx5	DIVERGENT_PROMOTER	0.735	0.407	1415.73	575.89	0.299	1215.48	363.50
A_68_P30861546	chr16:72663403-72663447	NM_019413:31	Robo1	INSIDE	0.735	0.455	1542.64	701.58	0.334	1207.14	403.63

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P21776097	chr2:157104828-157104872	NM_019642:17	Rpn2	INSIDE	0.735	0.492	2970.10	1462.75	0.362	2516.80	910.64
A_68_P30550102	chr16:11983916-11983960	NM_001174086:-267	Shisa9	PROMOTER	0.735	0.552	1039.13	573.25	0.405	786.39	318.80
A_68_P20456738	chr1:95531890-95531934	NM_021537:392	Stk25	INSIDE	0.735	0.435	2618.17	1139.22	0.320	2044.68	654.10
A_68_P27287714	chr10:80611346-80611390	NM_010731:12353	Zbtb7a	INSIDE	0.735	3.043	1863.48	5670.82	2.236	1281.71	2865.95
A_68_P27902562	chr11:70577949-70577993	NM_177565:22	Zfp3	INSIDE	0.735	0.593	1284.56	761.90	0.436	1000.50	436.43
A_68_P24540585	chr6:72184350-72184394	NM_153778:1199	Atoh8	INSIDE	0.734	0.629	1954.05	1228.88	0.462	1538.94	710.43
A_68_P30082170	chr15:25552222-25552266	NM_019472:-60	Myo10	PROMOTER	0.734	2.392	10089.63	24137.04	1.756	6288.85	11044.29
A_68_P22149842	chr3:54598425-54598471	NM_019483:38945	Smad9	INSIDE	0.734	2.264	538.91	1220.11	1.661	459.85	763.72
A_68_P30510294	chr16:4474965-4475009	NM_175347:48067	Srl	DOWNSTREAM	0.734	0.450	1173.45	527.48	0.330	968.41	319.38
A_68_P21890545	chr2:178141876-178141920	NM_177191:465	Sycp2	INSIDE	0.734	2.049	2217.97	4544.80	1.504	1689.33	2541.23
A_68_P28431150	chr12:52791936-52791980	NM_021710:6	Ap4s1	INSIDE	0.733	0.735	2875.79	2113.78	0.539	2351.11	1267.11
A_68_P30725227	chr16:45159318-45159362	NM_026402:399	Atg3	INSIDE	0.733	0.509	1447.87	737.09	0.373	1192.94	445.24
A_68_P21603778	chr2:125450808-125450852	NM_001081091:19	Cep152	INSIDE	0.733	0.715	6199.84	4434.33	0.524	4557.33	2390.20
A_68_P31113352	chr17:27083607-27083651	NM_026948:-7205	Cuta	PROMOTER	0.733	0.648	996.41	645.42	0.475	791.96	375.99
A_68_P24743885	chr6:110595746-110595790	NM_177328:177	Grm7	INSIDE	0.733	0.523	1156.01	604.95	0.384	940.53	360.81
A_68_P27880944	chr11:66907962-66908006	NM_001099635:16183	Myh3	INSIDE	0.733	2.703	497.53	1344.86	1.982	478.86	948.88
A_68_P23575371	chr5:31210102-31210146	NM_001134692:-29	Ost4	PROMOTER	0.733	0.480	1213.46	582.11	0.351	934.67	328.52
A_68_P25365848	chr7:107270096-107270140	NM_133692:-108	Pold3	PROMOTER	0.733	0.680	1283.68	872.82	0.499	1181.80	589.28
A_68_P26569721	chr9:62130111-62130155	NM_025721:-146	Spesp1	PROMOTER	0.733	2.215	702.65	1556.68	1.624	608.04	987.23
A_68_P23330838	chr4:135411699-135411743	NM_001080387:-286	Srsf10	PROMOTER	0.733	0.690	1178.39	812.78	0.506	884.46	447.16
A_68_P21492632	chr2:104968263-104968307	NM_144783:1599	Wt1	INSIDE	0.733	0.507	1516.18	768.13	0.371	1238.05	459.83
A_68_P32565628	chrX:98989774-98989818	ENSMUST00000151231:-198		DIVERGENT_PROMOTER	0.733	4.558	196.37	894.99	3.341	144.54	482.96
A_68_P24104843	chr5:133018201-133018245	NM_177047:-9	Auts2	PROMOTER	0.732	0.538	1584.04	852.42	0.394	1163.25	458.33
A_68_P28356776	chr12:36883470-36883514	NM_025840:-80	Bzw2	DIVERGENT_PROMOTER	0.732	0.710	3297.14	2340.35	0.520	2628.47	1365.87
A_68_P31423368	chr17:87845364-87845408	NM_007589:889	Calm2	INSIDE	0.732	2.042	27563.02	56296.76	1.495	21612.40	32309.69
A_68_P27446114	chr10:110357360-110357404	NM_007792:151	Csrp2	INSIDE	0.732	0.521	2924.13	1524.33	0.381	2285.41	871.54
A_68_P33007793	chr4_random:128741-128785	NM_001033326:18961	Dhrsx	INSIDE	0.732	1.925	1720.51	3312.23	1.409	1257.04	1770.88
A_68_P25958569	chr8:74249306-74249350	NM_028715:252	Fcho1	INSIDE	0.732	0.479	2105.72	1009.66	0.351	1609.95	565.35
A_68_P24444428	chr6:51419499-51419543	NM_016806:373	Hnrnpa2b1	INSIDE	0.732	0.524	1324.53	694.54	0.384	1055.90	405.42
A_68_P28748381	chr12:113412125-113412169	NM_001097621:27728	Kif26a	INSIDE	0.732	2.097	822.58	1725.27	1.535	702.55	1078.25
A_68_P25266320	chr7:87515606-87515650	NM_172903:633	Man2a2	INSIDE	0.732	0.601	1692.38	1017.45	0.440	1473.48	648.23
A_68_P27855152	chr11:62478459-62478505	NM_175002:16317	Mmgt2	INSIDE	0.732	2.476	1230.22	3045.92	1.813	897.55	1627.64
A_68_P32143072	chr19:46379792-46379836	NM_019408:-370	Nfkb2	PROMOTER	0.732	0.432	1338.96	579.09	0.317	1083.40	342.99
A_68_P31052339	chr17:12700068-12700112	NM_011395:480	Slc22a3	INSIDE	0.732	0.657	1867.82	1226.87	0.481	1422.62	683.59
A_68_P23332900	chr4:135804202-135804246	NM_011542:353	Tcea3	INSIDE	0.732	0.469	1229.78	576.18	0.343	1088.06	372.93
A_68_P25033085	chr7:31514372-31514419	NM_027215:158	Tmem147	INSIDE	0.732	2.442	683.31	1668.51	1.788	667.08	1192.76
A_68_P29437676	A_68_P29437676			Unknown	0.732	4.393	256.18	1125.31	3.215	628.33	2020.29
A_68_P23878952	chr5:90113527-90113571	NM_001081401:198811	Adamts3	INSIDE	0.731	2.426	454.01	1101.33	1.773	466.87	827.92
A_68_P30404626	chr15:85864596-85864640	NM_009886:-411	Celsr1	PROMOTER	0.731	0.464	1788.15	829.46	0.339	1499.85	508.85
A_68_P28745341	chr12:112908900-112908944	NM_021273:1627	Ckb	INSIDE	0.731	0.603	1086.49	654.70	0.440	893.41	393.32
A_68_P22152358	chr3:55046521-55046565	NM_001111053:95	Dclk1	INSIDE	0.731	0.561	1171.73	657.68	0.410	1028.00	421.62
A_68_P27690051	chr11:32543056-32543100	NM_134015:204	Fbxw11	INSIDE	0.731	0.659	1113.17	733.64	0.482	918.93	442.67
A_68_P25565906	chr7:144629538-144629582	NR_033611:204	Gm12669	INSIDE	0.731	0.591	1748.37	1033.55	0.432	1510.83	652.90
A_68_P28577466	chr12:81858386-81858430	NM_001008423:3294	Gm1568	INSIDE	0.731	2.007	1131.11	2269.65	1.466	861.16	1262.70
A_68_P20897049	chr1:186542249-186542293	NM_008250:14102	Hlx	DOWNSTREAM	0.731	0.518	1286.64	666.73	0.379	1073.75	406.51
A_68_P23752951	chr5:65195497-65195541	NM_008453:757	Klf3	INSIDE	0.731	0.606	1203.30	728.66	0.443	960.55	425.39
A_68_P26823921	chr9:110379166-110379210	NM_177771:10	Klhl18	INSIDE	0.731	0.462	1777.26	821.49	0.338	1350.38	456.43
A_68_P23567513	chr5:29761841-29761885	NM_001033457:656	Nom1	INSIDE	0.731	0.603	1385.36	834.81	0.441	1135.70	500.38
A_68_P28301678	chr12:27099581-27099625	NM_001081977:519	Rnf144a	INSIDE	0.731	0.364	3633.86	1323.13	0.266	2693.05	717.23
A_68_P31117592	chr17:27772360-27772404	NM_025963:-195	Rps10	PROMOTER	0.731	2.097	1745.21	3659.61	1.532	1565.47	2398.82
A_68_P21428682	chr2:92299796-92299840	NM_211358:133	Slc35c1	INSIDE	0.731	0.568	1365.13	775.95	0.416	967.01	401.94

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28050120	chr11:97224658-97224702	NM_138657:816	Socs7	INSIDE	0.731	0.519	1464.36	759.51	0.379	1082.23	410.54
A_68_P20456737	chr1:95531806-95531850	NM_021537:476	Stk25	INSIDE	0.731	0.628	2118.33	1331.00	0.459	1616.44	742.20
A_68_P21081131	chr2:26771732-26771776	NM_013678:-186	Surf2	PROMOTER	0.731	0.550	1339.48	737.21	0.402	1029.42	413.95
A_68_P23395559	chr4:148000804-148000848	NM_001003898:279	Tardbp	INSIDE	0.731	0.495	1299.99	643.76	0.362	1020.98	369.37
A_68_P31879126	chr18:83080440-83080484	NM_001177464:-3561	Zfp516	PROMOTER	0.731	0.596	1627.23	969.64	0.436	1286.50	560.63
A_68_P22314993	chr3:88447939-88447984	NM_001198912:22646	Arhgef2	INSIDE	0.730	3.396	533.25	1810.86	2.480	529.34	1312.88
A_68_P31001860	chr16:98144127-98144171	NM_174847:95	C2cd2	INSIDE	0.730	0.608	1436.86	873.60	0.444	1267.08	562.54
A_68_P22893527	chr4:47258362-47258406	NM_009928:37501	Col15a1	INSIDE	0.730	2.735	444.65	1216.09	1.998	476.01	950.92
A_68_P26658154	chr9:77955972-77956016	NM_023605:469	Fbxo9	INSIDE	0.730	0.420	1456.74	611.34	0.306	1126.44	344.96
A_68_P27278593	chr10:79198358-79198402	NM_008226:19002	Hcn2	INSIDE	0.730	2.195	1057.60	2321.40	1.602	960.91	1539.43
A_68_P29229616	chr13:94269682-94269726	NM_021310:59	Jmy	INSIDE	0.730	0.620	997.64	618.27	0.452	859.63	388.98
A_68_P30961943	chr16:91270119-91270163	NM_016968:127	Olig1	INSIDE	0.730	0.655	1037.24	678.90	0.478	715.41	342.06
A_68_P25972612	chr8:77737217-77737261	NM_029182:-604	Rasd2	PROMOTER	0.730	0.575	1037.15	596.20	0.419	865.12	362.81
A_68_P21101094	chr2:29917589-29917633	NM_001204875:-4383	Set	PROMOTER	0.730	0.649	931.57	604.35	0.474	787.60	373.05
A_68_P29879706	chr14:106295189-106295234	NM_011897:825	Spry2	INSIDE	0.730	0.613	1075.97	659.90	0.448	1048.06	469.19
A_68_P31056402	chr17:13898617-13898661	NM_022311:-237	Tcte2	PROMOTER	0.730	0.520	1287.85	669.45	0.379	1046.31	396.80
A_68_P30176276	chr15:43308988-43309032	NM_025736:236	Ttc35	INSIDE	0.730	0.619	998.62	618.58	0.452	691.14	312.52
A_68_P26216697	chr8:122434504-122434548	NM_009462:-225	Usp10	PROMOTER	0.730	0.620	2512.02	1557.68	0.453	2199.16	995.18
A_68_P22321213	chr3:89519038-89519082	NM_001038587:117	Adar	INSIDE	0.729	0.468	1699.68	795.95	0.342	1244.87	425.27
A_68_P29234320	chr13:95128962-95129006	NM_009680:70	Ap3b1	INSIDE	0.729	0.528	1627.44	859.83	0.385	1408.38	542.15
A_68_P26544128	chr9:57684324-57684368	NM_019689:-2305	Arid3b	PROMOTER	0.729	0.662	1698.33	1124.52	0.483	1408.74	679.73
A_68_P30388927	chr15:83357675-83357720	NM_007546:406	Bik	INSIDE	0.729	0.317	2292.07	725.67	0.231	1724.60	397.91
A_68_P24995608	chr7:20443293-20443337	NM_001033419:3334	Ceacam16	INSIDE	0.729	1.971	1047.32	2063.88	1.437	937.75	1347.93
A_68_P21319993	chr2:71367466-71367510	NM_010053:-13	Dlx1	PROMOTER	0.729	0.675	1582.09	1067.27	0.492	1113.15	547.26
A_68_P22248557	chr3:75750620-75750664	NM_175193:10111	Golim4	INSIDE	0.729	2.507	386.07	967.93	1.827	453.87	829.06
A_68_P26020945	chr8:87180658-87180702	NM_010499:6071	Ier2	DOWNSTREAM	0.729	0.672	1291.13	867.10	0.490	1027.75	503.38
A_68_P23637403	chr5:42152928-42152972	NM_007524:2509	Nkx3-2	INSIDE	0.729	2.186	939.08	2053.26	1.594	815.44	1300.20
A_68_P23201334	chr4:109149385-109149429	NM_013876:-296	Rnf11	PROMOTER	0.729	2.399	1504.44	3608.47	1.749	1220.93	2135.93
A_68_P26001116	chr8:83262423-83262467	NM_053124:914	Smarca5	INSIDE	0.729	0.637	829.84	528.52	0.464	808.72	375.36
A_68_P30452134	chr15:94234215-94234259	NM_177431:545	Adamts20	INSIDE	0.728	1.847	4300.23	7941.91	1.345	3108.86	4181.73
A_68_P27952857	chr11:79968086-79968130	NM_172133:445	Adap2	INSIDE	0.728	2.898	5612.81	16263.24	2.109	4343.35	9158.88
A_68_P25603236	chr7:151015869-151015913	NM_007856:6819	Dhcr7	INSIDE	0.728	0.538	1343.99	723.48	0.392	1008.76	395.09
A_68_P30672034	chr16:35768908-35768952	NM_153550:512	Dirc2	INSIDE	0.728	0.711	2075.77	1474.91	0.517	1784.89	923.02
A_68_P23164323	chr4:102787124-102787168	NM_001039081:-4848	Mier1	PROMOTER	0.728	0.645	2308.18	1489.19	0.470	1736.99	815.85
A_68_P20625773	chr1:135028384-135028428	NM_133819:664	Ppp1r15b	INSIDE	0.728	0.587	1366.41	802.11	0.427	1034.53	442.26
A_68_P22019227	chr3:28704574-28704618	NM_026517:164	Rpl22l1	INSIDE	0.728	0.441	1194.29	526.72	0.321	968.68	310.82
A_68_P25962754	chr8:75273669-75273713	NM_009188:26504	Sin3b	INSIDE	0.728	2.229	817.08	1820.90	1.622	680.00	1102.95
A_68_P23984908	chr5:111714055-111714099	NM_024477:405255	Ttc28	INSIDE	0.728	2.279	1091.13	2486.69	1.660	902.14	1497.47
A_68_P21622819	chr2:128891980-128892024	NM_027192:320	Ttl	INSIDE	0.728	0.660	1061.64	700.32	0.480	907.30	435.57
A_68_P25008266	chr7:25866428-25866472	NM_175477:4186	Zfp574	INSIDE	0.728	2.511	1484.50	3727.76	1.827	1220.65	2230.65
A_68_P25657384	chr8:11758629-11758673	NM_001113518:321	Arhgef7	INSIDE	0.727	0.607	1877.76	1140.00	0.441	1446.63	638.34
A_68_P28160636	chr11:116515196-116515240	NM_030206:409	Cygb	INSIDE	0.727	0.569	1537.01	875.06	0.414	1223.03	506.30
A_68_P25672218	chr8:14090222-14090266	NM_001034862:83	Erich1	INSIDE	0.727	0.588	1702.59	1000.38	0.427	1449.47	619.36
A_68_P21744414	chr2:151368303-151368347	NM_008019:90	Fkbp1a	INSIDE	0.727	0.693	1953.48	1354.35	0.504	1570.54	791.13
A_68_P30501630	chr15:102865341-102865385	NM_013553:537	Hoxc4	INSIDE	0.727	0.320	1947.38	623.16	0.233	1534.54	356.99
A_68_P27946740	chr11:78858340-78858384	NM_013571:101494	Ksr1	INSIDE	0.727	2.187	962.49	2105.12	1.590	843.46	1341.01
A_68_P25771672	chr8:35039940-35039984	NM_001042674:351	Rbpms	INSIDE	0.727	0.645	1149.59	741.54	0.469	1070.21	502.02
A_68_P24061231	chr5:124874924-124874968	NM_001081203:977	Sbno1	INSIDE	0.727	0.429	1705.12	731.13	0.312	1172.93	365.80
A_68_P20411723	chr1:88255233-88255277	NR_002851:-2352	Snord82	PROMOTER	0.727	0.639	3092.42	1975.33	0.465	2383.96	1107.49
A_68_P27253410	chr10:74388131-74388175			Unknown	0.727	0.649	1019.88	661.54	0.471	899.93	424.16
A_68_P22775166	chr4:21775651-21775695	NR_028384:-77	4930528A17Rik	PROMOTER	0.726	0.579	1118.53	647.08	0.420	982.88	413.00

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28068585	chr11:100389285-100389329	NM_001199296:8	Acly	INSIDE	0.726	0.422	1825.44	769.51	0.306	1350.08	413.08
A_68_P23999132	chr5:114064289-114064333	NM_008153:36089	Cmklr1	INSIDE	0.726	3.831	3808.84	14590.68	2.781	2486.06	6914.23
A_68_P32219575	chr19:59534436-59534480	NM_010132:1279	Emx2	INSIDE	0.726	0.574	1237.61	710.37	0.417	867.12	361.54
A_68_P32581184	chrX:102959900-102959944	NM_030614:107	Fgf16	INSIDE	0.726	2.257	817.00	1843.61	1.639	505.12	827.92
A_68_P26406139	chr9:32348076-32348120	NM_008026:855	Fli1	INSIDE	0.726	0.619	1003.44	620.84	0.449	908.47	408.04
A_68_P25196761	chr7:75098172-75098216	NM_010513:1052	Igf1r	INSIDE	0.726	0.562	1573.79	884.44	0.408	1281.11	522.68
A_68_P26065139	chr8:94882073-94882117	NM_018826:400	Irx5	INSIDE	0.726	0.459	1623.30	745.58	0.334	1287.46	429.42
A_68_P31556683	chr18:23910867-23910911	NM_001162941:-1337	Mapre2	PROMOTER	0.726	0.645	1567.35	1010.52	0.468	1251.24	585.91
A_68_P28246291	chr12:12946601-12946645	NM_008709:2020	Mycn	INSIDE	0.726	0.545	2001.94	1091.43	0.396	1632.13	645.61
A_68_P23527255	chr5:21181848-21181895	NM_178728:25292	Napepld	INSIDE	0.726	3.511	778.44	2733.38	2.550	605.52	1544.39
A_68_P29443157	chr14:20570549-20570593	NM_008695:92	Nid2	INSIDE	0.726	0.476	1258.67	599.71	0.346	1055.56	365.18
A_68_P25911983	chr8:64238848-64238892	NM_001081390:142617	Palld	INSIDE	0.726	2.786	1881.97	5243.79	2.023	1329.72	2690.63
A_68_P30346973	chr15:76062555-76062599	NM_001163542:-768	Plec	PROMOTER	0.726	0.397	1343.09	533.67	0.288	1077.52	310.76
A_68_P23365310	chr4:141220298-141220342	NM_001033150:-290	Plekhm2	PROMOTER	0.726	0.705	3434.16	2420.21	0.512	2590.37	1325.76
A_68_P27751867	chr11:43519036-43519080	NM_027557:23559	Pwwp2a	INSIDE	0.726	3.412	575.27	1962.55	2.476	476.34	1179.43
A_68_P22317139	chr3:88895370-88895414	NM_001083808:-1439	Rusc1	PROMOTER	0.726	0.375	1573.19	590.29	0.272	1277.21	347.71
A_68_P28469856	chr12:60113095-60113139	NM_009147:-112	Sec23a	DIVERGENT_PROMOTER	0.726	2.552	2382.29	6080.36	1.853	1786.13	3309.17
A_68_P27354561	chr10:93052055-93052099	NM_027246:327	Snrpf	INSIDE	0.726	0.594	1572.21	934.07	0.431	1214.94	523.94
A_68_P27923258	chr11:74739141-74739185	NM_001163311:138	Srr	INSIDE	0.726	0.671	2051.24	1377.33	0.488	1588.95	774.67
A_68_P23222803	chr4:114672646-114672690	NM_009185:-54	Stil	PROMOTER	0.726	2.772	439.73	1219.03	2.012	460.43	926.57
A_68_P22379763	chr3:102007843-102007887	NM_001165951:22	Vangl1	INSIDE	0.726	0.708	2178.67	1543.47	0.514	1869.83	961.19
A_68_P23610765	chr5:37358054-37358098	NM_011716:22145	Wfs1	INSIDE	0.726	2.103	2438.55	5127.22	1.526	1884.04	2875.12
A_68_P20350461	chr1:74829526-74829570	NM_009526:11083	Wnt6	INSIDE	0.726	3.505	6411.19	22469.51	2.543	4259.33	10832.63
A_68_P27288886	chr10:80787882-80787926	NM_027381:4057	2510012J08Rik	INSIDE	0.725	2.545	960.61	2444.53	1.846	859.70	1587.00
A_68_P30579425	chr16:18392661-18392705	NM_033474:44316	Arvcf	INSIDE	0.725	3.256	430.59	1402.20	2.360	516.79	1219.56
A_68_P27643055	chr11:22759832-22759876	NM_016888:-119	B3gnt2	PROMOTER	0.725	0.708	2446.67	1733.39	0.514	1999.02	1027.21
A_68_P24951536	chr7:4960475-4960519	NM_001110330:4348	Fiz1	INSIDE	0.725	2.257	801.86	1809.48	1.635	620.70	1015.09
A_68_P28456271	chr12:57446391-57446435	NM_145442:469	Mbip	INSIDE	0.725	0.637	1498.38	954.48	0.462	1183.34	546.69
A_68_P24224752	chr6:8159107-8159151	NM_145374:-98	Mios	PROMOTER	0.725	0.545	1524.88	831.58	0.395	1296.90	512.44
A_68_P27265100	chr10:76424357-76424401	NM_021568:314	Pcbp3	INSIDE	0.725	0.698	1178.78	822.39	0.506	899.86	454.98
A_68_P25505714	chr7:134615579-134615624	NM_145589:474	Prr14	INSIDE	0.725	0.595	953.39	567.68	0.432	762.13	328.88
A_68_P28945956	chr13:35998142-35998186	NM_145938:52	Rpp40	INSIDE	0.725	0.392	1535.69	602.67	0.285	1254.13	357.02
A_68_P20346580	chr1:74115002-74115046	NM_027884:55997	Tns1	INSIDE	0.725	0.636	2087.10	1327.26	0.461	1726.54	795.73
A_68_P26347946	chr9:21397416-21397460	NM_001205157:-163	Yipf2	PROMOTER	0.725	0.561	1870.46	1048.65	0.406	1520.99	618.19
A_68_P21962517	chr3:16083263-16083307	NM_001145919:102	Ythdf3	INSIDE	0.725	0.729	3048.18	2222.63	0.529	2510.01	1327.74
A_68_P26232969	chr8:124900303-124900347	NM_001029993:-191	Zc3h18	PROMOTER	0.725	0.435	1557.37	677.25	0.315	1218.96	384.38
A_68_P28881067	chr13:23461111-23461155	NM_001111107:-61	Zfp322a	PROMOTER	0.725	0.538	2214.96	1191.95	0.390	1627.99	635.28
A_68_P32906205	A_68_P32906205			Unknown	0.725	3.600	294.84	1061.53	2.611	267.52	698.39
A_68_P32134057	chr19:44809349-44809393			Unknown	0.725	0.623	1276.50	795.45	0.452	1205.40	544.56
A_68_P21151652	chr2:38863473-38863517	NM_028809:-164	Arpc5l	DIVERGENT_PROMOTER	0.724	0.591	1733.98	1023.98	0.427	1392.30	595.09
A_68_P30246247	chr15:57966117-57966161	NM_027435:499	Atad2	INSIDE	0.724	0.676	1828.16	1235.95	0.490	1578.61	773.15
A_68_P27281236	chr10:79605321-79605365	NM_025313:283	Atp5d	INSIDE	0.724	0.718	2994.40	2149.61	0.520	2273.14	1182.05
A_68_P29413809	chr14:13654279-13654328	NM_001042617:1290	Cadps	INSIDE	0.724	0.487	1275.96	621.37	0.352	1089.34	383.89
A_68_P20633195	chr1:136302482-136302526	NM_028057:-62	Cyb5r1	PROMOTER	0.724	0.562	1422.57	799.58	0.407	1326.68	539.53
A_68_P23416723	chr4:151505009-151505053	NM_019585:-1996	Espn	PROMOTER	0.724	0.433	1589.00	687.41	0.313	1365.09	427.71
A_68_P29702645	chr14:71041804-71041848	NM_008004:249	Fgf17	INSIDE	0.724	0.464	1140.24	529.50	0.336	953.06	320.39
A_68_P25766304	chr8:33995018-33995062	NM_001177589:65458	Gm3985	DOWNSTREAM	0.724	0.674	2432.88	1640.15	0.488	1792.19	875.33
A_68_P26807873	chr9:107240712-107240756	NM_133984:-53	Hemk1	DIVERGENT_PROMOTER	0.724	0.676	2187.57	1478.11	0.489	1638.98	801.25
A_68_P31936363	chr19:6914626-6914670	NM_019924:443	Rps6ka4	INSIDE	0.724	0.701	2019.36	1416.39	0.508	1506.29	765.37
A_68_P21843326	chr2:168578051-168578095	NM_175303:14629	Sall4	INSIDE	0.724	2.479	722.93	1791.90	1.796	619.20	1111.90
A_68_P24769158	chr6:115084990-115085034	NM_013681:93	Syn2	INSIDE	0.724	0.590	1155.87	682.44	0.427	974.73	416.56

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P30546424	chr16:11134701-11134745	NM_029582:-97	Txndc11	PROMOTER	0.724	0.618	2124.13	1313.17	0.447	1792.72	801.92
A_68_P24019918	chr5:117768976-117769020	NM_001033311:-276	Vsig10	PROMOTER	0.724	0.656	1275.68	837.32	0.475	1066.68	506.94
A_68_P32119204	chr19:42203483-42203527	NM_027106:-21	Avpi1	PROMOTER	0.723	0.598	2006.72	1199.15	0.432	1500.61	648.02
A_68_P25845473	chr8:49195312-49195356	NM_001161515:-32	Dctd	PROMOTER	0.723	0.546	1360.88	742.56	0.395	1002.96	395.71
A_68_P25006995	chr7:25655239-25655283	NM_027732:185	Dmrtc2	INSIDE	0.723	1.952	2884.94	5630.54	1.411	2332.56	3290.51
A_68_P25842940	chr8:48759447-48759491	NM_023503:1045	Ing2	INSIDE	0.723	0.672	1567.93	1053.26	0.486	1257.65	610.81
A_68_P24592784	chr6:83276117-83276161	NM_145571:106	Mobkl1b	INSIDE	0.723	0.528	1769.97	934.40	0.382	1482.24	566.09
A_68_P25954888	chr8:73437092-73437136	NM_173013:7242	Mtap1s	INSIDE	0.723	2.677	683.84	1830.83	1.936	619.43	1199.37
A_68_P21722729	chr2:147009831-147009875	NR_030769:34	Nkx2-2as	INSIDE	0.723	0.516	1165.88	601.81	0.373	948.28	354.00
A_68_P24754178	chr6:112439612-112439656	NM_001081147:168	Oxtr	INSIDE	0.723	0.617	1312.04	809.58	0.446	1144.24	510.31
A_68_P24980581	chr7:16858769-16858813	NM_001136270:251	Prr24	INSIDE	0.723	2.753	5266.99	14498.28	1.989	3841.92	7643.04
A_68_P21740963	chr2:150612754-150612798	NM_153781:245	Pygb	INSIDE	0.723	0.500	1332.57	665.82	0.361	1092.93	394.88
A_68_P25398381	chr7:114352789-114352833	NM_029660:-148	Rbmxl2	PROMOTER	0.723	1.905	1538.86	2931.71	1.377	1427.39	1966.18
A_68_P30578595	chr16:18249063-18249107	NM_001080999:109	Trmt2a	INSIDE	0.723	0.516	1058.52	546.66	0.373	810.33	302.63
A_68_P28917611	chr13:30637211-30637255	NM_025710:-47	Uqcrfs1	PROMOTER	0.723	0.595	1234.91	734.71	0.430	950.19	408.75
A_68_P29285951	chr13:104382683-104382727	BC099526:115009		INSIDE	0.723	2.281	2510.19	5725.30	1.649	2305.88	3801.85
A_68_P22503485	chr3:126300309-126300353	NM_001025438:440	Camk2d	INSIDE	0.722	0.693	1737.71	1205.09	0.500	1415.49	708.28
A_68_P27171226	chr10:59342593-59342637	NM_019965:276	Dnajb12	INSIDE	0.722	0.448	4791.16	2148.15	0.324	3910.47	1265.20
A_68_P25616320	chr8:4166752-4166796	NM_001039578:208	Evi5l	INSIDE	0.722	0.660	2131.01	1406.08	0.476	1685.31	802.97
A_68_P27290415	chr10:81007993-81008037	NM_010301:-223	Gna11	PROMOTER	0.722	0.643	2016.80	1296.83	0.464	1644.74	763.87
A_68_P24521961	chr6:67485251-67485297	NM_020047:542	Tacstd2	INSIDE	0.722	0.409	1551.17	634.54	0.296	1295.90	382.98
A_68_P31953437	chr19:10956463-10956507	NM_134142:-251	Tmem109	PROMOTER	0.722	0.451	1575.94	711.32	0.326	1156.95	377.26
A_68_P30302244	chr15:68090487-68090531	NM_001145888:-90	Zfat	PROMOTER	0.722	0.541	1139.57	616.28	0.391	1082.92	422.94
A_68_P28277949	chr12:19888314-19888358	ENSMUST00000103822:-9494		PROMOTER	0.722	2.760	1052.64	2905.42	1.993	1034.55	2061.88
A_68_P22859652	chr4:40895697-40895741	NM_029814:133	Chmp5	INSIDE	0.721	0.651	3551.89	2311.20	0.469	2606.32	1223.31
A_68_P28056292	chr11:98274199-98274243	NM_001003817:423	Erbb2	INSIDE	0.721	0.454	1283.62	582.49	0.327	1139.41	372.54
A_68_P29723691	chr14:75132032-75132076	NM_016903:-97	Esd	PROMOTER	0.721	0.677	2366.09	1601.63	0.488	1872.60	913.61
A_68_P29134817	chr13:72767989-72768033	NM_010574:1585	Irx2	INSIDE	0.721	0.653	1126.79	735.89	0.471	1044.53	491.57
A_68_P31354400	chr17:75404960-75405004	NM_019919:114	Ltbp1	INSIDE	0.721	0.486	3499.70	1699.32	0.350	2796.02	978.30
A_68_P21587250	chr2:122463614-122463658	NR_030547:-2902	Mir147	PROMOTER	0.721	0.554	1299.05	719.96	0.400	1149.60	459.48
A_68_P27568981	chr11:6428736-6428780	NM_178440:-7797	Myo1g	PROMOTER	0.721	0.598	1232.80	737.29	0.431	965.34	416.37
A_68_P26138124	chr8:108693007-108693051	NM_178798:254	Slc7a6	INSIDE	0.721	0.694	2550.07	1770.81	0.501	2102.15	1052.79
A_68_P28909016	chr13:29050255-29050299	NM_009238:-4725	Sox4	PROMOTER	0.721	0.674	1299.26	875.59	0.486	944.50	458.62
A_68_P24009037	chr5:115777935-115777979	NM_025573:771	Srsf9	INSIDE	0.721	0.636	1498.35	953.06	0.458	1200.46	550.24
A_68_P23608581	chr5:36924292-36924336	NM_133910:732	Tbc1d14	INSIDE	0.721	0.662	4456.69	2948.49	0.477	3334.78	1591.27
A_68_P30328130	chr15:72888613-72888657	NM_029640:-2392	Trappc9	PROMOTER	0.721	2.346	1403.91	3293.55	1.692	1079.29	1826.08
A_68_P29531323	chr14:35487371-35487415	NM_001004436:279	Wapal	INSIDE	0.721	0.692	1317.12	910.80	0.499	1136.07	566.73
A_68_P28730613	chr12:110132574-110132618	NM_177602:115	Wdr25	INSIDE	0.721	0.610	1638.80	1000.12	0.440	1288.58	566.68
A_68_P31002107	chr16:98183148-98183192	NM_001081684:616	Zfp295	INSIDE	0.721	0.520	1818.21	945.66	0.375	1511.68	566.97
A_68_P27271357	chr10:77441161-77441205	NM_026431:-212	1810043G02Rik	DIVERGENT_PROMOTER	0.720	0.483	1951.51	942.68	0.348	1717.07	597.32
A_68_P32053385	chr19:29596534-29596578	NR_015567:-79	A930007I19Rik	DIVERGENT_PROMOTER	0.720	0.737	2869.42	2115.98	0.531	2627.62	1394.73
A_68_P24513201	chr6:65621722-65621766	NM_172399:140	A930038C07Rik	INSIDE	0.720	0.723	3318.04	2400.39	0.521	2544.83	1326.45
A_68_P26200116	chr8:119517155-119517199	NM_026572:173	Gcsh	INSIDE	0.720	0.504	1696.26	854.39	0.363	1445.00	524.11
A_68_P27902204	chr11:70514324-70514368	NM_153103:297	Kif1c	INSIDE	0.720	0.443	1303.14	576.95	0.319	1109.21	353.36
A_68_P24126715	chr5:138070507-138070551	NM_001168652:178	Lrch4	INSIDE	0.720	0.685	1215.29	831.94	0.493	1012.01	498.74
A_68_P31259250	chr17:57074995-57075039	NM_022328:-205	Mllt1	PROMOTER	0.720	0.449	1321.39	592.84	0.323	1165.32	376.45
A_68_P30346760	chr15:76028479-76028523	NM_201394:-2360	Plec	PROMOTER	0.720	0.614	1070.98	657.66	0.442	945.58	418.34
A_68_P30379303	chr15:81560107-81560151	NM_001146174:221	Rangap1	INSIDE	0.720	0.393	1970.06	774.74	0.283	1525.51	431.85
A_68_P32289245	chrX:20195246-20195290	NM_001167776:384	Rbm10	INSIDE	0.720	2.587	3608.99	9337.43	1.864	1619.59	3018.40
A_68_P31207190	chr17:46624075-46624119	NM_001162864:528	Ttbk1	INSIDE	0.720	4.483	3248.45	14563.17	3.227	2079.66	6711.74
A_68_P20056409	chr1:16609431-16609475	NM_025773:-85	Ube2w	PROMOTER	0.720	0.346	2610.97	904.10	0.249	2344.68	584.60

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P23227951	chr4:115817250-115817294	NM_026547:-51	1520402A15Rik	DIVERGENT_PROMOTER	0.719	0.607	1179.98	716.58	0.437	1103.68	481.91
A_68_P27938082	chr11:77329483-77329527	NM_026185:886	Abhd15	INSIDE	0.719	0.533	1127.68	601.46	0.384	838.66	321.77
A_68_P23897556	chr5:93474347-93474391	NM_175270:-320	Ankrd56	PROMOTER	0.719	0.549	1587.32	871.67	0.395	1315.92	519.68
A_68_P24004688	chr5:115018396-115018440	NM_001004180:159	BC057022	INSIDE	0.719	0.528	1162.69	613.93	0.380	903.62	343.12
A_68_P22340620	chr3:94583224-94583268	NM_001037711:7191	Cgn	INSIDE	0.719	2.133	1002.28	2137.93	1.534	833.28	1278.22
A_68_P31286847	chr17:63230901-63230945	NM_010109:-256	Efna5	PROMOTER	0.719	0.659	1972.28	1300.33	0.474	1514.74	717.68
A_68_P30682388	chr16:37777040-37777084	NM_008047:-78	Fstl1	PROMOTER	0.719	0.526	4532.10	2385.99	0.378	3994.16	1511.69
A_68_P27182283	chr10:61245921-61245965	NM_207000:670	H2afy2	INSIDE	0.719	0.498	1813.66	903.99	0.358	1521.85	545.57
A_68_P28043963	chr11:96207399-96207443	NM_010458:2338	Hoxb3	INSIDE	0.719	0.711	1627.07	1156.80	0.511	1398.76	714.88
A_68_P28161573	chr11:116704755-116704799	NM_033398:-13	Jmjd6	DIVERGENT_PROMOTER	0.719	0.538	2060.65	1107.86	0.387	1508.39	583.27
A_68_P20634034	chr1:136457888-136457932	NM_152895:1156	Kdm5b	INSIDE	0.719	0.690	2098.96	1448.99	0.496	1856.95	921.90
A_68_P28696317	chr12:104480189-104480236	NM_133364:144	Prima1	INSIDE	0.719	2.038	5504.04	11217.00	1.466	3870.97	5675.53
A_68_P21752664	chr2:152880435-152880479	NM_001011732:22869	Xkr7	INSIDE	0.719	2.559	2806.39	7180.79	1.839	2288.67	4208.29
A_68_P22350125	chr3:96401803-96401847	NM_001024851:1266	Ankrd34a	INSIDE	0.718	0.546	983.70	537.03	0.392	770.48	301.93
A_68_P27067368	chr10:36694971-36695015	NM_008229:643	Hdac2	INSIDE	0.718	0.414	1714.73	709.38	0.297	1342.19	398.78
A_68_P26228652	chr8:124276907-124276951	NM_020605:22470	Jph3	INSIDE	0.718	3.509	1853.02	6502.49	2.519	1300.98	3276.98
A_68_P28035916	chr11:94852207-94852251	NM_172261:-297	Ppp1r9b	PROMOTER	0.718	0.589	2565.33	1510.08	0.423	1991.50	841.45
A_68_P28071924	chr11:100956580-100956624	NM_008949:113	Psmc3ip	INSIDE	0.718	0.683	1027.19	702.04	0.491	810.02	397.60
A_68_P26464015	chr9:43611634-43611678	NM_021424:58998	Pvrl1	INSIDE	0.718	3.630	1638.29	5946.65	2.607	1193.13	3110.42
A_68_P21769255	chr2:155891652-155891696	NM_139151:726	Spag4	INSIDE	0.718	0.600	1703.10	1021.05	0.431	1373.97	591.79
A_68_P24755318	chr6:112677438-112677482	NM_080448:219800	Srgap3	INSIDE	0.718	2.053	2175.65	4466.27	1.475	1721.84	2539.11
A_68_P27469158	chr10:114799283-114799327	NM_133683:14	Tmem19	INSIDE	0.718	0.494	1796.02	887.50	0.355	1479.01	524.89
A_68_P28703309	chr12:105685178-105685222			Unknown	0.718	2.408	1667.01	4014.48	1.729	1200.34	2075.13
A_68_P25933300	chr8:69010290-69010334	NM_025465:94	1810029B16Rik	INSIDE	0.717	0.553	2059.44	1137.95	0.396	1712.41	678.23
A_68_P23437420	chr4:154624071-154624115	NM_001190445:18	2610002J02Rik	INSIDE	0.717	0.668	995.52	665.49	0.479	851.02	407.95
A_68_P28724523	chr12:109154940-109154984	NM_001079883:86662	Bcl11b	INSIDE	0.717	3.145	792.49	2492.11	2.255	699.62	1577.63
A_68_P22264731	chr3:79432542-79432586	NM_025794:125	Etfdh	INSIDE	0.717	0.596	1236.80	736.82	0.427	1028.30	438.96
A_68_P23284715	chr4:127003542-127003595	NM_008126:2801	Gjb3	INSIDE	0.717	2.157	1169.71	2522.77	1.546	840.35	1299.07
A_68_P26463565	chr9:43552288-43552332	NM_021424:-348	Pvrl1	PROMOTER	0.717	0.648	1136.63	736.26	0.464	930.78	432.28
A_68_P20793342	chr1:167124624-167124668	NM_145512:-82	Sft2d2	PROMOTER	0.717	0.476	1387.72	660.89	0.342	1174.50	401.19
A_68_P31926781	chr19:5082721-5082765	NM_001001885:2735	Tmem151a	INSIDE	0.717	2.215	652.53	1445.61	1.588	536.66	852.31
A_68_P28470051	chr12:60162088-60162132	NM_030057:338	Trappc6b	INSIDE	0.717	0.494	3303.83	1632.28	0.354	2508.90	889.09
A_68_P25693344	chr8:17535329-17535373	NM_053171:35	Csmd1	INSIDE	0.716	0.647	3214.60	2080.06	0.463	2742.51	1270.97
A_68_P31424462	chr17:88072102-88072146	NM_008628:228	Msh2	INSIDE	0.716	0.599	1052.42	630.18	0.429	840.72	360.42
A_68_P27211071	chr10:66748168-66748213	NM_001036293:-161	Nrbf2	PROMOTER	0.716	0.562	1563.67	879.36	0.403	1247.18	502.43
A_68_P25090464	chr7:52241287-52241331	NM_019830:394	Prmt1	INSIDE	0.716	0.645	1700.71	1096.55	0.462	1414.14	653.24
A_68_P24536422	chr6:71390071-71390115	NM_024288:539	Rmnd5a	INSIDE	0.716	0.706	1871.57	1321.56	0.505	1556.39	786.63
A_68_P30601341	chr16:23108146-23108190	NR_030705:-857	Snord2	PROMOTER	0.716	0.530	1273.74	674.74	0.379	1043.15	395.42
A_68_P21706318	chr2:144096392-144096436	NM_024225:-106	Snx5	PROMOTER	0.716	0.660	897.31	592.44	0.473	735.52	347.61
A_68_P20254939	chr1:57832453-57832497	NM_144882:770	Spats2l	INSIDE	0.716	0.472	1176.24	555.26	0.338	969.32	327.53
A_68_P20353687	chr1:75384995-75385039	NM_001085370:2832	Speg	INSIDE	0.716	0.480	1580.00	758.47	0.344	1251.16	430.29
A_68_P23590344	chr5:34000777-34000821	NM_001040435:3	Tacc3	INSIDE	0.716	0.691	1594.79	1102.29	0.495	1283.49	635.10
A_68_P31953350	chr19:10944106-10944150	NM_133804:141	Tmem132a	INSIDE	0.716	0.605	1262.93	764.24	0.433	1016.41	440.47
A_68_P26170718	chr8:114400399-114400443	NM_025781:155	Tmem170	INSIDE	0.716	0.654	2599.20	1699.42	0.468	2204.55	1032.32
A_68_P22059398	chr3:36570005-36570050	NM_019510:19062	Trpc3	INSIDE	0.716	2.155	916.79	1975.25	1.543	742.68	1146.26
A_68_P27913322	chr11:72609852-72609896	NM_001045536:147	Zzef1	INSIDE	0.716	0.382	1757.70	671.21	0.273	1630.28	445.76
A_68_P27288863	chr10:80785224-80785268	NM_027381:1399	2510012J08Rik	INSIDE	0.715	2.137	1336.30	2855.41	1.528	1096.68	1675.40
A_68_P31206428	chr17:46464777-46464821	NM_145140:-2083	Abcc10	PROMOTER	0.715	0.585	1231.33	720.27	0.418	1094.04	457.71
A_68_P27750957	chr11:43342796-43342840	NM_001045530:533	Ccnjl	INSIDE	0.715	0.537	2303.45	1237.51	0.384	1728.76	664.29
A_68_P22412465	chr3:108209988-108210032	NM_001004177:8402	Celsr2	INSIDE	0.715	2.444	2383.87	5826.98	1.747	1833.46	3202.77
A_68_P22344502	chr3:95363644-95363703	NM_026489:75	Hormad1	INSIDE	0.715	2.543	488.09	1241.42	1.819	456.87	831.00

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26030504	chr8:89148137-89148181	NM_025827:217	Lonp2	INSIDE	0.715	0.607	1184.12	719.00	0.434	906.10	393.48
A_68_P21350019	chr2:76244929-76244973	NM_145525:356	Osbpl6	INSIDE	0.715	0.656	1996.46	1309.53	0.469	1700.36	797.31
A_68_P28936991	chr13:34254760-34254804	NM_001101430:-63	Psmg4	PROMOTER	0.715	0.540	1616.06	873.34	0.386	1256.10	485.04
A_68_P26926722	chr10:8605525-8605569	NM_175155:322	Sash1	INSIDE	0.715	0.665	1085.48	721.72	0.475	921.57	437.81
A_68_P27355931	chr10:93296360-93296404	NM_183199:2083	Usp44	INSIDE	0.715	0.709	1390.88	986.34	0.507	1054.12	534.17
A_68_P32672263	chrX:131023645-131023689	ENSMUST00000094550:-242		PROMOTER	0.715	2.831	6195.62	17540.71	2.024	2303.41	4661.40
A_68_P30367437	chr15:79435420-79435467	NM_010059:71	Dmc1	INSIDE	0.714	1.988	3791.31	7537.37	1.420	2684.81	3812.95
A_68_P31947675	chr19:10057125-10057169	NM_010239:-46	Fth1	PROMOTER	0.714	0.660	1194.43	788.75	0.472	948.54	447.43
A_68_P20294248	chr1:64782204-64782248	NM_001042659:2098	Fzd5	INSIDE	0.714	2.378	1569.19	3731.69	1.699	1269.15	2156.04
A_68_P21073107	chr2:25435061-25435105	NM_001005424:537	Gm996	INSIDE	0.714	0.469	1243.53	583.60	0.335	793.26	265.72
A_68_P23331346	chr4:135502630-135502674	NM_008254:285	Hmgcl	INSIDE	0.714	0.490	3139.75	1538.39	0.350	2222.26	777.92
A_68_P27262212	chr10:75931494-75931538	NM_019434:-199	Mcm3ap	PROMOTER	0.714	0.514	1658.69	852.92	0.367	1321.85	485.47
A_68_P23351224	chr4:138902115-138902159	NM_023536:6077	Mrto4	DOWNSTREAM	0.714	2.127	1917.64	4078.66	1.519	1507.45	2289.48
A_68_P28950789	chr13:36826888-36826932	NM_153529:-587	Nrn1	PROMOTER	0.714	2.410	1528.35	3682.98	1.720	1180.81	2030.98
A_68_P29055508	chr13:55614427-55614471	NM_001114088:352	Pdlim7	INSIDE	0.714	0.739	3019.28	2230.96	0.527	2188.30	1154.02
A_68_P29681985	chr14:67529671-67529715	NM_175498:-352	Pnma2	PROMOTER	0.714	0.496	1257.09	623.62	0.354	960.43	340.07
A_68_P26542155	chr9:57352313-57352357	NM_133982:426	Rpp25	INSIDE	0.714	0.664	905.51	601.25	0.474	854.63	405.05
A_68_P30351143	chr15:76742152-76742196	NM_001168276:13704	Zfp647	INSIDE	0.714	2.099	1000.32	2099.20	1.497	829.38	1241.98
A_68_P24463221	chr6:54379963-54380009	NR_033635:229	9130019P16Rik	INSIDE	0.713	0.406	1518.12	615.91	0.289	1264.40	365.66
A_68_P25007186	chr7:25689296-25689340	NM_001130152:-46	Arhgef1	PROMOTER	0.713	0.565	1015.19	573.43	0.402	860.75	346.44
A_68_P31159492	chr17:35654278-35654322	NM_146248:240	Cchcr1	INSIDE	0.713	2.315	1458.32	3376.28	1.651	1050.44	1734.27
A_68_P28992094	chr13:43880579-43880623	NM_009856:125	Cd83	INSIDE	0.713	0.471	1221.21	575.64	0.336	1002.21	337.06
A_68_P20910359	chr1:188791248-188791292	NM_033077:-24	D1Pas1	PROMOTER	0.713	2.679	1458.98	3909.11	1.911	1026.85	1961.91
A_68_P28186833	chr11:120657765-120657809	NM_026824:-77	Dus1l	PROMOTER	0.713	0.588	1619.11	952.78	0.419	1233.97	517.59
A_68_P32213522	chr19:58530442-58530494	NM_010279:-1512	Gfra1	PROMOTER	0.713	0.648	1015.72	658.05	0.462	704.83	325.74
A_68_P27862296	chr11:63735472-63735516	NM_018805:292	Hs3st3b1	INSIDE	0.713	0.303	2175.38	659.19	0.216	1670.01	361.01
A_68_P22165650	chr3:57650817-57650861	NM_019410:841	Pfn2	INSIDE	0.713	0.638	2189.75	1397.99	0.455	1639.74	746.47
A_68_P24117606	chr5:136209349-136209397	NM_008898:44289	Por	INSIDE	0.713	2.103	1276.39	2684.66	1.500	957.66	1436.75
A_68_P27430000	chr10:107598668-107598712	NM_027892:-765	Ppp1r12a	PROMOTER	0.713	0.499	1164.56	581.53	0.356	943.33	335.94
A_68_P24983171	chr7:17357272-17357316	NM_009201:-9400	Slc1a5	PROMOTER	0.713	2.338	1319.10	3084.01	1.667	1216.77	2028.50
A_68_P21901049	chr2:179777225-179777269	NM_178750:59	Ss18l1	INSIDE	0.713	0.565	2361.06	1334.01	0.403	1975.80	795.55
A_68_P27556190	chr11:4087152-4087196	NM_134023:339	Tbc1d10a	INSIDE	0.713	0.710	2447.34	1738.40	0.507	1770.03	897.05
A_68_P22162495	chr3:56941018-56941062			Unknown	0.713	3.215	3142.14	10101.48	2.293	2403.48	5512.03
A_68_P28094597	chr11:105026745-105026789	ENSMUST00000118770:1168		INSIDE	0.713	3.458	910.67	3148.94	2.467	809.26	1996.10
A_68_P23193446	chr4:107562348-107562392	NM_028754:-133	0610037L13Rik	PROMOTER	0.712	0.677	972.55	658.00	0.482	829.90	399.79
A_68_P28104773	chr11:106889018-106889062	NM_001163473:-496	1810010H24Rik	PROMOTER	0.712	0.633	827.60	523.95	0.451	702.02	316.35
A_68_P30927367	chr16:85080337-85080381	NM_001198823:93594	App	INSIDE	0.712	2.813	6074.52	17087.59	2.003	3972.32	7954.94
A_68_P25592836	chr7:149268658-149268702	NM_008748:12509	Dusp8	INSIDE	0.712	2.769	1890.58	5235.47	1.971	1626.26	3204.81
A_68_P24002950	chr5:114724269-114724313	NM_148935:-520	Foxn4	PROMOTER	0.712	0.657	2188.64	1438.64	0.468	1703.39	797.45
A_68_P28563527	chr12:79327853-79327897	NM_145965:233	Gphn	INSIDE	0.712	0.623	1344.51	837.80	0.444	1093.59	485.52
A_68_P27893905	chr11:69049315-69049359	NM_008192:1188	Gucy2e	INSIDE	0.712	0.630	1907.68	1201.82	0.448	1423.52	638.17
A_68_P23352996	chr4:139161037-139161081	NM_001205173:30424	Iffo2	INSIDE	0.712	2.201	2043.27	4497.04	1.567	1432.48	2244.17
A_68_P24129312	chr5:138635953-138635997	NM_177878:433	Mblac1	INSIDE	0.712	0.538	1349.87	725.74	0.383	1180.28	452.01
A_68_P24810878	chr6:122824602-122824646	NM_026267:50	Necap1	INSIDE	0.712	0.635	1307.38	829.67	0.452	1114.25	503.20
A_68_P28184541	chr11:120298583-120298627	NM_001195023:410	Nploc4	INSIDE	0.712	0.621	1931.94	1200.43	0.442	1547.01	684.27
A_68_P25846473	chr8:49361893-49361937	NM_001145937:398130	Odz3	INSIDE	0.712	2.967	2291.75	6798.66	2.112	1784.01	3768.33
A_68_P22484175	chr3:122433462-122433506	NM_153422:1409	Pde5a	INSIDE	0.712	0.514	2649.99	1363.15	0.366	2023.01	740.68
A_68_P23575727	chr5:31262311-31262358	NM_016703:400	Preb	INSIDE	0.712	0.619	2299.07	1422.59	0.440	1896.79	835.08
A_68_P27968803	chr11:82684639-82684683	NM_001164570:-414	Rffl	PROMOTER	0.712	0.618	5448.62	3365.58	0.440	4602.42	2025.37
A_68_P20464814	chr1:97564183-97564227	NM_009183:-33	St8sia4	PROMOTER	0.712	0.618	850.43	525.57	0.440	742.27	326.67
A_68_P31162742	chr17:36282712-36282756	NR_033517:772	2410017I17Rik	INSIDE	0.711	0.620	2633.82	1632.75	0.440	2193.41	966.12

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27789372	chr11:50415234-50415278	NM_175643:-330	Adamts2	PROMOTER	0.711	0.413	1367.99	565.07	0.294	1064.76	312.51
A_68_P31605186	chr18:33099273-33099317	NM_009793:600	Camk4	INSIDE	0.711	0.502	1050.90	527.53	0.357	803.93	286.99
A_68_P23873438	chr5:89104430-89104474	NM_001098476:153	Grsf1	INSIDE	0.711	0.660	1046.86	690.45	0.469	959.90	449.82
A_68_P28744814	chr12:112812598-112812642	NM_021516:-100	Mark3	PROMOTER	0.711	0.568	1933.40	1098.24	0.404	1822.14	735.71
A_68_P21076474	chr2:25977754-25977798	NM_026495:555	Nacc2	INSIDE	0.711	0.482	1223.14	589.39	0.343	1018.32	348.93
A_68_P31256047	chr17:56567658-56567702	NM_011218:48223	Ptprs	INSIDE	0.711	2.576	917.82	2364.21	1.831	869.78	1592.46
A_68_P27687433	chr11:32113469-32113513	NM_010117:8803	Rhbdf1	INSIDE	0.711	2.372	555.89	1318.50	1.687	611.66	1031.93
A_68_P20451969	chr1:94807947-94807991	NM_181405:567	Rnpepl1	INSIDE	0.711	0.487	1612.45	785.94	0.347	1299.90	450.79
A_68_P25090598	chr7:52262643-52262687	NM_001008422:8955	Scaf1	INSIDE	0.711	2.315	1076.37	2491.80	1.646	736.24	1212.10
A_68_P28636743	chr12:93017325-93017369	NM_175367:7530	Ston2	INSIDE	0.711	0.582	1326.52	772.47	0.414	1096.22	453.95
A_68_P29428733	chr14:17198192-17198236	NM_009409:495	Top2b	INSIDE	0.711	0.542	2327.94	1261.60	0.385	2086.84	803.95
A_68_P23610766	chr5:37358119-37358163	NM_011716:22081	Wfs1	INSIDE	0.711	3.129	318.68	997.08	2.224	295.79	657.81
A_68_P31295067	A_68_P31295067			Unknown	0.711	2.299	911.53	2096.00	1.635	921.75	1506.94
A_68_P25953982	chr8:73300805-73300849	NR_029440:66	2010320M18Rik	INSIDE	0.710	0.445	1277.69	568.94	0.316	854.23	269.92
A_68_P26764411	chr9:99394814-99394872	NM_028768:74476	Armc8	INSIDE	0.710	2.276	984.81	2241.56	1.616	796.42	1287.35
A_68_P25522112	chr7:137663073-137663117	NM_013799:-41	Ate1	PROMOTER	0.710	0.509	1291.47	657.23	0.361	1101.38	397.76
A_68_P26523446	chr9:53823019-53823063	NM_177769:68	Elmod1	INSIDE	0.710	0.585	1505.49	880.88	0.415	1282.08	532.54
A_68_P28419953	chr12:50484336-50484380	NM_008241:365	Foxg1	INSIDE	0.710	0.670	1326.52	888.86	0.476	1162.22	552.94
A_68_P29247527	chr13:97441130-97441174	NM_008255:-261	Hmgcr	PROMOTER	0.710	0.588	882.91	519.56	0.418	703.03	293.77
A_68_P21137727	chr2:35946843-35946887	NM_001083126:12716	Lhx6	INSIDE	0.710	0.569	1883.20	1071.58	0.404	1449.53	585.25
A_68_P32181720	chr19:53384971-53385016	NM_001008542:-2	Mxi1	PROMOTER	0.710	2.256	2341.61	5282.94	1.602	1728.57	2769.97
A_68_P29479229	chr14:26513511-26513556	NM_134084:-122	Ppif	PROMOTER	0.710	0.561	1672.47	939.01	0.399	1339.00	533.93
A_68_P23441764	chr4:155367553-155367597	NM_011341:552	Sdf4	INSIDE	0.710	0.660	1021.27	674.15	0.469	985.87	462.37
A_68_P27099069	chr10:42894720-42894764	NM_172419:233	9030612E09Rik	INSIDE	0.709	0.657	1043.47	685.50	0.465	857.93	399.37
A_68_P26864198	chr9:117950126-117950170	NM_001048146:532	Azi2	INSIDE	0.709	0.631	936.23	590.60	0.447	737.99	330.17
A_68_P23892221	chr5:92512692-92512736	NM_001080794:-131	G3bp2	PROMOTER	0.709	0.540	1594.29	861.05	0.383	1345.16	515.22
A_68_P26804351	chr9:106550055-106550099	NM_001160353:8364	Grm2	INSIDE	0.709	2.347	767.81	1801.78	1.663	669.91	1114.00
A_68_P24038736	chr5:120890309-120890353	NM_008499:8436	Lhx5	INSIDE	0.709	0.536	1545.14	827.51	0.379	1185.98	450.08
A_68_P28915540	chr13:30228458-30228502	NM_153546:122	Mboat1	INSIDE	0.709	0.634	1335.97	847.46	0.450	1174.74	528.05
A_68_P31107420	chr17:26088528-26088572	NM_001039038:-6674	Nhlrc4	PROMOTER	0.709	0.407	1473.22	599.18	0.288	1204.05	347.14
A_68_P23936338	chr5:102094059-102094103	NM_144955:-350	Nkx6-1	PROMOTER	0.709	0.629	978.88	615.56	0.446	828.51	369.14
A_68_P31257078	chr17:56723736-56723780	NM_001029979:248	Safb2	INSIDE	0.709	0.424	1439.76	610.77	0.301	1280.40	384.88
A_68_P23361255	chr4:140517166-140517210	NM_023374:3	Sdhb	INSIDE	0.709	0.684	1119.46	765.61	0.485	877.73	425.67
A_68_P21099538	chr2:29658204-29658248	NM_011989:27	Slc27a4	INSIDE	0.709	0.602	2004.04	1206.28	0.427	1531.54	653.68
A_68_P26154343	chr8:111480556-111480607	NM_007496:242038	Zfhx3	INSIDE	0.709	3.569	8587.49	30645.91	2.531	5705.29	14440.56
A_68_P31016356	chr17:5342041-5342085	NM_001085355:346989	Arid1b	INSIDE	0.708	2.703	1018.77	2753.31	1.914	802.26	1535.24
A_68_P20433333	chr1:91889782-91889826	NM_139152:21348	Asb18	INSIDE	0.708	2.175	950.83	2068.31	1.540	762.64	1174.66
A_68_P21094143	chr2:28771470-28771514	NM_019446:449	Barhl1	INSIDE	0.708	0.647	1707.53	1105.43	0.458	1493.11	684.35
A_68_P24925495	chr6:145814801-145814845	NM_024469:-962	Bhlhe41	PROMOTER	0.708	0.369	1855.57	683.94	0.261	1304.31	340.25
A_68_P26323901	chr9:15432521-15432565	NM_181816:-165	Ccdc67	PROMOTER	0.708	0.638	2626.85	1674.93	0.451	1967.95	888.02
A_68_P25827833	chr8:46095432-46095479	NM_001081286:59894	Fat1	INSIDE	0.708	2.546	693.16	1764.69	1.801	612.56	1103.53
A_68_P28080762	chr11:102527342-102527386	NM_001127576:463	Gm1564	INSIDE	0.708	2.789	865.85	2414.50	1.973	824.15	1626.01
A_68_P20080972	chr1:21951304-21951348	NM_001160139:697	Kcnq5	INSIDE	0.708	0.326	2032.00	662.79	0.231	1663.56	384.07
A_68_P26815589	chr9:108481413-108481457	NM_028944:18497	P4htm	INSIDE	0.708	0.471	1930.19	908.26	0.333	1479.69	493.00
A_68_P20139010	chr1:34529780-34529824	NM_011206:13212	Ptpn18	INSIDE	0.708	0.615	2653.67	1630.68	0.435	2119.68	922.68
A_68_P27406628	chr10:102830256-102830300	NM_175328:-198	Slc6a15	PROMOTER	0.708	0.703	2118.31	1488.99	0.497	1682.88	837.22
A_68_P26002685	chr8:83538307-83538351	NM_027554:477	Usp38	INSIDE	0.708	0.601	1416.41	851.42	0.425	1093.39	465.16
A_68_P24957693	chr7:6930088-6930132	NR_036631:-737	Zim3	PROMOTER	0.708	2.937	2073.03	6089.15	2.079	1650.34	3430.72
A_68_P22291859	chr3:84386912-84386956	NM_001081093:-387	Arfip1	PROMOTER	0.707	0.689	1155.08	796.00	0.487	842.36	410.59
A_68_P21566791	chr2:118727169-118727213	NM_001045523:-160	Bahd1	PROMOTER	0.707	0.457	1293.57	591.01	0.323	1090.81	352.32
A_68_P24055345	chr5:123821191-123821247	NM_029850:26762	Bcl7a	INSIDE	0.707	2.813	929.98	2615.85	1.988	734.08	1459.33

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P22412462	chr3:108209734-108209778	NM_001004177:8656	Celsr2	INSIDE	0.707	2.426	441.17	1070.49	1.716	388.28	666.35
A_68_P25609690	chr7:152047867-152047911	NM_010202:598	Fgf4	INSIDE	0.707	0.527	1410.30	743.14	0.373	1120.01	417.54
A_68_P21338893	chr2:74536131-74536175	NM_013555:333	Hoxd9	INSIDE	0.707	0.421	1729.65	727.92	0.297	1308.52	389.19
A_68_P32028426	chr19:25311621-25311665	NM_181404:-49	Kank1	PROMOTER	0.707	0.475	1372.93	652.63	0.336	1089.42	366.28
A_68_P23972005	chr5:108877904-108877948	NM_172883:-16	Mfsd7a	PROMOTER	0.707	0.670	1178.24	789.07	0.474	922.86	437.06
A_68_P22860679	chr4:41082140-41082184	NM_026275:-891	Ube2r2	PROMOTER	0.707	0.383	1381.99	528.77	0.271	1077.74	291.54
A_68_P32403977	chrX:55292060-55292104	NM_009575:8278	Zic3	DOWNSTREAM	0.707	2.581	1977.52	5104.11	1.826	1094.75	1998.59
A_68_P31932458	chr19:6061153-6061197	NM_013859:-32	Znhit2-ps	PROMOTER	0.707	0.425	1965.45	834.90	0.300	1569.84	471.60
A_68_P26430751	chr9:37267846-37267890			Unknown	0.707	0.472	3564.97	1682.51	0.334	2419.55	807.70
A_68_P32364026	chrX:45694076-45694120	NM_178782:-436	Bcorl1	PROMOTER	0.706	2.613	988.48	2583.00	1.845	455.76	840.68
A_68_P28944868	chr13:35832908-35832952	NM_001123386:-340	Cdyl	PROMOTER	0.706	0.453	1430.11	647.79	0.320	1155.12	369.23
A_68_P27190984	chr10:62892485-62892529	NM_177612:-339	Ctnna3	PROMOTER	0.706	0.368	1991.76	732.47	0.260	1506.87	391.44
A_68_P25416681	chr7:118172726-118172772	NM_009431:284	Ctr9	INSIDE	0.706	0.734	2710.97	1989.23	0.518	2001.34	1036.56
A_68_P27093486	chr10:41917452-41917496	NM_019740:79074	Foxo3	INSIDE	0.706	2.255	2589.70	5838.62	1.591	1851.55	2945.22
A_68_P27288384	chr10:80720348-80720392	NM_010768:81	Matk	INSIDE	0.706	0.617	1763.43	1088.65	0.436	1585.56	691.10
A_68_P31626419	chr18:37128747-37128791	NM_009957:-4809	Pcdha7	PROMOTER	0.706	2.080	1125.06	2340.46	1.469	798.92	1173.99
A_68_P26464016	chr9:43611710-43611754	NM_021424:59074	Pvrl1	INSIDE	0.706	4.179	1853.83	7747.84	2.952	1233.76	3642.35
A_68_P29194040	chr13:85429148-85429192	NM_145452:-79	Rasa1	PROMOTER	0.706	0.475	2358.92	1120.54	0.335	2012.07	674.78
A_68_P26348417	chr9:21490581-21490625	NM_001174078:69990	Smarca4	INSIDE	0.706	3.773	3313.48	12502.17	2.665	2400.34	6396.96
A_68_P28160199	chr11:116442326-116442370	NM_173755:413	Ube2o	INSIDE	0.706	0.540	1960.53	1058.85	0.381	1720.38	655.63
A_68_P20350709	chr1:74863629-74863673			Unknown	0.706	0.609	1135.90	691.46	0.430	865.85	372.34
A_68_P21761084	chr2:154375582-154375626	NM_029305:965	1700003F12Rik	INSIDE	0.705	0.439	1195.37	525.03	0.310	1069.38	331.19
A_68_P32710891	chrX:139401598-139401642	NM_019496:-349	Ammecr1	PROMOTER	0.705	5.326	1461.29	7782.83	3.755	918.83	3450.35
A_68_P21617373	chr2:127952615-127952659	NM_009754:863	Bcl2l11	INSIDE	0.705	0.463	1378.18	638.50	0.327	1135.63	370.82
A_68_P23767824	chr5:67818279-67818323	NM_001164806:738	Bend4	INSIDE	0.705	0.674	1035.32	697.77	0.475	1043.75	495.83
A_68_P24605097	chr6:85401585-85401629	NM_007638:108	Cct7	INSIDE	0.705	0.477	1988.85	948.60	0.336	1643.56	552.99
A_68_P31473578	chr18:6490125-6490169	NM_027497:708	Epc1	INSIDE	0.705	0.519	1314.68	681.87	0.366	1121.59	410.10
A_68_P21641077	chr2:132403236-132403280	NM_001042671:726	Gpcpd1	INSIDE	0.705	0.421	1403.50	590.25	0.297	1103.26	327.15
A_68_P23349534	chr4:138631170-138631214	NM_021358:-488	Htr6	PROMOTER	0.705	0.562	1012.93	568.86	0.396	906.90	358.91
A_68_P24660677	chr6:95068035-95068079	NM_001008785:157	Kbtbd8	INSIDE	0.705	0.621	4376.85	2717.60	0.438	3307.18	1447.31
A_68_P27056939	chr10:34138119-34138163	NM_176968:194	Nt5dc1	INSIDE	0.705	0.545	1401.00	763.33	0.384	1074.94	412.86
A_68_P31652785	chr18:42110533-42110577	NM_029942:294	Prelid2	INSIDE	0.705	0.569	1503.90	855.83	0.401	1157.17	464.50
A_68_P31542485	chr18:21159693-21159737	NM_019706:-127	Rnf138	PROMOTER	0.705	0.692	1419.40	982.49	0.488	1211.26	591.07
A_68_P22615130	chr3:146183915-146183959	NM_027371:451	Rpf1	INSIDE	0.705	0.636	978.58	622.39	0.448	778.91	349.26
A_68_P28086213	chr11:103511657-103511703	NM_001033212:858	Rprml	INSIDE	0.705	2.321	2463.95	5718.22	1.636	1628.59	2663.60
A_68_P30572150	chr16:17132494-17132538	NM_022324:-40	Sdf2l1	PROMOTER	0.705	0.513	1040.52	533.75	0.362	866.93	313.46
A_68_P30656973	chr16:33251896-33251940	NM_080557:377	Snx4	INSIDE	0.705	0.542	1392.96	754.76	0.382	1145.61	437.81
A_68_P27288946	chr10:80795962-80796006	NM_009325:4509	Tbxa2r	INSIDE	0.705	3.265	4109.92	13416.84	2.300	2783.01	6401.65
A_68_P24248064	chr6:13557588-13557632	NM_028990:453	Tmem168	INSIDE	0.705	0.606	1660.13	1005.53	0.427	1508.38	644.49
A_68_P24428348	chr6:48569845-48569889	NM_173429:6688	Zfp775	INSIDE	0.705	2.657	1149.03	3053.42	1.874	969.29	1815.99
A_68_P22148831	chr3:54437065-54437110	ENSMUST00000172420:1727		INSIDE	0.705	2.552	919.53	2346.93	1.801	772.42	1390.82
A_68_P22410428	chr3:107889363-107889407	NM_028779:161	Ampd2	INSIDE	0.704	0.579	2048.07	1184.83	0.407	1531.89	623.51
A_68_P32536865	chrX:91226290-91226336	NR_028320:12318	AU015836	DOWNSTREAM	0.704	2.421	1133.27	2743.12	1.705	495.40	844.66
A_68_P29122631	chr13:70776356-70776400	NM_144837:134	BC018507	INSIDE	0.704	0.428	1223.55	523.45	0.301	917.19	276.05
A_68_P20350881	chr1:74902348-74902392	NM_009872:768	Cdk5r2	INSIDE	0.704	0.562	2402.43	1349.55	0.395	1842.81	728.39
A_68_P26785470	chr9:103267147-103267191	NM_001134427:141	Cdv3	INSIDE	0.704	0.492	1823.41	896.73	0.346	1560.83	540.43
A_68_P20641220	chr1:137625770-137625814	NM_007791:19	Csrp1	INSIDE	0.704	0.698	3202.68	2235.30	0.491	2434.53	1195.96
A_68_P25268784	chr7:87948360-87948404	NM_016721:-165	Iqgap1	PROMOTER	0.704	0.610	1421.18	866.94	0.430	1117.54	480.14
A_68_P30359966	chr15:78267556-78267601	NM_001081367:8521	Kctd17	INSIDE	0.704	2.087	2693.88	5621.90	1.469	1819.10	2672.59
A_68_P22220265	chr3:69120566-69120610	NM_178726:-251	Ppm1l	PROMOTER	0.704	0.695	2022.59	1404.80	0.489	1567.48	766.63
A_68_P27835785	chr11:59063460-59063505	NM_009522:40771	Wnt3a	INSIDE	0.704	3.007	316.13	950.51	2.116	318.97	674.93

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26082677	chr8:97851977-97852021	NM_024467:3852	Zfp319	INSIDE	0.704	2.414	638.24	1540.71	1.699	565.76	961.02
A_68_P28736924	chr12:111427791-111427835	AK044800:2027		INSIDE	0.704	0.618	976.46	603.26	0.435	870.84	378.55
A_68_P25786362	chr8:37612307-37612351	AK076528:2179		DOWNSTREAM	0.704	0.543	987.44	535.82	0.382	832.29	318.13
A_68_P22478798	chr3:121517570-121517614	NM_008991:541	Abcd3	INSIDE	0.703	0.485	1106.14	536.74	0.341	849.26	289.80
A_68_P22510090	chr3:127398655-127398699	NM_027808:84769	Alpk1	INSIDE	0.703	0.463	1403.07	649.66	0.325	1221.11	397.42
A_68_P24872960	chr6:136467629-136467673	NM_019426:279	Atf7ip	INSIDE	0.703	0.685	1940.08	1328.57	0.482	1677.66	807.82
A_68_P32260372	chrX:11668383-11668427	NM_001168321:69077	Bcor	INSIDE	0.703	0.712	2248.46	1601.15	0.501	1061.34	531.24
A_68_P30540369	chr16:9995886-9995933	NM_008170:-3283	Grin2a	PROMOTER	0.703	0.647	787.14	509.42	0.455	713.83	324.59
A_68_P21750890	chr2:152560836-152560880	NM_010495:-1151	Id1	PROMOTER	0.703	0.704	1884.20	1326.14	0.495	1496.02	740.64
A_68_P26537267	chr9:56468392-56468441	NM_181074:64644	Lingo1	INSIDE	0.703	3.880	401.81	1558.89	2.727	316.11	862.16
A_68_P22370683	chr3:100490054-100490098	NM_010763:-680	Man1a2	PROMOTER	0.703	0.631	1675.24	1057.85	0.444	1445.14	641.84
A_68_P20940228	chr1:193645578-193645622	NM_010892:249	Nek2	INSIDE	0.703	0.583	937.32	546.29	0.410	689.34	282.36
A_68_P25367281	chr7:107520218-107520262	NM_028292:166	Ppme1	INSIDE	0.703	0.681	1142.22	777.31	0.478	1040.68	497.80
A_68_P22382660	chr3:102539302-102539346	NM_027533:632	Tspan2	INSIDE	0.703	0.720	2166.37	1560.46	0.506	1716.05	869.09
A_68_P23547925	chr5:25036093-25036137	NR_027388:279	1700096K18Rik	INSIDE	0.702	0.573	1709.67	979.34	0.402	1347.77	541.74
A_68_P23441291	chr4:155266628-155266672	NM_207223:667	Acap3	INSIDE	0.702	0.449	1196.21	537.65	0.315	949.75	299.45
A_68_P30822063	chr16:64851412-64851456	NM_178647:-476	Cggbp1	PROMOTER	0.702	0.551	1489.22	821.12	0.387	1289.20	499.24
A_68_P26129634	chr8:107165624-107165668	NM_026753:-18	Fam96b	PROMOTER	0.702	0.575	1062.66	611.08	0.403	776.41	313.24
A_68_P22522352	chr3:129534495-129534539	NM_026578:-202	Gar1	DIVERGENT_PROMOTER	0.702	0.488	1372.49	670.45	0.343	1104.54	378.62
A_68_P24135225	chr5:139856460-139856504	NM_030258:-138	Gpr146	PROMOTER	0.702	0.683	1453.06	992.69	0.479	1217.99	583.91
A_68_P25044870	chr7:35440785-35440829	NM_146188:-2946	Kctd15	PROMOTER	0.702	0.645	1091.76	704.66	0.453	903.45	409.20
A_68_P32559511	chrX:97624538-97624586	NM_001163191:211	Otud6a	INSIDE	0.702	2.971	697.79	2072.93	2.087	300.63	627.32
A_68_P25173479	chr7:70902673-70902717	NM_130880:313037	Otud7a	INSIDE	0.702	0.377	1408.50	530.75	0.265	1136.56	300.75
A_68_P25357342	chr7:105851579-105851623	NM_028410:-272	Prkrir	PROMOTER	0.702	0.510	2049.24	1044.85	0.358	1741.61	623.76
A_68_P28328449	chr12:31596572-31596616	NM_013709:61	Sh3yl1	INSIDE	0.702	0.645	1047.94	675.90	0.452	881.03	398.64
A_68_P26398843	chr9:30939371-30939415	NM_011176:-8	St14	PROMOTER	0.702	0.670	972.07	650.89	0.470	906.49	426.12
A_68_P26238821	chr8:125778775-125778819	NM_020497:702	Zfp276	INSIDE	0.702	0.557	1448.04	805.93	0.391	1109.20	433.42
A_68_P22931102	chr4:54958062-54958106	NM_172867:-2732	Zfp462	PROMOTER	0.702	0.560	1172.08	656.62	0.393	930.91	365.84
A_68_P25447475	chr7:123451082-123451126	ENSMUST00000106605:786		INSIDE	0.702	0.698	2082.21	1453.44	0.490	2002.29	981.02
A_68_P28314430	chr12:29360205-29360249	NM_134052:155	Adi1	INSIDE	0.701	0.425	1311.42	557.70	0.298	1116.03	332.47
A_68_P30459964	chr15:95621741-95621785	NM_175344:489	Ano6	INSIDE	0.701	0.677	1313.87	888.98	0.474	1199.40	568.91
A_68_P32573913	chrX:100818988-100819035	NR_028381:82	B230206F22Rik	INSIDE	0.701	0.624	1682.10	1050.16	0.438	598.45	262.06
A_68_P26808318	chr9:107302722-107302766	NM_001174047:534	Cacna2d2	INSIDE	0.701	0.590	1616.89	953.23	0.413	1133.35	468.19
A_68_P24325870	chr6:29298179-29298223	NM_007594:82	Calu	INSIDE	0.701	0.496	1716.18	852.06	0.348	1355.27	471.43
A_68_P21099938	chr2:29725051-29725095	NM_207298:59	Cercam	INSIDE	0.701	0.714	2528.96	1804.80	0.500	1963.50	982.72
A_68_P23203735	chr4:109650901-109650945	NM_172296:293	Dmrta2	INSIDE	0.701	0.704	1659.33	1168.34	0.493	1439.06	709.83
A_68_P26166325	chr8:113580098-113580142	NM_028274:-118	Exosc6	PROMOTER	0.701	0.506	1081.80	547.31	0.355	1016.24	360.49
A_68_P25531563	chr7:139158857-139158901	NM_173410:736	Gpr26	INSIDE	0.701	0.690	1103.51	761.95	0.484	1026.91	496.72
A_68_P31156856	chr17:35115532-35115587	NM_013558:5912	Hspa1l	INSIDE	0.701	4.215	2744.03	11565.93	2.954	1836.22	5423.27
A_68_P25042627	chr7:34981438-34981482	NM_026549:206	Pdcd2l	INSIDE	0.701	0.621	911.56	566.04	0.435	797.34	346.83
A_68_P25050417	chr7:36432045-36432089	NM_019746:435	Pdcd5	INSIDE	0.701	0.683	1031.15	704.23	0.479	871.40	417.05
A_68_P30343543	chr15:75543756-75543800	NM_001163465:9061	Rhpn1	INSIDE	0.701	2.812	1548.75	4355.21	1.970	1207.13	2377.98
A_68_P26631313	chr9:72961503-72961547	NM_198609:249	Rsl24d1	INSIDE	0.701	0.523	981.58	513.09	0.366	766.38	280.70
A_68_P22353009	chr3:96962896-96962945	NM_019800:221	Acp6	INSIDE	0.700	0.686	1135.65	778.80	0.480	1031.05	495.18
A_68_P31838822	chr18:75856443-75856487	NM_201354:886	Ctif	INSIDE	0.700	0.382	1559.24	596.27	0.268	1354.11	362.26
A_68_P28525536	chr12:72418903-72418947	NM_001190466:8054	Dact1	INSIDE	0.700	2.259	707.69	1598.35	1.580	713.25	1127.14
A_68_P26468514	chr9:44413289-44413333	NM_001110826:336	Ddx6	INSIDE	0.700	0.436	2568.01	1119.06	0.305	2142.02	653.36
A_68_P26584119	chr9:64659071-64659115	NM_001162917:275	Dennd4a	INSIDE	0.700	0.406	1913.08	776.95	0.284	1408.73	400.31
A_68_P25051002	chr7:36539157-36539201	NM_178704:295	Dpy19l3	INSIDE	0.700	0.451	4388.61	1978.98	0.316	3664.63	1157.23
A_68_P26135494	chr8:108228360-108228404	NM_198299:3686	E130303B06Rik	INSIDE	0.700	2.177	1028.01	2237.77	1.525	814.34	1241.57
A_68_P31928725	chr19:5448265-5448309	NM_010235:589	Fosl1	INSIDE	0.700	0.509	2548.84	1298.38	0.356	1856.84	661.82

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28463197	chr12:58644329-58644373	NM_008259:2758	Foxa1	INSIDE	0.700	0.602	2470.64	1486.82	0.421	1927.60	812.46
A_68_P28748141	chr12:113384025-113384069	NM_001097621:-372	Kif26a	PROMOTER	0.700	0.610	2136.05	1302.14	0.427	1469.28	627.02
A_68_P28594552	chr12:85112991-85113035	NM_001205343:8429	Papln	INSIDE	0.700	1.937	3397.39	6579.09	1.356	2820.17	3824.58
A_68_P23468798	chr5:8623006-8623050	NM_198620:-76	Rundc3b	PROMOTER	0.700	0.348	2390.32	831.95	0.244	1803.85	439.51
A_68_P26533462	chr9:55786156-55786200	NM_001081341:-256	Scaper	PROMOTER	0.700	0.673	986.07	663.68	0.471	829.85	391.20
A_68_P31619488	chr18:35821775-35821819	NM_029485:44	Spata24	INSIDE	0.700	0.714	2155.34	1539.01	0.500	1726.88	863.49
A_68_P28100096	chr11:106054873-106054917	NM_028126:-32	Strada	PROMOTER	0.700	0.433	2224.64	962.69	0.303	1592.87	482.54
A_68_P23974103	chr5:109204294-109204338	NM_026109:20066	Tmed11	DOWNSTREAM	0.700	4.515	459.36	2073.86	3.162	437.15	1382.30
A_68_P25009660	chr7:26100723-26100767	NM_183311:9618	Tmem145	INSIDE	0.700	0.554	2427.52	1345.66	0.388	2012.01	780.68
A_68_P21751499	chr2:152673945-152673989	NM_001141975:267	Tpx2	INSIDE	0.700	0.637	1234.55	786.11	0.446	1060.79	472.97
A_68_P25358212	chr7:105987224-105987268	NM_009519:-108	Wnt11	PROMOTER	0.700	0.481	1290.54	620.35	0.336	961.61	323.57
A_68_P21105304	chr2:30656752-30656796	NM_198000:453	1700001O22Rik	INSIDE	0.699	2.034	3417.32	6952.47	1.423	2537.40	3609.48
A_68_P24045787	chr5:122110769-122110813	NM_028227:196	Brap	INSIDE	0.699	0.512	1200.60	614.55	0.358	1045.49	374.08
A_68_P27308087	chr10:84849473-84849517	NM_028709:-64	Btbd11	PROMOTER	0.699	0.626	2521.06	1578.55	0.438	2031.06	888.66
A_68_P24791292	chr6:119058938-119058982	NM_001159533:-753	Cacna1c	PROMOTER	0.699	0.672	1223.48	822.05	0.469	936.33	439.55
A_68_P25092033	chr7:52496504-52496548	NM_007645:-2317	Cd37	PROMOTER	0.699	0.571	1083.78	618.92	0.399	849.17	339.21
A_68_P23611444	chr5:37482900-37482944	NM_178394:40827	Jakmip1	INSIDE	0.699	0.647	1581.10	1023.65	0.453	1275.07	577.27
A_68_P24758107	chr6:113145188-113145232	NM_177763:168	Lhfpl4	INSIDE	0.699	0.664	1299.63	863.19	0.465	1138.19	528.70
A_68_P21037815	chr2:17950260-17950305	NR_028378:1407	LOC100034739	INSIDE	0.699	0.583	1657.92	967.06	0.408	1314.01	535.98
A_68_P23956959	chr5:106161218-106161263	NM_178701:31412	Lrrc8d	INSIDE	0.699	0.439	1295.35	569.20	0.307	910.22	279.73
A_68_P31259248	chr17:57074657-57074701	NM_022328:133	Mllt1	INSIDE	0.699	0.437	2129.07	931.07	0.306	1704.40	520.95
A_68_P22289191	chr3:83959735-83959779	NM_029797:-48	Mnd1	PROMOTER	0.699	15.833	5893.51	93312.28	11.064	4650.31	51449.07
A_68_P21775758	chr2:157030220-157030264	NM_011249:28	Rbl1	INSIDE	0.699	0.584	1486.33	868.26	0.408	1190.57	486.25
A_68_P20353661	chr1:75381740-75381784	NM_001085370:-422	Speg	PROMOTER	0.699	2.347	5763.08	13527.64	1.642	3864.58	6343.90
A_68_P20620970	chr1:134257180-134257224	NM_178874:30656	Tmcc2	INSIDE	0.699	2.433	2472.56	6014.97	1.702	1808.51	3077.28
A_68_P27798800	chr11:52174442-52174486	NM_011694:-152	Vdac1	PROMOTER	0.699	0.586	1619.19	948.35	0.409	1319.10	540.04
A_68_P21219430	chr2:52280336-52280380	NM_182994:36	Arl5a	INSIDE	0.698	3.327	384.91	1280.58	2.321	377.39	875.86
A_68_P27643063	chr11:22760679-22760723	NM_001169114:-364	B3gnt2	PROMOTER	0.698	0.655	2078.47	1360.83	0.457	1785.90	816.37
A_68_P30480363	chr15:99301136-99301180	NM_029236:4003	Bcdin3d	INSIDE	0.698	2.669	509.18	1359.13	1.863	479.80	893.70
A_68_P22338533	chr3:94167492-94167536	NM_001136117:1149	C2cd4d	INSIDE	0.698	0.518	1296.63	671.80	0.361	1126.38	407.18
A_68_P26224704	chr8:123652972-123653016	NM_008024:1410	Foxl1	INSIDE	0.698	0.653	1266.48	827.18	0.456	1004.31	458.13
A_68_P31614302	chr18:34879775-34879820	NM_010280:244	Gfra3	INSIDE	0.698	0.592	1106.57	654.86	0.413	811.33	335.36
A_68_P21395215	chr2:84726754-84726798	NM_199223:73	Rtn4rl2	INSIDE	0.698	0.518	1288.11	666.64	0.361	1073.81	387.98
A_68_P25962574	chr8:75247287-75247331	NM_001113248:122	Sin3b	INSIDE	0.698	0.374	3283.74	1228.96	0.261	2456.71	641.46
A_68_P21115066	chr2:32237310-32237354	NM_198001:103	1110008P14Rik	INSIDE	0.697	0.603	889.30	535.82	0.420	660.80	277.51
A_68_P23562890	chr5:28791591-28791635	NR_015562:-1911	9530036O11Rik	PROMOTER	0.697	0.582	968.63	563.71	0.405	905.60	367.17
A_68_P23335795	chr4:136326956-136327004	NM_010142:64870	Ephb2	INSIDE	0.697	2.449	783.68	1919.59	1.708	663.37	1132.98
A_68_P24863966	chr6:134819841-134819893	NM_001167697:18011	Gpr19	INSIDE	0.697	2.503	692.27	1732.76	1.745	499.76	872.05
A_68_P27902198	chr11:70513486-70513530	NM_213729:149	Inca1	INSIDE	0.697	0.688	1726.77	1188.32	0.480	1348.04	646.65
A_68_P27234952	chr10:70810826-70810870	NM_027184:308	Ipmk	INSIDE	0.697	0.701	4909.12	3439.73	0.488	3668.05	1791.30
A_68_P24137693	chr5:140276198-140276242	NM_010757:8731	Mafk	INSIDE	0.697	2.139	1292.44	2764.97	1.491	989.49	1475.64
A_68_P32252893	chrX:10295189-10295233	NM_001166635:720	Mid1ip1	INSIDE	0.697	3.624	811.67	2941.23	2.526	282.11	712.70
A_68_P23401740	chr4:149029433-149029477	NM_001164052:7971	Pik3cd	INSIDE	0.697	2.573	1302.84	3352.23	1.794	920.73	1651.77
A_68_P29055231	chr13:55574123-55574167	NM_001030296:8517	Prr7	INSIDE	0.697	0.454	1655.72	750.91	0.316	1282.55	405.58
A_68_P31256437	chr17:56615365-56615409	NM_011218:517	Ptprs	INSIDE	0.697	0.603	2791.05	1683.58	0.420	2136.84	897.88
A_68_P22392371	chr3:104442921-104442965	NM_009196:352	Slc16a1	INSIDE	0.697	0.467	1128.11	526.97	0.326	1054.45	343.28
A_68_P25956521	chr8:73891201-73891245	NM_025917:107	Use1	INSIDE	0.697	0.474	1638.25	777.13	0.330	1159.60	383.14
A_68_P26736551	chr9:94438921-94438965	NM_001033145:-442	1190002N15Rik	PROMOTER	0.696	0.473	1867.19	883.29	0.329	1429.46	470.96
A_68_P21516956	chr2:109563795-109563839	NM_001048142:30097	Bdnf	INSIDE	0.696	3.682	1650.35	6076.83	2.565	1222.16	3134.37
A_68_P29501751	chr14:30535961-30536005	NM_009785:-932	Cacna2d3	PROMOTER	0.696	0.558	1979.53	1104.23	0.388	1609.18	624.66
A_68_P27367737	chr10:95403162-95403206	NM_001001932:-112	Eea1	PROMOTER	0.696	0.715	1850.86	1323.35	0.498	1405.40	699.38

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P21603045	chr2:125332058-125332102	NM_007993:94	Fbn1	INSIDE	0.696	0.565	1621.50	916.59	0.394	1496.76	589.20
A_68_P29083949	chr13:60278471-60278515	NM_008086:404	Gas1	INSIDE	0.696	0.624	2201.09	1373.66	0.434	1819.50	790.16
A_68_P27973895	chr11:83665005-83665049	NM_009330:656	Hnf1b	INSIDE	0.696	0.695	1386.97	963.94	0.483	1187.46	574.10
A_68_P27845571	chr11:60745673-60745717	NM_008928:136	Map2k3	INSIDE	0.696	0.594	2179.34	1293.99	0.414	1663.21	687.79
A_68_P31618904	chr18:35722537-35722581	NM_010771:747	Matr3	INSIDE	0.696	0.661	2846.50	1881.63	0.460	2141.72	985.59
A_68_P24137288	chr5:140212139-140212183	NM_174850:127	Micall2	INSIDE	0.696	0.623	1451.27	904.52	0.433	1082.32	469.18
A_68_P30376708	chr15:81021101-81021145	NM_001082536:65	Mkl1	INSIDE	0.696	0.371	4904.97	1821.46	0.259	3769.04	974.71
A_68_P26824825	chr9:110532716-110532765	NM_183276:23925	Nbeal2	INSIDE	0.696	3.030	941.40	2852.73	2.108	726.92	1532.44
A_68_P27710219	chr11:35860895-35860940	NM_011856:896828	Odz2	INSIDE	0.696	3.937	737.49	2903.25	2.738	527.71	1445.05
A_68_P25361260	chr7:106497298-106497342	NM_001111043:4429	Serpinh1	INSIDE	0.696	2.289	998.53	2285.90	1.593	709.01	1129.30
A_68_P30004450	chr15:9070068-9070112	NM_013787:117	Skp2	INSIDE	0.696	0.631	1746.56	1101.38	0.439	1312.45	575.97
A_68_P28042073	chr11:95896364-95896408	NM_033568:156	Snf8	INSIDE	0.696	0.469	1985.98	932.04	0.326	1587.99	518.33
A_68_P24155792	chr5:144031402-144031446	NM_017467:277	Zfp316	INSIDE	0.696	0.580	3890.05	2255.93	0.404	3150.94	1271.44
A_68_P21341873	chr2:74976122-74976166	ENSMUST00000143898:-289		PROMOTER	0.696	0.698	1831.51	1277.55	0.485	1602.37	777.86
A_68_P24768720	chr6:114987629-114987673	NM_026894:242	1500001M20Rik	INSIDE	0.695	0.572	1332.11	761.66	0.397	1167.24	463.55
A_68_P20789366	chr1:166388627-166388671	NM_009721:-162	Atp1b1	PROMOTER	0.695	0.558	2387.22	1331.26	0.387	1897.03	734.95
A_68_P27796928	chr11:51817669-51817713	NM_001166655:-32	Cdkl3	DIVERGENT_PROMOTER	0.695	0.550	953.29	524.44	0.383	782.29	299.29
A_68_P27927582	chr11:75493063-75493107	NM_133656:273	Crk	INSIDE	0.695	0.345	1622.06	559.91	0.240	1180.93	283.49
A_68_P30578862	chr16:18289475-18289519	NM_033324:-235	Dgcr8	PROMOTER	0.695	0.464	2814.07	1306.61	0.323	2400.82	774.39
A_68_P20947554	chr1:194979527-194979571	NM_016851:243	Irf6	INSIDE	0.695	0.596	3148.43	1876.23	0.414	2828.12	1170.77
A_68_P26531898	chr9:55393314-55393358	NM_027397:4381	Isl2	INSIDE	0.695	0.636	1245.19	791.73	0.442	1023.87	452.59
A_68_P28814400	chr13:9093008-9093052	NM_172585:-120	Larp4b	PROMOTER	0.695	0.608	1561.75	949.58	0.423	1305.95	552.06
A_68_P25948237	chr8:72356566-72356610	NM_001024954:-14	Pbx4	PROMOTER	0.695	0.612	1092.52	668.66	0.425	936.71	398.29
A_68_P26145654	chr8:110112041-110112085	NM_010817:320	Psmd7	INSIDE	0.695	0.663	2121.68	1405.97	0.460	1739.62	800.96
A_68_P22527927	chr3:130433279-130433323	NM_001199350:-53	Rpl34-ps1	PROMOTER	0.695	0.516	1318.87	679.94	0.358	1069.49	383.14
A_68_P23993056	chr5:113006473-113006517	NM_019982:-289	Sez6l	PROMOTER	0.695	0.565	1855.15	1047.71	0.392	1357.50	532.77
A_68_P31501879	chr18:12802846-12802890	NM_028341:827	Ttc39c	INSIDE	0.695	0.614	1130.41	694.33	0.427	872.02	372.50
A_68_P31253705	chr17:56214152-56214198	NM_024432:238	Ubxn6	INSIDE	0.695	4.386	6177.25	27091.23	3.049	4582.01	13969.99
A_68_P30660862	chr16:33966764-33966808	NM_009471:303	Umps	INSIDE	0.695	0.492	1842.53	907.08	0.342	1414.82	484.11
A_68_P31403206	chr17:84587417-84587461	NM_001001806:-151	Zfp36l2	PROMOTER	0.695	0.483	1157.99	559.22	0.336	951.40	319.45
A_68_P23971467	chr5:108795517-108795561	ENSMUST00000100944:-3338		PROMOTER	0.695	0.508	2314.48	1176.54	0.353	1975.71	698.10
A_68_P20504208	chr1:107560530-107560574	NM_029349:115	2310035C23Rik	INSIDE	0.694	0.614	1185.82	728.60	0.427	983.00	419.38
A_68_P31336383	chr17:72132310-72132354	NM_030179:1046	Clip4	INSIDE	0.694	0.665	1190.94	791.64	0.461	1150.68	530.48
A_68_P31620538	chr18:36020156-36020200	NM_133687:30707	Cxxc5	INSIDE	0.694	2.083	1139.80	2373.93	1.446	955.47	1381.23
A_68_P31953772	chr19:11015670-11015714	NM_009962:4043	Gpr44	INSIDE	0.694	0.676	2282.94	1542.28	0.469	1715.31	804.06
A_68_P23592019	chr5:34339056-34339100	NM_001001985:446	Nat8l	INSIDE	0.694	0.633	3594.93	2277.22	0.440	2551.28	1122.35
A_68_P26551395	chr9:58883489-58883533	NM_001042752:738	Neo1	INSIDE	0.694	0.716	2348.32	1681.07	0.497	1695.94	842.58
A_68_P31161704	chr17:36054019-36054063	NM_001163818:-100	Ppp1r10	PROMOTER	0.694	0.504	1098.47	553.85	0.350	841.09	294.20
A_68_P23649338	chr5:44492651-44492695	NM_001163584:-6665	Prom1	PROMOTER	0.694	0.645	1320.77	852.34	0.448	1169.60	523.49
A_68_P21152634	chr2:39045653-39045697	NM_178778:576	Scai	INSIDE	0.694	0.460	1672.26	770.05	0.320	1192.58	381.33
A_68_P27181919	chr10:61177928-61177972	NM_001039194:-60	Aifm2	PROMOTER	0.693	2.677	3183.89	8524.00	1.855	2581.25	4789.35
A_68_P20411443	chr1:88199921-88199965	NM_145222:147	B3gnt7	INSIDE	0.693	0.597	1258.97	752.19	0.414	989.70	409.53
A_68_P28450018	chr12:56086184-56086228	NM_013815:1117	Baz1a	INSIDE	0.693	0.724	2881.07	2084.80	0.501	2378.49	1192.55
A_68_P26531722	chr9:55359661-55359705	NM_145615:368	Etfa	INSIDE	0.693	0.604	944.16	570.48	0.418	836.55	350.05
A_68_P21569908	chr2:119302816-119302860	NM_026574:527	Ino80	INSIDE	0.693	0.478	1490.84	712.26	0.331	1236.47	409.36
A_68_P23278936	chr4:125911491-125911535	NM_001145970:22051	Mtap7d1	INSIDE	0.693	2.956	693.43	2049.59	2.047	631.87	1293.59
A_68_P28077767	chr11:102007085-102007129	NM_178053:-573	Nags	PROMOTER	0.693	0.554	1377.22	763.25	0.384	970.32	372.74
A_68_P30346577	chr15:76007094-76007138	NM_201394:19024	Plec	INSIDE	0.693	2.386	785.02	1872.96	1.652	620.97	1026.03
A_68_P24464321	chr6:54545667-54545711	NM_001001335:-7452	Plekha8	PROMOTER	0.693	0.437	1181.73	516.25	0.303	956.64	289.69
A_68_P25477639	chr7:129303337-129303384	NM_011121:410	Plk1	INSIDE	0.693	0.575	1484.84	853.44	0.398	1140.34	454.22
A_68_P25950464	chr8:72735989-72736033	NM_001007570:170	Slc25a42	INSIDE	0.693	0.668	4560.05	3044.74	0.463	3095.10	1431.68

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25807976	chr8:41984580-41984627	NM_001044740:36857	Slc7a2	INSIDE	0.693	2.514	463.99	1166.51	1.742	400.86	698.33
A_68_P31620630	chr18:36033185-36033229			Unknown	0.693	0.601	5132.45	3083.65	0.416	3761.46	1566.34
A_68_P24641622	chr6:91793552-91793596			Unknown	0.693	0.652	1449.33	945.37	0.452	1251.69	565.93
A_68_P28123543	chr11:110198733-110198777	NM_147219:276	Abca5	INSIDE	0.692	0.711	4231.15	3006.85	0.491	3635.03	1786.42
A_68_P25948485	chr8:72406884-72406928	NM_026818:4385	Cilp2	INSIDE	0.692	0.681	1214.26	827.45	0.472	1055.45	498.01
A_68_P28610003	chr12:87763757-87763801	NM_011934:1185	Esrrb	INSIDE	0.692	0.543	2123.21	1153.81	0.376	1653.20	621.43
A_68_P31677414	chr18:46685686-46685730	NM_173423:-83	Fem1c	PROMOTER	0.692	2.904	4249.78	12340.96	2.010	3517.58	7070.26
A_68_P20240345	chr1:55145369-55145413	NM_008303:399	Hspe1	INSIDE	0.692	0.481	1214.46	584.10	0.333	1044.30	347.64
A_68_P25656261	chr8:11561742-11561794	NM_011919:5703	Ing1	INSIDE	0.692	2.925	3040.76	8894.59	2.025	2076.39	4205.51
A_68_P24609841	chr6:86338705-86338755	NM_025823:8414	Pcyox1	INSIDE	0.692	2.391	756.37	1808.36	1.654	535.22	885.15
A_68_P29337691	chr13:113717612-113717656	NM_028151:-46	Skiv2l2	DIVERGENT_PROMOTER	0.692	0.668	1399.33	934.31	0.462	1208.62	558.82
A_68_P24954135	chr7:6083578-6083622	NM_001013012:23973	Zfp787	INSIDE	0.692	3.262	2246.21	7327.51	2.258	1565.21	3534.68
A_68_P28680483	chr12:101425716-101425760	ENSMUST00000146364:-439		PROMOTER	0.692	0.623	1424.75	887.18	0.431	1158.85	499.47
A_68_P22859203	chr4:40801292-40801336	NM_022305:-283	B4galt1	PROMOTER	0.691	0.459	2317.05	1062.95	0.317	1958.69	621.30
A_68_P20786426	chr1:165924837-165924881	NM_201364:54	BC055324	INSIDE	0.691	0.575	1506.08	865.49	0.397	1246.67	495.04
A_68_P26080205	chr8:97436931-97436975	NM_001033533:5046	Ccdc102a	INSIDE	0.691	0.660	1001.81	661.48	0.456	791.03	360.75
A_68_P27750958	chr11:43342876-43342920	NM_001045530:613	Ccnjl	INSIDE	0.691	0.643	2385.19	1533.76	0.444	1837.33	816.56
A_68_P25024699	chr7:29766684-29766728	NM_028659:127	Eif3k	INSIDE	0.691	0.584	1714.18	1000.36	0.403	1258.74	507.44
A_68_P24004043	chr5:114894003-114894047	NM_029956:12	Mmab	INSIDE	0.691	0.736	2863.32	2107.10	0.509	2466.02	1254.84
A_68_P22422568	chr3:109945463-109945507	NM_001163348:906	Ntng1	INSIDE	0.691	0.554	1776.81	984.45	0.383	1375.22	526.41
A_68_P26798483	chr9:105546867-105546912	NM_001081309:1565	Pik3r4	INSIDE	0.691	2.113	1690.32	3572.08	1.460	1350.12	1970.95
A_68_P30778985	chr16:56038024-56038068	NM_029092:-159	Rg9mtd1	PROMOTER	0.691	0.676	1089.63	736.80	0.467	828.97	387.21
A_68_P30686022	chr16:38446053-38446100	NM_007414:6693	Adprh	INSIDE	0.690	3.477	516.64	1796.44	2.399	512.40	1229.15
A_68_P22449317	chr3:116126878-116126922	NM_001080818:50	Cdc14a	INSIDE	0.690	0.667	1819.45	1213.53	0.460	1146.50	527.46
A_68_P25047615	chr7:35904906-35904950	NM_007678:617	Cebpa	INSIDE	0.690	0.530	2320.93	1230.11	0.366	1867.45	683.07
A_68_P24159778	chr5:144934748-144934792	NM_001081109:73466	Lmtk2	INSIDE	0.690	2.652	1056.32	2801.79	1.829	911.55	1667.41
A_68_P30346591	chr15:76008957-76009001	NM_201394:17162	Plec	INSIDE	0.690	2.736	818.69	2239.59	1.888	726.04	1370.64
A_68_P27673279	chr11:29072650-29072694	NM_134034:-234	Smek2	PROMOTER	0.690	0.421	2075.22	873.27	0.290	1518.24	440.73
A_68_P21628393	chr2:130004733-130004777	NM_009225:346	Snrpb	INSIDE	0.690	0.622	1462.71	909.49	0.429	1139.74	489.28
A_68_P25003661	chr7:24919152-24919197	NM_019941:-7	Zfp235	PROMOTER	0.690	0.589	983.89	579.72	0.407	774.86	315.20
A_68_P27284379	chr10:80085336-80085380	NM_134002:-166	Csnk1g2	PROMOTER	0.689	0.395	1415.55	559.53	0.272	1139.00	310.05
A_68_P27288001	chr10:80653093-80653137	NM_007828:6452	Dapk3	INSIDE	0.689	2.265	4338.70	9826.34	1.560	3144.48	4905.15
A_68_P33015622	chr1_random:50759-50807	NM_026866:134556	Disp1	INSIDE	0.689	3.139	1088.41	3416.35	2.162	822.92	1779.07
A_68_P23445682	chr5:3543936-3543980	NM_001042501:126	Fam133b	INSIDE	0.689	0.516	1504.37	776.36	0.356	1407.47	500.67
A_68_P29697251	chr14:70205056-70205100	NM_153514:274	Rhobtb2	INSIDE	0.689	0.388	2278.64	883.05	0.267	1870.58	499.51
A_68_P21776098	chr2:157104921-157104965	NM_019642:109	Rpn2	INSIDE	0.689	0.610	1177.65	718.29	0.420	1005.45	422.26
A_68_P31334601	chr17:71824126-71824170	NM_028887:535	Smchd1	INSIDE	0.689	0.585	1090.80	638.57	0.403	947.73	382.31
A_68_P29733544	chr14:76814636-76814680	NM_207652:-969	Tsc22d1	PROMOTER	0.689	2.141	4360.16	9334.01	1.475	2852.08	4205.57
A_68_P28155491	chr11:115675906-115675950	NM_029557:-124	Tsen54	DIVERGENT_PROMOTER	0.689	0.578	1803.69	1042.37	0.398	1408.51	560.77
A_68_P29440559	chr14:19725789-19725833	NM_144839:331	Ube2e2	INSIDE	0.689	0.559	1276.37	713.40	0.385	1030.76	396.93
A_68_P24158010	chr5:144493382-144493426	NM_029749:-255	Usp42	PROMOTER	0.689	0.377	1453.16	547.58	0.260	1225.92	318.18
A_68_P28599074	chr12:85912374-85912418	NM_007701:1595	Vsx2	INSIDE	0.689	0.367	2598.98	954.91	0.253	2077.80	525.90
A_68_P29662309	chr14:64225736-64225780	NM_173393:392	Xkr6	INSIDE	0.689	0.691	2284.73	1578.46	0.476	1806.55	860.55
A_68_P29477501	chr14:26280580-26280624	NM_183208:1932	Zmiz1	INSIDE	0.689	0.560	974.73	545.44	0.386	698.28	269.37
A_68_P26626260	chr9:71981061-71981105			Unknown	0.689	3.304	657.21	2171.44	2.275	642.22	1461.30
A_68_P22509002	chr3:127201649-127201693	ENSMUST00000104965:249		INSIDE	0.689	0.688	1294.56	890.14	0.474	1171.78	554.91
A_68_P23336493	chr4:136436510-136436556	NM_009777:5560	C1qb	INSIDE	0.688	2.554	524.82	1340.45	1.756	440.42	773.51
A_68_P25020923	chr7:29062778-29062822	NM_001177427:76	Eid2b	INSIDE	0.688	0.670	1109.22	742.63	0.461	787.32	362.89
A_68_P22478234	chr3:121426543-121426587	NM_010171:110	F3	INSIDE	0.688	0.521	1752.31	912.41	0.358	1407.16	503.98
A_68_P20091642	chr1:24106929-24106973	NM_026604:230	Fam135a	INSIDE	0.688	0.388	1541.03	597.91	0.267	1282.51	342.26
A_68_P32095554	chr19:37509531-37509575	NM_008245:222	Hhex	INSIDE	0.688	0.479	2204.80	1056.21	0.330	1836.93	605.79

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28091894	chr11:104469397-104469441	NM_016780:105	Itgb3	INSIDE	0.688	0.612	3183.72	1949.19	0.421	2525.38	1064.26
A_68_P29863083	chr14:103380887-103380931	NM_177715:946	Kctd12	INSIDE	0.688	0.697	1479.74	1031.64	0.480	1162.28	557.40
A_68_P26224547	chr8:123632165-123632209	NM_001166482:93	Mthfsd	INSIDE	0.688	0.398	1659.24	660.00	0.274	1284.05	351.30
A_68_P30514377	chr16:5203908-5203952	NM_013796:175	Nagpa	INSIDE	0.688	0.682	2948.51	2010.90	0.469	2342.15	1098.32
A_68_P21079204	chr2:26358051-26358095	NM_008714:1270	Notch1	INSIDE	0.688	0.587	1450.35	851.25	0.404	1345.02	543.23
A_68_P29509960	chr14:31952198-31952242	NM_027289:4182	Nt5dc2	INSIDE	0.688	2.285	1396.78	3191.19	1.572	1103.15	1733.64
A_68_P31923510	chr19:4510696-4510740	NM_001162946:247	Pcx	INSIDE	0.688	0.568	1546.08	878.66	0.391	1327.53	518.89
A_68_P30397298	chr15:84685375-84685419	NM_001081166:1163	Phf21b	INSIDE	0.688	0.338	1618.44	547.79	0.233	1283.76	298.84
A_68_P26809841	chr9:107501260-107501304	NM_009153:6451	Sema3b	INSIDE	0.688	3.127	1309.33	4094.29	2.150	944.77	2031.46
A_68_P22044436	chr3:33698679-33698723	NM_025978:-416	Ttc14	PROMOTER	0.688	0.639	1293.25	826.52	0.440	993.26	437.05
A_68_P22038453	chr3:32409465-32409509	NM_144519:-27	Zfp639	PROMOTER	0.688	0.562	2077.22	1167.39	0.387	1741.25	673.70
A_68_P28033906	chr11:94462930-94462974	NM_153807:148	Acsf2	INSIDE	0.687	0.588	1170.92	688.57	0.404	896.55	361.96
A_68_P27952856	chr11:79968014-79968058	NM_172133:373	Adap2	INSIDE	0.687	2.141	1729.17	3701.90	1.470	1391.69	2045.46
A_68_P25589623	chr7:148748286-148748330	NM_007459:230	Ap2a2	INSIDE	0.687	0.418	1614.50	675.53	0.287	1296.35	372.45
A_68_P24818643	chr6:125046676-125046720	NM_145979:518	Chd4	INSIDE	0.687	0.673	1123.22	756.09	0.462	860.94	397.85
A_68_P24057006	chr5:124134216-124134260	NM_019765:62	Clip1	INSIDE	0.687	0.552	5661.85	3123.99	0.379	4627.60	1754.33
A_68_P29863558	chr14:103469714-103469758	NM_001033242:304	Cln5	INSIDE	0.687	0.535	1411.50	754.88	0.367	1233.00	452.99
A_68_P30349378	chr15:76437639-76437683	NM_001164173:361	Cpsf1	INSIDE	0.687	0.517	1702.09	880.66	0.356	1259.14	447.65
A_68_P26504864	chr9:50467840-50467884	NM_145614:23	Dlat	INSIDE	0.687	0.526	1505.41	792.43	0.362	1282.19	463.85
A_68_P26531905	chr9:55394153-55394197	NM_027397:5219	Isl2	DOWNSTREAM	0.687	0.505	1800.88	910.18	0.347	1606.19	557.71
A_68_P26228657	chr8:124277495-124277539	NM_020605:23058	Jph3	INSIDE	0.687	4.170	3494.70	14572.88	2.863	2389.38	6840.43
A_68_P20637315	chr1:136982242-136982286	NM_001033409:19589	Lgr6	INSIDE	0.687	3.991	571.95	2282.63	2.741	486.93	1334.82
A_68_P27181451	chr10:61088741-61088785	NM_001177511:30531	Npffr1	INSIDE	0.687	0.625	1350.13	843.68	0.429	1159.09	497.59
A_68_P25614472	chr8:3537844-3537888	NM_001122818:22483	Pnpla6	INSIDE	0.687	3.459	1058.54	3661.45	2.376	901.47	2142.26
A_68_P20770874	chr1:163181125-163181169	NM_007453:151	Prdx6	INSIDE	0.687	0.682	1467.11	1000.13	0.468	1099.00	514.40
A_68_P23328082	chr4:134908937-134908981	NM_001130477:171	Srrm1	INSIDE	0.687	0.556	2728.00	1516.43	0.382	2165.13	826.53
A_68_P21844028	chr2:168719852-168719896	ENSMUST00000029064:32506		INSIDE	0.687	3.184	469.61	1495.03	2.186	399.41	872.95
A_68_P27279763	chr10:79389909-79389953	NM_007880:114	Arid3a	INSIDE	0.686	0.697	1103.67	769.51	0.478	791.61	378.75
A_68_P27272487	chr10:77632541-77632585	NM_138601:-49	D10Jhu81e	PROMOTER	0.686	0.528	1205.85	637.03	0.362	1006.37	364.45
A_68_P23392615	chr4:147514553-147514597	NM_027985:-24	Mad2l2	DIVERGENT_PROMOTER	0.686	0.643	932.85	599.43	0.441	765.24	337.21
A_68_P26581618	chr9:64234628-64234672	NM_172522:1218	Megf11	INSIDE	0.686	0.713	1478.72	1054.17	0.489	1119.08	547.26
A_68_P22314351	chr3:88340661-88340705	NR_035434:-378	Mir1905	PROMOTER	0.686	0.712	2102.36	1497.33	0.488	1573.99	768.56
A_68_P26742497	chr9:95460516-95460560	NM_198414:303	Paqr9	INSIDE	0.686	0.541	1199.90	649.19	0.371	992.47	368.54
A_68_P30481497	chr15:99481812-99481856	NM_012025:218	Racgap1	INSIDE	0.686	0.703	7033.81	4947.07	0.483	5319.72	2568.43
A_68_P30137689	chr15:36212841-36212885	NM_013923:40	Rnf19a	INSIDE	0.686	0.708	3102.26	2196.52	0.486	2332.65	1133.61
A_68_P26239789	chr8:125935544-125935588	NM_023279:103	Tubb3	INSIDE	0.686	0.678	1435.94	973.15	0.465	1174.95	545.94
A_68_P32143657	chr19:46470296-46470340	NM_016860:-93	Actr1a	DIVERGENT_PROMOTER	0.685	0.500	1520.75	759.86	0.342	1257.93	430.51
A_68_P28153393	chr11:115281149-115281196	NM_027862:61	Atp5h	INSIDE	0.685	0.676	1394.60	942.79	0.463	1047.24	485.24
A_68_P27254396	chr10:74524768-74524812	NM_001081412:1150	Bcr	INSIDE	0.685	0.495	1293.97	640.28	0.339	968.38	328.05
A_68_P31792973	chr18:67800987-67801031	NM_001081073:-18	Cep76	DIVERGENT_PROMOTER	0.685	0.651	2122.86	1381.19	0.446	1753.55	781.87
A_68_P24141812	chr5:141000260-141000310	NM_021528:18722	Chst12	INSIDE	0.685	2.690	748.42	2013.00	1.843	788.60	1453.51
A_68_P26885387	chr9:121668671-121668715	NR_033503:369	E530011L22Rik	INSIDE	0.685	0.632	4950.83	3130.05	0.433	3533.14	1531.19
A_68_P20562791	chr1:122503854-122503898	NM_010133:4813	En1	INSIDE	0.685	0.564	1037.42	585.58	0.387	749.34	289.67
A_68_P22013061	chr3:27610037-27610081	NM_173182:-697	Fndc3b	PROMOTER	0.685	0.573	1231.53	705.33	0.393	1172.40	460.27
A_68_P32141592	chr19:46077977-46078021	NM_176785:31	Hps6	INSIDE	0.685	0.576	965.38	556.22	0.395	738.42	291.54
A_68_P26346747	chr9:21172590-21172634	NM_001042708:166	Ilf3	INSIDE	0.685	0.421	1835.08	773.26	0.288	1383.28	399.04
A_68_P28073803	chr11:101286414-101286458	NM_172566:38	Rundc1	INSIDE	0.685	0.640	1201.68	769.29	0.439	1001.24	439.37
A_68_P30580603	chr16:18586991-18587035	NM_011532:50	Tbx1	INSIDE	0.685	0.498	1855.40	924.03	0.341	1449.38	494.48
A_68_P30479873	chr15:99223693-99223737	NM_001171035:65	Tmbim6	INSIDE	0.685	0.587	2305.89	1353.42	0.402	1906.03	766.28
A_68_P25957036	chr8:74005119-74005163	NM_001164679:4826	Ano8	INSIDE	0.684	2.072	1901.72	3939.49	1.416	1441.20	2041.16
A_68_P26055742	chr8:93432780-93432824	NM_177224:80069	Chd9	INSIDE	0.684	0.422	1842.60	778.01	0.289	1534.03	443.35

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P21320137	chr2:71384228-71384272	NM_010054:561	Dlx2	INSIDE	0.684	0.596	1863.59	1110.85	0.408	1431.78	583.95
A_68_P28593018	chr12:84828295-84828339	NM_058212:342	Dpf3	INSIDE	0.684	0.671	970.97	651.44	0.459	831.32	381.34
A_68_P28563523	chr12:79327207-79327251	NM_145965:-413	Gphn	PROMOTER	0.684	0.623	1232.30	767.38	0.426	1118.05	476.12
A_68_P26458696	chr9:42752203-42752247	NM_175481:230	Grik4	INSIDE	0.684	2.811	10571.76	29719.22	1.922	6798.45	13067.18
A_68_P20156380	chr1:37932346-37932395	NM_001037918:3320	Lipt1	INSIDE	0.684	3.693	704.10	2600.02	2.526	556.02	1404.40
A_68_P24137692	chr5:140276072-140276116	NM_010757:8605	Mafk	INSIDE	0.684	3.104	1174.45	3645.28	2.122	847.35	1797.68
A_68_P26227634	chr8:124114601-124114645	NM_026160:255	Map1lc3b	INSIDE	0.684	0.629	1826.77	1149.90	0.431	1507.59	649.39
A_68_P30086027	chr15:26239002-26239046	NM_177597:198	Marchf11	INSIDE	0.684	0.541	2497.35	1351.91	0.370	1881.62	697.04
A_68_P27896369	chr11:69476075-69476120	NM_011900:47	Mpdu1	INSIDE	0.684	0.698	1395.52	973.43	0.477	1202.53	573.41
A_68_P27940739	chr11:77796004-77796048	NM_174852:-291	Phf12	PROMOTER	0.684	0.413	1315.05	543.70	0.283	1036.51	292.97
A_68_P31127301	chr17:29459054-29459101	NM_023734:3251	Pi16	INSIDE	0.684	2.188	1317.53	2882.93	1.496	986.47	1475.51
A_68_P21831533	chr2:166539060-166539104	NM_177782:250	Prex1	INSIDE	0.684	0.666	918.15	611.73	0.456	817.45	372.48
A_68_P31023474	chr17:7165620-7165665	NM_147155:-137	Tagap1	PROMOTER	0.684	0.750	5775.71	4331.47	0.513	4062.05	2082.87
A_68_P26013517	chr8:85689748-85689792	NM_001111304:520	Tbc1d9	INSIDE	0.684	0.393	1849.57	726.16	0.269	1446.57	388.66
A_68_P25798748	chr8:40069239-40069283	NM_030254:340	Tusc3	INSIDE	0.684	0.393	1620.47	636.33	0.268	1401.12	376.12
A_68_P31161378	chr17:36003437-36003481	NM_175242:-101	2310014H01Rik	PROMOTER	0.683	0.659	2041.26	1345.76	0.450	1511.59	680.22
A_68_P31668412	chr18:44821284-44821328	NR_026853:-12	A930012L18Rik	PROMOTER	0.683	0.616	2755.43	1696.61	0.421	2247.16	945.34
A_68_P21516585	chr2:109514331-109514375	NM_007540:-504	Bdnf	PROMOTER	0.683	0.503	1666.72	837.60	0.343	1481.70	508.31
A_68_P32128429	chr19:43827379-43827423	NM_144874:90	Cox15	INSIDE	0.683	0.476	1425.18	678.47	0.325	1198.57	389.44
A_68_P31193020	chr17:44242569-44242613	NM_199016:167	Enpp4	INSIDE	0.683	0.616	1657.03	1021.38	0.421	1296.27	545.61
A_68_P32461570	chrX:70473796-70473840	NM_007978:174	F8a	INSIDE	0.683	3.165	467.24	1478.61	2.161	305.25	659.68
A_68_P20863431	chr1:180267832-180267876	NM_016805:61	Hnrnpu	INSIDE	0.683	0.572	954.12	546.20	0.391	931.67	364.04
A_68_P28161478	chr11:116688959-116689003	NM_026280:380	Mxra7	INSIDE	0.683	0.688	1117.54	769.30	0.470	1018.09	478.74
A_68_P30392998	chr15:83998328-83998372	NM_054088:105	Pnpla3	INSIDE	0.683	0.580	1021.09	592.64	0.396	816.65	323.67
A_68_P26811066	chr9:107673364-107673408	NM_148930:-53	Rbm5	PROMOTER	0.683	0.543	2115.91	1148.85	0.371	1556.64	577.47
A_68_P26660235	chr9:78435636-78435680	NM_172773:176	Slc17a5	INSIDE	0.683	0.670	2850.55	1911.08	0.458	2277.65	1042.94
A_68_P29269472	chr13:101421231-101421275	NM_027139:-45	Taf9	DIVERGENT_PROMOTER	0.683	0.327	2726.81	891.91	0.223	2284.93	510.24
A_68_P31108363	chr17:26250594-26250638	NM_021793:356	Tmem8	INSIDE	0.683	0.495	2667.25	1319.09	0.338	1976.85	667.47
A_68_P23340751	chr4:137150480-137150524	NM_130879:399	Usp48	INSIDE	0.683	0.324	1611.24	521.97	0.221	1172.50	259.45
A_68_P31630977	chr18:38095349-38095393	NM_007858:-305	Diap1	PROMOTER	0.682	0.542	953.84	517.09	0.370	714.07	263.98
A_68_P31827572	chr18:73914245-73914289	NM_053255:-133	Elac1	PROMOTER	0.682	0.685	1442.75	988.80	0.467	1232.23	575.74
A_68_P24951533	chr7:4960089-4960133	NM_001110330:4734	Fiz1	INSIDE	0.682	2.549	466.31	1188.54	1.737	459.07	797.52
A_68_P26592537	chr9:66198093-66198137	NM_145617:-142	Herc1	PROMOTER	0.682	0.444	1236.08	548.43	0.302	1055.67	319.31
A_68_P21078496	chr2:26264414-26264458	NM_033134:272	Inpp5e	INSIDE	0.682	0.600	1585.31	951.67	0.410	1347.95	551.99
A_68_P21812074	chr2:163202123-163202167	NM_021566:21565	Jph2	INSIDE	0.682	2.388	852.58	2036.02	1.629	727.26	1184.62
A_68_P22082262	chr3:40754266-40754310	NM_001040399:-264	Larp1b	PROMOTER	0.682	3.077	243.58	749.49	2.098	291.33	611.28
A_68_P22314130	chr3:88306601-88306645	NM_019390:-9401	Lmna	PROMOTER	0.682	0.377	2143.13	807.09	0.257	1775.63	455.77
A_68_P27536529	chr10:126981436-126981480	NM_008512:76746	Lrp1	INSIDE	0.682	2.357	1246.14	2936.61	1.607	901.22	1448.18
A_68_P26821061	chr9:109834270-109834314	NM_001205331:15	Mtap4	INSIDE	0.682	0.569	1076.57	612.58	0.388	937.57	363.64
A_68_P28671528	chr12:99927345-99927391	NM_011877:45487	Ptpn21	INSIDE	0.682	3.075	1040.43	3199.62	2.099	800.26	1679.48
A_68_P29041947	chr13:53206939-53206983	NM_013846:174518	Ror2	INSIDE	0.682	2.194	1132.70	2484.95	1.497	847.10	1268.27
A_68_P23295436	chr4:128866519-128866563	NM_029036:186	S100pbp	INSIDE	0.682	2.532	592.36	1499.77	1.727	483.99	835.68
A_68_P28635989	chr12:92886073-92886119	NM_175367:138780	Ston2	INSIDE	0.682	2.861	364.22	1042.12	1.952	313.49	611.99
A_68_P22359921	chr3:98186541-98186585	NM_172863:159	Zfp697	INSIDE	0.682	0.349	1534.49	535.82	0.238	1409.56	335.53
A_68_P30489505	chr15:100908652-100908696	AK078004:-795		PROMOTER	0.682	0.665	7103.47	4721.38	0.453	5646.55	2558.60
A_68_P29040996	chr13:53024696-53024740	NM_016709:328	Auh	INSIDE	0.681	0.620	2462.52	1525.86	0.422	1843.06	777.26
A_68_P27737179	chr11:40568476-40568520	NM_009831:290	Ccng1	INSIDE	0.681	0.712	2324.27	1654.79	0.485	1708.80	828.93
A_68_P27934406	chr11:76659626-76659671	NM_007754:862	Cpd	INSIDE	0.681	0.423	1330.18	563.23	0.288	1053.81	303.88
A_68_P21010260	chr2:12223375-12223419	NM_001001309:151	Itga8	INSIDE	0.681	0.555	1890.76	1048.90	0.378	1500.04	566.42
A_68_P21095673	chr2:29050527-29050571	NM_133500:53012	Ntng2	INSIDE	0.681	0.581	2275.90	1321.25	0.395	1701.50	672.65
A_68_P23341303	chr4:137237621-137237665	NM_001081155:25	Rap1gap	INSIDE	0.681	0.312	2655.98	827.77	0.212	2099.42	445.45

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P29989754	chr15:6659137-6659181	NM_030168:778	Rictor	INSIDE	0.681	0.605	949.48	574.20	0.412	673.27	277.44
A_68_P29041943	chr13:53206522-53206567	NM_013846:174934	Ror2	INSIDE	0.681	2.219	1106.53	2455.46	1.511	927.54	1401.53
A_68_P31150659	chr17:33961437-33961481	NM_016844:-15	Rps28	DIVERGENT_PROMOTER	0.681	0.577	1458.42	841.06	0.393	1072.94	421.23
A_68_P28177381	chr11:119216624-119216668	NM_018822:178	Sgsh	INSIDE	0.681	0.711	1447.07	1029.54	0.485	1149.41	557.09
A_68_P30019345	chr15:11925242-11925286	NM_011294:498	Sub1	INSIDE	0.681	0.414	2084.12	862.90	0.282	1677.98	473.37
A_68_P23337643	chr4:136604702-136604746	NM_198248:-114	Zbtb40	PROMOTER	0.681	0.724	1864.32	1349.77	0.493	1594.32	785.73
A_68_P26232725	chr8:124860203-124860247	NM_009569:54184	Zfpm1	INSIDE	0.681	0.555	3646.95	2025.30	0.378	2603.81	984.11
A_68_P24631970	chr6:90320418-90320462	NM_030260:953	Zxdc	INSIDE	0.681	0.686	1972.03	1352.55	0.467	1492.59	696.90
A_68_P33005932	A_68_P33005932			Unknown	0.681	5.456	116.03	633.09	3.718	160.59	596.99
A_68_P21567210	chr2:118801995-118802039	AK184532:42052		INSIDE	0.681	0.662	1334.51	882.86	0.450	1016.25	457.67
A_68_P23367953	chr4:141697540-141697586	NM_144531:68561	9030409G11Rik	INSIDE	0.680	2.758	474.41	1308.24	1.875	458.82	860.23
A_68_P21072310	chr2:25316302-25316346	NM_153557:290	BC029214	INSIDE	0.680	0.632	2882.94	1822.78	0.430	2327.04	1000.96
A_68_P21777899	chr2:157391883-157391927	NM_016916:193	Blcap	INSIDE	0.680	0.527	1269.24	669.07	0.359	1182.05	423.87
A_68_P23576265	chr5:31371305-31371351	NM_023525:14145	Cad	INSIDE	0.680	2.507	569.35	1427.48	1.704	451.39	769.26
A_68_P27289852	chr10:80926846-80926890	NM_176954:18586	Celf5	INSIDE	0.680	0.616	1056.66	650.64	0.419	914.86	383.12
A_68_P21489014	chr2:104250060-104250104	NM_001033347:409	D430041D05Rik	INSIDE	0.680	0.697	1415.77	986.84	0.474	1164.78	551.74
A_68_P32053974	chr19:29700925-29700969	NM_001081213:21964	Ermp1	INSIDE	0.680	3.253	13512.39	43952.77	2.212	10204.22	22574.45
A_68_P24642400	chr6:91929179-91929223	NM_172731:-7903	Fgd5	PROMOTER	0.680	0.710	2869.45	2036.06	0.482	2025.80	976.82
A_68_P29726035	chr14:75530811-75530855	NM_027581:-142	Lrrc63	DIVERGENT_PROMOTER	0.680	0.657	2243.06	1473.69	0.447	1972.90	880.97
A_68_P25353896	chr7:105260083-105260127	NM_008663:7899	Myo7a	INSIDE	0.680	0.697	1164.64	811.86	0.474	1138.79	539.49
A_68_P27889090	chr11:68199498-68199542	NM_008744:808	Ntn1	INSIDE	0.680	0.595	1017.31	605.20	0.404	908.58	367.39
A_68_P30402710	chr15:85565486-85565530	NM_001113418:-485	Ppara	PROMOTER	0.680	0.527	2242.95	1181.33	0.358	1707.17	611.15
A_68_P21833060	chr2:166821691-166821735	NM_001109905:66	Stau1	INSIDE	0.680	0.663	5938.79	3938.57	0.451	4525.85	2041.43
A_68_P28078907	chr11:102180135-102180179	NM_001044383:-1555	Ubtf	PROMOTER	0.680	0.629	961.92	605.47	0.428	885.87	379.44
A_68_P31118861	chr17:27994021-27994065	NM_001080769:591	Uhrf1bp1	INSIDE	0.680	0.448	1403.28	628.58	0.304	1113.50	338.96
A_68_P28336340	chr12:33063936-33063980	NM_001162903:305	2010109K11Rik	INSIDE	0.679	0.434	2102.73	912.95	0.295	1794.44	529.32
A_68_P25637835	chr8:8689975-8690019	NM_176849:541	Arglu1	INSIDE	0.679	0.444	2065.29	916.57	0.302	1692.06	510.25
A_68_P28175723	chr11:118942602-118942646	NM_007625:4927	Cbx4	INSIDE	0.679	2.237	2542.35	5687.64	1.519	1876.51	2850.68
A_68_P29613441	chr14:55260479-55260523	NM_199470:-299	Cdh24	PROMOTER	0.679	0.561	2836.98	1592.71	0.381	2137.26	814.50
A_68_P29134803	chr13:72766020-72766064	NR_030701:-30	D430050G20	DIVERGENT_PROMOTER	0.679	0.666	3082.56	2051.93	0.452	2198.05	992.88
A_68_P26527198	chr9:54547611-54547655	NM_021422:267	Dnaja4	INSIDE	0.679	0.433	1915.56	828.66	0.294	1400.73	411.65
A_68_P25420896	chr7:118923422-118923466	NM_173739:47	Galntl4	INSIDE	0.679	0.505	1217.92	615.12	0.343	1021.08	350.01
A_68_P24126243	chr5:137972158-137972202	NM_010312:2277	Gnb2	INSIDE	0.679	0.686	2618.44	1795.22	0.465	1991.97	926.94
A_68_P25198321	chr7:75310168-75310212	NM_010513:213048	Igf1r	INSIDE	0.679	2.696	1200.76	3237.15	1.830	1026.42	1878.52
A_68_P24052689	chr5:123330434-123330478	NM_013910:19903	Kdm2b	INSIDE	0.679	1.999	3467.76	6931.33	1.356	2705.29	3669.68
A_68_P21105340	chr2:30663727-30663771	NM_170592:252	Mettl11a	INSIDE	0.679	0.655	817.43	535.02	0.445	584.50	259.87
A_68_P24051801	chr5:123157862-123157906	NM_011026:319	P2rx4	INSIDE	0.679	0.529	1081.87	572.28	0.359	986.88	354.20
A_68_P27431035	chr10:107769451-107769495	NM_054056:228	Pawr	INSIDE	0.679	0.416	1831.20	761.38	0.282	1597.66	451.00
A_68_P24991408	chr7:19680755-19680799	NM_011383:884	Six5	INSIDE	0.679	0.591	1115.63	658.95	0.401	954.73	382.66
A_68_P31334604	chr17:71824355-71824399	NM_028887:307	Smchd1	INSIDE	0.679	0.610	3243.74	1977.51	0.414	2541.53	1052.20
A_68_P22543376	chr3:133207147-133207191	NM_001040400:186	Tet2	INSIDE	0.679	0.273	3611.66	987.41	0.186	2830.56	525.58
A_68_P27780291	chr11:48663201-48663245	NM_053166:23583	Trim7	INSIDE	0.679	4.081	3594.36	14669.74	2.771	2409.65	6677.11
A_68_P31982213	chr19:16854797-16854841	NM_173028:599	Vps13a	INSIDE	0.679	0.595	1902.90	1132.87	0.404	1731.95	699.78
A_68_P20628768	chr1:135557603-135557647	NM_001166552:-162	Zbed6	PROMOTER	0.679	0.691	1815.98	1255.22	0.469	1618.23	759.55
A_68_P29097413	chr13:64253752-64253796	NM_175494:733	Zfp367	INSIDE	0.679	0.472	1744.61	822.76	0.320	1360.91	435.67
A_68_P31093091	chr17:23837170-23837214	ENSMUST00000062827:22558		DOWNSTREAM	0.679	0.572	1041.64	595.33	0.388	813.31	315.64
A_68_P26276393	chr9:4309429-4309473	NM_026276:44	Aasdhppt	INSIDE	0.678	0.389	1496.94	582.82	0.264	1257.07	331.89
A_68_P23797911	chr5:73882756-73882800	NM_001190733:514	Dcun1d4	INSIDE	0.678	2.701	11644.76	31456.87	1.831	7834.46	14346.24
A_68_P27690045	chr11:32542304-32542348	NM_134015:-548	Fbxw11	PROMOTER	0.678	0.636	1120.59	712.38	0.431	966.68	416.55
A_68_P20842584	chr1:176431990-176432034	NM_019445:57	Fmn2	INSIDE	0.678	0.491	1840.10	903.75	0.333	1593.60	530.96
A_68_P24990859	chr7:19590097-19590141	NM_178757:705	Irf2bp1	INSIDE	0.678	0.680	1755.85	1193.45	0.461	1413.60	651.31

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P22467635	chr3:119486116-119486160	NM_019550:168	Ptbp2	INSIDE	0.678	0.459	1290.02	591.48	0.311	1093.67	340.04
A_68_P23074275	chr4:85160223-85160267	ENSMUST00000147066:14		INSIDE	0.678	0.372	1982.97	737.85	0.252	1561.58	393.76
A_68_P24810289	chr6:122714619-122714677	ENSMUST00000171541:15327		INSIDE	0.678	0.586	1168.37	684.87	0.397	954.13	379.15
A_68_P23573762	chr5:30950209-30950253	NM_175675:-81	4930471M23Rik	PROMOTER	0.677	0.639	2107.64	1346.21	0.432	1767.61	763.86
A_68_P28153582	chr11:115309493-115309537	NM_001033775:7656	4933422H20Rik	INSIDE	0.677	2.583	1058.05	2733.01	1.749	819.46	1433.43
A_68_P20443145	chr1:93437221-93437265	NM_023046:-414	Asb1	PROMOTER	0.677	0.637	1057.67	673.37	0.431	983.46	424.13
A_68_P27543825	chr10:128346978-128347022	NM_007653:79	Cd63	INSIDE	0.677	0.683	2144.45	1464.58	0.463	1855.31	858.09
A_68_P23094807	chr4:88940152-88940196	NM_009877:349	Cdkn2a	INSIDE	0.677	0.610	1421.78	867.07	0.413	1136.51	469.57
A_68_P23543722	chr5:24256716-24256760	NM_153076:6923	Crygn	DOWNSTREAM	0.677	0.656	1246.78	817.69	0.444	954.40	423.59
A_68_P21374007	chr2:80156093-80156137	NM_024181:492	Dnajc10	INSIDE	0.677	0.558	1432.89	799.80	0.378	1146.38	433.41
A_68_P24533271	chr6:70795056-70795100	NM_010121:558	Eif2ak3	INSIDE	0.677	0.665	1911.05	1270.61	0.450	1478.53	665.97
A_68_P27784883	chr11:49607746-49607790	NM_013529:112	Gfpt2	INSIDE	0.677	0.702	1282.49	900.36	0.475	1129.16	536.33
A_68_P25656231	chr8:11558343-11558389	NM_011919:2301	Ing1	INSIDE	0.677	0.726	2273.58	1650.52	0.491	1759.02	864.48
A_68_P27787506	chr11:50050605-50050649	NM_008521:1347	Ltc4s	INSIDE	0.677	0.361	1576.91	569.57	0.245	1388.43	339.49
A_68_P31109171	chr17:26390076-26390120	NM_025881:244	Luc7l	INSIDE	0.677	0.697	2158.07	1504.63	0.472	1977.61	933.80
A_68_P28089840	chr11:104092393-104092437	NM_001038609:-335	Mapt	PROMOTER	0.677	0.619	2129.17	1317.92	0.419	1609.56	674.35
A_68_P22532369	chr3:131227486-131227530	NM_011863:-223	Papss1	PROMOTER	0.677	0.646	1566.13	1012.40	0.437	1313.60	574.68
A_68_P29773647	chr14:84846157-84846201	NM_001013753:2809	Pcdh17	INSIDE	0.677	0.643	3141.64	2021.12	0.435	2418.45	1052.70
A_68_P27838988	chr11:59601147-59601191	NM_183139:-9	Pld6	PROMOTER	0.677	0.469	3032.00	1421.66	0.317	2325.61	737.73
A_68_P31934551	chr19:6413350-6413399	NM_011242:12792	Rasgrp2	INSIDE	0.677	2.945	1176.72	3465.49	1.993	916.58	1826.51
A_68_P26986175	chr10:20032280-20032325	NM_001025392:28	Bclaf1	INSIDE	0.676	0.485	1391.03	674.28	0.328	1262.70	413.96
A_68_P30793140	chr16:58728114-58728158	NM_171826:-20	Cldnd1	DIVERGENT_PROMOTER	0.676	2.562	12167.32	31168.94	1.731	8479.00	14679.90
A_68_P26137276	chr8:108535235-108535279	NM_028038:130	Ddx28	INSIDE	0.676	0.602	1041.66	626.73	0.407	822.05	334.21
A_68_P25592939	chr7:149280544-149280588	NM_008748:623	Dusp8	INSIDE	0.676	0.500	1989.12	994.60	0.338	1580.34	533.93
A_68_P27286410	chr10:80393339-80393383	NM_008655:525	Gadd45b	INSIDE	0.676	0.618	1942.04	1200.41	0.418	1525.67	637.36
A_68_P24186284	chr5:150438995-150439039	NM_013559:-126	Hsph1	PROMOTER	0.676	0.692	1299.90	899.95	0.468	925.49	433.23
A_68_P25656232	chr8:11558421-11558465	NM_011919:2377	Ing1	INSIDE	0.676	0.535	1490.09	797.77	0.362	1088.50	394.00
A_68_P20864296	chr1:180458833-180458877	NM_001161665:-401	Kif26b	PROMOTER	0.676	0.642	1212.57	777.93	0.433	916.61	397.26
A_68_P31930677	chr19:5757705-5757749	NM_008520:16823	Ltbp3	INSIDE	0.676	2.457	988.10	2428.06	1.661	748.51	1242.94
A_68_P30452810	chr15:94353750-94353801	NM_172437:20163	Pus7l	INSIDE	0.676	2.563	485.10	1243.46	1.733	464.68	805.32
A_68_P20441530	chr1:93195184-93195228	NM_016717:292	Scly	INSIDE	0.676	0.393	2856.82	1122.13	0.265	2200.85	584.12
A_68_P31682229	chr18:47526349-47526393	NM_018744:2152	Sema6a	INSIDE	0.676	0.689	1643.14	1131.91	0.466	1268.83	590.91
A_68_P30250396	chr15:58654501-58654545	NM_175212:460	Tmem65	INSIDE	0.676	3.526	437.07	1541.01	2.382	444.98	1059.97
A_68_P25502139	chr7:133920603-133920647	NM_025347:136	Ypel3	INSIDE	0.676	0.653	1015.14	662.75	0.441	977.14	431.25
A_68_P24951671	chr7:4981772-4981816	NM_001033383:9817	Zfp865	INSIDE	0.676	2.134	1420.09	3030.21	1.443	959.34	1383.93
A_68_P24476146	chr6:56602385-56602429			Unknown	0.676	0.543	1276.57	693.62	0.367	1076.72	395.27
A_68_P31062777	chr17:15080325-15080369	NM_001083880:158	1600012H06Rik	INSIDE	0.675	0.532	2438.49	1297.91	0.359	1847.23	663.96
A_68_P27291407	chr10:81590879-81590923	NM_001163064:143	AU041133	INSIDE	0.675	0.635	4459.76	2831.21	0.428	3864.80	1654.99
A_68_P24053126	chr5:123402327-123402371	NM_001005866:36194	Kdm2b	INSIDE	0.675	0.414	2137.11	883.85	0.279	1817.09	507.45
A_68_P30000045	chr15:8394103-8394149	NM_027707:337	Nipbl	INSIDE	0.675	0.658	1078.92	709.99	0.444	870.82	386.53
A_68_P30650137	chr16:31933143-31933187	NM_172822:-772	Pigz	PROMOTER	0.675	0.597	1360.04	812.25	0.403	1079.71	435.01
A_68_P31162031	chr17:36116088-36116132	NR_028516:-142	Prr3	PROMOTER	0.675	0.586	1125.22	658.85	0.395	1002.57	396.46
A_68_P27688272	chr11:32247924-32247968	NM_177364:136	Sh3pxd2b	INSIDE	0.675	0.627	3910.49	2451.21	0.423	2798.88	1184.19
A_68_P25807974	chr8:41984291-41984335	NM_001044740:36566	Slc7a2	INSIDE	0.675	2.142	1073.23	2299.31	1.445	874.63	1263.93
A_68_P28307259	chr12:28026905-28026949	NM_009234:657	Sox11	INSIDE	0.675	0.461	1436.43	662.36	0.311	1018.36	317.16
A_68_P31106584	chr17:25970012-25970056	NM_019719:272	Stub1	INSIDE	0.675	0.561	3601.70	2019.91	0.378	2722.32	1030.01
A_68_P23074274	chr4:85160094-85160138	ENSMUST00000147066:-114		PROMOTER	0.675	0.662	2306.52	1527.86	0.447	1748.61	782.34
A_68_P22953602	chr4:58925740-58925784	NM_172381:-165	AI314180	PROMOTER	0.674	0.578	1405.53	812.86	0.390	1187.37	462.84
A_68_P23873914	chr5:89194174-89194218	NM_007832:159	Dck	INSIDE	0.674	0.645	2333.25	1504.19	0.435	1917.54	833.61
A_68_P24477005	chr6:56782354-56782398	NM_012056:324	Fkbp9	INSIDE	0.674	0.521	1127.65	587.23	0.351	872.46	306.27
A_68_P27826628	chr11:57458677-57458721	NM_134189:-245	Galnt10	PROMOTER	0.674	0.655	2338.56	1531.00	0.442	1777.49	784.84

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28291802	chr12:25516979-25517023	NM_001083341:537	Mboat2	INSIDE	0.674	0.637	1029.89	656.28	0.430	839.91	360.83
A_68_P31826508	chr18:73732324-73732368	NM_001039214:-12	Mex3c	PROMOTER	0.674	0.623	901.53	561.54	0.420	797.44	335.01
A_68_P32823841	chrX:166435161-166435205	NM_183151:117629	Mid1	DOWNSTREAM	0.674	0.640	2516.88	1611.81	0.432	2567.56	1108.99
A_68_P28185950	chr11:120521651-120521695	NM_175263:479	Notum	INSIDE	0.674	0.485	1372.41	665.38	0.327	1122.43	366.93
A_68_P21117162	chr2:32597241-32597285	NM_013781:20671	Sh2d3c	INSIDE	0.674	0.460	1720.84	791.12	0.310	1521.71	471.58
A_68_P23610943	chr5:37380278-37380322	NM_011716:-79	Wfs1	PROMOTER	0.674	0.586	1056.70	618.78	0.395	968.76	382.51
A_68_P25701518	chr8:18950728-18950772	NM_001113350:223	Xkr5	INSIDE	0.674	0.529	1835.33	971.49	0.357	1616.69	577.17
A_68_P25614205	chr8:3493317-3493361	NM_080461:201	Zfp358	INSIDE	0.674	0.638	3019.06	1927.14	0.430	2491.40	1071.18
A_68_P22970310	chr4:63071641-63071685	NM_001045514:-7183	Akna	PROMOTER	0.673	0.422	1693.42	715.39	0.284	1284.67	365.45
A_68_P21219425	chr2:52279775-52279819	NM_182994:598	Arl5a	INSIDE	0.673	0.668	982.28	656.53	0.450	944.34	424.84
A_68_P31103787	chr17:25571314-25571358	NM_001163691:-608	Cacna1h	PROMOTER	0.673	0.500	1986.83	993.12	0.337	1598.56	538.03
A_68_P28614429	chr12:88488100-88488144	NM_010363:-545	Gstz1	PROMOTER	0.673	0.602	980.32	590.44	0.405	828.68	335.74
A_68_P32672783	chrX:131136007-131136051	NM_019868:204	Hnrnph2	INSIDE	0.673	2.555	2147.96	5488.15	1.720	932.06	1602.80
A_68_P28452665	chr12:56701584-56701628	NM_020287:1703	Insm2	INSIDE	0.673	0.526	979.73	515.70	0.354	800.68	283.70
A_68_P20593980	chr1:129102101-129102145	NM_145128:560	Mgat5	INSIDE	0.673	0.492	2176.46	1070.08	0.331	1689.23	558.60
A_68_P23278938	chr4:125911658-125911702	NM_001145970:21883	Mtap7d1	INSIDE	0.673	2.423	1312.99	3181.86	1.630	1040.03	1695.01
A_68_P26803471	chr9:106355871-106355915	NM_021567:-295	Pcbp4	PROMOTER	0.673	0.484	3334.46	1614.78	0.326	2598.75	846.98
A_68_P26544598	chr9:57787782-57787826	NM_011352:-137	Sema7a	PROMOTER	0.673	0.654	1667.16	1091.11	0.440	1302.63	573.74
A_68_P31487559	chr18:9958109-9958153	NM_153552:-47	Thoc1	PROMOTER	0.673	0.566	1293.21	732.15	0.381	1183.79	450.86
A_68_P24155795	chr5:144031809-144031857	NM_017467:-131	Zfp316	PROMOTER	0.673	0.608	2429.36	1477.76	0.409	1826.44	747.81
A_68_P25027726	chr7:30303717-30303761	ENSMUST00000141713:-485		PROMOTER	0.673	0.636	929.82	591.29	0.428	885.19	378.78
A_68_P26870478	chr9:119012095-119012152	NM_177117:528	Dlec1	INSIDE	0.672	0.626	862.25	539.44	0.420	678.61	285.21
A_68_P28914773	chr13:30075688-30075732	NM_010093:2222	E2f3	INSIDE	0.672	0.608	2516.02	1528.53	0.408	1884.76	769.44
A_68_P25641014	chr8:9207981-9208030	NM_173446:563018	Fam155a	INSIDE	0.672	3.605	1035.43	3732.32	2.423	729.95	1769.02
A_68_P23977822	chr5:110536969-110537013	NM_145147:226	Gtpbp6	INSIDE	0.672	0.732	2295.58	1681.25	0.492	1713.24	842.97
A_68_P23340286	chr4:137074294-137074338	NM_008305:49599	Hspg2	INSIDE	0.672	2.609	626.62	1635.10	1.753	602.12	1055.73
A_68_P23334810	chr4:136158767-136158811	NM_133872:-150	Kdm1a	DIVERGENT_PROMOTER	0.672	0.651	973.15	633.29	0.437	864.43	378.11
A_68_P27535071	chr10:126726102-126726146	NM_033072:-297	Mbd6	DIVERGENT_PROMOTER	0.672	0.728	1876.37	1366.01	0.490	1556.32	761.93
A_68_P23615748	chr5:38218732-38218776	NM_010835:-2930	Msx1	PROMOTER	0.672	0.680	1232.69	838.41	0.457	885.30	404.77
A_68_P22752866	chr4:15941305-15941349	NM_145950:-302	Osgin2	PROMOTER	0.672	0.377	1735.32	653.54	0.253	1459.46	369.14
A_68_P28513106	chr12:70259912-70259956	NM_009093:239	Rps29	INSIDE	0.672	0.699	1322.93	924.22	0.469	960.12	450.65
A_68_P23436706	chr4:154525048-154525092	NM_011385:71574	Ski	DOWNSTREAM	0.672	0.643	1075.26	691.70	0.432	852.30	368.42
A_68_P27340415	chr10:90634726-90634770	NM_001080129:-421	Tmpo	PROMOTER	0.672	0.700	1173.66	822.08	0.471	1031.83	485.61
A_68_P24007967	chr5:115577345-115577390	NM_175352:7617	Unc119b	INSIDE	0.672	4.107	3752.64	15412.48	2.761	2353.45	6498.28
A_68_P24643833	chr6:92164652-92164696	NM_030081:131	Zfyve20	INSIDE	0.672	0.590	4597.05	2713.97	0.396	3662.02	1451.90
A_68_P28788256	chr13:3477776-3477820	NR_015522:250	2810429I04Rik	INSIDE	0.671	0.628	3107.97	1952.97	0.422	2423.23	1021.56
A_68_P28724525	chr12:109155176-109155220	NM_001079883:86426	Bcl11b	INSIDE	0.671	2.821	1042.14	2940.16	1.893	903.58	1710.57
A_68_P21762929	chr2:154718235-154718279	NM_026030:386	Eif2s2	INSIDE	0.671	0.537	1062.37	570.97	0.361	785.70	283.53
A_68_P26313786	chr9:13632306-13632350	NM_176836:158	Fam76b	INSIDE	0.671	0.599	2504.57	1500.57	0.402	2098.29	843.62
A_68_P22791942	chr4:25726695-25726739	NM_010243:434	Fut9	INSIDE	0.671	0.686	1460.39	1001.93	0.460	1132.65	521.24
A_68_P24449526	chr6:52210086-52210130	NM_008264:766	Hoxa13	INSIDE	0.671	0.615	1502.30	923.27	0.412	1156.60	477.07
A_68_P27282937	chr10:79858218-79858268	NM_013595:3982	Mbd3	INSIDE	0.671	2.430	1160.12	2819.24	1.629	866.65	1412.13
A_68_P21706648	chr2:144157388-144157432	NM_152947:-312	Ovol2	PROMOTER	0.671	0.491	1783.53	876.51	0.330	1488.88	490.83
A_68_P22356949	chr3:97692477-97692521	NM_001039376:132	Pde4dip	INSIDE	0.671	0.598	1195.17	714.52	0.401	948.92	380.51
A_68_P29054896	chr13:55516436-55516480	NM_029303:135	Pfn3	INSIDE	0.671	0.456	2073.06	945.06	0.306	1519.38	464.51
A_68_P31142309	chr17:31992389-31992433	NM_010831:327	Sik1	INSIDE	0.671	0.729	4139.42	3018.26	0.490	3216.83	1574.91
A_68_P20087503	chr1:23263704-23263748	ENSMUST00000097807:-481		PROMOTER	0.671	0.499	1977.17	985.63	0.335	1647.42	551.12
A_68_P32678565	chrX:132420534-132420578	NM_001098222:167	Bhlhb9	INSIDE	0.670	2.230	1544.96	3445.00	1.494	797.82	1192.24
A_68_P30778320	chr16:55905833-55905877	NM_028815:29107	Cep97	INSIDE	0.670	2.862	380.98	1090.21	1.918	356.28	683.46
A_68_P27564953	chr11:5688605-5688649	NM_001146308:141	Dbnl	INSIDE	0.670	0.695	2021.36	1403.86	0.465	1567.56	728.93
A_68_P24607366	chr6:85911499-85911543	NM_028099:141	Dusp11	INSIDE	0.670	0.621	866.20	537.54	0.416	726.14	302.05

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28923679	chr13:31651001-31651045	NM_008239:984	Foxq1	INSIDE	0.670	0.669	2172.00	1452.05	0.448	1561.09	698.77
A_68_P26165492	chr8:113426392-113426436	NM_181666:-55	Fuk	PROMOTER	0.670	0.566	1644.99	931.16	0.379	1458.43	553.00
A_68_P31116576	chr17:27610068-27610113	NM_001013385:30159	Grm4	INSIDE	0.670	3.990	4281.32	17081.76	2.671	2957.50	7900.55
A_68_P27924562	chr11:74979450-74979494	NM_001098203:2182	Hic1	INSIDE	0.670	0.487	1104.94	537.62	0.326	842.19	274.44
A_68_P31108916	chr17:26340305-26340349	NM_001081069:420	Rgs11	INSIDE	0.670	0.588	1233.03	724.99	0.394	1057.55	416.67
A_68_P25581865	chr7:147222114-147222158	NM_133755:113	Tubgcp2	INSIDE	0.670	0.693	2465.37	1707.82	0.464	2077.08	963.56
A_68_P28087343	chr11:103673531-103673575	NM_009521:38064	Wnt3	INSIDE	0.670	4.641	2433.84	11295.21	3.107	1734.84	5390.88
A_68_P20826056	chr1:173016015-173016059	BC100368:10398		DOWNSTREAM	0.670	0.564	1640.33	925.20	0.378	1252.34	473.36
A_68_P28836956	chr13:14156155-14156199	NM_194262:118	Arid4b	INSIDE	0.669	0.690	1919.69	1325.30	0.462	1563.90	722.57
A_68_P25083581	chr7:50931799-50931843	NM_145582:4420	Ctu1	INSIDE	0.669	2.401	2120.58	5091.69	1.606	1452.51	2332.23
A_68_P23335796	chr4:136327079-136327123	NM_010142:64750	Ephb2	INSIDE	0.669	2.233	1845.17	4120.32	1.493	1478.72	2207.49
A_68_P23968410	chr5:108150495-108150539	NM_010278:2847	Gfi1	INSIDE	0.669	0.649	1001.29	649.95	0.434	891.94	387.34
A_68_P21339415	chr2:74601471-74601515	NM_010467:456	Hoxd1	INSIDE	0.669	0.708	2539.99	1797.15	0.474	2083.43	986.57
A_68_P29356812	chr13:117100315-117100359	NM_021459:-440	Isl1	PROMOTER	0.669	0.613	919.63	563.65	0.410	921.77	377.86
A_68_P28549422	chr12:76697372-76697416	NM_012024:-207	Ppp2r5e	PROMOTER	0.669	0.614	4111.37	2525.91	0.411	3356.09	1379.87
A_68_P27478502	chr10:116386947-116386991	NM_001003950:468	Rab3ip	INSIDE	0.669	0.509	1179.86	600.15	0.340	942.38	320.46
A_68_P26714893	chr9:89803729-89803773	NM_001039655:-862	Rasgrf1	PROMOTER	0.669	0.659	856.26	564.24	0.441	715.42	315.48
A_68_P20149051	chr1:36614518-36614562	NM_001126047:686	Sema4c	INSIDE	0.669	0.645	1130.29	728.96	0.431	949.38	409.44
A_68_P31120331	chr17:28216591-28216635	NM_013687:917	Tcp11	INSIDE	0.669	0.714	1324.09	945.25	0.477	1091.45	521.14
A_68_P31323661	chr17:69732210-69732254	NM_009547:-1085	Zfp161	PROMOTER	0.669	0.661	1152.64	761.38	0.442	970.05	428.87
A_68_P31744350	chr18:58996079-58996123	NM_175506:-317	Adamts19	PROMOTER	0.668	0.581	1351.03	784.35	0.388	1235.00	478.76
A_68_P21617370	chr2:127952278-127952322	NM_009754:527	Bcl2l11	INSIDE	0.668	0.557	1199.21	667.56	0.372	939.33	349.06
A_68_P27089721	chr10:41239063-41239107	NM_016898:-221	Cd164	PROMOTER	0.668	0.442	1478.47	654.22	0.295	1128.98	333.50
A_68_P26665705	chr9:79566838-79566882	NM_007730:-375	Col12a1	PROMOTER	0.668	0.695	3230.21	2245.78	0.464	2319.51	1077.35
A_68_P28120302	chr11:109582605-109582649	NM_153782:944	Fam20a	INSIDE	0.668	0.580	1847.27	1072.02	0.388	1591.69	616.80
A_68_P21229089	chr2:54288691-54288735	NM_173030:-85	Galnt13	PROMOTER	0.668	0.640	1762.61	1128.40	0.428	1599.03	684.31
A_68_P27915399	chr11:72951333-72951377	NM_010353:442	Gsg2	INSIDE	0.668	0.643	1027.53	660.99	0.430	834.13	358.28
A_68_P23807228	chr5:75472072-75472116	NM_133256:469	Gsx2	INSIDE	0.668	0.707	2024.06	1430.51	0.472	1638.57	773.77
A_68_P31935408	chr19:6531356-6531400	NM_001205234:112641	Nrxn2	INSIDE	0.668	0.583	1603.83	935.12	0.389	1334.63	519.47
A_68_P25406004	chr7:116226565-116226609	NM_001038624:252	Ric3	INSIDE	0.668	0.517	1077.58	556.82	0.345	787.70	272.01
A_68_P26896298	chr9:123587851-123587896	NM_139142:77	Slc6a20a	INSIDE	0.668	0.415	3054.71	1267.00	0.277	2432.20	673.39
A_68_P22311543	chr3:87862306-87862350	NM_144897:89	Apoa1bp	INSIDE	0.667	0.475	2288.20	1085.86	0.317	1695.77	537.05
A_68_P27534325	chr10:126602946-126602990	NM_027739:82	B4galnt1	INSIDE	0.667	0.488	1792.27	874.65	0.326	1549.71	504.52
A_68_P30588535	chr16:20621603-20621647	NM_028420:-273	Camk2n2	DIVERGENT_PROMOTER	0.667	0.443	1624.09	719.47	0.295	1327.82	392.09
A_68_P26019094	chr8:86794146-86794190	NM_026350:91	Ccdc130	INSIDE	0.667	0.639	2432.78	1555.21	0.426	1849.34	788.59
A_68_P21318133	chr2:71050301-71050345	NM_001198877:320	Dync1i2	INSIDE	0.667	0.585	905.85	529.99	0.390	735.70	287.24
A_68_P26765225	chr9:99530050-99530094	NM_028258:59	Dzip1l	INSIDE	0.667	0.573	1786.88	1024.12	0.382	1503.61	574.42
A_68_P32135375	chr19:45005538-45005582	NM_001081225:-48	Fam178a	PROMOTER	0.667	0.425	1610.73	685.16	0.284	1193.66	338.90
A_68_P21517947	chr2:109757830-109757874	NM_172671:49	Lgr4	INSIDE	0.667	0.625	1149.45	718.29	0.417	966.96	402.85
A_68_P26758565	chr9:98325194-98325238	NM_011254:1837	Rbp1	INSIDE	0.667	0.517	2718.74	1405.67	0.345	2031.16	700.18
A_68_P25962580	chr8:75247857-75247901	NM_001113248:692	Sin3b	INSIDE	0.667	0.564	1820.03	1027.17	0.376	1543.99	580.83
A_68_P27226084	chr10:69285147-69285191	NM_146005:288713	Ank3	INSIDE	0.666	2.148	2256.07	4846.37	1.430	1692.90	2420.42
A_68_P24205537	chr6:4550857-4550901	NM_145398:-187	Casd1	PROMOTER	0.666	0.598	1044.51	624.91	0.398	851.82	339.45
A_68_P27176102	chr10:60150451-60150495	NM_023370:8766	Cdh23	INSIDE	0.666	0.559	970.33	542.53	0.373	843.33	314.16
A_68_P21639430	chr2:132089195-132089239	NM_138651:224	Cds2	INSIDE	0.666	0.568	964.42	547.35	0.378	782.88	295.74
A_68_P28688787	chr12:103214342-103214386	NM_016856:181	Cpsf2	INSIDE	0.666	0.622	2682.38	1667.29	0.414	2038.61	843.77
A_68_P25616894	chr8:4258857-4258901	NM_183315:396	Ctxn1	INSIDE	0.666	0.634	1584.26	1005.21	0.422	1240.33	523.97
A_68_P33007791	chr4_random:128451-128495	NM_001033326:18671	Dhrsx	INSIDE	0.666	2.468	7810.77	19279.26	1.644	5480.38	9007.71
A_68_P29683688	chr14:67853251-67853295	NM_010095:1144	Ebf2	INSIDE	0.666	0.603	1322.62	797.41	0.401	1084.90	435.48
A_68_P22291219	chr3:84284726-84284770	NM_001033301:-387	Fhdc1	PROMOTER	0.666	0.447	2105.73	940.81	0.297	1601.10	476.27
A_68_P32026439	chr19:24975135-24975179	NM_008022:643	Foxd4	INSIDE	0.666	0.698	2978.11	2077.88	0.465	2138.93	993.63

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P24868563	chr6:135683062-135683116	NM_008171:440441	Grin2b	INSIDE	0.666	3.710	1775.75	6588.79	2.471	1180.46	2916.88
A_68_P25270819	chr7:88358500-88358544	NM_008803:-167	Pde8a	PROMOTER	0.666	0.579	1813.83	1049.79	0.386	1581.86	609.83
A_68_P27110003	chr10:44877999-44878045	NM_011156:91003	Prep	INSIDE	0.666	2.654	526.78	1397.88	1.768	385.35	681.48
A_68_P31232584	chr17:51318828-51318872	NM_028162:-176	Tbc1d5	PROMOTER	0.666	0.618	1991.74	1231.86	0.412	1666.78	686.17
A_68_P26593987	chr9:66439772-66439816	NM_144937:993	Usp3	INSIDE	0.666	0.520	1052.45	547.37	0.347	874.53	303.08
A_68_P28708614	chr12:106575757-106575801	ENSMUST00000138649:576		INSIDE	0.666	0.541	1331.24	720.65	0.361	1005.08	362.46
A_68_P26913681	chr10:6079865-6079909	NM_031185:326	Akap12	INSIDE	0.665	0.659	1348.73	889.00	0.438	1308.06	573.28
A_68_P31948448	chr19:10175771-10175815	NM_019699:201	Fads2	INSIDE	0.665	0.622	1068.35	664.43	0.414	824.89	341.19
A_68_P25827401	chr8:46036029-46036073	NM_001081286:489	Fat1	INSIDE	0.665	2.649	1533.08	4060.58	1.763	1253.18	2208.91
A_68_P27839121	chr11:59623157-59623201	NM_146018:97	Flcn	INSIDE	0.665	0.491	2653.43	1302.98	0.327	1880.19	614.39
A_68_P26466893	chr9:44113911-44113955	NM_172162:-178	Hinfp	PROMOTER	0.665	0.436	1731.62	755.54	0.290	1237.93	359.38
A_68_P25474217	chr7:128643986-128644031	NM_001081327:108199	Hs3st2	INSIDE	0.665	2.244	1612.51	3618.03	1.493	1081.08	1613.60
A_68_P33003685	chr1_random:342475-342519	NM_177389:417	Mia3	INSIDE	0.665	3.332	950.43	3167.27	2.217	815.73	1808.72
A_68_P22339047	chr3:94247097-94247141	NM_030116:-139	Mrpl9	DIVERGENT_PROMOTER	0.665	0.700	1718.75	1203.68	0.466	1528.25	711.60
A_68_P29110672	chr13:68720676-68720720	NM_172480:300	Mtrr	INSIDE	0.665	0.641	1667.98	1068.62	0.426	1104.70	470.95
A_68_P26521206	chr9:53345098-53345142	NM_001081152:-31	Npat	DIVERGENT_PROMOTER	0.665	0.515	1476.63	761.04	0.343	1089.94	373.51
A_68_P30473047	chr15:97923923-97923967	NM_144851:-108	Senp1	PROMOTER	0.665	0.647	1402.42	907.98	0.430	1117.88	481.06
A_68_P25017446	chr7:28258643-28258687	NM_133210:-194	Sertad3	PROMOTER	0.665	0.425	1727.41	734.53	0.283	1521.32	430.17
A_68_P27628894	chr11:19820464-19820508	NM_033523:-3958	Spred2	PROMOTER	0.665	2.904	294.59	855.42	1.932	379.16	732.65
A_68_P30244924	chr15:57743688-57743732	NM_001167679:-43	Wdr67	PROMOTER	0.665	0.704	1461.45	1028.98	0.468	1213.96	568.55
A_68_P23611948	chr5:37554605-37554649	AK036147:539		INSIDE	0.665	0.570	1301.86	742.67	0.379	1075.42	408.09
A_68_P23255467	chr4:120887341-120887385	ENSMUST00000056635:327		INSIDE	0.665	0.704	4992.08	3516.16	0.468	3955.74	1853.07
A_68_P31305849	chr17:66729099-66729143	NM_001114098:69970	1110012J17Rik	INSIDE	0.664	2.326	1921.71	4469.38	1.544	1357.88	2095.95
A_68_P31632918	chr18:38410055-38410099	NR_027904:143	1700086O06Rik	INSIDE	0.664	0.533	1071.74	570.96	0.354	893.60	316.12
A_68_P24908452	chr6:143048181-143048225	NM_001109688:425	5730419I09Rik	INSIDE	0.664	0.479	1960.53	938.78	0.318	1721.28	547.51
A_68_P30284265	chr15:64753968-64754012	NM_009623:-132	Adcy8	PROMOTER	0.664	0.712	2819.75	2007.06	0.472	2311.08	1091.54
A_68_P28923675	chr13:31650511-31650560	NM_008239:497	Foxq1	INSIDE	0.664	0.607	1112.82	675.23	0.403	946.63	381.14
A_68_P20451396	chr1:94727977-94728021	NM_016696:-264	Gpc1	PROMOTER	0.664	0.381	2725.04	1037.67	0.253	2281.88	577.30
A_68_P28727298	chr12:109557168-109557212	NM_001044380:12711	Hhipl1	INSIDE	0.664	4.705	1516.50	7134.36	3.125	1142.63	3570.46
A_68_P21107803	chr2:31101353-31101397	NM_019681:-68	Ncs1	PROMOTER	0.664	0.440	1396.79	614.35	0.292	1184.54	345.76
A_68_P31127304	chr17:29459396-29459440	NM_023734:3592	Pi16	INSIDE	0.664	3.213	1425.74	4581.14	2.133	1020.44	2176.48
A_68_P27682732	chr11:31271512-31271556	NM_011491:-1473	Stc2	PROMOTER	0.664	0.474	2672.53	1266.60	0.315	1977.73	622.37
A_68_P30542067	chr16:10395304-10395348	NM_001099275:215	Tekt5	INSIDE	0.664	0.689	1815.48	1251.03	0.458	1387.89	635.07
A_68_P24136182	chr5:140023230-140023274	NM_013702:3401	Uncx	INSIDE	0.664	0.389	1861.09	723.76	0.258	1418.20	366.30
A_68_P31203277	chr17:45942900-45942944	AK053380:16350		DOWNSTREAM	0.664	0.615	1171.19	720.86	0.409	1061.95	433.86
A_68_P31922428	chr19:4305887-4305931	NM_130863:47	Adrbk1	INSIDE	0.663	0.669	1755.30	1173.42	0.443	1417.95	628.83
A_68_P30502657	chr15:103013103-103013147	NM_001110216:32659	Cbx5	DOWNSTREAM	0.663	0.512	1157.92	592.32	0.339	1091.68	370.28
A_68_P28776182	chr12:119082285-119082329	NM_146040:-27	Cdca7l	PROMOTER	0.663	0.391	1820.37	710.99	0.259	1573.66	407.71
A_68_P25949230	chr8:72520586-72520630	NM_001113345:-330	Gatad2a	PROMOTER	0.663	0.589	1082.30	637.93	0.391	865.19	338.15
A_68_P26508624	chr9:51087195-51087239	NM_001195681:-557	Gm684	PROMOTER	0.663	0.738	2252.09	1662.84	0.489	1680.64	822.31
A_68_P28635712	chr12:92826632-92826677	NM_031391:1435	Gtf2a1	INSIDE	0.663	0.683	1034.83	706.39	0.453	948.48	429.29
A_68_P25101371	chr7:54051634-54051678	NM_008186:193	Gtf2h1	INSIDE	0.663	0.589	1266.18	745.54	0.391	959.92	374.94
A_68_P27340037	chr10:90564728-90564779	NM_027078:18970	Ikbip	INSIDE	0.663	2.282	1345.04	3069.80	1.513	1012.31	1531.59
A_68_P31383812	chr17:80976478-80976522	NM_001081357:150933	Map4k3	DOWNSTREAM	0.663	0.648	1188.54	770.31	0.430	947.73	407.50
A_68_P24118745	chr5:136438525-136438569	NM_001160366:11800	Srcrb4d	INSIDE	0.663	0.660	4244.66	2802.70	0.438	3021.76	1323.39
A_68_P22728294	chr4:11083669-11083713	NM_001199105:103	Trp53inp1	INSIDE	0.663	0.473	1751.11	828.77	0.314	1542.51	484.14
A_68_P24688741	chr6:99828483-99828532	ENSMUST00000074759:-80		PROMOTER	0.663	2.630	817.49	2150.01	1.743	645.29	1125.02
A_68_P22148833	chr3:54437305-54437349	ENSMUST00000172420:1966		INSIDE	0.663	2.541	557.80	1417.12	1.683	505.96	851.73
A_68_P25610226	chr7:152128254-152128298	NM_007631:-2446	Ccnd1	PROMOTER	0.662	0.407	1574.16	639.92	0.269	1284.45	345.41
A_68_P28067607	chr11:100216626-100216670	NM_010404:807	Hap1	INSIDE	0.662	0.663	931.14	617.47	0.439	778.26	341.72
A_68_P28043569	chr11:96160876-96160920	NM_008269:414	Hoxb6	INSIDE	0.662	0.559	1057.54	590.81	0.370	903.37	334.06

						Sham group			TiO$_2$-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P32095250	chr19:37450569-37450613	NM_010615:-302	Kif11	PROMOTER	0.662	0.600	936.98	561.73	0.397	721.13	286.01
A_68_P30433474	chr15:90880547-90880591	NM_001109040:-189	Kif21a	PROMOTER	0.662	0.603	1332.70	803.69	0.399	1122.47	448.16
A_68_P20454694	chr1:95202421-95202465	NM_178051:5	Mterfd2	INSIDE	0.662	0.577	1626.22	938.73	0.382	1052.21	401.83
A_68_P21952653	chr3:13472808-13472852	NM_001163328:1176	Ralyl	INSIDE	0.662	0.669	2071.17	1384.94	0.442	1586.41	701.86
A_68_P25094661	chr7:52968968-52969012	NM_020011:1587	Sphk2	INSIDE	0.662	2.561	1056.76	2706.28	1.695	892.29	1512.06
A_68_P30342960	chr15:75447074-75447118	NM_001044718:-18	Zfp41	PROMOTER	0.662	0.658	5546.32	3649.34	0.436	3908.26	1702.44
A_68_P25417176	chr7:118266442-118266486	NR_015573:-275	1700012D14Rik	PROMOTER	0.661	0.473	1157.80	547.26	0.312	1034.55	323.09
A_68_P25375960	chr7:109044724-109044768	NM_027532:-182	3200002M19Rik	PROMOTER	0.661	0.649	1096.91	712.10	0.429	1002.42	430.31
A_68_P31524846	chr18:16966832-16966876	NM_007664:704	Cdh2	INSIDE	0.661	0.602	908.10	546.70	0.398	793.88	315.98
A_68_P30677441	chr16:36828287-36828331	NM_001113401:37	Eaf2	INSIDE	0.661	0.640	806.69	516.26	0.423	706.70	299.12
A_68_P28839394	chr13:14705133-14705177	NM_029271:150	Mrpl32	INSIDE	0.661	0.567	912.05	517.10	0.375	814.12	305.27
A_68_P27539152	chr10:127472516-127472560	NM_001113199:137	Naca	INSIDE	0.661	0.541	1584.53	857.07	0.357	1252.56	447.78
A_68_P21628852	chr2:130099893-130099937	NM_024193:-233	Nop56	PROMOTER	0.661	0.545	1054.58	575.08	0.360	795.64	286.66
A_68_P26365996	chr9:25060486-25060530	NM_001205367:469	Septin7	INSIDE	0.661	0.556	1312.34	729.21	0.367	1069.71	392.71
A_68_P25092883	chr7:52650953-52650997	NM_009224:43	Snrnp70	INSIDE	0.661	0.674	1737.70	1170.49	0.445	1471.32	655.14
A_68_P32203589	chr19:56948890-56948934	NM_172840:7	Vwa2	INSIDE	0.661	0.555	1557.43	863.66	0.367	1261.95	462.79
A_68_P30401337	chr15:85374375-85374419	NM_001163634:34104	Wnt7b	INSIDE	0.661	2.597	787.40	2045.23	1.717	678.17	1164.31
A_68_P27534515	chr10:126627015-126627059	NM_001166413:-157	Arhgef25	PROMOTER	0.660	0.701	1586.51	1112.37	0.463	1074.10	497.23
A_68_P21576978	chr2:120557105-120557149	NM_026891:127	Cdan1	INSIDE	0.660	0.514	2920.88	1501.20	0.339	2432.31	825.35
A_68_P28076812	chr11:101846260-101846304	NM_028207:-177	Dusp3	DIVERGENT_PROMOTER	0.660	0.493	1421.69	701.35	0.325	1094.23	356.06
A_68_P21109954	chr2:31428423-31428467	NM_001033389:200	Fubp3	INSIDE	0.660	0.417	1273.80	531.61	0.275	1152.89	317.49
A_68_P23274589	chr4:125167651-125167695	NM_001081097:-402	Grik3	PROMOTER	0.660	0.456	1142.11	521.06	0.301	986.64	297.01
A_68_P27083090	chr10:39977304-39977348	NM_026113:145	Gtf3c6	INSIDE	0.660	0.706	1785.25	1261.18	0.466	1542.72	718.81
A_68_P22375208	chr3:101255145-101255189	NM_207205:74119	Igsf3	INSIDE	0.660	2.628	1387.42	3646.05	1.733	1171.12	2029.91
A_68_P31051124	chr17:12511856-12511901	NM_011948:-352	Map3k4	PROMOTER	0.660	0.508	1315.65	668.69	0.335	1125.73	377.64
A_68_P21744134	chr2:151319923-151319967	NM_198326:-99	Nsfl1c	PROMOTER	0.660	0.649	897.33	582.70	0.428	697.84	298.98
A_68_P20618103	chr1:133763971-133764015	NM_144875:139	Rab7l1	INSIDE	0.660	0.596	1245.37	742.01	0.393	1040.68	409.25
A_68_P29982091	chr15:5066504-5066548	NM_026069:-86	Rpl37	DIVERGENT_PROMOTER	0.660	0.527	1313.48	692.63	0.348	1118.21	389.18
A_68_P24431878	chr6:49214131-49214175	NM_198102:-101	Tra2a	PROMOTER	0.660	0.547	1378.24	753.33	0.361	1225.96	442.04
A_68_P28743067	chr12:112513239-112513283	NM_033603:3939	Amn	INSIDE	0.659	0.444	2108.31	935.35	0.292	1697.05	496.39
A_68_P22350123	chr3:96401551-96401595	NM_001024851:1014	Ankrd34a	INSIDE	0.659	0.357	1442.42	514.58	0.235	1071.90	251.88
A_68_P31751922	chr18:60686064-60686108	NM_026302:212	Dctn4	INSIDE	0.659	0.611	1171.49	715.57	0.403	921.77	371.06
A_68_P30361874	chr15:78543529-78543573	NM_183141:4993	Elfn2	INSIDE	0.659	0.436	2396.17	1045.86	0.287	1940.54	557.78
A_68_P28187037	chr11:120686073-120686117	NM_007988:-233	Fasn	PROMOTER	0.659	0.547	2938.89	1607.96	0.361	2277.31	820.98
A_68_P21059044	chr2:22478107-22478151	NM_008078:282	Gad2	INSIDE	0.659	0.563	2920.10	1644.43	0.371	2196.90	814.91
A_68_P20729266	chr1:155746790-155746834	NM_008131:-262	Glul	PROMOTER	0.659	0.418	1419.85	593.41	0.276	1090.54	300.51
A_68_P32281779	chrX:17739627-17739671	NM_009483:-144	Kdm6a	PROMOTER	0.659	0.414	2101.22	869.94	0.273	751.51	205.12
A_68_P21706642	chr2:144156624-144156668	NM_152947:452	Ovol2	INSIDE	0.659	0.463	1783.17	826.18	0.305	1626.83	496.36
A_68_P26022868	chr8:87489665-87489709	NM_027187:224	Rnaseh2a	INSIDE	0.659	0.554	2412.21	1337.52	0.366	1650.17	603.15
A_68_P30370942	chr15:80064643-80064687	NM_178719:155	Smcr7l	INSIDE	0.659	0.560	1635.09	915.58	0.369	1271.94	469.21
A_68_P31093841	chr17:23956616-23956662	NM_175229:16485	Srrm2	INSIDE	0.659	2.506	862.34	2161.44	1.652	613.74	1013.66
A_68_P31213960	chr17:47874243-47874287	NM_001161723:-615	Tcfeb	PROMOTER	0.659	0.682	2676.72	1826.49	0.450	2273.36	1022.84
A_68_P26867067	chr9:118468644-118468695	NM_018748:53234	Golga4	INSIDE	0.658	2.225	881.75	1962.18	1.465	798.09	1169.49
A_68_P26585801	chr9:64949612-64949656	NM_020043:333	Igdcc4	INSIDE	0.658	0.627	1439.01	901.83	0.412	1230.41	507.04
A_68_P20391651	chr1:82280179-82280223	NM_010570:7814	Irs1	INSIDE	0.658	0.653	5226.48	3411.42	0.430	3985.50	1712.03
A_68_P20714216	chr1:153191544-153191588	NM_001039511:-61	Ivns1abp	PROMOTER	0.658	0.439	1428.02	627.33	0.289	1103.53	318.97
A_68_P22303238	chr3:86351126-86351170	NM_011839:1057	Mab21l2	INSIDE	0.658	0.321	1866.19	598.95	0.211	1307.52	276.08
A_68_P27924625	chr11:74986839-74986883	NR_029794:-29	Mir212	DIVERGENT_PROMOTER	0.658	0.565	2361.24	1333.63	0.372	2102.63	781.59
A_68_P22220260	chr3:69120137-69120181	NM_178726:-681	Ppm1l	PROMOTER	0.658	0.580	1565.18	907.78	0.382	1400.32	534.54
A_68_P22345836	chr3:95623356-95623400	NM_001081293:-502	Rprd2	PROMOTER	0.658	0.625	918.79	574.31	0.411	845.16	347.61
A_68_P24152941	chr5:143177960-143178004	NM_146257:-72	Slc29a4	PROMOTER	0.658	2.270	11641.00	26427.90	1.495	7524.11	11247.90

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27636581	chr11:21271108-21271152	NM_139297:-248	Ugp2	PROMOTER	0.658	0.547	1452.35	794.69	0.360	1201.24	432.29
A_68_P30476370	chr15:98602905-98602961	NM_011718:5649	Wnt10b	INSIDE	0.658	0.648	983.34	637.23	0.426	799.76	340.80
A_68_P31054976	chr17:13185515-13185559	NM_175394:-131	Wtap	PROMOTER	0.658	0.434	1511.65	656.75	0.286	1108.73	317.01
A_68_P20876215	chr1:182413252-182413296	NM_001081227:361	6330403A02Rik	INSIDE	0.657	0.646	793.94	512.70	0.425	663.82	281.80
A_68_P24760450	chr6:113555022-113555066	NM_133937:279	6720456B07Rik	INSIDE	0.657	0.482	3223.92	1555.53	0.317	2566.48	814.00
A_68_P24540591	chr6:72184914-72184958	NM_153778:635	Atoh8	INSIDE	0.657	0.687	2346.58	1611.95	0.451	1756.77	792.80
A_68_P28181191	chr11:119803923-119803967	NM_001037754:-461	Baiap2	PROMOTER	0.657	0.387	1383.14	535.48	0.254	1139.96	290.04
A_68_P22449313	chr3:116126350-116126394	NM_001080818:578	Cdc14a	INSIDE	0.657	0.574	1449.04	832.43	0.377	1155.72	436.23
A_68_P26221733	chr8:123191825-123191869	NM_010926:166	Cox4nb	INSIDE	0.657	0.444	1290.41	573.13	0.292	1065.41	310.74
A_68_P21071852	chr2:25251736-25251780	NM_009849:365	Entpd2	INSIDE	0.657	0.679	1003.25	681.27	0.446	736.79	328.75
A_68_P23118613	chr4:94281110-94281154	NM_026319:-78	Ift74	PROMOTER	0.657	0.505	2146.78	1083.81	0.332	1823.82	605.34
A_68_P25005382	chr7:25316864-25316908	NM_153134:1220	Irgq	INSIDE	0.657	0.592	1466.50	868.70	0.389	1098.25	427.25
A_68_P24536430	chr6:71391224-71391268	NM_024288:-615	Rmnd5a	PROMOTER	0.657	0.712	1828.65	1301.86	0.468	1256.83	587.82
A_68_P23312650	chr4:132066273-132066317	NM_144907:77	Sesn2	INSIDE	0.657	0.640	1179.23	754.89	0.420	958.86	403.05
A_68_P31841969	chr18:76401128-76401172	NM_010754:-428	Smad2	PROMOTER	0.657	0.581	3962.36	2300.73	0.382	3061.97	1168.17
A_68_P28012997	chr11:90499182-90499226	NM_011505:218	Stxbp4	INSIDE	0.657	0.648	1058.56	686.34	0.426	718.26	306.10
A_68_P26421202	chr9:35007602-35007646	NM_001177846:-74	Tirap	PROMOTER	0.657	0.573	1140.89	653.58	0.376	972.80	366.21
A_68_P29211817	chr13:90229380-90229424	NM_025335:131	Tmem167	INSIDE	0.657	0.513	1928.84	989.87	0.337	1446.10	487.23
A_68_P30503432	chr15:103144711-103144755	NM_013866:25785	Zfp385a	INSIDE	0.657	2.208	1289.63	2847.64	1.450	944.34	1368.97
A_68_P27100908	chr10:43260523-43260567	NM_026411:256	1700021F05Rik	INSIDE	0.656	0.624	1409.83	879.04	0.409	1221.30	499.63
A_68_P23154900	chr4:101092304-101092348	NM_009647:19	Ak4	INSIDE	0.656	0.687	1672.17	1148.10	0.451	1431.01	645.01
A_68_P22350132	chr3:96402437-96402481	NM_001024851:1900	Ankrd34a	INSIDE	0.656	0.660	2265.19	1495.18	0.433	1805.69	781.54
A_68_P25588255	chr7:148524764-148524808	NR_027770:-104	Deaf1	DIVERGENT_PROMOTER	0.656	0.645	1280.83	826.61	0.423	1036.09	438.71
A_68_P29644188	chr14:60997183-60997227	NM_001164705:82	Fam123a	INSIDE	0.656	0.550	1771.93	975.27	0.361	1433.61	517.39
A_68_P27278459	chr10:79180444-79180488	NM_008226:1088	Hcn2	INSIDE	0.656	0.655	1170.31	766.08	0.429	940.59	403.81
A_68_P23252660	chr4:120370742-120370786	NM_001081142:49017	Kcnq4	INSIDE	0.656	3.128	4023.88	12586.34	2.052	2870.52	5890.80
A_68_P29856570	chr14:102129092-102129136	NM_201529:-30	Lmo7	PROMOTER	0.656	0.543	1325.98	719.70	0.356	1049.77	373.79
A_68_P29274934	chr13:102464406-102464450	NM_001024955:-1826	Pik3r1	PROMOTER	0.656	0.608	966.97	588.13	0.399	900.07	359.29
A_68_P30010836	chr15:10415930-10415974	NM_011232:164	Rad1	INSIDE	0.656	0.690	1309.92	903.80	0.452	1088.47	492.49
A_68_P22572455	chr3:138738714-138738758	NM_001040690:-573	Rap1gds1	PROMOTER	0.656	0.377	1539.73	581.21	0.248	1233.78	305.44
A_68_P20793340	chr1:167124392-167124436	NM_145512:150	Sft2d2	INSIDE	0.656	0.691	1278.22	883.79	0.453	1099.45	498.32
A_68_P31926801	chr19:5085238-5085283	NM_001001885:217	Tmem151a	INSIDE	0.656	0.555	1342.06	744.73	0.364	1171.07	426.35
A_68_P27804721	chr11:53244209-53244253	NM_025352:103	Uqcrq	INSIDE	0.656	0.376	1433.16	539.11	0.247	1209.03	298.46
A_68_P25505644	chr7:134592579-134592625	NM_175163:70	Zfp689	INSIDE	0.656	0.528	1421.16	749.72	0.346	1004.56	347.43
A_68_P27269569	chr10:77127129-77127173			Unknown	0.656	2.122	5450.30	11563.49	1.392	4134.26	5753.76
A_68_P20447503	chr1:94077585-94077629	AK155250:-688		PROMOTER	0.656	0.634	1170.32	742.21	0.416	986.34	410.35
A_68_P22037673	chr3:32264387-32264431	NR_027966:-2	4930429B21Rik	PROMOTER	0.655	0.458	4313.59	1976.21	0.300	3350.07	1005.86
A_68_P28183224	chr11:120095621-120095666	NM_198423:1383	Bahcc1	INSIDE	0.655	0.647	2464.21	1595.23	0.424	1712.63	726.58
A_68_P30337596	chr15:74347238-74347282	NM_174991:635	Bai1	INSIDE	0.655	0.607	1736.25	1053.94	0.398	1380.84	549.00
A_68_P30836891	chr16:67620592-67620636	NM_001145977:539	Cadm2	INSIDE	0.655	0.618	1691.84	1046.08	0.405	1262.79	511.09
A_68_P24125355	chr5:137799146-137799190	NM_001159571:7832	Ephb4	INSIDE	0.655	2.823	615.22	1736.53	1.848	566.27	1046.42
A_68_P27897908	chr11:69727660-69727704	NM_019726:-11	Gps2	PROMOTER	0.655	0.503	2695.71	1356.48	0.330	1950.72	642.99
A_68_P27897812	chr11:69715753-69715797	NM_001013414:395	Neurl4	INSIDE	0.655	0.546	1649.75	900.96	0.358	1233.32	441.15
A_68_P31935004	chr19:6481505-6481549	NM_001205234:62789	Nrxn2	INSIDE	0.655	2.154	3802.31	8188.49	1.411	2531.56	3573.21
A_68_P24931167	chr6:146837167-146837211	NM_001170433:173	Ppfibp1	INSIDE	0.655	0.692	2211.77	1530.32	0.453	1846.75	836.77
A_68_P32150072	chr19:47538682-47538726	NM_001164717:197	Sh3pxd2a	INSIDE	0.655	0.608	1522.14	924.88	0.398	1241.86	493.98
A_68_P21311407	chr2:69699641-69699685	NM_001110145:44	Ssb	INSIDE	0.655	0.470	1500.34	705.40	0.308	1358.31	418.06
A_68_P25591626	chr7:149088429-149088473	NM_023764:-139	Tollip	PROMOTER	0.655	0.646	1001.20	646.50	0.423	830.74	351.32
A_68_P27356012	chr10:93309036-93309080	NM_183199:14759	Usp44	INSIDE	0.655	3.048	1192.22	3633.63	1.996	1052.88	2101.65
A_68_P31204662	chr17:46168262-46168306	NM_001110266:-6172	Vegfa	PROMOTER	0.655	0.559	1009.01	563.57	0.366	853.50	312.15
A_68_P24631969	chr6:90320325-90320370	NM_030260:860	Zxdc	INSIDE	0.655	0.533	1114.63	594.15	0.349	916.81	320.28

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27842897	chr11:60231302-60231346	NM_025757:678	4933439F18Rik	INSIDE	0.654	0.655	1006.25	659.05	0.429	775.80	332.46
A_68_P31055160	chr17:13153437-13153481	NM_009338:133	Acat2	INSIDE	0.654	0.483	1171.71	566.14	0.316	1001.83	316.34
A_68_P21492617	chr2:104966415-104966459	NR_015462:231	AI314831	INSIDE	0.654	0.614	1321.80	812.21	0.402	1146.31	460.51
A_68_P28449511	chr12:55963765-55963809	NM_007688:78	Cfl2	INSIDE	0.654	0.440	1716.52	755.81	0.288	1482.68	426.90
A_68_P25948512	chr8:72410079-72410123	NM_026818:1191	Cilp2	INSIDE	0.654	0.443	2700.09	1196.23	0.290	1845.91	535.14
A_68_P25776076	chr8:35869953-35869997	NM_176933:-689	Dusp4	PROMOTER	0.654	0.571	2564.91	1464.14	0.373	1967.69	734.05
A_68_P25957388	chr8:74066580-74066624	NM_028617:-226	Fam125a	DIVERGENT_PROMOTER	0.654	0.603	1064.35	641.34	0.394	853.31	336.09
A_68_P31106284	chr17:25929403-25929447	NM_145410:-195	Fam173a	PROMOTER	0.654	0.688	1331.38	916.06	0.450	1013.23	456.00
A_68_P26682080	chr9:83039935-83039979	NM_026122:258	Hmgn3	INSIDE	0.654	0.656	1783.67	1170.60	0.429	1385.19	594.39
A_68_P27449324	chr10:110943649-110943693	NM_009344:329	Phlda1	INSIDE	0.654	0.539	1081.33	582.49	0.352	903.72	318.26
A_68_P31411759	chr17:86020803-86020847	NM_011381:651	Six3	INSIDE	0.654	0.595	2238.44	1332.71	0.389	1756.08	683.90
A_68_P26239786	chr8:125935222-125935266	NM_023279:-219	Tubb3	PROMOTER	0.654	0.589	1583.80	932.19	0.385	1419.24	546.12
A_68_P26232281	chr8:124805601-124805645	NM_009569:-418	Zfpm1	PROMOTER	0.654	3.113	7093.42	22079.62	2.037	4233.43	8622.50
A_68_P26802099	chr9:106150157-106150201	NM_020559:107	Alas1	INSIDE	0.653	0.720	1662.89	1196.94	0.470	1261.48	593.12
A_68_P32364065	chrX:45698842-45698886	NM_178782:4330	Bcorl1	INSIDE	0.653	2.914	865.54	2521.90	1.904	483.93	921.37
A_68_P31152205	chr17:34255338-34255382	NR_037970:1485	Brd2	INSIDE	0.653	0.581	1894.32	1101.27	0.380	1315.29	499.50
A_68_P26519509	chr9:53056349-53056393	NM_029936:-153	Ddx10	PROMOTER	0.653	0.537	1522.99	817.41	0.351	1233.91	432.66
A_68_P31769416	chr18:63546211-63546255	NM_001039485:605	Fam38b	INSIDE	0.653	0.626	1508.79	945.19	0.409	1172.54	479.91
A_68_P23222252	chr4:114581006-114581050	NM_008593:475	Foxd2	INSIDE	0.653	0.663	984.16	652.19	0.433	828.85	358.66
A_68_P30500861	chr15:102773323-102773367	NM_010463:6061	Hoxc12	DOWNSTREAM	0.653	0.703	1594.27	1121.45	0.460	1243.25	571.40
A_68_P20229134	chr1:52874442-52874486	NM_008384:68	Inpp1	INSIDE	0.653	0.730	2012.80	1468.90	0.476	1592.47	758.51
A_68_P26222126	chr8:123259917-123259961	NM_008320:-337	Irf8	PROMOTER	0.653	0.582	1630.42	949.18	0.380	1302.79	495.12
A_68_P30366727	chr15:79316080-79316124	NM_008427:19569	Kcnj4	INSIDE	0.653	2.056	3781.89	7776.96	1.343	2686.58	3607.71
A_68_P27528049	chr10:125403615-125403659	NM_177152:362	Lrig3	INSIDE	0.653	0.628	1397.99	877.79	0.410	1190.24	488.34
A_68_P31151557	chr17:34162040-34162084	NR_029800:-25	Mir219-1	PROMOTER	0.653	0.618	3317.33	2050.15	0.404	2651.31	1070.63
A_68_P20010809	chr1:5906460-5906507	NM_010342:996	Npbwr1	INSIDE	0.653	2.274	1096.84	2494.24	1.484	766.36	1137.20
A_68_P23354400	chr4:139377667-139377712	NM_011039:11194	Pax7	INSIDE	0.653	0.693	2436.09	1687.37	0.452	1808.82	817.53
A_68_P31097499	chr17:24607735-24607779	NM_025954:339	Pgp	INSIDE	0.653	0.483	1351.18	652.43	0.315	1073.26	338.44
A_68_P24059427	chr5:124573452-124573496	NM_011256:92953	Pitpnm2	INSIDE	0.653	2.145	1806.45	3873.94	1.401	1175.89	1647.64
A_68_P27899473	chr11:70028070-70028114	NM_153081:681	Slc16a11	INSIDE	0.653	0.449	1495.14	671.05	0.293	1262.84	370.40
A_68_P21116356	chr2:32462749-32462793	NM_001025310:290	St6galnac6	INSIDE	0.653	0.443	2138.72	946.90	0.289	1637.68	473.42
A_68_P21652098	chr2:134469794-134469838	NM_029148:41	Tmx4	INSIDE	0.653	0.491	1576.93	775.03	0.321	1270.80	407.65
A_68_P31624558	chr18:36719345-36719389	NM_175375:-890	Ankhd1	PROMOTER	0.652	0.443	1562.32	691.96	0.289	1311.14	378.84
A_68_P27334198	chr10:89512597-89512641	NM_001128086:176365	Anks1b	INSIDE	0.652	3.116	369.75	1152.02	2.032	365.58	743.02
A_68_P27284501	chr10:80101148-80101192	NM_001159591:8770	Csnk1g2	INSIDE	0.652	2.188	1736.53	3798.94	1.427	1321.42	1885.63
A_68_P23582162	chr5:32438904-32438948	NM_008037:82	Fosl2	INSIDE	0.652	0.693	1512.24	1047.93	0.451	1175.62	530.76
A_68_P26224615	chr8:123641830-123641874	NM_013519:1782	Foxc2	INSIDE	0.652	0.439	1379.86	606.37	0.286	1020.43	292.22
A_68_P24533908	chr6:70906504-70906548	NM_001101464:-73	Foxi3	PROMOTER	0.652	0.571	1723.25	984.33	0.373	1304.38	486.08
A_68_P27536903	chr10:127031018-127031062	NM_008512:27164	Lrp1	INSIDE	0.652	2.582	1667.49	4305.84	1.683	1242.84	2091.36
A_68_P26204794	chr8:120325573-120325617	NM_026758:235	Mphosph6	INSIDE	0.652	0.561	1212.15	679.99	0.366	1011.10	369.93
A_68_P30295277	chr15:66801273-66801317	NM_008681:-91	Ndrg1	PROMOTER	0.652	0.392	1920.63	753.31	0.256	1429.87	365.71
A_68_P20370402	chr1:78193529-78193573	NM_001159520:161	Pax3	INSIDE	0.652	0.595	1505.07	895.51	0.388	1258.59	488.35
A_68_P26573398	chr9:62828411-62828455	NM_019663:254	Pias1	INSIDE	0.652	0.686	3303.73	2264.88	0.447	2612.06	1167.71
A_68_P29055170	chr13:55565739-55565783	NM_001030296:133	Prr7	INSIDE	0.652	0.555	1054.47	585.21	0.362	875.87	317.12
A_68_P28137851	chr11:112646227-112646271	NM_011448:2725	Sox9	INSIDE	0.652	0.476	3114.77	1483.97	0.310	2500.51	776.27
A_68_P29560589	chr14:41779724-41779768	NM_145928:350	Tspan14	INSIDE	0.652	0.589	1931.70	1138.56	0.384	1656.26	636.34
A_68_P25947839	chr8:72273658-72273702	NM_001200023:181	Zfp963	INSIDE	0.652	0.357	2152.55	767.40	0.232	1797.64	417.73
A_68_P31961512	chr19:12670749-12670793	NR_015503:286	A330040F15Rik	INSIDE	0.651	0.371	1868.62	693.37	0.242	1442.61	348.69
A_68_P22482404	chr3:122123031-122123075	NM_013867:355	Bcar3	INSIDE	0.651	0.688	1892.26	1301.59	0.448	1459.46	653.58
A_68_P22413865	chr3:108456942-108456986	NM_001177770:57	Clcc1	INSIDE	0.651	0.330	1817.88	600.02	0.215	1674.97	360.17
A_68_P32094200	chr19:37249204-37249248	NM_198300:32557	Cpeb3	INSIDE	0.651	0.667	3503.09	2337.36	0.434	2782.03	1207.72

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P20137270	chr1:34234710-34234761	NM_133833:166066	Dst	INSIDE	0.651	3.787	212.75	805.64	2.467	206.01	508.22
A_68_P24449858	chr6:52263643-52263687	NM_007966:173	Evx1	INSIDE	0.651	0.440	1586.70	698.08	0.286	1311.23	375.36
A_68_P30093915	chr15:27610984-27611028	NM_198301:247	Fam105a	INSIDE	0.651	0.684	2057.35	1406.39	0.445	1708.53	760.09
A_68_P23274595	chr4:125168487-125168531	NM_001081097:434	Grik3	INSIDE	0.651	0.648	1355.65	879.12	0.422	1100.74	464.36
A_68_P26215168	chr8:122157059-122157103	NM_025734:2500	Kcng4	INSIDE	0.651	2.357	818.18	1928.32	1.534	766.81	1176.59
A_68_P31406961	chr17:85189534-85189578	NM_028233:570	Lrpprc	INSIDE	0.651	0.624	1016.38	634.34	0.407	766.49	311.60
A_68_P25025263	chr7:29870710-29870754	NR_035489:-2019	Mir1963	PROMOTER	0.651	2.608	4466.52	11647.53	1.698	2906.53	4936.17
A_68_P23615664	chr5:38208449-38208493	NM_010835:7354	Msx1	DOWNSTREAM	0.651	2.478	2092.20	5184.99	1.614	1476.33	2383.32
A_68_P31112724	chr17:26978218-26978262	NM_008700:270	Nkx2-5	INSIDE	0.651	0.639	2373.49	1517.28	0.416	2003.61	833.68
A_68_P32107646	chr19:40345679-40345723	NM_016861:406	Pdlim1	INSIDE	0.651	0.346	2015.46	697.52	0.225	1704.07	384.19
A_68_P21006492	chr2:11424861-11424905	NM_001177752:-1165	Pfkfb3	PROMOTER	0.651	0.537	1161.10	623.36	0.349	958.88	335.11
A_68_P23531277	chr5:21851025-21851070	NM_011261:-524	Reln	PROMOTER	0.651	0.661	1497.21	990.22	0.430	1294.20	556.98
A_68_P31936299	chr19:6904994-6905038	NM_019924:10075	Rps6ka4	INSIDE	0.651	0.447	1447.70	646.70	0.291	1061.00	308.55
A_68_P23165023	chr4:102888044-102888088	NM_177732:-577	Slc35d1	PROMOTER	0.651	0.694	1415.28	982.17	0.452	1125.28	508.43
A_68_P22863908	chr4:41660593-41660637	NM_027278:-65	2810432D09Rik	PROMOTER	0.650	0.535	1473.68	788.48	0.348	1281.32	445.32
A_68_P22479596	chr3:121656435-121656479	NM_172525:213	Arhgap29	INSIDE	0.650	0.600	1067.93	640.26	0.390	917.44	357.48
A_68_P24980778	chr7:16897508-16897552	NM_133234:2599	Bbc3	INSIDE	0.650	0.515	1396.88	719.35	0.335	1236.23	413.85
A_68_P24008375	chr5:115644484-115644528	NM_013879:-8376	Cabp1	PROMOTER	0.650	0.403	1287.34	519.41	0.262	1078.13	282.69
A_68_P31186622	chr17:43013421-43013465	NM_009847:-69	Cd2ap	PROMOTER	0.650	0.721	1637.03	1179.64	0.468	1520.31	712.00
A_68_P30026215	chr15:13103074-13103118	NM_007666:298	Cdh6	INSIDE	0.650	0.710	5232.29	3715.88	0.462	3839.97	1773.12
A_68_P29196857	chr13:86186094-86186138	NM_007749:284	Cox7c	INSIDE	0.650	0.505	1146.09	579.31	0.328	1081.14	355.01
A_68_P32093242	chr19:37093220-37093264	NM_198300:188541	Cpeb3	DOWNSTREAM	0.650	0.735	2543.40	1870.48	0.478	2135.53	1020.16
A_68_P24817420	chr6:124811153-124811197	NM_013533:2761	Gpr162	INSIDE	0.650	2.824	1192.47	3368.01	1.834	939.70	1723.85
A_68_P20240344	chr1:55145241-55145285	NM_008303:271	Hspe1	INSIDE	0.650	0.475	1246.14	592.43	0.309	1020.33	315.22
A_68_P21613745	chr2:127307805-127307849	NM_001111331:409	Kcnip3	INSIDE	0.650	0.441	2650.19	1168.26	0.287	2148.46	615.97
A_68_P26588950	chr9:65524268-65524312	NM_010952:-64	Oaz2-ps	PROMOTER	0.650	0.614	1028.55	631.76	0.399	831.67	331.97
A_68_P25957674	chr8:74115987-74116031	NM_025396:-74	Pgls	PROMOTER	0.650	0.586	1398.98	819.98	0.381	1063.00	404.72
A_68_P24176178	chr5:148674084-148674130	NM_025624:1903	Pomp	INSIDE	0.650	2.514	645.38	1622.69	1.635	512.61	838.38
A_68_P31868104	chr18:81182542-81182586	NM_178280:753	Sall3	INSIDE	0.650	0.534	1422.10	759.78	0.348	1067.28	370.91
A_68_P28540844	chr12:75065711-75065755	NM_178392:216	Snapc1	INSIDE	0.650	0.627	1423.89	893.06	0.408	1175.17	479.01
A_68_P28307234	chr12:28023843-28023887	NM_009234:3719	Sox11	INSIDE	0.650	0.673	1241.04	834.66	0.437	1084.51	474.32
A_68_P29672990	chr14:65977418-65977462	NM_199029:-72	Zfp395	PROMOTER	0.650	0.548	1234.36	676.50	0.356	1021.31	363.56
A_68_P30394507	chr15:84237076-84237131	NM_001163145:40424	1810041L15Rik	INSIDE	0.649	5.609	2320.61	13015.88	3.642	1346.29	4902.97
A_68_P27904028	chr11:70846735-70846779	NM_134022:363	6330403K07Rik	INSIDE	0.649	0.578	1180.96	682.81	0.376	949.72	356.62
A_68_P26134606	chr8:108089561-108089605	NM_013477:358	Atp6v0d1	INSIDE	0.649	0.568	2506.60	1424.01	0.369	1834.28	676.18
A_68_P28936242	chr13:34129507-34129551	NM_026512:19	Bphl	INSIDE	0.649	0.542	1096.78	594.95	0.352	982.49	345.68
A_68_P22550733	chr3:134875756-134875800	NM_173762:252	Cenpe	INSIDE	0.649	0.648	991.59	642.34	0.420	773.26	324.99
A_68_P23807227	chr5:75471945-75471989	NM_133256:341	Gsx2	INSIDE	0.649	0.448	1377.26	616.42	0.291	1001.14	290.99
A_68_P22793478	chr4:26273773-26273817	NM_172865:5	Manea	INSIDE	0.649	0.589	2829.43	1667.16	0.383	2197.29	840.60
A_68_P31107419	chr17:26088437-26088481	NM_001039038:-6582	Nhlrc4	PROMOTER	0.649	0.705	1543.19	1087.78	0.458	1224.04	560.00
A_68_P31633050	chr18:38428628-38428672	NM_017378:15405	Pcdh12	INSIDE	0.649	2.673	409.14	1093.71	1.736	411.17	713.73
A_68_P22356948	chr3:97692392-97692436	NM_001039376:216	Pde4dip	INSIDE	0.649	0.684	2626.34	1796.39	0.444	2051.58	910.16
A_68_P31139420	chr17:31523449-31523493	NM_001163748:292	Pde9a	INSIDE	0.649	0.538	1767.14	951.56	0.349	1459.95	509.92
A_68_P20138941	chr1:34516537-34516581	NM_011206:-32	Ptpn18	PROMOTER	0.649	0.553	1213.68	671.17	0.359	976.21	350.26
A_68_P31846732	chr18:77493370-77493414	NM_013666:68807	St8sia5	INSIDE	0.649	2.348	2710.63	6364.55	1.524	1865.98	2843.82
A_68_P27281037	chr10:79578104-79578148	NM_011492:-1154	Stk11	PROMOTER	0.649	0.530	1828.89	969.27	0.344	1251.59	430.62
A_68_P24760947	chr6:113647724-113647768	NM_001033463:254	Tatdn2	INSIDE	0.649	0.524	1236.48	648.06	0.340	1076.77	366.41
A_68_P31487558	chr18:9957999-9958043	NM_153552:-157	Thoc1	PROMOTER	0.649	0.503	1773.60	891.31	0.326	1342.73	437.60
A_68_P24007966	chr5:115577255-115577310	NM_175352:7702	Unc119b	INSIDE	0.649	5.250	1870.32	9818.65	3.406	1256.12	4278.53
A_68_P24059260	chr5:124540242-124540286	NM_019875:5543	Abcb9	INSIDE	0.648	2.562	3085.29	7904.10	1.661	2247.29	3731.71
A_68_P20437266	chr1:92500005-92500049	NM_133805:27	Cops8	INSIDE	0.648	0.582	1136.15	661.69	0.378	937.25	353.96

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27898577	chr11:69834947-69834991	NM_001109752:2862	Dlg4	INSIDE	0.648	0.513	1313.67	674.23	0.333	1020.02	339.38
A_68_P30512413	chr16:4879317-4879361	NM_145359:513	Fam100a	INSIDE	0.648	0.533	1151.90	614.17	0.346	819.29	283.16
A_68_P28432638	chr12:53072168-53072212	NM_177171:118	Heatr5a	INSIDE	0.648	0.462	1801.20	832.51	0.300	1625.66	487.10
A_68_P26824826	chr9:110532797-110532841	NM_183276:23847	Nbeal2	INSIDE	0.648	2.812	2334.25	6563.42	1.822	1637.31	2983.00
A_68_P27095770	chr10:42311388-42311432	NM_152229:-8016	Nr2e1	PROMOTER	0.648	0.515	1520.31	782.29	0.333	1203.04	401.11
A_68_P29009464	chr13:46822934-46822978	NM_175749:262	Nup153	INSIDE	0.648	0.433	1908.64	826.99	0.281	1480.98	416.03
A_68_P26528578	chr9:54798480-54798524	NM_011966:-163	Psma4	PROMOTER	0.648	0.718	1755.06	1259.28	0.465	1265.83	588.51
A_68_P25510686	chr7:135561251-135561295	NM_026418:414	Rgs10	INSIDE	0.648	0.707	1356.19	958.84	0.458	1082.84	496.08
A_68_P30725222	chr16:45158683-45158727	NM_028756:82	Slc35a5	INSIDE	0.648	0.611	843.81	515.92	0.396	757.76	300.05
A_68_P20551183	chr1:120207585-120207629	NM_011650:103	Tsn	INSIDE	0.648	0.539	1932.44	1042.17	0.349	1603.20	560.27
A_68_P25877023	chr8:55163035-55163079	NM_009506:171	Vegfc	INSIDE	0.648	0.603	2737.76	1650.89	0.391	2305.21	901.17
A_68_P30141374	chr15:36868599-36868643			Unknown	0.648	0.365	3879.51	1416.42	0.236	3206.83	758.20
A_68_P20141344	chr1:34986763-34986807			Unknown	0.648	2.861	587.06	1679.65	1.855	567.90	1053.67
A_68_P28189253	chr11:121066168-121066212	NM_025402:-228	1110031I02Rik	DIVERGENT_PROMOTER	0.647	0.674	2836.41	1911.52	0.436	2309.43	1007.33
A_68_P21013689	chr2:12931615-12931659	NM_153155:855	C1ql3	INSIDE	0.647	0.672	974.19	655.09	0.435	849.89	369.68
A_68_P25325434	chr7:99709780-99709824	NM_001162918:144	Ccdc90b	INSIDE	0.647	0.703	1190.19	836.67	0.454	937.76	426.20
A_68_P29083946	chr13:60278080-60278124	NM_008086:794	Gas1	INSIDE	0.647	2.797	346.02	967.97	1.810	347.89	629.57
A_68_P25458544	chr7:125634804-125634848	NM_001033380:663	Itpripl2	INSIDE	0.647	0.423	1217.89	514.67	0.273	962.69	263.22
A_68_P24126543	chr5:138042018-138042062	NM_030037:228	Mospd3	INSIDE	0.647	0.583	1499.36	874.05	0.377	1140.88	430.06
A_68_P20956471	chr1:196446176-196446220	NM_008882:176	Plxna2	INSIDE	0.647	0.518	2147.75	1112.04	0.335	1680.28	562.98
A_68_P25092648	chr7:52616935-52616979	NM_029741:5433	Ppfia3	INSIDE	0.647	0.546	1744.66	952.09	0.353	1343.74	474.37
A_68_P25007068	chr7:25669351-25669396	NM_023133:-359	Rps19	PROMOTER	0.647	0.695	2395.65	1665.50	0.450	1762.43	793.30
A_68_P26894025	chr9:123168633-123168677	NM_001002267:1253	Tmem158	INSIDE	0.647	0.704	1365.83	961.32	0.455	1099.05	500.15
A_68_P22362400	chr3:98945013-98945057	NM_027462:22	Wars2	INSIDE	0.647	0.586	1480.70	867.95	0.379	1232.09	467.18
A_68_P23591878	chr5:34279071-34279115	NM_011914:-185	Whsc2	PROMOTER	0.647	0.718	1656.32	1189.28	0.465	1213.21	563.55
A_68_P31509663	chr18:14128717-14128761	NM_145492:2504	Zfp521	INSIDE	0.647	0.709	1369.05	970.87	0.459	1248.48	573.06
A_68_P31620891	chr18:36080181-36080225	AK021191:7417		DOWNSTREAM	0.647	0.505	1741.27	879.53	0.327	1247.52	407.89
A_68_P24735710	chr6:108733170-108733214	NM_026011:140	Arl8b	INSIDE	0.646	0.535	1523.38	815.54	0.346	1278.76	442.11
A_68_P23396583	chr4:148179764-148179808	NM_027195:1286	Casz1	INSIDE	0.646	0.546	2151.18	1175.23	0.353	1743.54	615.11
A_68_P20613762	chr1:133026314-133026358	NM_145508:8475	Dyrk3	INSIDE	0.646	2.760	1035.86	2858.97	1.782	860.35	1532.86
A_68_P29512329	chr14:32308482-32308526	NM_028932:240	Eaf1	INSIDE	0.646	0.459	1287.20	590.78	0.296	1039.79	308.20
A_68_P26761439	chr9:98857310-98857354	NM_012020:1307	Foxl2	INSIDE	0.646	0.380	2619.83	996.83	0.246	2193.86	538.88
A_68_P28206069	chr12:5381867-5381911	NM_001164493:600	Klhl29	INSIDE	0.646	0.571	1469.22	839.34	0.369	1153.24	425.71
A_68_P27845569	chr11:60745467-60745511	NM_008928:-70	Map2k3	DIVERGENT_PROMOTER	0.646	0.328	1578.99	517.62	0.212	1136.75	240.67
A_68_P25475988	chr7:129008709-129008753	NM_011325:106	Scnn1b	INSIDE	0.646	0.428	1252.92	536.83	0.277	933.48	258.50
A_68_P23311790	chr4:131885707-131885751	NM_027925:-275	Trnau1ap	PROMOTER	0.646	0.615	1618.76	995.18	0.397	1438.11	570.86
A_68_P27790811	chr11:50641126-50641170	NM_013922:85	Zfp354c	INSIDE	0.646	0.575	2899.51	1666.58	0.372	2099.59	780.08
A_68_P23588918	chr5:33785513-33785557			Unknown	0.646	8.238	2820.06	23230.67	5.318	1850.53	9840.73
A_68_P25024594	chr7:29747163-29747207	NM_021895:115	Actn4	INSIDE	0.645	0.570	1895.95	1081.05	0.368	1565.62	575.77
A_68_P29514241	chr14:32644334-32644378	NM_001024604:-755	Ankrd28	PROMOTER	0.645	0.404	1801.85	728.03	0.260	1310.82	341.36
A_68_P30896823	chr16:78577179-78577223	NM_025967:-287	D16Ertd472e	PROMOTER	0.645	0.681	1168.17	795.47	0.439	1059.91	465.78
A_68_P29335930	chr13:113442131-113442175	NM_001145885:366	Ddx4	INSIDE	0.645	2.608	2026.92	5286.71	1.681	1708.42	2872.61
A_68_P23595699	chr5:35003466-35003510	NM_001080743:461	Grk4	INSIDE	0.645	0.613	1008.96	618.42	0.395	790.34	312.33
A_68_P20877853	chr1:182724319-182724363	NM_008210:19394	H3f3a	DOWNSTREAM	0.645	0.523	1074.31	561.60	0.337	838.95	282.98
A_68_P26567942	chr9:61794410-61794454	NM_024245:174	Kif23	INSIDE	0.645	0.691	1252.07	865.46	0.446	1080.95	482.19
A_68_P21095672	chr2:29050439-29050483	NM_133500:53100	Ntng2	INSIDE	0.645	0.730	2161.13	1577.79	0.471	1866.60	878.51
A_68_P21322074	chr2:71711897-71711941	NM_172665:590	Pdk1	INSIDE	0.645	0.552	1129.30	623.13	0.356	993.73	353.69
A_68_P27287756	chr10:80616365-80616414	NM_021501:14076	Pias4	DOWNSTREAM	0.645	3.573	1617.64	5780.39	2.304	1166.31	2686.76
A_68_P21750261	chr2:152453185-152453229	NM_009047:463	Rem1	INSIDE	0.645	0.444	1860.67	826.16	0.287	1469.94	421.20
A_68_P31067730	chr17:15962490-15962534	NM_178615:1038	Rgmb	INSIDE	0.645	0.417	2151.37	897.58	0.269	1632.10	439.16
A_68_P28555624	chr12:77810657-77810701	NM_013675:856	Spnb1	INSIDE	0.645	0.303	2647.47	801.05	0.195	2209.99	431.34

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P32791361	chrX:159326363-159326407	NM_025932:10	Syap1	INSIDE	0.645	5.291	1302.62	6892.50	3.411	603.29	2058.07
A_68_P22485526	chr3:122687380-122687424	NM_133857:-37	Usp53	PROMOTER	0.645	0.448	3046.44	1364.61	0.289	2356.61	680.60
A_68_P27292201	chr10:81817091-81817135	DQ459435:113		INSIDE	0.645	0.430	2416.43	1039.41	0.277	1901.22	527.09
A_68_P32143656	chr19:46470216-46470260	NM_016860:-13	Actr1a	DIVERGENT_PROMOTER	0.644	0.418	2256.12	942.36	0.269	1745.71	469.68
A_68_P28047528	chr11:96777981-96778025	NM_030248:-207	Cdk5rap3	PROMOTER	0.644	0.630	1635.48	1030.65	0.406	1163.80	471.95
A_68_P29651206	chr14:62266896-62266940	NR_028264:34292	Dleu2	INSIDE	0.644	0.700	1475.22	1033.22	0.451	1259.92	568.46
A_68_P23969234	chr5:108298178-108298222	NM_007964:5926	Evi5	INSIDE	0.644	0.636	1399.66	890.76	0.410	1169.91	479.42
A_68_P27865440	chr11:64249134-64249178	NM_178870:323	Hs3st3a1	INSIDE	0.644	0.627	2304.24	1444.40	0.404	1736.33	700.61
A_68_P28185372	chr11:120433823-120433867	NM_011032:406	P4hb	INSIDE	0.644	0.651	1657.79	1079.68	0.420	1330.17	558.10
A_68_P22301214	chr3:85946197-85946241	NR_004418:-1609	Rnu73b	PROMOTER	0.644	0.562	960.79	540.23	0.362	815.47	295.20
A_68_P30255521	chr15:59480987-59481031	NM_144549:800	Trib1	INSIDE	0.644	0.711	2941.36	2089.94	0.458	2130.32	975.09
A_68_P21434081	chr2:93174589-93174633	NM_183180:34	Tspan18	INSIDE	0.644	0.636	822.85	523.40	0.409	729.18	298.47
A_68_P26184809	chr8:117045830-117045874	NM_019573:82301	Wwox	INSIDE	0.644	2.694	1201.00	3235.35	1.734	870.81	1509.62
A_68_P26184811	chr8:117045980-117046026	NM_019573:82451	Wwox	INSIDE	0.644	2.941	853.03	2508.99	1.895	616.44	1168.19
A_68_P30344504	chr15:75672213-75672257	NM_172121:104	Zc3h3	INSIDE	0.644	0.488	1641.17	800.63	0.314	1138.16	357.45
A_68_P25081793	chr7:50568397-50568441	NM_027264:213	Zfp715	INSIDE	0.644	0.507	5156.42	2612.85	0.326	4186.34	1366.36
A_68_P20637766	chr1:137043169-137043217	NM_026823:-218	Arl8a	PROMOTER	0.643	0.668	1332.89	889.74	0.429	1043.44	447.63
A_68_P27171640	chr10:59414686-59414730	NM_029083:-190	Ddit4	PROMOTER	0.643	0.621	1703.05	1058.42	0.400	1477.74	590.80
A_68_P20567558	chr1:123464212-123464256	NM_025860:323	Ddx18	INSIDE	0.643	0.666	1561.56	1039.62	0.428	1340.21	573.95
A_68_P24620313	chr6:88143671-88143715	NM_008090:-4965	Gata2	PROMOTER	0.643	0.694	1209.74	839.92	0.446	872.92	389.45
A_68_P22649021	chr3:151828589-151828633	NM_016867:254	Gipc2	INSIDE	0.643	0.612	1020.89	625.26	0.394	880.87	347.06
A_68_P24538442	chr6:71781548-71781592	NM_029673:246	Immt	INSIDE	0.643	0.674	1186.21	799.41	0.433	1013.46	439.12
A_68_P23120704	chr4:94717633-94717677	NM_010591:1259	Jun	INSIDE	0.643	0.606	1291.57	782.50	0.389	973.89	379.20
A_68_P29701297	chr14:70843346-70843390	NR_029802:52	Mir320	INSIDE	0.643	0.627	994.33	623.54	0.403	780.89	314.73
A_68_P29507574	chr14:31528289-31528333	NM_001166531:-42	Sfmbt1	PROMOTER	0.643	0.676	961.67	650.19	0.435	775.40	337.34
A_68_P27688273	chr11:32248073-32248117	NM_177364:284	Sh3pxd2b	INSIDE	0.643	0.738	4627.14	3415.56	0.475	3784.82	1797.77
A_68_P30464706	chr15:96472084-96472128	NM_134086:287	Slc38a1	INSIDE	0.643	0.621	1270.19	788.24	0.399	996.93	397.86
A_68_P27327920	chr10:88349166-88349210	NM_145423:452	Slc5a8	INSIDE	0.643	0.410	1537.83	630.03	0.263	1071.91	282.16
A_68_P28307238	chr12:28024309-28024353	NM_009234:3253	Sox11	INSIDE	0.643	0.665	1290.02	857.63	0.427	1168.43	499.42
A_68_P24760940	chr6:113646921-113646965	NM_001033463:-550	Tatdn2	PROMOTER	0.643	0.310	1943.88	603.41	0.200	1473.06	294.21
A_68_P31113562	chr17:27109927-27109971	NM_001005916:-175	Zbtb9	PROMOTER	0.643	0.410	1334.08	547.14	0.264	1046.96	276.11
A_68_P21481086	chr2:102914077-102914121	NM_019735:267	Apip	INSIDE	0.642	0.564	964.81	544.20	0.362	866.22	313.63
A_68_P22202884	chr3:65762093-65762137	NM_019937:33	Ccnl1	INSIDE	0.642	0.497	2814.84	1398.89	0.319	2196.65	700.89
A_68_P30328265	chr15:72921187-72921231	NM_053068:367	Chrac1	INSIDE	0.642	0.448	1281.58	573.79	0.288	1000.24	287.65
A_68_P21731577	chr2:148506945-148506989	NM_028986:111	Gzf1	INSIDE	0.642	0.737	2375.53	1750.12	0.473	1693.37	800.84
A_68_P23593812	chr5:34679442-34679486	NM_011278:426	Rnf4	INSIDE	0.642	0.533	1152.43	614.50	0.342	904.59	309.47
A_68_P27693351	chr11:33102254-33102303	NM_019916:1310	Tlx3	INSIDE	0.642	4.137	2358.31	9756.09	2.658	1525.60	4054.39
A_68_P20827191	chr1:173224816-173224860	NM_025388:275	Ufc1	INSIDE	0.642	0.613	2240.32	1372.98	0.394	1628.28	641.14
A_68_P30476409	chr15:98608492-98608536	NM_011718:67	Wnt10b	INSIDE	0.642	0.733	1990.71	1460.02	0.471	1581.59	744.93
A_68_P20412114	chr1:88330989-88331033	NM_027966:8107	1700019O17Rik	DOWNSTREAM	0.641	0.597	2890.85	1724.47	0.382	2337.87	893.83
A_68_P28182350	chr11:119960353-119960397	NM_001110242:127	1810043H04Rik	INSIDE	0.641	0.643	2765.61	1779.32	0.412	2015.50	830.58
A_68_P27835193	chr11:58977324-58977368	NM_173785:-102	A230051G13Rik	PROMOTER	0.641	0.710	1345.47	955.91	0.456	1036.07	472.19
A_68_P27765618	chr11:45869772-45869816	NM_009616:306	Adam19	INSIDE	0.641	0.640	1923.87	1232.24	0.411	1518.19	623.73
A_68_P29449128	chr14:21612623-21612667	NM_001039138:666	Camk2g	INSIDE	0.641	0.738	3410.83	2517.97	0.473	2557.73	1209.41
A_68_P23999718	chr5:114185852-114185896	NM_001010825:84	Ficd	INSIDE	0.641	0.455	3096.15	1410.16	0.292	2435.03	711.35
A_68_P31161697	chr17:36053340-36053384	NM_025878:-48	Mrps18b	DIVERGENT_PROMOTER	0.641	0.574	1546.78	887.48	0.368	1262.04	464.16
A_68_P26821060	chr9:109834141-109834185	NM_001205331:-115	Mtap4	PROMOTER	0.641	0.661	1010.27	667.28	0.423	961.08	406.93
A_68_P21820255	chr2:164705460-164705507	NM_146129:616	Pcif1	INSIDE	0.641	0.500	1254.20	627.53	0.321	880.58	282.51
A_68_P27954273	chr11:80241942-80241986	NM_178616:-152	Psmd11	PROMOTER	0.641	0.624	1819.27	1135.26	0.400	1508.78	603.12
A_68_P29144761	chr13:74304464-74304508	NM_001081060:45524	Slc9a3	DOWNSTREAM	0.641	0.647	1075.95	695.72	0.415	865.52	358.83
A_68_P23271163	chr4:124614216-124614260	NM_177573:-53	9930104L06Rik	DIVERGENT_PROMOTER	0.640	0.656	1168.39	766.73	0.420	927.63	389.38

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P24098745	chr5:132014699-132014743	NM_177047:1003493	Auts2	INSIDE	0.640	0.421	1656.56	697.87	0.270	1591.66	429.26
A_68_P20265713	chr1:59820408-59820452	NM_007561:-1050	Bmpr2	PROMOTER	0.640	0.492	1359.20	669.18	0.315	1108.33	349.36
A_68_P24831080	chr6:127105235-127105279	NM_009829:-4190	Ccnd2	PROMOTER	0.640	0.712	1507.40	1073.68	0.456	1322.49	603.22
A_68_P27796702	chr11:51781404-51781448	NM_029976:294	Cdkn2aipnl	INSIDE	0.640	0.453	1411.50	638.77	0.290	1139.71	330.17
A_68_P28186831	chr11:120657508-120657552	NM_026824:179	Dus1l	INSIDE	0.640	0.632	861.08	544.18	0.404	746.98	301.96
A_68_P20433001	chr1:91827813-91827857	NM_010262:-83	Gbx2	PROMOTER	0.640	0.642	1031.45	662.60	0.411	724.71	297.74
A_68_P31631086	chr18:38114645-38114689	NM_010411:-24	Hdac3	DIVERGENT_PROMOTER	0.640	0.468	2185.66	1021.91	0.299	1667.69	499.29
A_68_P28004885	chr11:89160628-89160672	NM_008711:3223	Nog	DOWNSTREAM	0.640	0.524	1607.08	841.78	0.335	1359.69	455.88
A_68_P30421723	chr15:88693456-88693500	NM_145478:855	Pim3	INSIDE	0.640	0.693	1434.73	994.80	0.444	1103.85	489.91
A_68_P22014196	chr3:27837925-27837969	NM_001164056:345	Pld1	INSIDE	0.640	0.604	1984.92	1198.54	0.386	1581.36	610.92
A_68_P28190285	chr11:121249100-121249144	NM_139147:443	Rab40b	INSIDE	0.640	0.592	2051.82	1214.50	0.379	1551.46	588.11
A_68_P22727924	chr4:11003258-11003303	NM_001085493:71	2310030N02Rik	INSIDE	0.639	0.508	1185.00	602.42	0.325	1010.87	328.61
A_68_P30387340	chr15:83081767-83081811	NM_001170954:373	A4galt	INSIDE	0.639	0.488	1467.01	715.23	0.311	1375.72	428.41
A_68_P20395061	chr1:82836417-82836461	NM_010472:381	Agfg1	INSIDE	0.639	0.503	2044.72	1029.10	0.321	1736.66	558.30
A_68_P25089687	chr7:52107857-52107901	NM_026270:3282	Akt1s1	INSIDE	0.639	2.612	1327.96	3469.01	1.668	938.04	1564.97
A_68_P31746196	chr18:59334709-59334753	NM_001081328:-263	Chsy3	PROMOTER	0.639	0.574	2107.12	1208.92	0.366	1680.18	615.52
A_68_P21087493	chr2:27741935-27741979	NM_015734:12	Col5a1	INSIDE	0.639	0.633	1692.94	1071.61	0.405	1321.68	534.64
A_68_P27281160	chr10:79594459-79594503	NM_001195268:5652	Dos	INSIDE	0.639	0.649	1352.83	877.60	0.414	1025.43	424.80
A_68_P26543335	chr9:57556330-57556374	NM_153799:-23	Edc3	PROMOTER	0.639	0.622	1894.48	1178.32	0.398	1420.47	564.74
A_68_P31493012	chr18:11048533-11048577	NM_010258:-3953	Gata6	PROMOTER	0.639	0.605	1283.71	777.13	0.387	1095.99	423.72
A_68_P23329327	chr4:135129537-135129581	NM_001013756:-23	Grhl3	PROMOTER	0.639	0.499	1064.11	531.15	0.319	890.80	283.90
A_68_P30367930	chr15:79521605-79521649	NM_013818:301	Gtpbp1	INSIDE	0.639	0.354	2153.79	762.88	0.226	1851.95	418.93
A_68_P25528244	chr7:138553556-138553600	NM_175115:414	Ikzf5	INSIDE	0.639	0.435	1298.19	564.92	0.278	1130.82	314.23
A_68_P20935802	chr1:192850220-192850264	NM_001081259:-173	Mfsd7b	PROMOTER	0.639	0.549	952.00	523.08	0.351	736.89	258.77
A_68_P30364397	chr15:78940024-78940068	NM_177461:634	Micall1	INSIDE	0.639	0.394	1481.73	584.52	0.252	1163.41	293.34
A_68_P30961694	chr16:91226413-91226457	NM_016967:640	Olig2	INSIDE	0.639	0.545	2814.15	1535.09	0.349	2091.87	729.27
A_68_P21839349	chr2:167906063-167906107	NM_021409:-419	Pard6b	PROMOTER	0.639	0.437	1735.05	758.43	0.280	1323.04	369.83
A_68_P21322065	chr2:71710952-71710996	NM_172665:-354	Pdk1	PROMOTER	0.639	0.668	901.20	601.73	0.427	682.81	291.47
A_68_P23649331	chr5:44491778-44491823	NM_001163584:-5793	Prom1	PROMOTER	0.639	0.449	2239.47	1004.57	0.286	1784.79	511.32
A_68_P31196983	chr17:44871711-44871755	NM_001145920:1865	Runx2	INSIDE	0.639	0.512	1047.42	536.45	0.327	806.88	264.25
A_68_P25588799	chr7:148623331-148623375	NM_001177576:-2859	Slc25a22	PROMOTER	0.639	0.564	2863.01	1613.45	0.360	2015.33	725.84
A_68_P31160312	chr17:35804249-35804293	NM_175137:267	Vars2	INSIDE	0.639	0.659	2132.19	1404.93	0.421	1507.83	635.08
A_68_P25947576	chr8:72149308-72149352	NM_001045553:-256	Zfp868	PROMOTER	0.639	0.748	3835.41	2867.80	0.478	3162.71	1511.47
A_68_P31111771	chr17:26813342-26813386	NM_025272:24	Atp6v0e	INSIDE	0.638	0.477	1213.59	578.99	0.304	925.51	281.80
A_68_P32111334	chr19:40906541-40906585	NM_172839:794	Ccnj	INSIDE	0.638	0.367	1696.24	621.81	0.234	1386.38	324.13
A_68_P32053973	chr19:29700840-29700884	NM_001081213:22048	Ermp1	INSIDE	0.638	3.951	5484.76	21669.41	2.521	4005.10	10097.35
A_68_P24423937	chr6:47544969-47545013	NM_001146689:39	Ezh2	INSIDE	0.638	0.644	1090.33	701.77	0.410	976.73	400.80
A_68_P25828172	chr8:46136729-46136773	NM_001081286:101189	Fat1	INSIDE	0.638	2.472	3628.42	8967.89	1.576	2402.99	3787.61
A_68_P26520288	chr9:53192430-53192474	NM_212445:325	Kdelc2	INSIDE	0.638	0.632	1068.40	675.49	0.404	857.41	346.03
A_68_P31113145	chr17:27054067-27054111	NM_053173:53	Kifc5b	INSIDE	0.638	0.565	1547.45	873.86	0.360	1163.83	419.41
A_68_P27282836	chr10:79844946-79844990	NM_198615:5428	Mex3d	INSIDE	0.638	2.635	587.52	1547.81	1.682	514.30	864.85
A_68_P22083009	chr3:40887619-40887663	NM_027558:-672	Pgrmc2	PROMOTER	0.638	0.606	1226.19	743.43	0.387	1036.50	400.86
A_68_P22558738	chr3:136332932-136332976	NM_008913:-779	Ppp3ca	PROMOTER	0.638	0.400	1495.87	597.87	0.255	1261.42	321.47
A_68_P30572149	chr16:17132425-17132469	NM_022324:30	Sdf2l1	INSIDE	0.638	0.561	2784.40	1561.61	0.358	2256.50	807.17
A_68_P28038653	chr11:95275248-95275292	NM_025287:-126	Spop	PROMOTER	0.638	2.705	2310.60	6250.27	1.726	1571.40	2712.43
A_68_P24543641	chr6:72739120-72739164	NM_001079822:-192	Tcf7l1	PROMOTER	0.638	0.497	3199.68	1591.50	0.317	2630.69	834.83
A_68_P24130232	chr5:138883088-138883132	NM_028130:407	Zfp157	INSIDE	0.638	0.559	1125.68	628.75	0.356	895.87	319.00
A_68_P20262082	chr1:59176751-59176795	NM_001037812:-122	Als2cr4	PROMOTER	0.637	0.626	1856.35	1162.14	0.399	1222.12	487.50
A_68_P28524149	chr12:72170902-72170957	NM_001081195:53976	Arid4a	INSIDE	0.637	3.138	1242.63	3899.38	1.997	930.82	1859.19
A_68_P28072388	chr11:101035404-101035448	NM_007721:1331	Ccr10	INSIDE	0.637	0.568	1405.57	798.95	0.362	1007.15	364.74
A_68_P27191665	chr10:63046368-63046418	NM_001164376:126134	Ctnna3	INSIDE	0.637	2.627	760.18	1996.91	1.674	593.57	993.89

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25776088	chr8:35871210-35871254	NM_176933:569	Dusp4	INSIDE	0.637	0.602	2469.37	1486.92	0.384	1867.02	716.31
A_68_P24586428	chr6:81991724-81991768	NM_145570:125	Fam176a	INSIDE	0.637	0.633	1449.43	917.63	0.403	1219.75	491.76
A_68_P32016080	chr19:23215457-23215501	NM_010638:-237	Klf9	PROMOTER	0.637	0.486	1225.61	595.08	0.309	1048.53	324.25
A_68_P28587835	chr12:83718196-83718240	NM_015812:194	Rgs6	INSIDE	0.637	0.584	1606.29	937.43	0.372	1389.97	517.07
A_68_P20233542	chr1:53841734-53841778	NM_133810:303	Stk17b	INSIDE	0.637	0.424	1870.82	793.03	0.270	1607.60	433.96
A_68_P27340413	chr10:90634459-90634503	NM_001080129:-153	Tmpo	PROMOTER	0.637	0.532	1631.07	868.20	0.339	1314.71	445.66
A_68_P20826009	chr1:173003701-173003745	ENSMUST00000164179:-8656		PROMOTER	0.637	0.635	6207.37	3943.81	0.405	5287.46	2141.38
A_68_P20596874	chr1:129670673-129670717	NM_028399:-46	Ccnt2	PROMOTER	0.636	0.622	2718.22	1689.58	0.395	2117.80	837.57
A_68_P32097099	chr19:37772682-37772726	NM_007811:407	Cyp26a1	INSIDE	0.636	0.685	1552.26	1062.66	0.436	1380.23	601.39
A_68_P23936294	chr5:102088064-102088108	NM_144955:5644	Nkx6-1	DOWNSTREAM	0.636	0.667	1836.63	1225.65	0.424	1509.94	640.58
A_68_P22310058	chr3:87598739-87598783	NM_001033124:324	Ntrk1	INSIDE	0.636	0.691	2699.07	1863.82	0.439	2215.10	972.96
A_68_P22488132	chr3:123150107-123150151	NM_008939:298	Prss12	INSIDE	0.636	0.483	1826.65	883.10	0.307	1507.45	463.51
A_68_P25362155	chr7:106631960-106632004	NR_002172:-540	Snord15a	PROMOTER	0.636	0.445	1544.64	686.94	0.283	1260.32	356.51
A_68_P28974246	chr13:40833476-40833520	NM_011547:-4306	Tcfap2a	PROMOTER	0.636	0.687	1336.42	917.93	0.437	1185.03	517.86
A_68_P27286219	chr10:80363610-80363656	NM_013895:82	Timm13	INSIDE	0.636	0.464	1142.84	529.86	0.295	897.89	264.69
A_68_P26247733	chr8:127317798-127317842	NM_198632:902	Trim67	INSIDE	0.636	0.644	2690.72	1732.42	0.409	2128.66	871.68
A_68_P23409803	chr4:150432014-150432058	NM_009498:26	Vamp3	INSIDE	0.636	0.349	1524.16	532.27	0.222	1315.57	292.32
A_68_P29220644	chr13:91947270-91947314	NM_145453:9	Zcchc9	INSIDE	0.636	0.501	1717.52	860.32	0.319	1415.02	450.99
A_68_P31113295	chr17:27076389-27076433	NM_026307:3	Cuta	INSIDE	0.635	0.361	1600.29	578.07	0.229	1269.62	291.24
A_68_P21570230	chr2:119372732-119372776	NM_172857:609	Exd1	INSIDE	0.635	0.549	1903.16	1044.28	0.349	1615.08	563.12
A_68_P21073096	chr2:25433798-25433842	NM_001005424:1799	Gm996	INSIDE	0.635	0.678	1034.05	701.41	0.431	814.96	351.21
A_68_P24156244	chr5:144131752-144131796	NM_133355:6188	Grid2ip	INSIDE	0.635	0.524	1618.60	848.49	0.333	1291.53	429.81
A_68_P29725079	chr14:75347435-75347479	NM_001033439:228	Lrch1	INSIDE	0.635	0.681	2126.09	1447.08	0.432	1683.23	727.52
A_68_P29681981	chr14:67529271-67529315	NM_175498:-752	Pnma2	PROMOTER	0.635	0.474	1667.09	790.64	0.301	1256.84	378.67
A_68_P27506870	chr10:121484975-121485019	NM_001081037:-747	Srgap1	PROMOTER	0.635	0.710	1308.03	929.24	0.451	1135.09	512.18
A_68_P26013519	chr8:85689979-85690023	NM_001111304:750	Tbc1d9	INSIDE	0.635	0.650	1327.87	862.60	0.413	1162.47	479.86
A_68_P26706400	chr9:87625023-87625067	NM_023814:1051	Tbx18	INSIDE	0.635	0.436	1733.04	755.80	0.277	1521.64	421.40
A_68_P26721507	chr9:91259790-91259834	NM_009573:825	Zic1	INSIDE	0.635	0.461	1301.45	600.40	0.293	1053.38	308.39
A_68_P25509657	chr7:135381773-135381817	NM_177001:-249	9130023H24Rik	PROMOTER	0.634	0.692	2857.26	1976.81	0.439	2169.56	952.30
A_68_P32186060	chr19:54121227-54121271	NM_007417:1577	Adra2a	INSIDE	0.634	0.689	1199.32	826.91	0.437	916.79	400.61
A_68_P29050149	chr13:54676413-54676457	NM_019968:61	Arl10	INSIDE	0.634	0.544	2082.33	1132.56	0.345	1714.75	591.28
A_68_P20786425	chr1:165924761-165924805	NM_201364:130	BC055324	INSIDE	0.634	0.637	5119.83	3263.62	0.404	3884.09	1570.60
A_68_P27894658	chr11:69182004-69182048	NM_146019:902	Chd3	INSIDE	0.634	0.650	2150.42	1398.55	0.413	1538.82	634.86
A_68_P24775469	chr6:116158491-116158535	NM_026585:462	D6Wsu116e	INSIDE	0.634	0.541	1295.52	700.46	0.343	1087.33	372.83
A_68_P21762934	chr2:154718701-154718745	NM_026030:-80	Eif2s2	PROMOTER	0.634	0.632	983.75	622.14	0.401	747.45	299.69
A_68_P26893205	chr9:123022399-123022443	NM_001081188:72	Exosc7	INSIDE	0.634	0.444	1766.43	783.61	0.281	1468.20	413.17
A_68_P23451685	chr5:4757093-4757137	NM_021457:1102	Fzd1	INSIDE	0.634	0.616	1047.22	644.60	0.390	825.75	322.38
A_68_P21609431	chr2:126501251-126501295	NM_207669:-49	Gabpb1	PROMOTER	0.634	0.630	2080.23	1309.89	0.399	1921.36	767.08
A_68_P25462321	chr7:126328077-126328121	NM_001024138:-210	Gpr139	PROMOTER	0.634	0.569	1096.54	623.49	0.360	757.26	272.78
A_68_P21536546	chr2:113597904-113597948	NM_011824:879	Grem1	INSIDE	0.634	0.527	1857.10	978.87	0.334	1209.25	404.16
A_68_P24589797	chr6:82723544-82723588	NM_013820:882	Hk2	INSIDE	0.634	0.700	1367.97	957.22	0.443	1086.57	481.83
A_68_P24431635	chr6:49168267-49168311	NM_023670:-3335	Igf2bp3	PROMOTER	0.634	0.694	1529.37	1061.34	0.440	1187.27	522.47
A_68_P26815429	chr9:108462952-108462996	NM_011830:143	Impdh2	INSIDE	0.634	0.703	3132.35	2201.00	0.446	2559.36	1140.39
A_68_P24360135	chr6:35127937-35127981	NM_027513:343	Nup205	INSIDE	0.634	0.579	1249.82	724.04	0.368	1063.37	390.85
A_68_P26554372	chr9:59464905-59464949	NM_001205239:-164	Parp6	PROMOTER	0.634	0.673	1353.16	910.63	0.427	1197.47	510.94
A_68_P28160473	chr11:116485490-116485534	NM_001167680:54	Rhbdf2	INSIDE	0.634	0.579	1372.87	794.50	0.367	1102.26	404.22
A_68_P22957030	chr4:59562123-59562167	NM_144904:92	Rod1	INSIDE	0.634	0.596	2044.82	1218.47	0.378	1536.07	579.98
A_68_P20022705	chr1:9535306-9535350	NM_021511:-160	Rrs1	PROMOTER	0.634	0.525	1044.51	548.22	0.333	846.96	281.96
A_68_P24974126	chr7:13595184-13595228	NM_001024699:-57	Zbtb45	PROMOTER	0.634	0.606	1005.90	609.91	0.384	753.09	289.51
A_68_P23339578	chr4:136944088-136944132	ENSMUST00000078305:-7097		PROMOTER	0.634	0.617	1364.89	841.92	0.391	1110.30	433.94
A_68_P27928205	chr11:75608766-75608811	NM_007873:771	Doc2b	INSIDE	0.633	0.689	1849.08	1273.82	0.436	1455.04	634.03

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P30497455	chr15:102189021-102189065	NM_130458:7660	Sp7	INSIDE	0.633	0.631	899.42	567.58	0.399	732.98	292.80
A_68_P25195709	chr7:74904507-74904551	NM_183312:100	Synm	INSIDE	0.633	0.428	3143.10	1344.47	0.271	2529.27	684.46
A_68_P24053752	chr5:123526651-123526695	NM_001039723:389	Tmem120b	INSIDE	0.633	0.294	1826.77	537.00	0.186	1374.88	255.77
A_68_P20893085	chr1:185857220-185857264	NM_028516:635	1700056E22Rik	INSIDE	0.632	0.641	1625.01	1041.74	0.405	1221.15	494.90
A_68_P24464807	chr6:54632035-54632079	NM_026629:291	2410066E13Rik	INSIDE	0.632	0.590	1040.73	613.55	0.373	893.50	333.04
A_68_P25655856	chr8:11497567-11497611	NM_026995:21	Carkd	INSIDE	0.632	0.426	1901.22	809.80	0.269	1558.69	419.41
A_68_P24791601	chr6:119125187-119125231	NM_001033379:-62	Dcp1b	PROMOTER	0.632	0.555	1294.89	718.25	0.351	1091.87	382.79
A_68_P31928718	chr19:5447671-5447715	NM_010235:-5	Fosl1	PROMOTER	0.632	0.622	1066.72	663.68	0.393	950.71	373.71
A_68_P26228651	chr8:124276830-124276874	NM_020605:22394	Jph3	INSIDE	0.632	4.407	713.02	3142.37	2.786	541.11	1507.67
A_68_P25507196	chr7:134913351-134913395	NM_198424:44	Orai3	INSIDE	0.632	0.601	964.23	579.78	0.380	772.09	293.24
A_68_P20611336	chr1:132612197-132612241	NM_001162416:-1065	Pfkfb2	PROMOTER	0.632	0.719	1983.00	1426.16	0.454	1578.71	717.52
A_68_P24604963	chr6:85382060-85382104	NM_144918:113	Smyd5	INSIDE	0.632	0.612	1158.73	708.80	0.387	828.46	320.23
A_68_P23062262	chr4:83063627-83063671	NM_029949:1	Snapc3	INSIDE	0.632	0.477	1983.02	945.11	0.301	1568.90	472.77
A_68_P20304765	chr1:66863691-66863735	NM_001122738:457	1110028C15Rik	INSIDE	0.631	0.632	979.39	619.21	0.399	800.69	319.66
A_68_P31849681	chr18:78012952-78012997	NM_007505:468	Atp5a1	INSIDE	0.631	0.550	2082.15	1144.89	0.347	1835.81	636.47
A_68_P21572764	chr2:119853205-119853250	NM_001114637:9	Jmjd7	INSIDE	0.631	0.580	1744.85	1011.54	0.366	1471.50	538.00
A_68_P24660675	chr6:95067758-95067802	NM_001008785:-119	Kbtbd8	PROMOTER	0.631	0.493	1453.92	716.41	0.311	1223.34	380.35
A_68_P20593981	chr1:129102201-129102245	NM_145128:660	Mgat5	INSIDE	0.631	0.377	2212.75	834.77	0.238	1756.59	417.87
A_68_P32143106	chr19:46383535-46383579	NM_001177370:3137	Nfkb2	INSIDE	0.631	0.567	1753.43	994.37	0.358	1356.57	485.49
A_68_P25500411	chr7:133572604-133572648	NM_030566:346	Rabep2	INSIDE	0.631	0.375	1911.48	716.57	0.236	1552.20	367.06
A_68_P29448256	chr14:21493458-21493502	NM_001168273:-62	Sec24c	DIVERGENT_PROMOTER	0.631	0.497	1200.16	596.51	0.313	1039.54	325.78
A_68_P30964217	chr16:91660217-91660261	NM_019973:12170	Son	INSIDE	0.631	2.702	598.42	1617.13	1.705	534.39	910.91
A_68_P29286848	chr13:104564132-104564176	NM_172592:-9492	Srek1	PROMOTER	0.631	0.560	1868.39	1046.08	0.354	1663.54	588.15
A_68_P24037873	chr5:120752578-120752622			Unknown	0.631	0.565	1554.68	878.25	0.356	1259.76	448.82
A_68_P28753095	chr12:114115760-114115804	AK018992:-1757		PROMOTER	0.631	0.695	1249.18	868.25	0.439	1053.27	462.24
A_68_P23542801	chr5:24083043-24083087	NM_001190443:221	Abcf2	INSIDE	0.630	0.639	2154.11	1376.27	0.403	1492.52	601.00
A_68_P20429508	chr1:91351074-91351118	NM_001037136:-289	Agap1	PROMOTER	0.630	0.599	1031.65	617.65	0.377	954.07	359.59
A_68_P31541309	chr18:20904102-20904146	NM_019737:781	B4galt6	INSIDE	0.630	0.559	3266.39	1827.17	0.352	2408.73	848.99
A_68_P24990312	chr7:19477759-19477803	NM_001033314:17973	Ccdc61	INSIDE	0.630	0.421	1511.52	636.40	0.265	1289.45	341.99
A_68_P23342966	chr4:137514008-137514052	NM_199307:95879	Ece1	INSIDE	0.630	3.308	2803.57	9274.59	2.085	2035.51	4243.58
A_68_P26058236	chr8:93837616-93837660	NM_011936:215	Fto	INSIDE	0.630	0.579	1268.19	734.29	0.365	940.46	343.04
A_68_P25736445	chr8:28195931-28195975	NM_054044:-360	Gpr124	PROMOTER	0.630	0.559	1132.18	633.02	0.352	1019.07	359.21
A_68_P24008165	chr5:115608256-115608300	NM_175403:-93	Mlec	PROMOTER	0.630	0.384	2003.34	770.11	0.242	1630.56	395.04
A_68_P26985108	chr10:19868390-19868434	NM_001198635:-313	Mtap7	PROMOTER	0.630	0.627	960.34	601.97	0.395	830.65	328.19
A_68_P24819298	chr6:125141713-125141757	NM_146171:-130	Ncapd2	DIVERGENT_PROMOTER	0.630	0.547	1865.58	1021.21	0.345	1373.52	473.75
A_68_P22393113	chr3:104584603-104584647	NM_027982:651	Ppm1j	INSIDE	0.630	0.655	1650.21	1080.34	0.413	1328.57	548.04
A_68_P23440513	chr4:155144647-155144691	NM_147776:4002	Vwa1	INSIDE	0.630	0.560	1129.99	633.04	0.353	937.60	331.16
A_68_P25416834	chr7:118199064-118199108	NM_009431:26622	Ctr9	INSIDE	0.629	2.955	630.19	1862.12	1.860	559.19	1040.14
A_68_P24218731	chr6:6813573-6813617	NM_010057:261	Dlx6	INSIDE	0.629	0.518	3828.75	1984.03	0.326	3140.88	1023.77
A_68_P31929504	chr19:5568132-5568176	NM_001033448:81	Gm962	INSIDE	0.629	0.497	1629.72	810.65	0.313	1261.36	394.82
A_68_P27279739	chr10:79384461-79384505	NM_053244:4767	Kiss1r	INSIDE	0.629	0.411	1414.74	581.63	0.259	1146.57	296.50
A_68_P27536901	chr10:127030734-127030787	NM_008512:27444	Lrp1	INSIDE	0.629	2.985	1284.50	3833.85	1.877	943.04	1770.01
A_68_P31143941	chr17:32280371-32280415	NM_008716:23405	Notch3	INSIDE	0.629	0.633	1371.65	868.42	0.398	1249.43	497.62
A_68_P25957205	chr8:74031894-74031938	NM_032398:3752	Plvap	INSIDE	0.629	0.623	2304.19	1436.26	0.392	1844.09	722.71
A_68_P31205623	chr17:46339517-46339561	NM_030715:36	Polh	INSIDE	0.629	0.670	2337.58	1565.75	0.421	1891.15	797.00
A_68_P29507007	chr14:31438823-31438867	NM_011103:550	Prkcd	INSIDE	0.629	2.446	6147.13	15036.60	1.538	3438.11	5286.19
A_68_P21138067	chr2:35992191-35992235	NM_001159635:12	Rbm18	INSIDE	0.629	0.469	1495.94	701.46	0.295	1171.16	345.47
A_68_P29605238	chr14:52817188-52817232	NM_033618:-296	Supt16h	PROMOTER	0.629	0.713	1878.41	1339.91	0.449	1684.43	755.82
A_68_P28087055	chr11:103635334-103635379	NM_009521:-132	Wnt3	PROMOTER	0.629	0.568	1040.45	590.64	0.357	884.95	316.13
A_68_P26600191	chr9:67481194-67481238			Unknown	0.629	0.539	1794.58	968.01	0.339	1576.75	534.87
A_68_P23005994	chr4:70071277-70071321	NM_145990:103	Cdk5rap2	INSIDE	0.628	0.572	1910.35	1093.22	0.360	1466.55	527.45

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P24167577	chr5:147072524-147072578	NM_153599:29300	Cdk8	INSIDE	0.628	3.728	301.16	1122.79	2.340	284.14	664.76
A_68_P24141811	chr5:141000117-141000161	NM_021528:18576	Chst12	INSIDE	0.628	3.118	3628.19	11313.18	1.960	2600.06	5095.03
A_68_P25951442	chr8:72899053-72899099	NM_016685:1630	Comp	INSIDE	0.628	0.579	2072.65	1200.28	0.364	1575.08	572.82
A_68_P20157022	chr1:38055055-38055099	NM_198303:222	Eif5b	INSIDE	0.628	0.707	1327.07	938.31	0.444	1144.07	508.22
A_68_P32117376	chr19:41904363-41904407	NM_008043:-75	Frat1	PROMOTER	0.628	0.617	1990.52	1228.56	0.387	1661.84	643.79
A_68_P28158434	chr11:116142875-116142919	NM_010254:644	Galr2	INSIDE	0.628	0.435	1715.76	745.91	0.273	1323.62	361.38
A_68_P27565570	chr11:5802331-5802375	NM_010292:47250	Gck	INSIDE	0.628	0.650	837.86	544.37	0.408	744.34	303.83
A_68_P21338645	chr2:74506594-74506638	NM_008275:250	Hoxd13	INSIDE	0.628	0.617	3313.08	2045.71	0.388	2518.88	976.32
A_68_P26228499	chr8:124254393-124254437	NM_020605:-44	Jph3	PROMOTER	0.628	3.411	9864.62	33653.00	2.144	8324.80	17848.18
A_68_P23527432	chr5:21207260-21207304	NM_178728:-119	Napepld	PROMOTER	0.628	0.666	3288.87	2189.42	0.418	2663.73	1112.75
A_68_P24059409	chr5:124571234-124571278	NM_011256:95171	Pitpnm2	INSIDE	0.628	3.626	631.12	2288.74	2.276	551.76	1255.76
A_68_P24834768	chr6:127718939-127718983	NM_201371:-213	Prmt8	PROMOTER	0.628	0.541	1630.42	881.85	0.340	1227.04	416.85
A_68_P23294682	chr4:128735948-128735992	NM_029219:456	Rnf19b	INSIDE	0.628	0.564	3204.02	1808.51	0.355	2596.62	920.73
A_68_P24591261	chr6:83021489-83021533	NM_009392:-1291	Tlx2	DIVERGENT_PROMOTER	0.628	0.418	1760.59	735.92	0.262	1491.91	391.43
A_68_P26084569	chr8:98201452-98201496	ENSMUST00000041318:-510		PROMOTER	0.628	0.369	2092.09	771.70	0.232	1604.27	371.74
A_68_P31776698	chr18:64819777-64819821	NM_001001488:856	Atp8b1	INSIDE	0.627	2.636	1212.06	3194.80	1.652	1067.03	1762.54
A_68_P30348812	chr15:76342113-76342157	NM_010046:114	Dgat1	INSIDE	0.627	0.689	2411.73	1660.52	0.432	1886.27	814.94
A_68_P22481535	chr3:121977658-121977702	NM_153806:349	Dnttip2	INSIDE	0.627	0.644	2361.54	1521.84	0.404	1831.98	740.02
A_68_P24603562	chr6:85138183-85138227	NM_010131:280	Emx1	INSIDE	0.627	0.674	1104.60	744.62	0.423	943.13	398.48
A_68_P24002948	chr5:114724032-114724076	NM_148935:-284	Foxn4	PROMOTER	0.627	0.538	1086.21	584.61	0.338	861.39	290.73
A_68_P25953468	chr8:73223214-73223258	NM_010592:1599	Jund	INSIDE	0.627	0.512	1154.87	591.68	0.321	776.61	249.48
A_68_P25174079	chr7:71036675-71036719	NM_021366:47105	Klf13	INSIDE	0.627	2.450	789.09	1933.59	1.537	659.13	1013.13
A_68_P23006658	chr4:70196288-70196332	NM_172694:-348	Megf9	PROMOTER	0.627	0.437	1205.86	527.14	0.274	1004.73	275.61
A_68_P24610519	chr6:86475835-86475879	NM_011865:303	Pcbp1	INSIDE	0.627	0.549	1089.32	598.13	0.344	781.72	268.95
A_68_P30496839	chr15:102077744-102077788	NM_001042727:-983	Rarg	PROMOTER	0.627	0.484	1077.53	522.05	0.304	882.94	268.37
A_68_P25262216	chr7:86762430-86762474	NM_019799:91	Rhcg	INSIDE	0.627	0.550	1137.87	626.33	0.345	872.04	301.05
A_68_P26344895	chr9:20780976-20781020	NM_010333:239	S1pr2	INSIDE	0.627	0.379	1860.91	705.48	0.238	1518.23	360.79
A_68_P25100828	chr7:53965985-53966029	NM_030233:15	Saal1	INSIDE	0.627	0.632	1392.36	880.50	0.396	1171.80	464.41
A_68_P31868115	chr18:81184119-81184163	NM_178280:-823	Sall3	PROMOTER	0.627	0.600	2579.41	1548.67	0.377	2060.63	776.29
A_68_P25023458	chr7:29551865-29551909	NM_001122765:116	Sirt2	INSIDE	0.627	0.640	1524.09	974.95	0.401	1180.08	473.61
A_68_P29211818	chr13:90229540-90229584	NM_025335:291	Tmem167	INSIDE	0.627	0.577	1913.81	1104.10	0.362	1438.59	520.70
A_68_P24007965	chr5:115577169-115577225	NM_175352:7788	Unc119b	INSIDE	0.627	3.482	399.10	1389.78	2.182	342.83	748.07
A_68_P28153350	chr11:115274720-115274764	NM_027862:6491	Atp5h	DOWNSTREAM	0.626	0.324	1681.50	544.65	0.203	1313.19	266.33
A_68_P30532560	chr16:8424805-8424849	NM_029070:403	Cldn26	INSIDE	0.626	0.568	1407.49	799.30	0.356	1205.20	428.55
A_68_P22998988	chr4:68615056-68615100	NM_019967:353	Dbc1	INSIDE	0.626	0.560	1044.33	584.64	0.351	699.53	245.32
A_68_P26249220	chr8:127578421-127578465	NM_174853:348	Disc1	INSIDE	0.626	0.636	1507.71	959.49	0.398	1281.30	510.18
A_68_P29651453	chr14:62308585-62308640	NR_028264:-7402	Dleu2	PROMOTER	0.626	0.658	1112.26	731.90	0.412	960.19	395.76
A_68_P29582178	chr14:48037787-48037833	NM_144553:272	Dlgap5	INSIDE	0.626	0.587	1015.43	596.15	0.368	726.20	266.99
A_68_P23970975	chr5:108698202-108698246	NM_026106:309	Dr1	INSIDE	0.626	0.692	1479.65	1023.38	0.433	1373.15	594.14
A_68_P27479719	chr10:116584876-116584920	NM_177798:632	Frs2	INSIDE	0.626	0.734	2670.68	1961.34	0.460	1711.13	786.38
A_68_P29073062	chr13:58503740-58503784	NM_025279:115	Hnrnpk	INSIDE	0.626	0.613	898.64	550.43	0.384	755.18	289.67
A_68_P21203200	chr2:49474749-49474793	NM_008449:-63	Kif5c	PROMOTER	0.626	0.582	1030.88	599.73	0.364	858.34	312.44
A_68_P21817648	chr2:164230100-164230144	NM_013592:-8	Matn4	PROMOTER	0.626	0.426	1891.65	806.02	0.267	1543.94	412.07
A_68_P31629954	chr18:37927868-37927912	NM_033595:2657	Pcdhga12	INSIDE	0.626	2.467	799.41	1972.00	1.544	724.94	1119.06
A_68_P22386744	chr3:103379702-103379746	NM_018800:521	Syt6	INSIDE	0.626	0.631	840.40	530.69	0.395	752.89	297.67
A_68_P22342447	chr3:94944410-94944458	NM_027206:1848	Tnfaip8l2	INSIDE	0.626	5.217	2252.92	11753.35	3.264	1502.71	4904.67
A_68_P31102171	chr17:25325763-25325807	NM_001197024:440	Unkl	INSIDE	0.626	0.446	1153.78	514.61	0.279	1027.76	287.03
A_68_P22970353	chr4:63077625-63077669	NM_001008797:16710	Whrn	INSIDE	0.626	2.656	3032.62	8053.90	1.661	2170.31	3605.79
A_68_P31615278	chr18:35047273-35047317			Unknown	0.626	0.587	1840.24	1079.92	0.367	1573.37	577.90
A_68_P24183981	chr5:150040843-150040887	AK155259:18394		DOWNSTREAM	0.626	0.656	1546.10	1013.86	0.411	1369.89	562.72
A_68_P24172796	chr5:148086210-148086254	NR_038157:-3135	2210019I11Rik	PROMOTER	0.625	0.522	1982.01	1035.05	0.326	1761.65	575.12

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31114504	chr17:27270575-27270620	NM_026063:239	2900010M23Rik	INSIDE	0.625	0.666	2784.56	1854.97	0.416	2154.48	896.31
A_68_P22149462	chr3:54539562-54539606	NM_025442:124	Alg5	INSIDE	0.625	0.553	1629.65	901.92	0.346	1252.56	432.93
A_68_P23345849	chr4:138011542-138011586	NM_025451:502	Camk2n1	INSIDE	0.625	0.631	1900.64	1199.08	0.394	1338.71	528.10
A_68_P27284472	chr10:80097247-80097291	NM_001159591:4868	Csnk1g2	INSIDE	0.625	2.677	2810.08	7522.39	1.673	1993.33	3334.83
A_68_P29110676	chr13:68721046-68721090	NM_027123:-56	Fastkd3	DIVERGENT_PROMOTER	0.625	0.626	2254.47	1411.85	0.391	1937.62	758.54
A_68_P23968440	chr5:108154062-108154106	NM_010278:-721	Gfi1	PROMOTER	0.625	0.488	1271.79	620.83	0.305	1042.16	317.71
A_68_P22405342	chr3:107082078-107082122	NM_026774:325	Hbxip	INSIDE	0.625	0.467	1942.45	907.77	0.292	1409.57	411.88
A_68_P29581906	chr14:47993698-47993742	NM_001145953:186	Lgals3	INSIDE	0.625	0.638	1990.11	1270.59	0.399	1817.17	725.14
A_68_P22289190	chr3:83959655-83959699	NM_029797:32	Mnd1	INSIDE	0.625	0.562	2696.81	1514.78	0.351	2103.73	738.87
A_68_P30132613	chr15:35225986-35226030	NM_054049:142	Osr2	INSIDE	0.625	0.547	1390.27	760.71	0.342	1015.68	347.19
A_68_P28291148	chr12:25393461-25393505	NM_009104:364	Rrm2	INSIDE	0.625	0.701	1467.99	1029.07	0.438	1087.94	476.86
A_68_P27804859	chr11:53270871-53270915	NM_027917:186	Shroom1	INSIDE	0.625	0.380	1868.92	710.80	0.238	1462.56	347.79
A_68_P30485728	chr15:100253426-100253470	NM_008732:38	Slc11a2	INSIDE	0.625	0.409	2542.12	1039.85	0.256	2195.62	561.25
A_68_P30342961	chr15:75447233-75447277	NM_001044718:140	Zfp41	INSIDE	0.625	0.412	1561.99	644.23	0.258	1111.18	286.26
A_68_P25007553	chr7:25740497-25740541			Unknown	0.625	0.352	1919.09	675.28	0.220	1598.64	351.47
A_68_P25438698	chr7:122071148-122071192	ENSMUST00000059737:70		INSIDE	0.625	2.853	1220.64	3482.95	1.784	995.47	1775.99
A_68_P23331981	chr4:135637926-135637970	ENSMUST00000121307:-7061		PROMOTER	0.625	0.477	2704.07	1289.31	0.298	2176.79	649.00
A_68_P27317703	chr10:86521047-86521091	NM_029685:278	1700113H08Rik	INSIDE	0.624	0.575	1156.61	665.29	0.359	870.51	312.44
A_68_P27282039	chr10:79723618-79723662	NM_010255:73	Gamt	INSIDE	0.624	0.614	1077.94	662.22	0.383	887.24	339.90
A_68_P25504680	chr7:134376542-134376586	NR_030674:80	Gm4532	INSIDE	0.624	0.614	1378.69	846.77	0.383	1128.24	432.07
A_68_P26458695	chr9:42752086-42752130	NM_175481:346	Grik4	INSIDE	0.624	3.936	10800.17	42505.35	2.454	6227.14	15282.22
A_68_P25279939	chr7:90014474-90014518	NM_175366:-1346	Mex3b	PROMOTER	0.624	0.515	3217.05	1657.68	0.322	2574.17	827.85
A_68_P26068080	chr8:95351388-95351432	NM_008610:184	Mmp2	INSIDE	0.624	0.530	1233.21	653.13	0.330	971.02	320.76
A_68_P20795497	chr1:167564136-167564180	NM_001001880:514	Mpzl1	INSIDE	0.624	0.675	1095.66	739.84	0.421	918.17	386.86
A_68_P28457446	chr12:57635707-57635751	NM_001146198:365	Nkx2-1	INSIDE	0.624	0.522	1497.94	781.79	0.325	1359.08	442.38
A_68_P30826536	chr16:65815148-65815192	NM_028572:-707	Vgll3	PROMOTER	0.624	0.624	1090.77	680.92	0.390	952.90	371.16
A_68_P30344506	chr15:75672397-75672441	NM_172121:-80	Zc3h3	PROMOTER	0.624	0.469	1120.24	524.92	0.292	858.42	250.86
A_68_P27830258	chr11:58120752-58120796	NM_001040686:204	Zfp692	INSIDE	0.624	0.616	1151.09	708.82	0.384	948.30	364.10
A_68_P27851352	chr11:61770486-61770530	ENSMUST00000136971:197		INSIDE	0.624	0.628	1093.46	686.80	0.392	980.30	384.11
A_68_P26920085	chr10:7382878-7382922	NR_030698:-268	A630066F11Rik	PROMOTER	0.623	0.672	1249.75	840.30	0.419	1076.44	450.76
A_68_P26129050	chr8:107065100-107065144	NM_053070:416	Car7	INSIDE	0.623	0.616	1457.84	898.37	0.384	1326.11	509.07
A_68_P22964275	chr4:62069685-62069729	NM_139291:-49	Cdc26	DIVERGENT_PROMOTER	0.623	0.508	1093.77	555.39	0.316	846.94	268.04
A_68_P30486145	chr15:100325764-100325808	NM_153407:-116	Csrnp2	PROMOTER	0.623	0.631	1488.54	939.42	0.393	1158.38	455.09
A_68_P22398584	chr3:105490057-105490101	NM_017397:411	Ddx20	INSIDE	0.623	0.625	955.34	596.94	0.389	797.36	310.28
A_68_P21905657	chr2:180436282-180436326	NM_175551:501	Dido1	INSIDE	0.623	0.561	2040.66	1144.36	0.349	1441.47	503.53
A_68_P28120310	chr11:109583554-109583598	NM_153782:-6	Fam20a	PROMOTER	0.623	0.464	1323.81	613.60	0.289	1052.51	303.71
A_68_P21059051	chr2:22478980-22479024	NM_008078:1156	Gad2	INSIDE	0.623	0.728	2507.45	1824.41	0.453	1952.96	885.11
A_68_P24620284	chr6:88140062-88140106	NM_008090:-8573	Gata2	PROMOTER	0.623	0.709	1936.62	1372.21	0.441	1468.86	648.11
A_68_P28888886	chr13:24853737-24853781	NM_020567:48	Gmnn	INSIDE	0.623	0.652	3986.32	2598.08	0.406	3025.99	1229.46
A_68_P31116575	chr17:27610002-27610046	NM_001013385:30225	Grm4	INSIDE	0.623	4.118	2069.05	8520.77	2.567	1431.83	3675.22
A_68_P28083512	chr11:102993647-102993691	NM_001130516:-984	Hexim2	PROMOTER	0.623	0.519	1413.27	733.25	0.323	1164.68	376.68
A_68_P27390318	chr10:99478125-99478169	NM_013598:-311	Kitl	PROMOTER	0.623	0.632	1060.59	670.45	0.394	856.22	336.99
A_68_P24929767	chr6:146591034-146591078	NM_025315:-44	Med21	DIVERGENT_PROMOTER	0.623	0.583	1030.87	600.65	0.363	804.04	292.07
A_68_P22582958	chr3:140874353-140874397	NM_008811:945	Pdha2	INSIDE	0.623	2.348	2156.64	5063.04	1.462	1808.41	2643.97
A_68_P21110387	chr2:31495883-31495927	NM_001123362:348	Prdm12	INSIDE	0.623	0.525	1190.86	625.01	0.327	996.20	325.67
A_68_P22411525	chr3:108059789-108059833	NM_011967:-33	Psma5	PROMOTER	0.623	0.488	1245.34	607.81	0.304	1061.12	322.83
A_68_P20927662	chr1:191552465-191552509	NM_008976:340	Ptpn14	INSIDE	0.623	0.503	1091.33	548.52	0.313	858.56	268.81
A_68_P31120667	chr17:28279215-28279259	NM_001004366:-234	Scube3	PROMOTER	0.623	0.574	2709.46	1553.88	0.357	2254.63	804.92
A_68_P28051297	chr11:97413036-97413080	NM_018873:23382	Srcin1	INSIDE	0.623	0.633	817.06	517.33	0.394	635.78	250.71
A_68_P31207576	chr17:46692058-46692102	NM_020493:1031	Srf	INSIDE	0.623	0.725	3690.55	2677.11	0.452	2324.42	1050.17
A_68_P28974165	chr13:40824171-40824219	NM_001122948:1618	Tcfap2a	INSIDE	0.623	0.702	1295.96	909.52	0.437	1130.91	494.40

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P20620972	chr1:134257371-134257415	NM_178874:30466	Tmcc2	INSIDE	0.623	3.221	3614.04	11639.46	2.005	2309.75	4632.10
A_68_P20804420	chr1:169238624-169238668	NM_001039483:-154	Tmco1	PROMOTER	0.623	0.542	1321.98	716.47	0.338	1038.25	350.73
A_68_P23111977	chr4:93002257-93002301	NM_026954:-76	Tusc1	PROMOTER	0.623	0.432	1974.38	853.07	0.269	1522.63	410.16
A_68_P23590585	chr5:34037821-34037865	AK172441:87544		INSIDE	0.623	0.598	1576.61	942.50	0.373	1240.98	462.38
A_68_P21113214	chr2:31939681-31939725	NM_175511:-477	Fam78a	PROMOTER	0.622	0.593	1617.40	959.38	0.369	1278.06	471.64
A_68_P29145567	chr13:74454737-74454781	NM_011051:16	Pdcd6	INSIDE	0.622	0.375	1578.31	592.15	0.233	1210.49	282.42
A_68_P30513991	chr16:5132312-5132356	NM_008909:240	Ppl	INSIDE	0.622	0.653	5131.29	3349.38	0.406	3921.83	1592.24
A_68_P21721814	chr2:146838725-146838769	NM_011917:-49	Xrn2	PROMOTER	0.622	0.549	1238.50	679.61	0.342	930.84	317.94
A_68_P21334161	chr2:73730794-73730838	NM_001025093:-131	Atf2	PROMOTER	0.621	0.592	1565.67	927.41	0.368	1036.41	381.19
A_68_P22393605	chr3:104667362-104667406	NM_009797:39	Capza1	INSIDE	0.621	0.739	2537.34	1875.67	0.459	2024.34	928.75
A_68_P27262972	chr10:76059240-76059284	NM_146007:26887	Col6a2	INSIDE	0.621	2.423	1159.92	2810.02	1.504	990.29	1489.82
A_68_P24816932	chr6:124719430-124719474	NM_013509:75	Eno2	INSIDE	0.621	0.617	3958.17	2442.02	0.383	2813.88	1078.75
A_68_P23795929	chr5:73524595-73524639	NM_028194:123241	Fryl	INSIDE	0.621	2.907	717.25	2084.89	1.804	617.36	1113.74
A_68_P27286342	chr10:80380790-80380834	NM_010722:178	Lmnb2	INSIDE	0.621	0.559	1287.32	720.17	0.347	1064.87	369.65
A_68_P23439841	chr4:155027081-155027125	NM_011985:391	Mmp23	INSIDE	0.621	0.721	3407.25	2456.30	0.448	2512.20	1125.54
A_68_P22129477	chr3:51212635-51212679	NM_025523:221	Ndufc1	INSIDE	0.621	0.612	1563.98	957.33	0.380	1247.67	473.94
A_68_P28265956	chr12:16660397-16660441	NM_008747:143	Ntsr2	INSIDE	0.621	0.465	1150.11	535.29	0.289	961.02	277.93
A_68_P23593807	chr5:34678844-34678888	NM_011278:-172	Rnf4	PROMOTER	0.621	0.616	1394.05	859.07	0.383	1193.81	457.20
A_68_P24176374	chr5:148706152-148706196	NM_027872:204	Slc46a3	INSIDE	0.621	0.561	1055.09	592.00	0.349	888.81	309.76
A_68_P31677780	chr18:46757146-46757190	NM_025698:21	Tmed7	INSIDE	0.621	0.524	1358.72	712.29	0.325	1254.78	408.22
A_68_P32217661	chr19:59241208-59241252	NM_009501:3289	Vax1	INSIDE	0.621	0.630	866.15	545.71	0.391	762.10	298.23
A_68_P29019863	chr13:48608843-48608887	NM_001164576:-59	Zfp169	PROMOTER	0.621	0.678	1016.38	688.98	0.421	884.39	372.36
A_68_P30150545	chr15:38591758-38591802	NM_025494:122	Atp6v1c1	INSIDE	0.620	0.584	1683.06	983.12	0.362	1387.33	502.20
A_68_P28419969	chr12:50486658-50486702	NM_008241:2687	Foxg1	INSIDE	0.620	0.691	2377.01	1642.31	0.428	1716.69	735.02
A_68_P24501230	chr6:63206331-63206375	NM_008167:-498	Grid2	PROMOTER	0.620	0.455	1381.44	628.56	0.282	1105.87	311.82
A_68_P31849647	chr18:78006501-78006545	NM_146089:-3	Haus1	DIVERGENT_PROMOTER	0.620	0.536	1708.20	915.30	0.332	1483.02	493.02
A_68_P24449040	chr6:52154168-52154212	NM_010453:396	Hoxa5	INSIDE	0.620	0.622	3048.81	1897.39	0.386	2375.59	915.95
A_68_P27284101	chr10:80040251-80040295	NM_078477:-231	Klf16	PROMOTER	0.620	0.532	2891.93	1539.90	0.330	2218.23	732.89
A_68_P27500772	chr10:120415468-120415512	NM_001081193:896	Lemd3	INSIDE	0.620	0.574	977.29	561.25	0.356	794.67	282.79
A_68_P32226999	chr19:60832637-60832681	NM_178421:769	Nanos1	INSIDE	0.620	0.686	1576.41	1081.76	0.425	1332.58	566.66
A_68_P27131118	chr10:50615055-50615099	NM_011376:-380	Sim1	PROMOTER	0.620	0.677	1119.43	757.96	0.419	930.01	390.13
A_68_P28957974	chr13:38085985-38086029	NM_025965:53	Ssr1	INSIDE	0.620	0.464	1318.20	611.17	0.287	1236.17	355.27
A_68_P27693350	chr11:33102180-33102224	NM_019916:1386	Tlx3	INSIDE	0.620	2.714	6440.35	17478.25	1.684	4142.87	6974.99
A_68_P31406131	chr17:85075545-85075589	NM_031884:6697	Abcg5	INSIDE	0.619	0.430	1248.70	537.12	0.266	968.77	257.85
A_68_P31599403	chr18:31919740-31919784	NM_153515:229	Ammecr1l	INSIDE	0.619	0.683	1004.46	686.51	0.423	796.59	337.11
A_68_P30371905	chr15:80202995-80203040	NM_001044308:85350	Cacna1i	INSIDE	0.619	6.483	113.92	738.50	4.011	142.16	570.23
A_68_P27495202	chr10:119526727-119526771	NM_080446:23273	Helb	INSIDE	0.619	2.400	1052.84	2526.84	1.486	871.14	1294.48
A_68_P27497203	chr10:119851890-119851938	NM_010441:62077	Hmga2	INSIDE	0.619	3.041	1188.53	3614.42	1.883	922.28	1736.95
A_68_P21345222	chr2:75497220-75497264	NM_053263:-73	Hnrnpa3	PROMOTER	0.619	0.489	1143.12	558.50	0.302	996.67	301.31
A_68_P20240341	chr1:55144942-55144986	NM_008303:-27	Hspe1	DIVERGENT_PROMOTER	0.619	0.470	1872.90	879.42	0.291	1633.71	475.15
A_68_P28041914	chr11:95866847-95866891	NM_009951:390	Igf2bp1	INSIDE	0.619	0.704	1657.30	1166.79	0.436	1324.37	577.04
A_68_P25187998	chr7:73533035-73533079	NM_146191:171	Lrrk1	INSIDE	0.619	0.453	2351.17	1064.01	0.280	2026.61	567.49
A_68_P31556681	chr18:23910710-23910754	NM_001162942:-101	Mapre2	PROMOTER	0.619	0.570	1000.45	570.56	0.353	907.80	320.23
A_68_P27695167	chr11:33413838-33413882	NM_023146:-114	Ranbp17	PROMOTER	0.619	0.547	1762.37	964.25	0.339	1472.20	498.76
A_68_P21612305	chr2:127073731-127073775	NM_175145:42	Tmem127	INSIDE	0.619	0.476	1722.70	819.82	0.295	1265.67	372.99
A_68_P24624900	chr6:88852416-88852460	NM_011906:194	Tpra1	INSIDE	0.619	0.412	1630.70	672.01	0.255	1328.12	338.55
A_68_P25507823	chr7:135019837-135019881	NM_146259:479	Zfp668	INSIDE	0.619	0.639	1201.88	768.49	0.396	966.17	382.61
A_68_P24631971	chr6:90320525-90320569	NM_030260:1059	Zxdc	INSIDE	0.619	0.692	1515.49	1048.08	0.428	1144.78	489.68
A_68_P30351330	chr15:76779157-76779201	NM_054099:205	1110038F14Rik	INSIDE	0.618	0.466	1212.67	565.59	0.288	1047.35	301.82
A_68_P26234306	chr8:125100834-125100878	NM_009698:-49	Aprt	PROMOTER	0.618	2.571	9686.04	24899.64	1.589	6517.89	10354.67
A_68_P27188615	chr10:62411987-62412031	NM_177372:2232	Dna2	INSIDE	0.618	2.596	910.51	2363.28	1.605	760.06	1220.14

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26025443	chr8:88079254-88079298	NM_019794:-106	Dnaja2	PROMOTER	0.618	0.555	1859.01	1031.32	0.343	1720.93	590.43
A_68_P24952006	chr7:5032174-5032218	NM_010147:290	Epn1	INSIDE	0.618	0.674	1203.37	811.37	0.417	1007.89	419.94
A_68_P21221946	chr2:52717355-52717399	NM_172409:475	Fmnl2	INSIDE	0.618	0.490	2710.32	1329.41	0.303	2104.41	638.12
A_68_P25661163	chr8:12385271-12385315	NR_027975:-478	Gm5607	PROMOTER	0.618	0.694	1255.05	870.74	0.429	981.76	420.97
A_68_P24111875	chr5:134660308-134660352	NM_053266:423	Gtf2ird2	INSIDE	0.618	0.494	2700.07	1333.23	0.305	2069.94	631.95
A_68_P26021786	chr8:87295957-87296001	NM_001081981:2290	Nfix	INSIDE	0.618	0.439	1489.51	653.41	0.271	1071.33	290.47
A_68_P20335742	chr1:72301442-72301486	NM_023523:29424	Pecr	DOWNSTREAM	0.618	0.387	2902.68	1123.65	0.239	2134.24	510.80
A_68_P25115500	chr7:57167143-57167187	NM_148931:95	Slc6a5	INSIDE	0.618	0.599	1270.30	760.81	0.370	959.40	355.32
A_68_P22336402	chr3:93248746-93248790	NM_001163098:2517	Tchh	INSIDE	0.618	0.715	1596.61	1141.44	0.442	1243.86	549.45
A_68_P24542638	chr6:72566666-72566710	NM_009444:54	Tgoln2	INSIDE	0.618	0.711	2406.13	1709.67	0.439	1943.97	854.01
A_68_P31926780	chr19:5082631-5082675	NM_001001885:2825	Tmem151a	INSIDE	0.618	2.379	950.57	2261.20	1.469	759.18	1115.50
A_68_P26644654	chr9:75406902-75406946	NM_016963:540	Tmod3	INSIDE	0.618	0.550	1637.02	900.32	0.340	1383.47	469.90
A_68_P25508614	chr7:135153815-135153862	NM_001079932:5947	Trim72	INSIDE	0.618	2.597	1699.77	4413.51	1.604	1251.21	2007.20
A_68_P22948240	chr4:57968866-57968910	NM_011660:395	Txn1	INSIDE	0.618	0.562	1046.69	588.20	0.347	910.36	316.27
A_68_P32117276	chr19:41876224-41876268	NM_001163495:328	Arhgap19	INSIDE	0.617	0.495	1654.12	818.59	0.305	1309.43	399.97
A_68_P24118896	chr5:136470915-136470959	NM_023742:190	Dtx2	INSIDE	0.617	0.645	2522.89	1627.48	0.398	2062.38	821.34
A_68_P24112568	chr5:134790208-134790252	NM_001080746:386	Gtf2i	INSIDE	0.617	0.617	2532.59	1563.75	0.381	2013.74	767.02
A_68_P25965604	chr8:75876534-75876578	NM_010687:-101	Large	PROMOTER	0.617	0.495	1383.28	684.59	0.306	1184.68	361.93
A_68_P31734234	chr18:57292707-57292751	NM_001001979:-15	Megf10	PROMOTER	0.617	0.485	1416.03	687.00	0.299	1027.76	307.71
A_68_P30722301	chr16:44558812-44558856	NR_037242:-592	Mir3081	PROMOTER	0.617	0.662	1582.35	1046.83	0.408	1317.74	538.01
A_68_P22312503	chr3:88018770-88018821	NR_037276:-297	Mir3093	PROMOTER	0.617	0.495	1146.59	567.86	0.306	811.73	248.22
A_68_P22898164	chr4:48058319-48058363	NM_015743:-5779	Nr4a3	PROMOTER	0.617	0.558	2232.91	1246.65	0.345	1848.83	637.15
A_68_P26142833	chr8:109572050-109572094	NM_026513:442	Pdf	INSIDE	0.617	0.486	1244.49	605.28	0.300	975.92	293.09
A_68_P27282239	chr10:79755107-79755151	NM_009091:-47	Rps15	PROMOTER	0.617	0.562	1324.96	744.01	0.346	943.82	326.75
A_68_P31934219	chr19:6363498-6363542	NM_001110791:-169	Sf1	PROMOTER	0.617	0.631	1450.81	916.02	0.389	1059.31	412.36
A_68_P22872187	chr4:43536672-43536716	NM_009416:-434	Tpm2	PROMOTER	0.617	0.497	1160.65	576.55	0.306	917.73	281.16
A_68_P27056228	chr10:34017531-34017575	NM_030203:326	Tspyl4	INSIDE	0.617	0.630	1544.81	972.47	0.388	1238.09	480.83
A_68_P20349425	chr1:74634360-74634404	NM_029888:220	Zfp142	INSIDE	0.617	0.449	2720.49	1222.32	0.277	2035.70	564.19
A_68_P30499469	chr15:102568057-102568101			Unknown	0.617	2.888	2183.69	6306.93	1.781	1649.54	2938.28
A_68_P21840498	chr2:168107179-168107224	ENSMUST00000109191:-569		PROMOTER	0.617	0.437	2202.02	962.78	0.270	1665.42	448.93
A_68_P30261323	chr15:60655040-60655084	NR_030696:543	9930014A18Rik	INSIDE	0.616	0.454	1534.45	696.58	0.280	1241.21	347.00
A_68_P27285631	chr10:80270128-80270172	NM_007445:2158	Amh	INSIDE	0.616	0.443	1418.57	628.69	0.273	984.36	268.53
A_68_P26595469	chr9:66682493-66682537	NM_026674:-1	Aph1c	PROMOTER	0.616	0.722	1603.34	1157.12	0.445	1297.80	577.33
A_68_P23155610	chr4:101223010-101223054	NM_001164583:-166	Dnajc6	PROMOTER	0.616	0.725	2314.37	1677.70	0.447	1849.94	826.56
A_68_P24979593	chr7:16684397-16684441	NM_025898:427	Napa	INSIDE	0.616	0.536	1795.96	962.56	0.330	1447.41	477.97
A_68_P20740066	chr1:157659774-157659818	NM_001024945:233	Qsox1	INSIDE	0.616	0.630	2087.28	1315.94	0.389	1556.18	604.64
A_68_P21867064	chr2:172826009-172826053	NM_175112:413	Rae1	INSIDE	0.616	0.612	1108.55	678.63	0.377	967.90	365.17
A_68_P26748151	chr9:96531280-96531324	NM_053268:620	Rasa2	INSIDE	0.616	0.558	2267.55	1265.27	0.344	2134.17	733.36
A_68_P21815998	chr2:163900092-163900136	NM_021420:201	Stk4	INSIDE	0.616	0.425	1468.72	623.74	0.262	1215.31	317.93
A_68_P25949499	chr8:72567227-72567271	NM_027481:537	Sugp1	INSIDE	0.616	0.530	1543.33	817.97	0.327	1335.24	436.21
A_68_P31260843	chr17:57415026-57415070	NM_001163815:-3474	Vav1	PROMOTER	0.616	0.575	2460.19	1414.40	0.354	2166.22	766.78
A_68_P20319174	chr1:69424426-69424470			Unknown	0.616	2.741	506.66	1388.83	1.689	515.58	870.68
A_68_P28153161	chr11:115243333-115243378	NM_001080929:126	Cdr2l	INSIDE	0.615	0.703	1343.15	943.86	0.432	1293.34	558.71
A_68_P31193443	chr17:44325522-44325566	NM_172621:24	Clic5	INSIDE	0.615	0.487	1461.95	711.75	0.299	1172.02	350.96
A_68_P26081252	chr8:97605501-97605545	NM_028805:422	Katnb1	INSIDE	0.615	2.298	1639.11	3766.25	1.412	1072.01	1513.75
A_68_P27509909	chr10:122116007-122116051	NM_176919:211	Ppm1h	INSIDE	0.615	0.681	1353.95	922.59	0.419	1184.77	496.89
A_68_P26347006	chr9:21216708-21216752	NM_021888:450	Qtrt1	INSIDE	0.615	0.495	1285.34	636.11	0.304	1167.96	355.36
A_68_P28580849	chr12:82433588-82433632	NM_001167920:557	Slc8a3	INSIDE	0.615	0.666	997.56	663.93	0.410	772.99	316.54
A_68_P20005798	chr1:4482441-4482485	NM_011441:4032	Sox17	INSIDE	0.615	0.428	1368.50	585.40	0.263	1140.95	300.06
A_68_P26447525	chr9:40965613-40965657	NM_176860:-57	Ubash3b	PROMOTER	0.615	0.411	1287.73	529.80	0.253	1161.68	293.92
A_68_P22362401	chr3:98945093-98945137	NM_027462:102	Wars2	INSIDE	0.615	0.591	1894.53	1120.60	0.363	1479.21	537.67

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28040434	chr11:95573914-95573958	ENSMUST00000107717:-50		PROMOTER	0.615	0.609	1551.86	944.87	0.374	1341.55	502.26
A_68_P26892247	chr9:122859927-122859971	NM_025419:170	1110059G10Rik	INSIDE	0.614	0.597	1193.62	712.33	0.366	952.22	348.99
A_68_P23293015	chr4:128444743-128444787	NM_001009819:8263	A3galt2	INSIDE	0.614	2.437	1056.13	2573.32	1.495	898.87	1343.67
A_68_P31939559	chr19:7457501-7457545	NM_001033139:-6	AI846148	PROMOTER	0.614	0.510	1834.51	936.50	0.313	1487.51	466.18
A_68_P24039813	chr5:121063452-121063497	NM_028041:336	Ddx54	INSIDE	0.614	0.453	1291.47	584.56	0.278	994.37	276.44
A_68_P30083648	chr15:25772800-25772844	NM_001034851:-196	Fam134b	PROMOTER	0.614	0.680	2093.85	1424.58	0.418	1793.37	748.82
A_68_P27543728	chr10:128328158-128328202	NM_010272:594	Gdf11	INSIDE	0.614	0.713	2342.09	1668.76	0.437	1895.11	828.69
A_68_P28055838	chr11:98210489-98210533	NM_144828:459	Ppp1r1b	INSIDE	0.614	0.536	3461.83	1855.57	0.329	2814.69	926.37
A_68_P22488130	chr3:123149844-123149888	NM_008939:36	Prss12	INSIDE	0.614	0.572	1247.95	713.78	0.351	1075.79	377.71
A_68_P23402407	chr4:149147586-149147630	NM_027460:768	Slc25a33	INSIDE	0.614	0.586	1141.88	668.64	0.360	946.72	340.62
A_68_P30499547	chr15:102577888-102577932			Unknown	0.614	0.568	1922.29	1091.84	0.349	1531.94	534.65
A_68_P23601494	chr5:35917751-35917795	NM_030208:-53	2310079F23Rik	DIVERGENT_PROMOTER	0.613	0.579	1261.35	730.68	0.355	978.75	347.82
A_68_P30462697	chr15:96118805-96118849	NM_175251:874	Arid2	INSIDE	0.613	2.922	759.14	2218.15	1.792	653.35	1170.67
A_68_P29265994	chr13:100670562-100670606	NM_001081493:54	Cartpt	INSIDE	0.613	0.490	1785.71	874.59	0.300	1439.31	432.37
A_68_P27894312	chr11:69137170-69137214	NM_172560:183	Cntrob	INSIDE	0.613	0.477	1808.54	863.43	0.293	1303.35	381.55
A_68_P21102914	chr2:30247811-30247855	NM_020329:-103	Dolpp1	PROMOTER	0.613	0.489	4399.74	2149.48	0.299	3276.44	981.06
A_68_P21007903	chr2:11698976-11699020	NM_015792:156	Fbxo18	INSIDE	0.613	0.626	3801.92	2380.95	0.384	2789.82	1071.73
A_68_P20170820	chr1:40382866-40382910	NM_133193:1417	Il1rl2	INSIDE	0.613	0.599	1729.41	1035.11	0.367	1317.23	483.15
A_68_P28155559	chr11:115685801-115685845	NM_145438:451	Llgl2	INSIDE	0.613	0.546	2563.04	1399.14	0.334	1948.82	651.73
A_68_P20185543	chr1:42908342-42908386	NM_023514:287	Mrps9	INSIDE	0.613	0.465	1569.81	729.99	0.285	1272.81	363.00
A_68_P29453027	chr14:22319300-22319344	NM_017479:316	Myst4	INSIDE	0.613	0.706	2117.96	1496.31	0.433	1647.68	713.30
A_68_P30344676	chr15:75714693-75714737	NM_172607:10197	Naprt1	DOWNSTREAM	0.613	0.702	1537.91	1080.22	0.431	1142.02	491.74
A_68_P22006131	chr3:26230237-26230281	NM_138666:573	Nlgn1	INSIDE	0.613	0.426	1343.22	571.62	0.261	998.03	260.19
A_68_P26742504	chr9:95461303-95461354	NM_198414:1093	Paqr9	INSIDE	0.613	2.623	1333.75	3498.63	1.608	977.47	1572.11
A_68_P20184674	chr1:42754743-42754787	NM_008900:774	Pou3f3	INSIDE	0.613	0.631	1701.20	1073.53	0.387	1494.22	578.41
A_68_P27631990	chr11:20443463-20443507	NM_021372:229	Sertad2	INSIDE	0.613	0.689	1889.90	1302.35	0.422	1447.47	611.00
A_68_P23243656	chr4:118781563-118781607	NM_011400:235	Slc2a1	INSIDE	0.613	0.601	1382.72	830.48	0.368	1175.39	432.70
A_68_P26924750	chr10:8238430-8238474	NM_177387:171	Ust	INSIDE	0.613	0.633	1249.79	791.26	0.388	1122.33	435.37
A_68_P26872302	chr9:119336590-119336634	NM_007397:24994	Acvr2b	INSIDE	0.612	2.514	1913.37	4810.10	1.537	1406.02	2161.67
A_68_P26399345	chr9:31019701-31019745	NM_001102455:-322	Aplp2	PROMOTER	0.612	0.534	1052.03	561.48	0.327	829.63	271.20
A_68_P30567432	chr16:15887571-15887615	NM_007679:214	Cebpd	INSIDE	0.612	0.562	3420.96	1921.32	0.344	2518.76	865.88
A_68_P22046077	chr3:33979970-33980014	NM_001026211:256	Dnajc19	INSIDE	0.612	0.558	1122.87	626.97	0.342	729.58	249.15
A_68_P23796634	chr5:73647594-73647638	NM_028194:241	Fryl	INSIDE	0.612	0.645	854.45	551.52	0.395	702.24	277.44
A_68_P31978254	chr19:16207846-16207890	NM_008139:548	Gnaq	INSIDE	0.612	0.495	1558.38	771.01	0.303	1272.35	385.25
A_68_P26811671	chr9:107804092-107804136	NM_028369:13655	Mon1a	INSIDE	0.612	0.601	994.45	597.82	0.368	768.57	282.58
A_68_P21821252	chr2:164859772-164859816	NM_144892:485	Ncoa5	INSIDE	0.612	0.593	930.67	552.14	0.363	804.09	291.83
A_68_P22771642	chr4:20705490-20705534	NM_172987:303	Nkain3	INSIDE	0.612	0.652	1130.86	737.18	0.399	956.36	381.83
A_68_P26129290	chr8:107115528-107115572	NM_001024606:183	Pdp2	INSIDE	0.612	0.632	3062.32	1936.90	0.387	2437.09	943.68
A_68_P20632580	chr1:136195843-136195887	NM_001144855:33641	Ppfia4	INSIDE	0.612	0.668	1158.23	773.15	0.409	951.89	388.86
A_68_P26136326	chr8:108379372-108379416	NM_021513:392	Thap11	INSIDE	0.612	0.724	1593.83	1153.63	0.443	1325.04	586.55
A_68_P21736743	chr2:149656066-149656110	NM_001085521:-430	Tmem90b	PROMOTER	0.612	0.634	1383.81	877.21	0.388	1006.57	390.19
A_68_P21568807	chr2:119114429-119114473	NM_172269:-27	Vps18	PROMOTER	0.612	0.443	1270.63	562.46	0.271	882.92	239.10
A_68_P21221053	chr2:52531826-52531870	NM_001037099:253	Cacnb4	INSIDE	0.611	0.486	1392.83	676.68	0.297	1086.75	322.45
A_68_P31156008	chr17:34974068-34974113	NM_001163770:127	Dom3z	INSIDE	0.611	0.503	1152.02	579.63	0.307	772.23	237.39
A_68_P24141307	chr5:140894611-140894655	NM_133916:-626	Eif3b	PROMOTER	0.611	0.418	1644.66	687.41	0.256	1499.27	383.16
A_68_P29150850	chr13:75845171-75845215	NM_138953:261	Ell2	INSIDE	0.611	0.560	2148.41	1202.57	0.342	1824.14	623.46
A_68_P28118149	chr11:109224381-109224425	NM_010303:295	Gna13	INSIDE	0.611	0.521	1186.78	618.62	0.318	840.02	267.48
A_68_P30501636	chr15:102866066-102866110	NM_013553:1263	Hoxc4	INSIDE	0.611	0.709	2052.98	1455.93	0.433	1530.93	663.51
A_68_P27865436	chr11:64248735-64248779	NM_178870:-77	Hs3st3a1	PROMOTER	0.611	0.517	1450.49	750.17	0.316	1056.21	333.60
A_68_P29130721	chr13:72100670-72100714	NM_010573:479	Irx1	INSIDE	0.611	0.650	1830.69	1189.90	0.397	1628.53	647.06
A_68_P31253054	chr17:56109780-56109824	NM_001159523:-102	Shd	PROMOTER	0.611	0.544	2327.83	1266.72	0.333	1596.29	530.99

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P29116718	chr13:69749922-69749966	NM_175283:397	Srd5a1	INSIDE	0.611	0.491	1683.52	826.10	0.300	1354.43	406.03
A_68_P20620971	chr1:134257276-134257320	NM_178874:30560	Tmcc2	INSIDE	0.611	3.302	7294.02	24086.94	2.019	4591.99	9270.90
A_68_P22693141	chr4:3501940-3501984	NM_028097:-47	Tmem68	DIVERGENT_PROMOTER	0.611	0.637	1267.27	807.37	0.390	883.29	344.10
A_68_P24431872	chr6:49213460-49213504	NM_198102:569	Tra2a	INSIDE	0.611	0.663	1617.45	1072.19	0.405	1375.13	556.98
A_68_P31156940	chr17:35137702-35137746	NM_011690:-127	Vars	PROMOTER	0.611	0.658	1243.88	819.07	0.402	1014.05	407.80
A_68_P30572230	chr16:17147040-17147084	NM_026940:3	Ydjc	INSIDE	0.611	0.601	883.12	530.49	0.367	695.06	255.05
A_68_P27256916	chr10:74980191-74980235	NM_175133:-145	1110038D17Rik	DIVERGENT_PROMOTER	0.610	0.716	1785.62	1279.09	0.437	1457.66	637.16
A_68_P26586895	chr9:65142202-65142246	NM_001044389:123	Clpx	INSIDE	0.610	0.495	1320.21	653.66	0.302	993.50	300.26
A_68_P22803188	chr4:28741959-28742006	NM_001122889:1688	Epha7	INSIDE	0.610	0.475	1383.03	657.36	0.290	1197.30	347.26
A_68_P29268695	chr13:101262403-101262447	NM_022011:140	Gtf2h2	INSIDE	0.610	0.714	3258.92	2328.09	0.435	2502.66	1089.91
A_68_P24186279	chr5:150438537-150438581	NM_013559:332	Hsph1	INSIDE	0.610	0.641	2614.15	1675.15	0.391	1852.45	724.07
A_68_P23819018	chr5:77380092-77380136	NM_025939:-321	Paics	PROMOTER	0.610	0.694	2442.61	1695.65	0.423	1747.29	739.64
A_68_P31936609	chr19:6983898-6983942	NM_012021:215	Prdx5	INSIDE	0.610	0.577	1095.19	631.95	0.352	840.94	295.98
A_68_P29568500	chr14:45609358-45609402	NM_008964:1595	Ptger2	INSIDE	0.610	0.611	1117.69	683.42	0.373	827.85	308.64
A_68_P26630344	chr9:72773728-72773772	NM_028116:294	Pygo1	INSIDE	0.610	0.607	1909.56	1159.73	0.371	1458.27	540.37
A_68_P27841330	chr11:59989954-59989998	NM_001037764:36393	Rai1	INSIDE	0.610	0.405	3478.04	1409.63	0.247	2566.04	634.55
A_68_P22345837	chr3:95623518-95623562	NM_001081293:-664	Rprd2	PROMOTER	0.610	0.691	1853.12	1280.45	0.422	1463.67	617.43
A_68_P21635216	chr2:131318279-131318323	NM_001177833:703	Smox	INSIDE	0.610	0.636	1055.27	671.38	0.388	808.80	313.76
A_68_P21626548	chr2:129627604-129627648	NR_029452:-431	4932416H05Rik	PROMOTER	0.609	0.560	2485.64	1392.84	0.342	1718.23	586.82
A_68_P26885918	chr9:121748458-121748502	NM_028384:99	Ccdc13	INSIDE	0.609	0.709	1349.44	956.93	0.432	1078.83	465.64
A_68_P29688239	chr14:68551910-68551954	NM_177780:-303	Dock5	PROMOTER	0.609	0.568	924.51	525.56	0.346	817.83	283.14
A_68_P29671617	chr14:65716487-65716531	NM_018788:435	Extl3	INSIDE	0.609	0.447	1700.67	759.39	0.272	1422.87	386.99
A_68_P32135377	chr19:45005799-45005843	NM_001081225:212	Fam178a	INSIDE	0.609	0.559	2677.66	1495.88	0.340	2182.19	741.87
A_68_P25668520	chr8:13468316-13468360	NM_019521:26197	Gas6	INSIDE	0.609	2.535	1674.75	4245.58	1.545	1151.97	1779.25
A_68_P24318684	chr6:28083743-28083787	NM_008174:605	Grm8	INSIDE	0.609	0.544	1165.14	633.31	0.331	960.59	317.93
A_68_P20556978	chr1:121319090-121319134	NM_008381:-287	Inhbb	PROMOTER	0.609	0.628	862.01	541.47	0.383	748.04	286.33
A_68_P26018638	chr8:86707466-86707510	NR_029821:-4628	Mir181c	PROMOTER	0.609	0.570	1613.66	920.38	0.348	1165.56	405.13
A_68_P31000878	chr16:97985324-97985368	NM_023663:16	Ripk4	INSIDE	0.609	0.500	2313.74	1156.23	0.304	1915.25	582.80
A_68_P28177384	chr11:119217045-119217089	NM_178743:196	Slc26a11	INSIDE	0.609	0.605	1646.79	996.71	0.369	1314.26	484.36
A_68_P22659972	chr3:153636247-153636291	NM_001081263:-131	Slc44a5	PROMOTER	0.609	0.592	962.49	569.93	0.361	806.88	291.12
A_68_P22889891	chr4:46663047-46663091	NM_198664:3	Tbc1d2	INSIDE	0.609	0.618	2097.59	1295.27	0.376	1552.68	584.26
A_68_P31620719	chr18:36048780-36048824			Unknown	0.609	0.403	1830.91	738.23	0.246	1525.10	374.46
A_68_P23637941	chr5:42235067-42235111	NM_001081422:466	Bod1l	INSIDE	0.608	0.500	1234.59	617.58	0.304	1086.26	330.62
A_68_P23351276	chr4:138908601-138908645	NM_001039200:115	C230096C10Rik	INSIDE	0.608	0.625	1153.69	720.54	0.380	790.46	300.24
A_68_P20740951	chr1:157820596-157820640	NM_001039184:-233	Cep350	PROMOTER	0.608	0.675	1368.22	923.57	0.410	1014.32	416.26
A_68_P24850800	chr6:131338648-131338692	NM_011733:-202	Csda	PROMOTER	0.608	0.474	1407.49	667.06	0.288	1216.73	350.56
A_68_P25616319	chr8:4166672-4166716	NM_001039578:128	Evi5l	INSIDE	0.608	0.490	2932.47	1437.51	0.298	2388.07	711.77
A_68_P27282041	chr10:79723845-79723889	NM_010255:-153	Gamt	DIVERGENT_PROMOTER	0.608	0.660	1685.06	1111.51	0.401	1312.24	526.41
A_68_P23417747	chr4:151661148-151661192	NM_008237:4601	Hes3	INSIDE	0.608	0.535	2896.06	1550.47	0.325	2289.36	745.00
A_68_P20058158	chr1:17087056-17087100	NM_020604:892	Jph1	INSIDE	0.608	0.604	1157.64	699.31	0.367	976.90	358.60
A_68_P25503046	chr7:134072788-134072832	NM_172747:418	Kctd13	INSIDE	0.608	0.679	1493.07	1014.50	0.413	1249.56	516.54
A_68_P20164265	chr1:39250200-39250244	NM_008719:-894	Npas2	PROMOTER	0.608	0.623	2167.63	1350.98	0.379	1748.67	662.81
A_68_P20134288	chr1:33726517-33726564	NM_008922:63	Prim2	INSIDE	0.608	0.507	1021.62	518.28	0.308	697.23	215.01
A_68_P20304094	chr1:66747456-66747500	NM_025683:12	Rpe	INSIDE	0.608	0.534	1472.35	785.78	0.325	1219.74	395.84
A_68_P26804660	chr9:106587656-106587700	NM_011573:320	Tex264	INSIDE	0.608	0.587	1043.54	612.71	0.357	872.80	311.83
A_68_P23186774	chr4:106511714-106511758	ENSMUST00000151369:8789		DOWNSTREAM	0.608	0.451	1198.88	541.18	0.274	1005.49	275.96
A_68_P23391468	chr4:147315734-147315778	NM_029841:753	2510039O18Rik	INSIDE	0.607	0.686	1454.28	997.18	0.416	1186.43	493.83
A_68_P27534003	chr10:126528845-126528889	NM_001033263:12904	Agap2	INSIDE	0.607	0.585	2525.24	1476.80	0.355	1894.39	672.92
A_68_P22069323	chr3:38354784-38354828	NM_001167883:28932	Ankrd50	INSIDE	0.607	2.767	733.56	2029.72	1.680	686.76	1153.66
A_68_P23262162	chr4:123020250-123020294	NM_007558:-226	Bmp8a	PROMOTER	0.607	0.528	1218.13	642.86	0.321	1020.81	327.24
A_68_P31932622	chr19:6085142-6085186	NM_026410:68	Cdca5	INSIDE	0.607	0.455	2496.54	1136.69	0.276	2019.11	557.75

						Sham group			TiO$_2$-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25951436	chr8:72898442-72898486	NM_016685:1018	Comp	INSIDE	0.607	0.631	1820.77	1149.15	0.383	1374.59	526.43
A_68_P31259843	chr17:57201503-57201547	NM_177638:-175	Crb3	DIVERGENT_PROMOTER	0.607	0.687	2382.63	1636.66	0.417	1768.01	737.28
A_68_P28924079	chr13:31718773-31718817	NM_010225:1110	Foxf2	INSIDE	0.607	0.700	4496.20	3149.18	0.425	3390.73	1440.90
A_68_P24757355	chr6:113027040-113027084	NR_027010:176	Gt(ROSA)26Sor	INSIDE	0.607	0.391	1817.88	711.35	0.238	1389.91	330.26
A_68_P31099379	chr17:24889503-24889547	NM_001012402:-423	Hs3st6	PROMOTER	0.607	0.650	1028.18	668.07	0.394	828.92	326.80
A_68_P26658578	chr9:78023836-78023880	NM_019987:62814	Ick	DOWNSTREAM	0.607	0.721	1741.92	1256.45	0.438	1372.60	601.28
A_68_P26228658	chr8:124277668-124277712	NM_020605:23232	Jph3	INSIDE	0.607	3.557	2747.82	9774.66	2.159	1848.26	3989.51
A_68_P32028425	chr19:25311521-25311565	NM_181404:-149	Kank1	PROMOTER	0.607	0.703	1355.53	953.17	0.426	1111.31	473.97
A_68_P21900915	chr2:179759580-179759624	NM_177727:-89	Lsm14b	PROMOTER	0.607	0.659	901.20	593.66	0.400	874.32	349.57
A_68_P26797102	chr9:105297505-105297549	NM_172461:91	Nek11	INSIDE	0.607	0.404	1654.00	667.97	0.245	1435.81	352.11
A_68_P24763851	chr6:114081597-114081641	NM_172890:384	Slc6a11	INSIDE	0.607	0.648	1224.23	793.89	0.394	1041.94	410.18
A_68_P27226083	chr10:69285075-69285119	NM_146005:288641	Ank3	INSIDE	0.606	2.579	1959.05	5052.22	1.563	1565.26	2446.25
A_68_P23252015	chr4:120242852-120242896	NM_016748:7	Ctps	INSIDE	0.606	0.510	1269.60	647.95	0.309	1139.09	352.38
A_68_P28463221	chr12:58647081-58647125	NM_008259:6	Foxa1	INSIDE	0.606	0.499	1992.93	993.54	0.302	1599.98	483.68
A_68_P21901246	chr2:179805450-179805494	NM_001083328:175	Gtpbp5	INSIDE	0.606	0.631	1197.29	756.00	0.382	882.63	337.49
A_68_P22405344	chr3:107082299-107082343	NM_026774:545	Hbxip	INSIDE	0.606	0.598	1435.14	858.53	0.363	1185.10	429.74
A_68_P23300617	chr4:129816677-129816721	NM_198959:-292	Hcrtr1	PROMOTER	0.606	0.656	1169.89	767.48	0.397	941.02	373.98
A_68_P22388055	chr3:103594904-103594948	NM_010432:272	Hipk1	INSIDE	0.606	0.677	1287.47	872.07	0.411	995.39	408.69
A_68_P30348454	chr15:76288272-76288316	NM_198885:427	Scx	INSIDE	0.606	0.519	1891.00	981.97	0.315	1523.61	479.34
A_68_P20585380	chr1:127457355-127457399	NM_028787:-216	Slc35f5	PROMOTER	0.606	0.427	1335.57	570.20	0.259	1127.49	291.80
A_68_P21749219	chr2:152240057-152240101	NM_175126:702	Zcchc3	INSIDE	0.606	0.611	1622.07	991.19	0.370	1373.36	508.34
A_68_P27172917	chr10:59649185-59649231	NM_016803:32800	Chst3	INSIDE	0.605	2.849	1161.45	3308.62	1.725	971.49	1675.68
A_68_P32145202	chr19:46728964-46729014	NM_001177813:31098	D19Wsu162e	INSIDE	0.605	3.450	2587.61	8926.64	2.086	1851.03	3860.42
A_68_P26015687	chr8:86132654-86132698	NM_018808:603	Dnajb1	INSIDE	0.605	0.595	1336.38	794.62	0.360	1176.46	423.12
A_68_P29002205	chr13:45602874-45602918	NM_025508:59	Gmpr	INSIDE	0.605	0.546	1397.33	763.28	0.330	1112.58	367.64
A_68_P26531866	chr9:55389590-55389634	NM_027397:657	Isl2	INSIDE	0.605	0.456	1252.05	571.38	0.276	1095.48	302.45
A_68_P30656039	chr16:33062880-33062924	NM_172823:296	Lmln	INSIDE	0.605	0.441	2475.71	1090.93	0.266	1927.64	513.59
A_68_P28457439	chr12:57634754-57634798	NM_001146198:1317	Nkx2-1	INSIDE	0.605	0.467	1609.36	751.63	0.283	1341.25	379.02
A_68_P28056108	chr11:98248019-98248063	NM_008890:95	Pnmt	INSIDE	0.605	0.728	1962.01	1429.14	0.440	1588.81	699.84
A_68_P24950722	chr7:4781562-4781606	NM_172737:14714	Shisa7	INSIDE	0.605	2.517	2137.86	5380.02	1.523	1644.26	2504.79
A_68_P22864088	chr4:41687513-41687565	NM_011014:648	Sigmar1	INSIDE	0.605	0.638	872.40	556.37	0.386	665.26	256.65
A_68_P27504460	chr10:121043018-121043071	NM_001081056:20328	Xpot	INSIDE	0.605	2.799	725.45	2030.52	1.694	566.97	960.58
A_68_P31092274	chr17:23684082-23684126	NM_001033496:17089	Zfp213	DOWNSTREAM	0.605	0.578	1127.59	651.49	0.349	909.99	317.95
A_68_P28747156	chr12:113205010-113205054	NM_027360:156	2010107E04Rik	INSIDE	0.604	0.507	1478.02	750.02	0.306	1230.96	376.99
A_68_P27320001	chr10:86955807-86955851	NM_008553:577	Ascl1	INSIDE	0.604	0.595	2074.22	1235.00	0.359	1735.27	623.81
A_68_P24248438	chr6:13628084-13628128	NM_175312:-140	B630005N14Rik	PROMOTER	0.604	0.604	3333.22	2014.92	0.365	2409.21	879.89
A_68_P30964663	chr16:91729071-91729122	NM_026994:-49	Cryzl1	DIVERGENT_PROMOTER	0.604	0.597	1606.66	959.02	0.361	1232.55	444.72
A_68_P27997845	chr11:87913051-87913095	NM_198013:425	Cuedc1	INSIDE	0.604	0.638	1295.02	826.82	0.386	1219.44	470.60
A_68_P26572463	chr9:62658873-62658917	NM_010193:561	Fem1b	INSIDE	0.604	0.724	2162.60	1565.76	0.437	1624.45	710.21
A_68_P31217285	chr17:48548234-48548282	NM_001110832:887	Nfya	INSIDE	0.604	0.543	1238.29	672.28	0.328	995.94	326.52
A_68_P29011093	chr13:47106234-47106282	NM_175340:3961	Nhlrc1	DOWNSTREAM	0.604	3.761	2716.80	10217.71	2.271	1867.85	4242.03
A_68_P27900565	chr11:70223680-70223724	NM_029231:-169	Pelp1	PROMOTER	0.604	0.542	3105.07	1684.38	0.327	2393.70	783.69
A_68_P21928444	chr3:7366471-7366516	NM_008862:-110	Pkia	PROMOTER	0.604	0.582	1249.51	726.84	0.352	978.78	344.14
A_68_P23981857	chr5:111209299-111209343	NM_001025561:295	Pus1	INSIDE	0.604	0.690	2104.92	1453.25	0.417	1734.51	723.61
A_68_P28069222	chr11:100501295-100501339	NM_177790:10691	Zfp385c	INSIDE	0.604	0.612	1173.82	718.80	0.370	897.51	331.73
A_68_P26351028	chr9:22064295-22064339	NM_181419:23	Zfp599	INSIDE	0.604	0.523	1647.92	861.06	0.316	1267.56	400.15
A_68_P30245927	chr15:57908540-57908584	NM_001042438:-518	Zhx1	PROMOTER	0.604	0.659	906.18	597.41	0.398	684.63	272.56
A_68_P22217911	chr3:68673203-68673247	NM_001167996:-283	1110032F04Rik	PROMOTER	0.603	0.508	1114.32	566.44	0.306	941.56	288.50
A_68_P21967930	chr3:17686893-17686937	NR_033490:-3006	2610100L16Rik	PROMOTER	0.603	0.621	1124.67	697.86	0.374	890.64	332.99
A_68_P30475231	chr15:98397707-98397751	NR_028442:-26	9330020H09Rik	PROMOTER	0.603	0.522	2177.89	1136.61	0.315	1624.71	511.56
A_68_P28084858	chr11:103222146-103222190	NM_001205236:2838	Arhgap27	INSIDE	0.603	0.558	1261.80	703.64	0.337	945.53	318.21

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P22314832	chr3:88425175-88425219	NM_001198912:-119	Arhgef2	PROMOTER	0.603	0.440	1225.51	538.80	0.265	984.79	261.27
A_68_P24639203	chr6:91422971-91423017	NM_133928:423	Chchd4	INSIDE	0.603	0.611	1014.68	619.91	0.368	765.80	282.03
A_68_P28158778	chr11:116196536-116196580	NM_008240:110	Foxj1	INSIDE	0.603	0.698	1889.70	1318.66	0.421	1406.04	591.32
A_68_P28577473	chr12:81859415-81859459	NM_001008423:2266	Gm1568	INSIDE	0.603	3.825	273.66	1046.71	2.308	341.37	787.73
A_68_P22907354	chr4:49858702-49858746	NM_001033351:-771	Grin3a	PROMOTER	0.603	0.582	1701.90	990.30	0.351	1147.95	402.82
A_68_P31158870	chr17:35457706-35457750	NM_010390:226	H2-Q1	INSIDE	0.603	0.547	1166.12	638.01	0.330	983.84	324.67
A_68_P20455838	chr1:95375093-95375137	NM_133808:271	Hdlbp	INSIDE	0.603	0.536	1707.94	915.49	0.323	1274.21	411.62
A_68_P27987932	chr11:86070867-86070911	NM_027421:182	Ints2	INSIDE	0.603	0.513	1126.92	578.10	0.310	851.72	263.63
A_68_P29240037	chr13:96095372-96095416	NR_035461:-5140	Mir1940	PROMOTER	0.603	0.517	2115.72	1093.90	0.312	1826.87	569.57
A_68_P22336828	chr3:93324960-93325004	NM_016740:565	S100a11	INSIDE	0.603	0.580	1343.79	779.27	0.350	1075.51	375.97
A_68_P24153575	chr5:143582152-143582196	NM_001122730:-3108	Tnrc18	PROMOTER	0.603	0.599	1074.49	643.17	0.361	846.95	305.86
A_68_P20877471	chr1:182656470-182656514	NM_133225:319	Acbd3	INSIDE	0.602	0.472	2000.22	943.87	0.284	1672.07	474.65
A_68_P27271774	chr10:77506231-77506275	NM_009646:73	Aire	INSIDE	0.602	0.694	2650.11	1838.64	0.418	2071.33	865.39
A_68_P23893979	chr5:92821310-92821354	NM_181728:60466	Art3	INSIDE	0.602	2.868	1474.08	4228.29	1.727	1177.63	2033.79
A_68_P24160783	chr5:145118513-145118557	NM_025833:447	Baiap2l1	INSIDE	0.602	0.630	2141.54	1348.14	0.379	1824.01	691.42
A_68_P20618861	chr1:133904468-133904512	NM_007923:309	Elk4	INSIDE	0.602	0.632	2302.05	1453.89	0.380	1819.24	691.20
A_68_P27996720	chr11:87684836-87684880	NM_007946:4180	Epx	INSIDE	0.602	2.771	723.69	2005.40	1.669	593.25	990.38
A_68_P26224342	chr8:123606667-123606711	NM_010426:-1685	Foxf1a	PROMOTER	0.602	0.463	1434.04	663.83	0.279	1035.19	288.39
A_68_P26035031	chr8:89996648-89996692	NR_033430:-40	Gm2694	DIVERGENT_PROMOTER	0.602	0.465	1283.10	596.31	0.280	1145.03	320.35
A_68_P28086531	chr11:103558931-103558975	NM_019650:72	Gosr2	INSIDE	0.602	0.456	1316.56	600.68	0.275	1112.71	305.66
A_68_P21957225	chr3:14533992-14534036	NM_001163579:227	Lrrcc1	INSIDE	0.602	0.606	2893.89	1754.91	0.365	2195.12	801.46
A_68_P27897807	chr11:69715139-69715183	NM_001013414:-219	Neurl4	DIVERGENT_PROMOTER	0.602	0.370	2029.20	751.82	0.223	1519.97	338.98
A_68_P31107657	chr17:26122228-26122272	NM_153140:36555	Rab11fip3	DOWNSTREAM	0.602	0.534	1205.51	643.56	0.321	1061.30	341.07
A_68_P27943642	chr11:78304280-78304324	NM_001168521:6954	Sarm1	INSIDE	0.602	0.680	1333.95	906.64	0.409	1015.98	415.37
A_68_P25372613	chr7:108470115-108470159	NM_019990:304	Stard10	INSIDE	0.602	0.601	1988.33	1195.02	0.362	1657.57	599.40
A_68_P26018926	chr8:86761267-86761311	NM_172503:-347	Zswim4	PROMOTER	0.602	0.548	1005.10	550.67	0.330	789.16	260.26
A_68_P29509891	chr14:31944757-31944801	NR_024069:-2662	2010107H07Rik	DIVERGENT_PROMOTER	0.601	5.677	1068.55	6065.94	3.414	867.90	2962.98
A_68_P27179426	chr10:60708843-60708887	NM_001081127:27322	Adamts14	INSIDE	0.601	2.570	1597.10	4104.40	1.544	1165.79	1800.06
A_68_P25597927	chr7:150153952-150153996	NM_008554:1195	Ascl2	INSIDE	0.601	0.661	3359.94	2222.43	0.397	2505.57	995.60
A_68_P28115684	chr11:108782304-108782348	NM_015732:664	Axin2	INSIDE	0.601	0.494	3204.51	1581.72	0.297	2628.61	779.86
A_68_P25501815	chr7:133839681-133839725	NM_175103:189	Bola2	INSIDE	0.601	0.393	1973.25	775.55	0.236	1391.41	328.75
A_68_P27155060	chr10:55948706-55948750	NM_001033385:-233	D630037F22Rik	PROMOTER	0.601	0.666	895.17	596.40	0.400	671.00	268.64
A_68_P24125311	chr5:137791525-137791569	NM_001159571:210	Ephb4	INSIDE	0.601	0.588	4521.60	2657.53	0.353	3480.29	1229.09
A_68_P27561149	chr11:4961389-4961433	NM_001190406:3920	Gas2l1	INSIDE	0.601	0.560	2634.12	1474.41	0.337	2254.87	758.77
A_68_P26821065	chr9:109834739-109834783	NM_001205331:483	Mtap4	INSIDE	0.601	0.735	2605.53	1914.22	0.441	1897.80	837.46
A_68_P29591677	chr14:49685584-49685628	NM_144535:-563	Mudeng	PROMOTER	0.601	0.570	2138.88	1220.06	0.343	1757.77	602.70
A_68_P29060115	chr13:56353410-56353454	NM_010896:92	Neurog1	INSIDE	0.601	0.682	2951.80	2013.31	0.410	2345.20	961.68
A_68_P28223705	chr12:8681057-8681101	NM_030723:-408	Pum2	PROMOTER	0.601	0.620	1390.83	862.72	0.373	982.46	366.01
A_68_P28830400	chr13:12198333-12198377	NM_023868:858	Ryr2	INSIDE	0.601	0.548	1628.34	891.62	0.329	1428.77	470.24
A_68_P24120066	chr5:136707860-136707905	NM_018825:12891	Sh2b2	INSIDE	0.601	2.852	1914.56	5460.69	1.713	1297.49	2222.73
A_68_P29729988	chr14:76186558-76186602	NM_026232:264	Slc25a30	INSIDE	0.601	0.525	1223.05	642.53	0.316	965.31	304.96
A_68_P25952901	chr8:73122626-73122673	NM_133772:9564	Ssbp4	INSIDE	0.601	2.646	2179.14	5766.93	1.591	1340.71	2133.65
A_68_P28339006	chr12:33638754-33638798	NM_013635:-33	Sypl	PROMOTER	0.601	0.482	1530.53	737.06	0.290	1198.52	347.09
A_68_P32147505	chr19:47149484-47149530	NM_177342:7269	Taf5	INSIDE	0.601	3.208	269.63	865.01	1.927	289.71	558.29
A_68_P24850991	chr6:131383858-131383902			Unknown	0.601	0.595	2288.24	1361.69	0.358	1976.50	706.73
A_68_P25087377	chr7:51684556-51684600	ENSMUST00000127790:191		INSIDE	0.601	0.488	2152.66	1051.28	0.294	1622.87	476.62
A_68_P30092466	chr15:27396756-27396800	NM_020332:347	Ank	INSIDE	0.600	0.632	3710.37	2345.48	0.379	2786.22	1055.95
A_68_P31678446	chr18:46887405-46887449	NM_033037:570	Cdo1	INSIDE	0.600	0.570	1542.13	879.69	0.342	1208.86	413.91
A_68_P26971606	chr10:17444088-17444133	NM_010828:1077	Cited2	INSIDE	0.600	0.664	1726.83	1146.50	0.398	1241.37	494.69
A_68_P27280209	chr10:79451266-79451310	NM_007725:-56	Cnn2	DIVERGENT_PROMOTER	0.600	0.498	1202.49	598.45	0.299	900.74	269.17
A_68_P24295435	chr6:23204086-23204130	NM_028462:-5844	Fezf1	PROMOTER	0.600	0.695	1354.26	940.63	0.417	1081.26	450.87

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27137650	chr10:52137866-52137910	NM_030250:536	Nus1	INSIDE	0.600	0.572	1525.12	872.76	0.343	1337.33	459.15
A_68_P22518783	chr3:128921672-128921716	NM_001042502:4840	Pitx2	INSIDE	0.600	0.588	887.59	522.06	0.353	736.64	259.96
A_68_P28190288	chr11:121249326-121249370	NM_139147:217	Rab40b	INSIDE	0.600	0.634	866.71	549.64	0.380	758.05	288.27
A_68_P30343544	chr15:75543867-75543911	NM_001163465:9171	Rhpn1	INSIDE	0.600	2.680	2917.76	7820.67	1.607	2077.65	3339.03
A_68_P20715112	chr1:153348264-153348308	NM_011277:-333	Rnf2	PROMOTER	0.600	0.662	1196.30	791.90	0.397	978.14	388.20
A_68_P31106589	chr17:25970569-25970614	NM_019719:-285	Stub1	PROMOTER	0.600	0.508	1234.01	627.21	0.305	958.01	291.94
A_68_P23441977	chr4:155409010-155409054	NM_029264:15894	Ttll10	INSIDE	0.600	0.598	988.82	590.88	0.358	850.24	304.68
A_68_P25469455	chr7:127778730-127778774	NM_025899:50	Uqcrc2	INSIDE	0.600	0.556	1663.72	924.96	0.333	1301.62	433.87
A_68_P20735709	chr1:156930520-156930564	ENSMUST00000128143:-146		PROMOTER	0.600	0.422	4388.75	1850.51	0.253	3340.67	845.51
A_68_P26541149	chr9:57110346-57110390	NM_028820:38	1700017B05Rik	INSIDE	0.599	0.630	1570.04	989.76	0.378	1379.00	520.84
A_68_P28184735	chr11:120328666-120328710	NM_197995:226	Arl16	INSIDE	0.599	0.697	1341.45	935.31	0.418	1020.53	426.48
A_68_P20941835	chr1:193960556-193960600	NR_033536:-201	Gm10516	PROMOTER	0.599	0.631	1911.71	1206.98	0.378	1339.15	506.58
A_68_P29842699	chr14:99698157-99698201	NM_009769:269	Klf5	INSIDE	0.599	0.627	1269.40	795.40	0.375	1196.09	448.72
A_68_P29266706	chr13:100785478-100785522	NM_030026:94	Mccc2	INSIDE	0.599	0.479	1263.17	604.47	0.286	969.08	277.61
A_68_P20352131	chr1:75121569-75121613	NM_029342:210	Nhej1	INSIDE	0.599	0.565	1094.85	618.55	0.338	909.93	307.82
A_68_P30656972	chr16:33251779-33251823	NM_080557:259	Snx4	INSIDE	0.599	0.405	1770.76	717.61	0.243	1379.56	334.67
A_68_P21117288	chr2:32612911-32612955	NM_152800:142	Tor2a	INSIDE	0.599	0.668	1061.59	709.04	0.400	876.03	350.28
A_68_P28280594	chr12:21423400-21423444	NM_011739:-125	Ywhaq	PROMOTER	0.599	0.456	1720.19	783.97	0.273	1289.76	351.84
A_68_P24798989	chr6:120481488-120481532	NM_144815:-193	Cecr5	PROMOTER	0.598	0.628	1119.77	702.70	0.376	763.89	286.89
A_68_P28684631	chr12:102137378-102137422	NM_001177674:334	Gpr68	INSIDE	0.598	0.509	1290.68	656.58	0.304	975.80	296.96
A_68_P30961691	chr16:91226111-91226155	NM_016967:338	Olig2	INSIDE	0.598	0.611	1189.41	726.43	0.365	904.05	330.23
A_68_P28107298	chr11:107341035-107341079	NM_025894:215	Psmd12	INSIDE	0.598	0.445	1765.52	785.03	0.266	1435.59	381.52
A_68_P22659666	chr3:153576060-153576104	NM_001163478:-152	Rabggtb	PROMOTER	0.598	0.434	1389.17	602.76	0.260	1050.59	272.66
A_68_P26809521	chr9:107457493-107457537	NM_019713:528	Rassf1	INSIDE	0.598	0.495	1189.45	588.53	0.296	931.76	275.71
A_68_P23820628	chr5:77694649-77694693	NM_011263:152	Rest	INSIDE	0.598	0.528	1795.51	947.91	0.316	1573.14	496.55
A_68_P27985547	chr11:85647100-85647150	NM_009324:1008	Tbx2	INSIDE	0.598	2.876	710.64	2044.07	1.719	539.30	926.94
A_68_P31006134	chr17:3557457-3557501	NM_146074:235	Tfb1m	INSIDE	0.598	0.658	2450.16	1611.56	0.393	1941.65	763.90
A_68_P29064233	chr13:56989277-56989325	NM_012035:7649	Trpc7	INSIDE	0.598	3.530	1275.13	4500.65	2.110	856.97	1807.91
A_68_P29560592	chr14:41780099-41780143	NM_145928:-24	Tspan14	PROMOTER	0.598	0.567	1621.41	918.61	0.339	1295.42	438.68
A_68_P26801828	chr9:106105584-106105628	NM_011876:168	Twf2	INSIDE	0.598	0.689	1170.24	806.50	0.412	1168.39	481.73
A_68_P23996380	chr5:113567336-113567380	NM_172884:24975	2900026A02Rik	INSIDE	0.597	0.491	1434.83	705.15	0.293	1109.33	325.36
A_68_P27910207	chr11:72028699-72028750	NM_001163728:85	4930563E22Rik	INSIDE	0.597	0.520	1367.10	711.38	0.310	1077.14	334.38
A_68_P28752832	chr12:114067540-114067584	NM_028023:38	Cdca4	INSIDE	0.597	0.529	3303.95	1748.13	0.316	2474.00	781.15
A_68_P25471450	chr7:128125237-128125281	NM_007672:568	Cdr2	INSIDE	0.597	0.664	1492.75	990.68	0.396	1161.96	460.64
A_68_P25948535	chr8:72413120-72413164	NM_026818:-1851	Cilp2	PROMOTER	0.597	0.479	1235.17	591.11	0.286	957.46	273.46
A_68_P21629316	chr2:130187590-130187634	NM_001110513:65938	Ebf4	INSIDE	0.597	0.645	2161.58	1394.12	0.385	1725.52	664.14
A_68_P28470864	chr12:60320947-60320991	NM_001033156:-498	Fbxo33	PROMOTER	0.597	0.493	1475.94	727.36	0.294	1217.60	358.41
A_68_P28604396	chr12:86827240-86827284	NM_010234:12412	Fos	DOWNSTREAM	0.597	0.620	1083.29	671.61	0.370	897.62	332.01
A_68_P26375211	chr9:27107465-27107509	NM_001033323:674	Igsf9b	INSIDE	0.597	0.520	2186.28	1137.52	0.310	1657.82	514.59
A_68_P27543981	chr10:128370721-128370765	NM_008398:-126	Itga7	PROMOTER	0.597	0.515	1877.83	966.34	0.307	1326.14	407.68
A_68_P27924619	chr11:74986101-74986145	NR_029794:-767	Mir212	DIVERGENT_PROMOTER	0.597	0.582	3777.86	2199.81	0.348	2972.84	1033.89
A_68_P24191782	chr5:151396383-151396427	NM_133898:696	N4bp2l1	INSIDE	0.597	0.551	1231.69	678.95	0.329	1028.45	338.20
A_68_P27290092	chr10:80958931-80958975	NM_134009:156	Ncln	INSIDE	0.597	0.544	3936.53	2141.26	0.325	2844.15	923.92
A_68_P31866297	chr18:80904269-80904314	NM_001164111:621	Nfatc1	INSIDE	0.597	0.618	1196.16	738.86	0.369	1035.19	381.56
A_68_P30000041	chr15:8393675-8393723	NM_027707:765	Nipbl	INSIDE	0.597	0.572	1360.81	777.79	0.341	1211.29	413.04
A_68_P31140479	chr17:31701231-31701275	NM_016670:-465	Pknox1	PROMOTER	0.597	0.542	1130.48	613.27	0.324	828.28	268.31
A_68_P23407014	chr4:149944046-149944090	NM_001085492:288044	Rere	INSIDE	0.597	0.590	2454.17	1448.36	0.352	1861.77	655.57
A_68_P21912147	chr2:181428245-181428289	NM_026446:363	Rgs19	INSIDE	0.597	0.587	1635.67	959.55	0.350	1612.89	565.09
A_68_P26596750	chr9:66896100-66896144	NM_001164252:-4444	Tpm1	PROMOTER	0.597	0.443	1696.14	752.00	0.264	1218.54	322.29
A_68_P25089670	chr7:52105704-52105748	NM_026270:1130	Akt1s1	INSIDE	0.596	0.546	998.05	545.25	0.325	857.57	279.07
A_68_P24759116	chr6:113328203-113328247	NM_001170485:118	Arpc4	INSIDE	0.596	0.626	924.00	578.23	0.373	765.03	285.30

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27278868	chr10:79240243-79240287	NM_031380:246	Fstl3	INSIDE	0.596	2.279	5870.34	13380.16	1.358	3783.22	5138.65
A_68_P20193920	chr1:44608775-44608819	NM_028450:281	Gulp1	INSIDE	0.596	0.647	1750.20	1133.25	0.386	1417.05	547.02
A_68_P29613101	chr14:55196302-55196346	NM_010590:174	Jub	INSIDE	0.596	0.558	3510.28	1958.95	0.333	2838.90	944.66
A_68_P25598743	chr7:150293354-150293398	NM_008434:218	Kcnq1	INSIDE	0.596	0.717	1531.70	1098.05	0.427	1262.71	539.38
A_68_P23842572	chr5:82223907-82223953	NM_198702:773313	Lphn3	INSIDE	0.596	2.820	711.71	2007.26	1.681	568.12	954.97
A_68_P25576399	chr7:146398944-146398988	NM_001143755:-207	Lrrc27	PROMOTER	0.596	0.649	991.03	643.50	0.387	789.55	305.75
A_68_P29330296	chr13:112515544-112515588	NM_172593:39181	Mier3	DOWNSTREAM	0.596	0.394	1640.41	646.06	0.235	1309.51	307.46
A_68_P22856642	chr4:40226159-40226203	NM_001033305:221	Ndufb6	INSIDE	0.596	0.436	2086.76	910.02	0.260	1462.95	380.38
A_68_P20413386	chr1:88567063-88567107	NM_010933:64	Nppc	INSIDE	0.596	0.569	1056.02	600.65	0.339	904.77	306.88
A_68_P23374051	chr4:142802693-142802737	NM_001081355:-102	Prdm2	PROMOTER	0.596	0.531	1841.54	977.22	0.316	1580.36	499.43
A_68_P29703310	chr14:71165976-71166021	NM_023045:437	Xpo7	INSIDE	0.596	0.516	1046.55	540.47	0.308	816.33	251.35
A_68_P22129250	chr3:51162734-51162778			Unknown	0.596	0.561	2229.30	1251.07	0.335	1913.56	640.43
A_68_P31961132	chr19:12575516-12575560	NM_172442:948	Dtx4	INSIDE	0.595	0.611	1741.39	1064.59	0.364	1392.13	506.25
A_68_P32397420	chrX:53985031-53985075	NM_001077361:-81	Fhl1	PROMOTER	0.595	2.929	2221.21	6506.14	1.743	1013.79	1767.47
A_68_P25715599	chr8:24348136-24348180	NM_024240:-18	Gins4	PROMOTER	0.595	0.634	1208.93	765.98	0.377	871.37	328.63
A_68_P31117100	chr17:27692460-27692504	NM_001025427:-1036	Hmga1	PROMOTER	0.595	0.692	1553.21	1074.37	0.412	1403.69	577.94
A_68_P27572319	chr11:7114101-7114145	NM_008343:-196	Igfbp3	PROMOTER	0.595	0.390	1367.48	533.25	0.232	1066.04	247.33
A_68_P30130467	chr15:34767012-34767056	NM_181317:-101	Kcns2	PROMOTER	0.595	0.588	992.19	583.30	0.350	860.67	301.10
A_68_P24114755	chr5:135583039-135583083	NM_021455:278	Mlxipl	INSIDE	0.595	0.605	1122.30	678.59	0.360	990.96	356.51
A_68_P22752527	chr4:15885475-15885519	NM_013752:383	Nbn	INSIDE	0.595	0.493	1053.71	519.57	0.293	793.14	232.50
A_68_P21151183	chr2:38781338-38781382	NM_010264:621	Nr6a1	INSIDE	0.595	0.691	2248.49	1553.46	0.411	1773.06	729.37
A_68_P28802625	chr13:6547192-6547238	NM_145131:-188	Pitrm1	PROMOTER	0.595	2.377	6069.01	14426.27	1.415	3902.82	5521.78
A_68_P23233548	chr4:116977181-116977225	NM_025739:192318	Rnf220	INSIDE	0.595	2.418	2800.74	6770.84	1.437	1868.70	2685.92
A_68_P21747680	chr2:151931345-151931389	NM_029688:-99	Srxn1	PROMOTER	0.595	0.646	2846.43	1838.72	0.385	2308.07	887.70
A_68_P30580616	chr16:18588788-18588832	NM_011532:-1748	Tbx1	PROMOTER	0.595	0.415	1778.89	738.00	0.247	1371.09	338.49
A_68_P26152538	chr8:111238302-111238346	NM_007496:-219	Zfhx3	PROMOTER	0.595	0.679	1081.35	734.45	0.404	944.21	381.59
A_68_P30339073	chr15:74539555-74539599	NR_033197:-14	4933427E11Rik	PROMOTER	0.594	0.475	1781.36	846.98	0.282	1168.47	329.98
A_68_P24455810	chr6:53238161-53238205	NR_015553:894	9430076C15Rik	INSIDE	0.594	0.428	1853.46	793.26	0.254	1447.77	367.84
A_68_P23260768	chr4:122782372-122782416	NM_007559:-13	Bmp8b	PROMOTER	0.594	0.539	1363.52	735.06	0.320	1135.02	363.35
A_68_P32139835	chr19:45734791-45734835	NM_013907:-129	Fbxw4	PROMOTER	0.594	0.573	1068.08	612.45	0.341	896.83	305.64
A_68_P23222200	chr4:114574734-114574778	NM_008593:6747	Foxd2	DOWNSTREAM	0.594	0.415	1753.67	727.13	0.246	1345.87	331.71
A_68_P23785052	chr5:71487399-71487443	NM_008066:-332	Gabra2	PROMOTER	0.594	0.547	1099.64	601.65	0.325	861.42	279.79
A_68_P25095548	chr7:53121361-53121405	NM_008172:669	Grin2d	INSIDE	0.594	0.662	1402.91	929.37	0.394	1222.04	480.94
A_68_P27806467	chr11:53584134-53584178	NM_001159396:182	Irf1	INSIDE	0.594	0.577	2049.85	1182.05	0.343	1649.48	565.15
A_68_P24003591	chr5:114830465-114830509	NM_001159941:28	Kctd10	INSIDE	0.594	0.449	1952.45	876.19	0.267	1600.68	426.94
A_68_P24993121	chr7:19989091-19989135	NM_146182:-3907	Klc3	DIVERGENT_PROMOTER	0.594	0.435	1409.77	612.81	0.258	1126.58	291.00
A_68_P31934666	chr19:6428995-6429039	NM_001205234:10279	Nrxn2	INSIDE	0.594	2.293	5391.29	12362.88	1.363	3511.12	4786.12
A_68_P31774689	chr18:64500435-64500479	NM_194268:439	Onecut2	INSIDE	0.594	0.667	3296.23	2200.05	0.396	2371.46	940.06
A_68_P30346620	chr15:76012400-76012444	NM_201394:13718	Plec	INSIDE	0.594	2.759	550.95	1520.08	1.640	466.16	764.39
A_68_P27921006	chr11:74335943-74335987	NM_001015046:67696	Rap1gap2	INSIDE	0.594	0.532	2306.35	1226.08	0.316	1703.70	538.42
A_68_P31097159	chr17:24551794-24551838	NM_001080127:197	Rnps1	INSIDE	0.594	0.663	1629.48	1080.65	0.394	1406.48	553.71
A_68_P31926384	chr19:5024260-5024304	NM_007854:277	Slc29a2	INSIDE	0.594	0.524	1656.91	868.73	0.312	1423.90	443.74
A_68_P20346581	chr1:74115086-74115133	NM_027884:55912	Tns1	INSIDE	0.594	0.542	1191.98	645.89	0.322	865.66	278.39
A_68_P23394410	chr4:147818444-147818488	NM_027873:394	Ubiad1	INSIDE	0.594	0.710	1967.05	1395.74	0.421	1672.34	704.34
A_68_P24091295	chr5:130418466-130418510	NM_001001327:506	Vkorc1l1	INSIDE	0.594	0.448	1611.24	721.77	0.266	1259.09	334.89
A_68_P23059228	chr4:82505265-82505309	NM_026647:279	Zdhhc21	INSIDE	0.594	0.362	1506.93	545.23	0.215	1274.73	273.96
A_68_P26199699	chr8:119445245-119445289	NM_026844:70	2310061C15Rik	INSIDE	0.593	0.631	1993.24	1257.71	0.374	1502.66	561.86
A_68_P26476278	chr9:45646743-45646787	NM_001145947:153	Bace1	INSIDE	0.593	0.651	1643.77	1069.63	0.386	1365.52	527.25
A_68_P26486124	chr9:47338813-47338857	NM_001025600:400	Cadm1	INSIDE	0.593	0.689	1720.45	1185.19	0.409	1558.50	637.17
A_68_P21628998	chr2:130120631-130120675	NM_001110513:-1022	Ebf4	PROMOTER	0.593	0.714	2592.44	1850.61	0.423	1876.95	794.32
A_68_P20938885	chr1:193399879-193399925	NM_178632:290	Ints7	INSIDE	0.593	0.450	1340.38	603.72	0.267	1058.05	282.71

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27922700	chr11:74645583-74645627	NM_010813:1179	Mnt	INSIDE	0.593	0.482	1154.05	556.61	0.286	1009.08	288.46
A_68_P24932173	chr6:146991217-146991261	NM_145573:-53	Mrps35	PROMOTER	0.593	0.358	1804.95	645.93	0.212	1586.10	336.34
A_68_P21842414	chr2:168415753-168415797	NM_001136073:-83	Nfatc2	PROMOTER	0.593	0.657	2148.69	1411.51	0.390	1208.10	470.89
A_68_P30474567	chr15:98268138-98268187	NM_146457:262	Olfr282	INSIDE	0.593	3.048	743.38	2265.76	1.809	609.24	1101.89
A_68_P29699779	chr14:70576599-70576643	NM_145978:859	Pdlim2	INSIDE	0.593	0.557	3028.68	1686.77	0.330	2376.19	784.84
A_68_P30344972	chr15:75751799-75751843	NM_025412:170	Pycrl	INSIDE	0.593	0.610	1528.07	932.19	0.362	1219.50	441.14
A_68_P30496838	chr15:102077585-102077629	NM_001042727:-823	Rarg	PROMOTER	0.593	0.414	1630.74	674.50	0.245	1351.07	331.20
A_68_P28159196	chr11:116273617-116273661	NM_027258:708	Rnf157	INSIDE	0.593	0.710	1436.28	1019.53	0.421	1107.91	466.62
A_68_P28051299	chr11:97413226-97413270	NM_018873:23192	Srcin1	INSIDE	0.593	0.608	889.92	541.50	0.361	809.41	291.86
A_68_P25232272	chr7:81159033-81159078	NM_009181:-487	St8sia2	PROMOTER	0.593	0.522	3343.28	1744.06	0.310	2614.63	809.38
A_68_P23962876	chr5:107125079-107125123	NM_026856:749	Zfp644	INSIDE	0.593	0.299	2493.51	746.29	0.178	2052.64	364.35
A_68_P24058184	chr5:124357527-124357571	NM_026603:265	Denr	INSIDE	0.592	0.638	1275.27	813.70	0.377	1045.85	394.79
A_68_P21425684	chr2:91803378-91803422	NM_138306:320	Dgkz	INSIDE	0.592	0.472	1509.86	713.20	0.280	1290.92	361.18
A_68_P25093408	chr7:52744206-52744250	NM_027903:-62	Dhdh	PROMOTER	0.592	0.591	1981.28	1171.77	0.350	1605.28	562.44
A_68_P30672035	chr16:35769023-35769067	NM_153550:398	Dirc2	INSIDE	0.592	0.411	1741.59	714.97	0.243	1510.92	367.51
A_68_P25026465	chr7:30089302-30089346	NM_013874:301	Dpf1	INSIDE	0.592	0.682	1670.30	1139.36	0.404	1269.35	512.71
A_68_P32143269	chr19:46402678-46402722	NM_133694:27	Fbxl15	INSIDE	0.592	0.569	950.84	541.30	0.337	834.76	281.20
A_68_P28377242	chr12:40949783-40949827	NM_013562:-28	Ifrd1	PROMOTER	0.592	0.410	2672.45	1096.43	0.243	1962.72	476.90
A_68_P27453320	chr10:111709075-111709123	NM_001025581:920	Kcnc2	INSIDE	0.592	0.552	990.86	547.40	0.327	709.97	232.23
A_68_P21147691	chr2:38212503-38212547	NM_010710:5697	Lhx2	INSIDE	0.592	0.527	1144.24	602.93	0.312	948.15	295.77
A_68_P25257803	chr7:86027612-86027656	NR_029826:-5528	Mir7-2	PROMOTER	0.592	0.595	1051.81	625.68	0.352	837.58	294.80
A_68_P27674921	chr11:29426434-29426478	NM_133767:0	Mtif2	INSIDE	0.592	0.496	1979.73	981.54	0.293	1667.20	489.31
A_68_P26345850	chr9:20988460-20988504	NM_183408:18325	Pde4a	INSIDE	0.592	0.536	1152.31	617.18	0.317	1038.81	329.58
A_68_P31067774	chr17:15967950-15967994	NM_178615:-4422	Rgmb	PROMOTER	0.592	0.579	2910.60	1684.44	0.342	2239.36	766.97
A_68_P22388655	chr3:103718078-103718124	NM_172684:58	Rsbn1	INSIDE	0.592	0.308	1704.85	525.40	0.183	1451.51	264.92
A_68_P29448257	chr14:21493552-21493596	NM_001168273:32	Sec24c	INSIDE	0.592	0.524	1383.50	725.40	0.310	1162.57	360.68
A_68_P28931376	chr13:32893858-32893902	NM_030215:-18	Wrnip1	PROMOTER	0.592	0.442	1884.77	833.81	0.262	1466.74	384.43
A_68_P23586719	chr5:33362030-33362074	NM_011738:588	Ywhah	INSIDE	0.592	0.440	1903.90	837.08	0.260	1523.40	396.55
A_68_P22510975	chr3:127540105-127540149	NM_145964:284	Ap1ar	INSIDE	0.591	0.647	1969.64	1275.09	0.383	1545.85	591.83
A_68_P26764915	chr9:99469261-99469305	NM_028768:36	Armc8	INSIDE	0.591	0.507	1275.98	647.07	0.300	944.09	283.19
A_68_P30404227	chr15:85809018-85809063	NM_009886:55167	Celsr1	INSIDE	0.591	2.968	311.14	923.41	1.755	375.22	658.46
A_68_P24058179	chr5:124357031-124357075	NM_026603:-231	Denr	PROMOTER	0.591	0.439	2534.45	1111.70	0.259	2046.88	530.57
A_68_P20558185	chr1:121545078-121545122	NM_145506:477	Epb4.1l5	INSIDE	0.591	0.534	1283.66	686.03	0.316	1047.29	330.86
A_68_P31207969	chr17:46765813-46765857	NM_175168:619	Ptk7	INSIDE	0.591	0.685	1632.20	1117.64	0.405	1424.66	576.74
A_68_P25425954	chr7:119822563-119822607	NM_001166584:-249	Tead1	PROMOTER	0.591	0.696	1116.05	776.37	0.411	827.84	340.06
A_68_P23970433	chr5:108561687-108561731	NM_028876:-98	Tmed5	DIVERGENT_PROMOTER	0.591	0.563	1286.53	724.64	0.333	1064.53	354.31
A_68_P22872184	chr4:43536297-43536341	NM_009416:-58	Tpm2	PROMOTER	0.591	0.647	1978.44	1279.19	0.382	1525.80	582.66
A_68_P27926185	chr11:75268208-75268252	NM_138950:-11	Wdr81	DIVERGENT_PROMOTER	0.591	0.590	998.65	589.12	0.349	725.60	252.95
A_68_P23318625	chr4:133189081-133189125	NM_001017968:242	Zdhhc18	INSIDE	0.591	0.727	1867.74	1358.58	0.430	1424.77	612.52
A_68_P32217859	chr19:59268751-59268795			Unknown	0.591	0.692	1552.77	1074.21	0.409	1214.18	496.59
A_68_P25007551	chr7:25740203-25740247			Unknown	0.591	0.501	2713.42	1358.79	0.296	2068.17	612.20
A_68_P23817352	chr5:77087407-77087451	ENSMUST00000125922:683		INSIDE	0.591	0.646	1029.33	664.65	0.382	900.77	343.76
A_68_P25415073	chr7:117912172-117912216	NM_009667:-3923	Ampd3	PROMOTER	0.590	0.708	1292.80	915.88	0.418	1120.65	468.80
A_68_P27228313	chr10:69652213-69652261	NM_001111121:92368	Ccdc6	INSIDE	0.590	3.830	1022.68	3916.45	2.259	799.74	1807.01
A_68_P23202007	chr4:109339070-109339115	NM_007671:-1115	Cdkn2c	PROMOTER	0.590	0.689	1117.88	770.49	0.407	936.38	380.95
A_68_P25592946	chr7:149281230-149281274	NM_008748:-63	Dusp8	PROMOTER	0.590	0.457	2086.08	952.95	0.269	1690.04	455.17
A_68_P26878190	chr9:120401831-120401875	NM_026892:129	Eif1b	INSIDE	0.590	0.643	2200.97	1414.61	0.379	1671.60	634.25
A_68_P23561108	chr5:28492702-28492746	NM_010134:489	En2	INSIDE	0.590	0.582	1171.21	681.86	0.344	1050.16	360.88
A_68_P31624334	chr18:36675661-36675705	NM_010415:-223	Hbegf	PROMOTER	0.590	0.491	2047.62	1006.16	0.290	1646.99	477.39
A_68_P21840415	chr2:168094408-168094454	NM_001081134:401	Kcng1	INSIDE	0.590	4.346	2995.93	13019.33	2.564	1963.66	5034.52
A_68_P27838142	chr11:59475681-59475726	NM_012027:-293	Mprip	PROMOTER	0.590	0.489	2725.32	1333.89	0.289	2117.86	611.96

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P29694907	chr14:69808925-69808969	NM_010921:198	Nkx3-1	INSIDE	0.590	0.638	1546.71	986.36	0.376	1204.94	453.06
A_68_P22593191	chr3:142545216-142545260	NM_178654:-270	Pkn2	PROMOTER	0.590	0.365	1598.84	582.80	0.215	1338.37	287.70
A_68_P30477113	chr15:98711795-98711839	NM_026967:29	Rhebl1	INSIDE	0.590	0.638	2410.21	1538.84	0.376	1874.16	705.52
A_68_P20250374	chr1:57026684-57026728	NM_139146:1472	Satb2	INSIDE	0.590	0.551	962.45	530.59	0.325	833.78	271.05
A_68_P22169678	chr3:58496243-58496287	NM_009174:46	Siah2	INSIDE	0.590	0.678	1708.09	1158.64	0.400	1488.06	595.39
A_68_P24951727	chr7:4990151-4990195	NM_001039532:-124	Zfp784	PROMOTER	0.590	0.495	1695.96	839.82	0.292	1174.83	343.22
A_68_P21040880	chr2:18610461-18610505	NM_007552:11838	Bmi1	DOWNSTREAM	0.589	0.633	1224.93	775.07	0.373	1105.97	412.53
A_68_P28071735	chr11:100931508-100931552	NM_013792:123	Naglu	INSIDE	0.589	0.655	3157.25	2067.87	0.386	2575.22	993.59
A_68_P25343523	chr7:103360337-103360381	NM_011858:1212	Odz4	INSIDE	0.589	0.648	1218.86	789.75	0.382	970.32	370.61
A_68_P23271482	chr4:124664450-124664494	NM_138683:799	Rspo1	INSIDE	0.589	0.534	1364.90	729.21	0.314	1093.02	343.75
A_68_P21099540	chr2:29658503-29658547	NM_011989:325	Slc27a4	INSIDE	0.589	0.635	2505.89	1590.11	0.374	2038.73	761.84
A_68_P27844726	chr11:60591168-60591212	NM_175491:164	Smcr8	INSIDE	0.589	0.522	1251.94	653.71	0.308	882.45	271.43
A_68_P28055911	chr11:98219606-98219650	NM_021547:-69	Stard3	PROMOTER	0.589	0.669	1966.85	1314.93	0.394	1854.60	730.57
A_68_P20156312	chr1:37921635-37921679	NM_207228:268	Tsga10	INSIDE	0.589	0.734	2196.50	1611.88	0.432	1827.78	789.63
A_68_P23340749	chr4:137150280-137150324	NM_130879:199	Usp48	INSIDE	0.589	0.550	1095.82	602.36	0.324	964.16	312.11
A_68_P20433089	chr1:91838165-91838209	AK051578:11351		DOWNSTREAM	0.589	0.737	2162.14	1593.01	0.434	1701.73	738.74
A_68_P28448909	chr12:55757202-55757246	NM_134054:335	1110002B05Rik	INSIDE	0.588	0.474	2137.50	1012.68	0.279	1647.80	459.13
A_68_P28073762	chr11:101278541-101278585	NM_144829:185	Aarsd1	INSIDE	0.588	0.663	2841.75	1882.70	0.389	2252.20	876.80
A_68_P28574815	chr12:81360407-81360451	NM_134156:930	Actn1	INSIDE	0.588	0.558	1566.46	874.72	0.328	1291.53	423.94
A_68_P21071034	chr2:25127984-25128028	NM_175300:21	Anapc2	INSIDE	0.588	0.520	1814.36	943.09	0.305	1493.07	456.13
A_68_P30579427	chr16:18392999-18393043	NM_033474:44654	Arvcf	INSIDE	0.588	0.577	1495.70	862.72	0.339	1055.92	357.93
A_68_P28596936	chr12:85534975-85535019	NM_001163502:-31	C130039O16Rik	PROMOTER	0.588	0.587	1200.40	704.15	0.345	1073.45	370.30
A_68_P29454308	chr14:22505922-22505966	NM_001013826:27854	Dupd1	INSIDE	0.588	0.575	1335.15	767.19	0.338	1088.89	367.69
A_68_P29941732	chr14:119324506-119324550	NM_025943:-2139	Dzip1	PROMOTER	0.588	0.519	1763.44	915.93	0.306	1422.85	434.86
A_68_P27281570	chr10:79649434-79649479	NM_007909:7230	Efna2	INSIDE	0.588	2.645	5708.01	15096.17	1.556	3752.70	5837.50
A_68_P24005878	chr5:115199611-115199670	NM_001077360:23860	Git2	INSIDE	0.588	3.829	817.22	3129.23	2.252	735.92	1657.63
A_68_P24448934	chr6:52142084-52142128	NM_008265:-404	Hoxa4	DIVERGENT_PROMOTER	0.588	0.393	1418.62	557.15	0.231	1199.19	277.16
A_68_P22312508	chr3:88019276-88019320	NR_029817:-221	Mir9-1	PROMOTER	0.588	0.675	3063.02	2066.37	0.397	2338.02	927.20
A_68_P26983365	chr10:19569569-19569613	NM_029529:1675	Slc35d3	INSIDE	0.588	0.572	1545.29	883.45	0.336	1185.10	398.63
A_68_P22149839	chr3:54598091-54598144	NM_019483:38614	Smad9	INSIDE	0.588	3.121	567.72	1771.93	1.836	545.08	1000.84
A_68_P25670892	chr8:13869760-13869804	NM_181854:142	Zfp828	INSIDE	0.588	0.622	1248.35	776.91	0.366	942.02	344.73
A_68_P27958481	chr11:80966909-80966953	NM_007384:-525	Accn1	PROMOTER	0.587	0.530	1433.96	760.52	0.311	1131.20	352.29
A_68_P32536866	chrX:91226350-91226409	NR_028320:12385	AU015836	DOWNSTREAM	0.587	3.387	761.39	2578.65	1.989	311.25	618.96
A_68_P28454005	chr12:56962212-56962256	NM_001037756:24882	Brms1l	INSIDE	0.587	2.506	3126.73	7837.02	1.472	2390.91	3518.38
A_68_P31613997	chr18:34810920-34810964	NM_178347:448	Cdc23	INSIDE	0.587	0.539	1317.81	710.65	0.316	1280.28	405.10
A_68_P24948002	chr7:4103289-4103333	NM_021454:12991	Cdc42ep5	INSIDE	0.587	0.550	1204.32	662.79	0.323	994.85	321.59
A_68_P21070567	chr2:25066910-25066954	NM_021393:77	Cobra1	INSIDE	0.587	0.613	2930.85	1797.52	0.360	2259.95	813.56
A_68_P30476595	chr15:98637338-98637382	NM_001013741:996	Ddn	INSIDE	0.587	0.527	1055.42	556.17	0.309	607.30	187.81
A_68_P25051306	chr7:36587684-36587728	NR_033567:96	E130304I02Rik	INSIDE	0.587	0.600	1063.82	638.82	0.353	839.10	295.97
A_68_P21374845	chr2:80287756-80287800	NM_011356:-225	Frzb	PROMOTER	0.587	0.598	1486.51	889.05	0.351	1228.64	431.51
A_68_P28156586	chr11:115836453-115836497	NM_001005608:436	Itgb4	INSIDE	0.587	0.690	1192.84	822.66	0.405	1019.21	412.34
A_68_P21077040	chr2:26061806-26061850	NM_001039653:248	Lhx3	INSIDE	0.587	0.674	1325.00	892.57	0.395	1011.50	400.02
A_68_P30504522	chr15:103333324-103333368	NM_008800:-382	Pde1b	PROMOTER	0.587	0.563	5703.82	3213.64	0.331	4299.93	1422.32
A_68_P31709379	chr18:52927884-52927928	NM_001199154:109	Sncaip	INSIDE	0.587	0.598	3074.14	1837.96	0.351	2558.60	897.60
A_68_P24001332	chr5:114443223-114443267	NM_198109:522	Ssh1	INSIDE	0.587	0.614	974.48	598.35	0.360	898.80	323.69
A_68_P24974288	chr7:13622741-13622791	NM_145578:561	Ube2m	INSIDE	0.587	3.217	3408.62	10964.70	1.887	2139.26	4036.39
A_68_P25075267	chr7:48155196-48155240	NM_021387:571	Vstm2b	INSIDE	0.587	0.600	1537.76	922.13	0.352	1083.43	381.25
A_68_P25063517	chr7:38557044-38557088	NM_172385:-2295	Zfp536	PROMOTER	0.587	0.596	1286.86	767.42	0.350	1140.18	399.32
A_68_P28787943	chr13:3358419-3358463			Unknown	0.587	0.572	1915.00	1096.27	0.336	1673.32	561.86
A_68_P29848869	chr14:100685216-100685260	AK021307:-1632		PROMOTER	0.587	0.662	1466.94	971.10	0.389	1239.62	482.10
A_68_P23996382	chr5:113567569-113567615	NM_172884:24741	2900026A02Rik	INSIDE	0.586	0.508	1928.01	979.69	0.298	1581.06	470.66

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P29113347	chr13:69137713-69137757	NM_153534:685	Adcy2	INSIDE	0.586	0.475	2924.73	1389.59	0.279	2510.56	699.32
A_68_P23818507	chr5:77287352-77287398	NM_001163793:17751	C530008M17Rik	INSIDE	0.586	2.378	1867.71	4441.86	1.394	1621.02	2258.91
A_68_P30371307	chr15:80118683-80118727	NM_001044308:1037	Cacna1i	INSIDE	0.586	0.546	1468.48	801.33	0.320	1132.34	362.15
A_68_P28925094	chr13:31898196-31898240	NM_008592:-296	Foxc1	PROMOTER	0.586	0.561	1913.30	1073.09	0.329	1442.34	474.33
A_68_P31151376	chr17:34115729-34115774	NR_004446:-15	H2-K2	DIVERGENT_PROMOTER	0.586	0.479	1184.32	567.85	0.281	896.88	252.05
A_68_P24637118	chr6:91106557-91106606	NM_144919:-227	Hdac11	PROMOTER	0.586	0.551	945.08	520.85	0.323	768.25	248.10
A_68_P24116584	chr5:135965213-135965257	NM_146001:55758	Hip1	INSIDE	0.586	0.687	1038.07	713.20	0.403	893.22	359.88
A_68_P20646087	chr1:138362972-138363016	NM_001081258:-1540	Kif14	PROMOTER	0.586	0.509	1568.30	797.99	0.298	1246.87	371.71
A_68_P31612701	chr18:34569089-34569133	NM_001163004:34	Pkd2l2	INSIDE	0.586	0.478	1227.35	587.13	0.280	1201.01	336.66
A_68_P28549414	chr12:76696397-76696441	NM_012024:769	Ppp2r5e	INSIDE	0.586	0.546	1307.02	713.63	0.320	1038.60	332.58
A_68_P23239264	chr4:117933534-117933578	NM_011213:30446	Ptprf	INSIDE	0.586	0.622	2082.68	1295.04	0.364	1607.52	585.38
A_68_P28187725	chr11:120812339-120812383	NM_001038653:1980	Slc16a3	INSIDE	0.586	0.481	1844.74	887.19	0.282	1489.49	419.73
A_68_P27086284	chr10:40603346-40603390	NM_031877:29	Wasf1	INSIDE	0.586	0.617	1123.31	692.57	0.361	904.19	326.61
A_68_P30511519	chr16:4679291-4679335	NM_030205:408	Coro7	INSIDE	0.585	0.743	2750.91	2044.13	0.435	2371.87	1031.09
A_68_P29688234	chr14:68551046-68551090	NM_177780:561	Dock5	INSIDE	0.585	0.514	1339.68	688.48	0.300	1156.66	347.46
A_68_P23120702	chr4:94717432-94717476	NM_010591:1459	Jun	INSIDE	0.585	0.436	1934.02	843.61	0.255	1533.51	391.60
A_68_P21076058	chr2:25915846-25915890	NM_001037098:32048	Nacc2	INSIDE	0.585	3.005	760.70	2285.96	1.759	618.06	1087.18
A_68_P20927663	chr1:191552534-191552578	NM_008976:410	Ptpn14	INSIDE	0.585	0.627	1222.18	765.79	0.367	994.35	364.73
A_68_P25025137	chr7:29849427-29849471	NM_009109:60722	Ryr1	INSIDE	0.585	3.562	488.34	1739.48	2.085	447.61	933.23
A_68_P24265240	chr6:17015458-17015502	NM_207176:332	Tes	INSIDE	0.585	0.500	1068.22	534.25	0.293	888.76	260.11
A_68_P20346582	chr1:74115236-74115286	NM_027884:55761	Tns1	INSIDE	0.585	0.486	1637.65	796.65	0.284	1178.01	335.06
A_68_P30214224	chr15:51871601-51871645	NM_175503:-30	Aard	PROMOTER	0.584	0.646	1498.65	967.89	0.377	1408.32	531.36
A_68_P26289572	chr9:7837195-7837239	NM_007465:-1961	Birc2	PROMOTER	0.584	0.612	1049.29	642.09	0.357	770.67	275.28
A_68_P32130738	chr19:44220823-44220867	NM_028607:92	Bloc1s2	INSIDE	0.584	0.550	1274.72	701.66	0.322	1090.56	350.70
A_68_P27533815	chr10:126500675-126500719	NM_009870:38	Cdk4	INSIDE	0.584	0.617	1119.52	690.68	0.360	881.74	317.42
A_68_P21603779	chr2:125450959-125451003	NM_001081091:-131	Cep152	PROMOTER	0.584	0.440	1192.28	525.10	0.257	954.54	245.33
A_68_P21820017	chr2:164658603-164658647	NM_001038492:252	Ctsa	INSIDE	0.584	0.619	1168.57	723.19	0.361	836.37	302.12
A_68_P31928719	chr19:5447756-5447800	NM_010235:81	Fosl1	INSIDE	0.584	0.663	1175.44	778.85	0.387	992.25	383.70
A_68_P30358260	chr15:78004836-78004880	NM_025931:-320	Ift27	PROMOTER	0.584	0.484	2458.65	1188.88	0.282	1884.91	532.31
A_68_P31927054	chr19:5117908-5117952	NM_008451:478	Klc2	INSIDE	0.584	0.569	1030.60	585.96	0.332	772.93	256.46
A_68_P27903938	chr11:70833216-70833260	NM_025993:126	Mis12	INSIDE	0.584	0.426	1984.46	845.79	0.249	1636.81	407.41
A_68_P28157575	chr11:115999733-115999777	NM_024177:428	Mrpl38	INSIDE	0.584	0.723	2131.30	1540.49	0.422	1658.02	700.46
A_68_P24990653	chr7:19548237-19548281	NM_001029877:37022	Nova2	INSIDE	0.584	0.596	864.84	515.06	0.348	716.69	249.28
A_68_P25809871	chr8:42325399-42325443	NM_023662:308	Pcm1	INSIDE	0.584	0.450	1836.14	826.68	0.263	1441.26	379.25
A_68_P29094161	chr13:63665111-63665155	NM_008957:1696	Ptch1	INSIDE	0.584	0.636	1075.76	683.74	0.371	814.33	302.29
A_68_P22753437	chr4:16090490-16090534	NM_138952:133	Ripk2	INSIDE	0.584	0.534	3360.68	1795.39	0.312	2760.93	861.70
A_68_P27160893	chr10:57252088-57252132	NM_019760:225	Serinc1	INSIDE	0.584	0.598	2679.26	1601.93	0.349	2042.17	713.07
A_68_P26229670	chr8:124431063-124431107	NM_011404:502	Slc7a5	INSIDE	0.584	0.556	1446.85	804.54	0.325	967.08	314.19
A_68_P23749449	chr5:64550826-64550870	NM_019636:-601	Tbc1d1	PROMOTER	0.584	0.723	1945.85	1406.56	0.422	1543.93	651.55
A_68_P30405821	chr15:86044775-86044819	NM_145476:-92	Tbc1d22a	PROMOTER	0.584	0.707	1291.53	913.22	0.413	1017.61	420.45
A_68_P24097673	chr5:131783669-131783713	NM_145218:-298	Wbscr17	PROMOTER	0.584	0.547	1383.22	756.17	0.319	1156.88	369.14
A_68_P27630624	chr11:20149666-20149710	NM_172260:-261	Cep68	PROMOTER	0.583	0.701	1895.69	1328.52	0.409	1310.85	535.75
A_68_P23797904	chr5:73881900-73881944	NM_001190733:-342	Dcun1d4	PROMOTER	0.583	0.535	1183.96	633.58	0.312	948.80	296.23
A_68_P21823221	chr2:165151623-165151667	NM_207705:-9251	Elmo2	PROMOTER	0.583	0.534	1692.06	904.29	0.311	1298.13	404.31
A_68_P30589022	chr16:20695936-20695980	NM_133778:829	Fam131a	INSIDE	0.583	0.481	1123.15	539.78	0.280	885.61	248.13
A_68_P32135379	chr19:45006013-45006057	NM_001081225:426	Fam178a	INSIDE	0.583	0.712	1613.59	1149.54	0.415	1325.25	550.36
A_68_P25361477	chr7:106530129-106530173	NM_201352:92	Gdpd5	INSIDE	0.583	0.713	4847.48	3456.02	0.415	3705.98	1539.77
A_68_P27897910	chr11:69727956-69728000	NM_019726:285	Gps2	INSIDE	0.583	0.475	2358.46	1120.53	0.277	2000.33	553.62
A_68_P31381050	chr17:80461904-80461948	NM_144802:-252	Hnrpll	PROMOTER	0.583	0.604	1043.17	630.03	0.352	867.92	305.53
A_68_P31618898	chr18:35721681-35721725	NM_010771:-109	Matr3	PROMOTER	0.583	0.687	1018.69	700.32	0.401	801.10	320.86
A_68_P23312412	chr4:132019695-132019742	NM_026039:118	Med18	INSIDE	0.583	0.639	1206.94	770.71	0.372	972.08	362.05

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P21842487	chr2:168427037-168427082	NM_001037178:96	Nfatc2	INSIDE	0.583	0.632	2127.20	1343.38	0.368	1665.96	612.90
A_68_P25144267	chr7:63217811-63217855	NM_023647:-12	Nipa2	DIVERGENT_PROMOTER	0.583	0.572	1925.68	1102.39	0.334	1670.82	557.86
A_68_P23417946	chr4:151687386-151687430	NM_001033489:5326	Rnf207	INSIDE	0.583	0.395	1871.00	738.27	0.230	1446.89	332.85
A_68_P25021896	chr7:29221702-29221746	NM_175021:-514	Samd4b	DIVERGENT_PROMOTER	0.583	0.559	1178.30	658.97	0.326	988.86	322.20
A_68_P32113654	chr19:41281095-41281139	NM_011904:148	Tll2	INSIDE	0.583	0.324	1788.52	579.01	0.189	1515.62	285.94
A_68_P25393298	chr7:112766252-112766301	NM_018880:15737	Trim3	INSIDE	0.583	3.635	900.14	3272.04	2.120	687.53	1457.72
A_68_P27553116	chr11:3549120-3549164	NR_002321:-331	Tug1	DIVERGENT_PROMOTER	0.583	0.551	1689.80	930.29	0.321	1397.58	448.47
A_68_P24084069	chr5:129106010-129106054	NR_015517:530	5930412G12Rik	INSIDE	0.582	0.549	1411.44	774.39	0.319	1193.13	381.14
A_68_P32186064	chr19:54121845-54121889	NM_007417:2195	Adra2a	INSIDE	0.582	0.467	4281.35	1999.14	0.272	3174.42	862.59
A_68_P27987612	chr11:86014370-86014414	NM_178309:303	Brip1	INSIDE	0.582	0.442	1329.23	586.89	0.257	1017.15	261.40
A_68_P28053991	chr11:97884084-97884128	NM_145121:-165	Cacnb1	DIVERGENT_PROMOTER	0.582	0.583	1340.27	781.35	0.339	1030.71	349.81
A_68_P22715816	chr4:8618846-8618890	NM_001081417:801	Chd7	INSIDE	0.582	0.588	1987.24	1168.28	0.342	1535.90	525.41
A_68_P22383904	chr3:102824419-102824463	NM_001161854:-28	Csde1	PROMOTER	0.582	0.712	1739.02	1238.71	0.414	1408.55	583.84
A_68_P22998987	chr4:68614912-68614956	NM_019967:497	Dbc1	INSIDE	0.582	0.588	4040.92	2377.58	0.343	2851.93	976.91
A_68_P21486502	chr2:103810841-103810885	NM_001142335:419	Lmo2	INSIDE	0.582	0.502	2107.53	1058.46	0.292	1592.02	465.02
A_68_P27855153	chr11:62478528-62478583	NM_175002:16390	Mmgt2	INSIDE	0.582	2.520	1615.21	4069.55	1.466	1313.96	1926.60
A_68_P23749118	chr5:64484258-64484302	NM_025700:92	Pgm1	INSIDE	0.582	0.435	1405.88	610.91	0.253	1098.24	277.77
A_68_P22778510	chr4:22415241-22415285	NM_008899:16	Pou3f2	INSIDE	0.582	0.557	1936.78	1078.50	0.324	1608.27	521.51
A_68_P31919102	chr19:3767890-3767935	NM_001167884:492	Suv420h1	INSIDE	0.582	0.368	1882.44	692.33	0.214	1476.78	316.13
A_68_P23291909	chr4:128263071-128263115	NM_177758:24250	Zscan20	INSIDE	0.582	2.509	1907.70	4786.37	1.460	1270.91	1855.73
A_68_P26351649	chr9:22193381-22193425	NM_028390:248	Anln	INSIDE	0.581	0.534	2202.16	1176.53	0.311	1832.55	569.23
A_68_P23237382	chr4:117602465-117602509	NM_009711:-118	Artn	PROMOTER	0.581	0.578	927.52	535.73	0.336	760.39	255.25
A_68_P26352023	chr9:22280042-22280086	NM_178415:-94	Bbs9	DIVERGENT_PROMOTER	0.581	0.453	2385.20	1080.37	0.263	1848.16	486.01
A_68_P29639450	chr14:60216642-60216686	NM_001168535:132	Cdadc1	INSIDE	0.581	0.529	1593.61	843.08	0.307	1313.86	403.51
A_68_P24483216	chr6:58781482-58781526	NM_028705:-2189	Herc3	PROMOTER	0.581	0.701	1869.26	1311.24	0.408	1596.32	650.82
A_68_P21814760	chr2:163679507-163679551	NM_001030292:43	Kcnk15	INSIDE	0.581	0.683	1483.07	1013.04	0.397	1168.80	463.49
A_68_P21820020	chr2:164658912-164658956	NM_001082974:162	Neurl2	INSIDE	0.581	0.624	2133.92	1331.60	0.363	1653.66	600.01
A_68_P20354547	chr1:75502266-75502310	NM_178884:739	Obsl1	INSIDE	0.581	0.691	1324.77	915.62	0.402	1148.24	461.21
A_68_P30213987	chr15:51823056-51823100	NM_009009:228	Rad21	INSIDE	0.581	0.625	1189.79	743.37	0.363	1281.63	465.47
A_68_P31303254	chr17:66234502-66234546	NM_001198949:-261	Ralbp1	PROMOTER	0.581	0.565	1492.42	842.92	0.328	1169.84	384.02
A_68_P25094672	chr7:52970422-52970466	NM_020011:133	Sphk2	INSIDE	0.581	0.611	1761.61	1077.13	0.355	1348.74	479.06
A_68_P29560588	chr14:41779590-41779634	NM_145928:484	Tspan14	INSIDE	0.581	0.520	1838.70	955.94	0.302	1504.30	454.60
A_68_P24129053	chr5:138596838-138596882	NM_019747:112	Zfp113	INSIDE	0.581	0.696	1327.08	923.33	0.404	1009.66	407.96
A_68_P30350970	chr15:76701410-76701454	NM_001007568:433	Zfp251	INSIDE	0.581	0.542	1337.07	724.17	0.315	1079.66	339.70
A_68_P24165132	chr5:146041465-146041509	NM_001081431:-2725	Zfp498	PROMOTER	0.581	0.514	1170.54	602.02	0.299	1047.64	313.04
A_68_P29455233	chr14:22668221-22668265	NM_026965:-110	Comtd1	PROMOTER	0.580	0.619	1182.20	732.35	0.359	892.59	320.72
A_68_P30109622	chr15:30576916-30576960	NM_008729:474591	Ctnnd2	INSIDE	0.580	0.676	6571.73	4443.22	0.392	5192.23	2037.84
A_68_P30477181	chr15:98724879-98724923	NM_007857:4071	Dhh	INSIDE	0.580	0.550	1153.09	634.29	0.319	1038.42	331.31
A_68_P23539567	chr5:23536236-23536280	NM_053090:243	Fam126a	INSIDE	0.580	0.532	1173.13	624.22	0.309	1009.61	311.81
A_68_P25181446	chr7:72301608-72301652	NM_183087:-216	Fam189a1	PROMOTER	0.580	0.633	1533.31	971.24	0.368	1321.13	485.66
A_68_P24173494	chr5:148211545-148211589	NM_010229:499	Flt3	INSIDE	0.580	0.536	1212.71	649.66	0.311	1069.32	332.11
A_68_P25965607	chr8:75876888-75876932	NM_010687:-455	Large	PROMOTER	0.580	0.640	3075.41	1967.19	0.371	2662.94	987.24
A_68_P31113238	chr17:27070074-27070118	NM_009343:25	Phf1	INSIDE	0.580	0.473	1647.89	778.89	0.274	1296.92	355.43
A_68_P22282899	chr3:82859431-82859475	NM_016784:-7	Plrg1	DIVERGENT_PROMOTER	0.580	0.691	1792.03	1238.57	0.401	1438.42	576.72
A_68_P25736232	chr8:28153444-28153488	NM_001039077:440	Prosc	INSIDE	0.580	0.637	1710.49	1089.82	0.370	1291.68	477.72
A_68_P26825589	chr9:110645592-110645636	NM_001083936:-500	Pth1r	PROMOTER	0.580	0.411	1991.10	817.54	0.238	1559.66	371.21
A_68_P21132195	chr2:35055732-35055776	NM_026697:886	Rab14	INSIDE	0.580	0.630	1690.96	1065.90	0.366	1391.18	508.67
A_68_P24983214	chr7:17367558-17367602	NM_009201:886	Slc1a5	INSIDE	0.580	0.568	2163.86	1229.99	0.330	1549.68	511.26
A_68_P26015637	chr8:86118596-86118640	NM_027179:-228	Tecr	PROMOTER	0.580	0.569	1785.36	1015.03	0.330	1281.21	422.42
A_68_P27188397	chr10:62349624-62349668	NM_027384:-6884	Tet1	PROMOTER	0.580	0.470	1401.47	658.65	0.273	1197.01	326.31
A_68_P29211816	chr13:90229293-90229337	NM_025335:43	Tmem167	INSIDE	0.580	0.594	2440.41	1450.01	0.345	1874.10	646.27

						Sham group			TiO$_2$-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P22881129	chr4:45120647-45120691	NM_001099675:317	Tomm5	INSIDE	0.580	0.725	3108.26	2254.27	0.421	2339.66	984.34
A_68_P26024221	chr8:87823033-87823077	NM_022997:342	Vps35	INSIDE	0.580	0.564	1183.96	668.26	0.327	1087.68	356.17
A_68_P20730831	chr1:156052030-156052074	NM_001204908:3736	Zfp648	INSIDE	0.580	0.635	1837.98	1167.92	0.368	1387.16	511.01
A_68_P31921019	chr19:4097126-4097170	NM_026373:-202	Cdk2ap2	PROMOTER	0.579	0.598	2421.43	1448.75	0.347	1777.27	616.17
A_68_P30475796	chr15:98493283-98493327	NM_001080981:16	Ddx23	INSIDE	0.579	0.691	2075.61	1433.25	0.400	1564.93	625.98
A_68_P27941031	chr11:77845557-77845601	NM_183286:-236	Dhrs13	PROMOTER	0.579	0.745	3029.23	2257.21	0.432	2349.80	1014.47
A_68_P31928290	chr19:5367444-5367500	NM_027236:660	Eif1ad	INSIDE	0.579	0.459	1233.97	566.61	0.266	1159.37	308.41
A_68_P25528910	chr7:138687411-138687455	NM_008257:956	Hmx3	INSIDE	0.579	0.611	2432.25	1486.29	0.354	1796.73	635.58
A_68_P24634428	chr6:90686241-90686285	NM_001134384:73855	Iqsec1	INSIDE	0.579	0.678	2612.91	1772.44	0.393	2089.01	820.01
A_68_P21811852	chr2:163165006-163165050	NM_021566:58681	Jph2	INSIDE	0.579	2.985	3279.26	9788.78	1.727	2219.38	3833.21
A_68_P28814398	chr13:9092754-9092798	NM_172585:-374	Larp4b	PROMOTER	0.579	0.462	2798.39	1293.94	0.268	2228.87	596.23
A_68_P26465869	chr9:43938100-43938144	NM_023061:-4618	Mcam	PROMOTER	0.579	0.651	1367.40	889.59	0.377	920.52	346.68
A_68_P31400333	chr17:84105260-84105304	NM_001171053:-220	Mta3	PROMOTER	0.579	0.580	2863.75	1660.20	0.336	2363.73	793.91
A_68_P29681978	chr14:67528942-67528986	NM_175498:-1080	Pnma2	PROMOTER	0.579	0.659	2916.67	1920.97	0.381	2155.40	821.28
A_68_P26783903	chr9:103014881-103014925	NM_173781:499	Rab6b	INSIDE	0.579	0.656	1862.64	1222.49	0.380	1492.34	567.03
A_68_P23328514	chr4:134990088-134990132	NM_022980:-390	Rcan3	PROMOTER	0.579	0.637	1470.26	936.68	0.369	1113.42	410.39
A_68_P32131187	chr19:44322861-44322905	NM_024450:45105	Scd3	DOWNSTREAM	0.579	0.483	1336.55	645.79	0.280	1158.84	324.23
A_68_P23212277	chr4:111392547-111392591	NM_026470:-46	Spata6	PROMOTER	0.579	0.722	2450.04	1768.02	0.418	1935.81	808.79
A_68_P21395954	chr2:84877657-84877701	NM_001136081:71	Ssrp1	INSIDE	0.579	0.680	1147.42	780.43	0.394	841.63	331.42
A_68_P23416141	chr4:151406800-151406844	NM_031867:5777	Tas1r1	INSIDE	0.579	2.881	2323.06	6692.06	1.668	1697.79	2831.10
A_68_P26713770	chr9:89599836-89599880	NM_025360:23	Tmed3	INSIDE	0.579	0.526	1640.26	863.54	0.305	1456.47	443.97
A_68_P28087330	chr11:103671857-103671901	NM_009521:36390	Wnt3	INSIDE	0.579	0.650	1416.30	921.02	0.377	1132.06	426.34
A_68_P21907109	chr2:180655229-180655273	NM_173761:391	Ythdf1	INSIDE	0.579	0.732	4037.06	2954.50	0.423	3038.38	1286.42
A_68_P20997496	chr2:9804242-9804286	NR_024257:1392	4930412O13Rik	INSIDE	0.578	0.432	1238.32	535.15	0.250	906.54	226.47
A_68_P31099615	chr17:24941244-24941288	NM_029197:-60	4930528F23Rik	PROMOTER	0.578	0.577	956.95	552.02	0.333	928.45	309.45
A_68_P30931274	chr16:85802529-85802573	NM_009621:810	Adamts1	INSIDE	0.578	0.515	1303.21	671.32	0.298	1028.77	306.50
A_68_P25190563	chr7:73984782-73984826	NM_001033877:184	Adamts17	INSIDE	0.578	0.708	2513.85	1779.56	0.409	1968.77	805.09
A_68_P21587096	chr2:122436805-122436849	NM_025961:187	Gatm	INSIDE	0.578	0.637	1149.79	732.57	0.368	992.33	365.34
A_68_P25581954	chr7:147234659-147234703	NM_010836:307	Msx3	INSIDE	0.578	0.504	2172.19	1094.67	0.291	1560.04	454.44
A_68_P21419238	chr2:90687606-90687650	NM_019758:317	Mtch2	INSIDE	0.578	0.484	1622.41	785.73	0.280	1170.82	327.70
A_68_P27638868	chr11:21896875-21896919	NM_011023:4758	Otx1	INSIDE	0.578	0.602	908.17	547.01	0.348	724.67	252.19
A_68_P31934460	chr19:6398732-6398778	NM_011242:-1828	Rasgrp2	PROMOTER	0.578	0.465	1130.32	525.27	0.268	897.33	240.83
A_68_P26522400	chr9:53619652-53619696	NM_028060:333	Slc35f2	INSIDE	0.578	0.536	1415.28	758.62	0.310	1195.29	370.62
A_68_P28137834	chr11:112644282-112644326	NM_011448:781	Sox9	INSIDE	0.578	0.511	1460.42	745.79	0.295	1178.99	347.99
A_68_P25065279	chr7:38870220-38870264	AK181724:37896		INSIDE	0.578	0.518	1871.57	969.62	0.299	1406.81	421.10
A_68_P28713546	chr12:107412574-107412618	BC156654:374736		DOWNSTREAM	0.578	0.432	1914.63	826.66	0.250	1554.94	388.09
A_68_P30547087	chr16:11254371-11254415	NM_001130008:26	Gspt1	INSIDE	0.577	0.614	3031.98	1860.73	0.354	2326.81	824.29
A_68_P25596368	chr7:149846445-149846489	NM_001122736:474	Igf2	INSIDE	0.577	0.370	1630.36	603.75	0.214	1179.04	252.07
A_68_P28832392	chr13:12553513-12553557	NM_001199043:471	Lgals8	INSIDE	0.577	0.611	1021.01	623.80	0.352	870.26	306.72
A_68_P31104862	chr17:25716282-25716326	NM_029624:186	Lmf1	INSIDE	0.577	0.708	1309.45	926.46	0.409	987.70	403.56
A_68_P29284641	chr13:104125004-104125048	NM_175171:-454	Mast4	PROMOTER	0.577	0.664	1558.60	1034.88	0.383	1257.14	481.27
A_68_P26024230	chr8:87823989-87824033	NM_001163791:480	Orc6	INSIDE	0.577	0.591	1130.55	668.43	0.341	913.64	311.66
A_68_P23696202	chr5:53060801-53060845	NM_172490:118	Sepsecs	INSIDE	0.577	0.299	1850.27	553.64	0.173	1378.19	237.74
A_68_P29879712	chr14:106295768-106295812	NM_011897:246	Spry2	INSIDE	0.577	0.442	1487.24	657.86	0.255	1204.45	307.63
A_68_P21303499	chr2:68309684-68309728	NM_016866:332	Stk39	INSIDE	0.577	0.458	1598.00	731.37	0.264	1365.24	360.73
A_68_P24001850	chr5:114541225-114541269	NM_026805:143	Svop	INSIDE	0.577	4.049	564.96	2287.46	2.338	415.58	971.69
A_68_P22411405	chr3:108029325-108029369	NM_008596:171	Sypl2	INSIDE	0.577	0.591	3969.92	2348.18	0.341	3288.41	1121.94
A_68_P30379763	chr15:81642166-81642210	NM_017376:345	Tef	INSIDE	0.577	4.365	785.27	3427.49	2.518	798.52	2010.95
A_68_P27780290	chr11:48663076-48663120	NM_053166:23459	Trim7	INSIDE	0.577	2.957	4750.74	14048.07	1.706	3224.86	5501.84
A_68_P24156073	chr5:144090815-144090859	NM_028379:69	Zdhhc4	INSIDE	0.577	0.577	3562.81	2054.34	0.333	3003.39	999.47
A_68_P31879119	chr18:83079657-83079701	NM_183033:-592	Zfp516	PROMOTER	0.577	0.687	1555.85	1069.20	0.397	1190.30	472.38

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31620977	chr18:36093125-36093169			Unknown	0.577	0.625	1026.76	642.06	0.361	821.13	296.34
A_68_P23947955	chr5:104121272-104121316	ENSMUST00000126335:-98		PROMOTER	0.577	0.610	1540.71	939.63	0.352	1314.96	462.88
A_68_P27978000	chr11:84339607-84339651	NR_038057:467	1500016L03Rik	INSIDE	0.576	0.596	1987.31	1184.09	0.343	1411.79	484.72
A_68_P30476329	chr15:98593570-98593614	NM_007478:-43	Arf3	PROMOTER	0.576	0.556	2638.09	1467.56	0.320	2215.02	709.90
A_68_P32260332	chrX:11664013-11664057	NM_029510:-6355	Bcor	PROMOTER	0.576	0.588	1667.60	981.30	0.339	737.01	249.92
A_68_P31936680	chr19:6996479-6996523	NM_007953:-202	Esrra	PROMOTER	0.576	0.541	1686.14	911.97	0.312	1451.94	452.29
A_68_P23892222	chr5:92512823-92512867	NM_011816:-83	G3bp2	PROMOTER	0.576	0.494	1504.75	742.84	0.285	1221.40	347.50
A_68_P27805436	chr11:53381255-53381299	NM_008443:396	Kif3a	INSIDE	0.576	0.531	1519.41	806.94	0.306	1138.73	348.14
A_68_P24595550	chr6:83745123-83745167	NM_001164187:-7	Nagk	PROMOTER	0.576	0.700	1824.13	1277.32	0.404	1476.84	595.96
A_68_P22009787	chr3:27081688-27081732	NM_178772:-215	Nceh1	PROMOTER	0.576	0.702	2056.24	1443.40	0.404	1651.64	667.85
A_68_P28863267	chr13:19714988-19715032	NM_016687:-33	Sfrp4	DIVERGENT_PROMOTER	0.576	0.589	1211.63	713.85	0.340	957.44	325.14
A_68_P27804858	chr11:53270789-53270833	NM_027917:104	Shroom1	INSIDE	0.576	0.401	1370.05	549.13	0.231	1092.37	252.36
A_68_P30572953	chr16:17278195-17278239	NM_177473:1824	Tmem191c	INSIDE	0.576	0.630	1052.54	663.41	0.363	834.60	302.99
A_68_P22887152	chr4:46151235-46151279	NM_173033:91	Tstd2	INSIDE	0.576	0.516	2509.76	1294.07	0.297	1766.84	525.10
A_68_P30351332	chr15:76779347-76779391	NM_054099:395	1110038F14Rik	INSIDE	0.575	0.453	1546.39	700.56	0.261	1351.00	352.07
A_68_P30977033	chr16:93683476-93683520	NM_173047:35	Cbr3	INSIDE	0.575	0.313	1765.34	552.66	0.180	1377.70	248.14
A_68_P23241428	chr4:118293645-118293692	NR_029469:-5340	D4Ertd617e	PROMOTER	0.575	0.694	1313.45	911.38	0.399	963.78	384.26
A_68_P23103759	chr4:91041388-91041432	NM_010486:-2664	Elavl2	PROMOTER	0.575	0.693	2443.92	1693.04	0.398	2132.77	848.93
A_68_P26657025	chr9:77765481-77765525	NM_134255:331	Elovl5	INSIDE	0.575	0.572	998.33	571.27	0.329	842.64	277.24
A_68_P32130261	chr19:44144105-44144149	NM_145502:50	Erlin1	INSIDE	0.575	0.546	1589.93	868.54	0.314	1403.40	440.59
A_68_P23979843	chr5:110877476-110877520	NM_001142642:24	Fbrsl1	INSIDE	0.575	0.491	1786.34	877.14	0.283	1389.15	392.50
A_68_P24326760	chr6:29424133-29424177	NM_001145360:2718	Gm9047	DOWNSTREAM	0.575	0.439	1592.23	699.21	0.252	1285.44	324.39
A_68_P32082884	chr19:34996996-34997040	NM_183046:171	Kif20b	INSIDE	0.575	0.534	1524.39	813.30	0.307	1149.54	352.94
A_68_P27977992	chr11:84338560-84338604	NM_008498:454	Lhx1	INSIDE	0.575	0.719	1637.36	1176.99	0.413	1242.14	513.35
A_68_P25972025	chr8:77633597-77633641	NM_008566:192	Mcm5	INSIDE	0.575	0.451	1369.88	617.36	0.259	1024.82	265.60
A_68_P26871811	chr9:119249105-119249149	NM_010851:32	Myd88	INSIDE	0.575	0.397	1622.18	643.73	0.228	1414.08	322.78
A_68_P20347698	chr1:74331582-74331626	NM_025580:-3	Pnkd	DIVERGENT_PROMOTER	0.575	0.566	1536.65	870.03	0.325	1145.16	372.56
A_68_P25500723	chr7:133618294-133618338	NM_011363:328	Sh2b1	INSIDE	0.575	0.689	1287.82	887.81	0.396	1062.67	420.92
A_68_P26717017	chr9:90165120-90165164	NM_194334:465	Tbc1d2b	INSIDE	0.575	0.698	2545.27	1777.14	0.402	1817.95	730.18
A_68_P24287933	chr6:21802094-21802138	NM_173007:399	Tspan12	INSIDE	0.575	0.711	1841.57	1309.71	0.409	1520.64	622.07
A_68_P20377582	chr1:79758038-79758082	NM_001111279:284	Wdfy1	INSIDE	0.575	0.683	4103.31	2801.99	0.393	2836.70	1114.77
A_68_P21332187	chr2:73367126-73367170	NM_153138:319	Wipf1	INSIDE	0.575	0.654	865.10	565.43	0.376	827.83	311.21
A_68_P21332193	chr2:73367805-73367850	NM_153138:-360	Wipf1	PROMOTER	0.575	0.529	1822.11	964.58	0.304	1528.39	464.90
A_68_P23364201	chr4:141020235-141020279	NM_009541:19669	Zbtb17	INSIDE	0.575	2.984	2071.46	6182.02	1.717	1603.27	2752.63
A_68_P24114265	chr5:135485654-135485698	NR_033794:351	Abhd11	INSIDE	0.574	0.617	1223.70	754.79	0.354	885.51	313.72
A_68_P22568796	chr3:138106098-138106142	NM_007410:-7	Adh5	PROMOTER	0.574	0.367	1963.40	720.78	0.211	1479.80	311.80
A_68_P26940377	chr10:11063537-11063581	NM_010146:316	Epm2a	INSIDE	0.574	0.541	1361.70	736.85	0.311	1256.73	390.51
A_68_P22603827	chr3:144232599-144232643	NM_011828:560	Hs2st1	INSIDE	0.574	0.592	1626.19	963.49	0.340	1213.11	412.60
A_68_P20074998	chr1:20880874-20880920	NM_028829:194	Paqr8	INSIDE	0.574	0.697	1920.11	1338.10	0.400	1499.85	599.83
A_68_P30397289	chr15:84684008-84684052	NM_001081166:2529	Phf21b	INSIDE	0.574	0.711	2450.67	1742.93	0.408	1998.97	815.55
A_68_P29982792	chr15:5192574-5192618	NM_001136079:1086	Ptger4	INSIDE	0.574	0.609	1175.28	715.29	0.349	1048.64	366.06
A_68_P21762357	chr2:154616385-154616429	NM_001139511:-439	Raly	PROMOTER	0.574	0.530	5463.18	2897.66	0.304	4104.39	1249.13
A_68_P20038597	chr1:12982588-12982632	NM_172841:-1394	Slco5a1	PROMOTER	0.574	0.592	1150.49	680.83	0.340	942.04	320.02
A_68_P31106586	chr17:25970234-25970278	NM_019719:50	Stub1	INSIDE	0.574	0.606	1580.31	957.97	0.348	1193.25	415.48
A_68_P20198785	chr1:45852285-45852329	NM_028599:-39	Wdr75	PROMOTER	0.574	0.557	1204.36	670.33	0.319	1004.44	320.88
A_68_P30495241	chr15:101807758-101807802			Unknown	0.574	0.612	839.96	513.71	0.351	627.35	220.06
A_68_P25471459	chr7:128126104-128126148	NM_028955:104	4933427G17Rik	INSIDE	0.573	0.600	1261.10	756.18	0.344	1044.62	359.02
A_68_P27815711	chr11:55274535-55274579	NM_009720:84	Atox1	INSIDE	0.573	0.421	1520.34	640.64	0.241	1224.27	295.63
A_68_P32364049	chrX:45696991-45697035	NM_178782:2478	Bcorl1	INSIDE	0.573	3.269	2293.72	7497.48	1.872	912.24	1708.07
A_68_P25843141	chr8:48799219-48799263	NM_172407:45	Cdkn2aip	INSIDE	0.573	0.616	3600.91	2218.30	0.353	2750.15	970.19
A_68_P32227330	chr19:60887752-60887797	NM_001167829:302	Fam45a	INSIDE	0.573	0.602	870.95	524.64	0.345	770.61	266.04

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26466888	chr9:44113383-44113427	NM_172162:350	Hinfp	INSIDE	0.573	0.728	1790.13	1302.75	0.417	1557.83	649.66
A_68_P31100627	chr17:25097854-25097898	NM_198937:-308	Hn1l	PROMOTER	0.573	0.514	1415.31	728.17	0.295	1145.61	337.48
A_68_P27765091	chr11:45758223-45758267	NM_028185:193	Lsm11	INSIDE	0.573	0.376	1929.95	725.05	0.215	1567.62	337.36
A_68_P28119819	chr11:109511596-109511640	NM_021880:-644	Prkar1a	PROMOTER	0.573	0.538	1105.98	594.70	0.308	836.18	257.86
A_68_P32109309	chr19:40588021-40588065	NM_178362:184	Sorbs1	INSIDE	0.573	0.468	1716.44	804.03	0.269	1455.53	390.82
A_68_P22894262	chr4:47366025-47366069	NM_009370:-130	Tgfbr1	PROMOTER	0.573	0.726	2531.27	1837.14	0.416	2232.68	929.32
A_68_P26596751	chr9:66896180-66896228	NM_001164252:-4526	Tpm1	PROMOTER	0.573	0.467	1734.19	810.51	0.268	1328.51	355.62
A_68_P30421911	chr15:88721121-88721165	ENSMUST00000172019:63706		INSIDE	0.573	0.597	1352.42	807.08	0.342	1126.91	385.52
A_68_P28115679	chr11:108781544-108781588	NM_015732:-96	Axin2	PROMOTER	0.572	0.627	1909.56	1196.62	0.358	1757.95	630.21
A_68_P20631266	chr1:135975629-135975675	NM_007570:80	Btg2	INSIDE	0.572	0.519	1236.30	641.90	0.297	944.69	280.50
A_68_P27089727	chr10:41239601-41239645	NM_016898:317	Cd164	INSIDE	0.572	0.479	1117.35	535.70	0.274	1158.53	317.56
A_68_P20240146	chr1:55109304-55109348	NM_001039710:-287	Coq10b	PROMOTER	0.572	0.604	1427.39	862.22	0.346	1131.81	391.22
A_68_P28069090	chr11:100480471-100480515	NM_019795:990	Dnajc7	INSIDE	0.572	0.689	4194.67	2891.82	0.394	3144.37	1239.33
A_68_P23336240	chr4:136390937-136390981	NM_010142:892	Ephb2	INSIDE	0.572	0.459	1492.56	684.86	0.262	1120.00	293.71
A_68_P26567939	chr9:61794038-61794082	NM_024245:546	Kif23	INSIDE	0.572	0.692	1333.40	922.34	0.395	1143.33	452.02
A_68_P22818618	chr4:32050821-32050865	NM_009316:-239	Map3k7	PROMOTER	0.572	0.362	2234.04	809.83	0.207	1848.73	383.14
A_68_P24643145	chr6:92042439-92042483	NM_011630:1049	Nr2c2	INSIDE	0.572	0.443	1697.54	752.66	0.254	1205.20	305.84
A_68_P26282994	chr9:6168621-6168669	NM_027924:33	Pdgfd	INSIDE	0.572	0.493	1583.15	781.21	0.282	1232.96	348.13
A_68_P30114432	chr15:31383420-31383464	NM_145852:2	Ropn1l	INSIDE	0.572	0.367	1671.99	614.10	0.210	1297.00	272.53
A_68_P29937400	chr14:118625343-118625387	NM_177753:10888	Sox21	DOWNSTREAM	0.572	0.509	1005.32	511.31	0.291	804.61	233.91
A_68_P32113659	chr19:41281622-41281669	NM_011904:-381	Tll2	PROMOTER	0.572	0.506	1114.07	563.53	0.289	704.58	203.69
A_68_P28881066	chr13:23461022-23461066	NM_001111107:27	Zfp322a	INSIDE	0.572	0.657	2833.68	1861.60	0.376	2303.79	866.40
A_68_P30385945	chr15:82818023-82818067	ENSMUST00000170562:4745		INSIDE	0.572	0.469	1347.10	631.13	0.268	1008.23	270.29
A_68_P29613716	chr14:55305799-55305843	NM_001085473:-52	Acin1	PROMOTER	0.571	0.413	2027.70	837.31	0.236	1701.80	400.98
A_68_P24383760	chr6:39523904-39523948	NM_178873:52	Adck2	INSIDE	0.571	0.606	3931.43	2382.30	0.346	2869.75	992.80
A_68_P24056167	chr5:123974295-123974339	NM_023232:-143	Diablo	PROMOTER	0.571	0.484	2310.52	1118.89	0.276	1973.22	545.19
A_68_P22311349	chr3:87826614-87826658	NM_022031:4797	Hapln2	INSIDE	0.571	0.590	1205.66	710.99	0.337	1032.84	347.79
A_68_P27185482	chr10:61803237-61803281	NM_001146100:-89	Hk1	DIVERGENT_PROMOTER	0.571	0.702	1982.39	1390.70	0.400	1654.77	662.31
A_68_P20453279	chr1:94998401-94998445	NM_001110315:20	Kif1a	INSIDE	0.571	0.610	1585.84	967.91	0.348	1191.72	414.97
A_68_P29350210	chr13:115880236-115880280	NM_134058:108	Pelo	INSIDE	0.571	0.428	1365.78	584.99	0.244	1293.53	316.15
A_68_P27949792	chr11:79404418-79404462	NM_175543:-273	Rab11fip4	PROMOTER	0.571	0.648	1053.99	683.13	0.370	778.13	288.13
A_68_P27096527	chr10:42481255-42481299	NM_153055:-25	Sec63	PROMOTER	0.571	0.585	1212.18	709.24	0.334	1047.00	349.96
A_68_P24385310	chr6:39822500-39822544			Unknown	0.571	0.529	1931.19	1021.31	0.302	1586.14	478.97
A_68_P30925086	chr16:84703745-84703789	ENSMUST00000164314:-9501		PROMOTER	0.571	0.673	3861.79	2600.48	0.385	3215.69	1236.75
A_68_P21061285	chr2:22924459-22924503	NM_001102437:-111	Acbd5	PROMOTER	0.570	0.701	2070.25	1452.17	0.400	1512.58	604.66
A_68_P26466977	chr9:44127873-44127917	NM_027909:471	C2cd2l	INSIDE	0.570	0.627	3836.44	2404.59	0.357	2957.77	1055.85
A_68_P24942889	chr6:148893354-148893400	NM_019643:1578	Fam60a	INSIDE	0.570	0.544	1192.04	648.66	0.310	907.54	281.66
A_68_P25661492	chr8:12431084-12431128	NR_027975:45336	Gm5607	INSIDE	0.570	0.713	3639.99	2594.08	0.406	2677.83	1087.00
A_68_P29071679	chr13:58230820-58230864	NM_029872:-925	Hnrnpa0	PROMOTER	0.570	0.490	1513.66	741.79	0.279	1149.29	321.01
A_68_P28067851	chr11:100258744-100258788	NM_010593:338	Jup	INSIDE	0.570	0.483	1464.57	706.93	0.275	1199.55	330.09
A_68_P28516077	chr12:70825553-70825597	NM_145443:287	L2hgdh	INSIDE	0.570	0.620	1226.48	760.61	0.354	1048.37	370.75
A_68_P20306026	chr1:67085213-67085257	NM_001190984:174	Lancl1	INSIDE	0.570	0.592	3031.06	1795.81	0.338	2374.70	801.63
A_68_P21571366	chr2:119584202-119584246	NM_008523:37	Ltk	INSIDE	0.570	0.636	1211.98	771.39	0.363	1037.16	376.53
A_68_P20449354	chr1:94370335-94370379	NM_024197:-21	Ndufa10	PROMOTER	0.570	0.602	980.29	589.81	0.343	669.35	229.49
A_68_P20147268	chr1:36326573-36326617	NM_153408:3676	Neurl3	INSIDE	0.570	3.028	2584.59	7827.19	1.726	1746.11	3013.23
A_68_P25528062	chr7:138514868-138514912	NM_001039534:231	Pstk	INSIDE	0.570	0.612	1795.30	1099.46	0.349	1420.24	496.16
A_68_P22858652	chr4:40704660-40704704	NM_021535:236	Smu1	INSIDE	0.570	0.652	2674.12	1742.33	0.372	2167.75	805.33
A_68_P21833056	chr2:166821240-166821285	NM_001109905:516	Stau1	INSIDE	0.570	0.595	1196.97	711.91	0.339	986.92	334.35
A_68_P31922242	chr19:4282667-4282711	NM_026720:449	Ankrd13d	INSIDE	0.569	0.487	1226.66	597.09	0.277	847.48	234.89
A_68_P29613437	chr14:55259966-55260010	NM_199470:213	Cdh24	INSIDE	0.569	0.679	3029.23	2055.85	0.386	2450.58	945.95
A_68_P25616318	chr8:4166571-4166615	NM_001039578:26	Evi5l	INSIDE	0.569	0.727	3763.31	2734.40	0.413	3072.69	1269.57

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27810087	chr11:54251592-54251636	NM_173753:-66	Fnip1	PROMOTER	0.569	0.658	2478.66	1632.10	0.375	2100.32	787.14
A_68_P20146390	chr1:36161035-36161084	NM_015818:35815	Hs6st1	INSIDE	0.569	2.857	777.68	2221.56	1.627	582.83	948.01
A_68_P26716013	chr9:90009639-90009683	NM_001039147:-2	Morf4l1	PROMOTER	0.569	0.544	1835.28	998.48	0.310	1452.06	449.68
A_68_P31161702	chr17:36053831-36053875	NM_175934:-3	Ppp1r10	DIVERGENT_PROMOTER	0.569	0.672	3400.04	2283.76	0.382	2415.44	923.69
A_68_P30574323	chr16:17530866-17530910	NM_026909:257	Thap7	INSIDE	0.569	0.514	1312.67	675.16	0.293	1058.94	310.03
A_68_P27469304	chr10:114822217-114822261	NM_001033261:224	Zfc3h1	INSIDE	0.569	0.723	1971.17	1424.91	0.411	1642.50	675.30
A_68_P26139677	chr8:108939449-108939493	NM_011764:232	Zfp90	INSIDE	0.569	0.531	1320.09	700.60	0.302	1016.72	306.91
A_68_P21533267	chr2:113057089-113057133	ENSMUST00000099579:93		INSIDE	0.569	0.611	865.52	528.56	0.348	790.99	275.02
A_68_P27292892	chr10:82085954-82085998	NM_001135567:-3	1190007I07Rik	DIVERGENT_PROMOTER	0.568	0.611	1061.20	648.32	0.347	864.90	300.19
A_68_P31610612	chr18:34166849-34166893	NM_013512:-10	Epb4.1l4a	PROMOTER	0.568	0.602	1215.32	731.69	0.342	930.00	317.78
A_68_P29671494	chr14:65696542-65696586	NM_018788:20379	Extl3	INSIDE	0.568	2.377	2904.76	6904.49	1.350	2132.45	2879.37
A_68_P22071616	chr3:38786996-38787040	NM_183221:1157	Fat4	INSIDE	0.568	0.666	1415.98	943.31	0.378	1074.47	406.55
A_68_P26467074	chr9:44143508-44143552	NM_010436:733	H2afx	INSIDE	0.568	0.539	1039.19	560.28	0.306	869.37	266.17
A_68_P22934416	chr4:55543231-55543275	NM_010637:2095	Klf4	INSIDE	0.568	0.675	1338.12	903.88	0.383	1075.42	412.35
A_68_P28206058	chr12:5380617-5380662	NM_001164493:1849	Klhl29	INSIDE	0.568	0.545	1529.67	834.43	0.310	1206.06	373.61
A_68_P31625586	chr18:36903899-36903943	NM_010885:282	Ndufa2	INSIDE	0.568	0.515	1076.74	554.72	0.293	943.88	276.09
A_68_P32099500	chr19:38172076-38172120	NM_181748:530	O3far1	INSIDE	0.568	0.513	2719.67	1395.86	0.291	2141.75	624.03
A_68_P26640622	chr9:74710098-74710142	NM_008262:393	Onecut1	INSIDE	0.568	0.691	2058.51	1423.29	0.393	1578.58	620.07
A_68_P21831539	chr2:166539726-166539770	NM_177782:-416	Prex1	PROMOTER	0.568	0.452	1321.79	597.79	0.257	1027.42	263.70
A_68_P31793418	chr18:67883645-67883689	NM_001127177:609	Ptpn2	INSIDE	0.568	0.573	2730.29	1565.13	0.326	2353.85	766.35
A_68_P23621603	chr5:38952428-38952472	NM_011715:384	Wdr1	INSIDE	0.568	0.543	1462.37	794.23	0.308	1059.71	326.78
A_68_P24118624	chr5:136409884-136409928	NM_018871:605	Ywhag	INSIDE	0.568	0.668	3287.17	2196.31	0.380	2580.55	979.53
A_68_P27674153	chr11:29274024-29274068	NM_176841:272	Ccdc88a	INSIDE	0.567	0.537	954.11	512.21	0.304	822.91	250.40
A_68_P25113816	chr7:56890828-56890872	NM_001005232:1355	Dbx1	INSIDE	0.567	0.631	828.80	522.87	0.358	700.60	250.47
A_68_P24131499	chr5:139230499-139230543	NM_030565:-514	Fam20c	PROMOTER	0.567	0.679	1326.13	900.41	0.385	1196.45	460.94
A_68_P25828173	chr8:46136798-46136846	NM_001081286:101261	Fat1	INSIDE	0.567	2.570	2112.83	5429.90	1.457	1471.99	2144.67
A_68_P23145525	chr4:99320580-99320624	NM_010425:-2387	Foxd3	PROMOTER	0.567	0.458	1131.51	518.60	0.260	984.49	256.00
A_68_P29952573	chr14:121310169-121310213	NM_023579:-225	Ipo5	PROMOTER	0.567	0.540	973.95	525.93	0.306	813.28	249.18
A_68_P20744278	chr1:158604428-158604472	NM_023141:20	Tor3a	INSIDE	0.567	0.435	1221.33	531.24	0.247	1085.85	267.91
A_68_P30959118	chr16:90810399-90810443	NM_029497:238	Urb1	INSIDE	0.567	0.716	1794.66	1285.74	0.406	1464.42	594.60
A_68_P31669248	chr18:44988658-44988702	NM_001163013:362	Ythdc2	INSIDE	0.567	0.428	1645.12	704.73	0.243	1200.46	291.34
A_68_P28881184	chr13:23488366-23488410	BC160303:76510		INSIDE	0.567	0.438	1520.84	666.28	0.248	1293.95	321.54
A_68_P27954544	chr11:80291421-80291465	NM_009871:895	Cdk5r1	INSIDE	0.566	0.593	1698.75	1008.11	0.336	1220.56	409.99
A_68_P22340673	chr3:94590302-94590346	NM_001037711:113	Cgn	INSIDE	0.566	0.543	4165.07	2260.24	0.307	3089.59	948.51
A_68_P25045003	chr7:35461137-35461181	NM_175140:136572	Chst8	INSIDE	0.566	0.593	1404.10	832.32	0.336	1336.94	448.61
A_68_P28684632	chr12:102137444-102137488	NM_001177674:268	Gpr68	INSIDE	0.566	0.504	2787.51	1405.18	0.285	1916.13	546.92
A_68_P28089853	chr11:104094131-104094175	NM_001038609:1403	Mapt	INSIDE	0.566	0.580	2669.04	1548.50	0.328	1732.60	568.89
A_68_P26885085	chr9:121628083-121628127	NM_010918:-194	Nktr	PROMOTER	0.566	0.471	1500.13	706.12	0.267	1164.19	310.30
A_68_P28600137	chr12:86113873-86113917	NM_023409:168	Npc2	INSIDE	0.566	0.524	3879.45	2034.68	0.297	3086.46	916.64
A_68_P31256423	chr17:56613777-56613821	NM_011218:2105	Ptprs	INSIDE	0.566	0.725	2457.40	1782.69	0.411	1862.73	764.70
A_68_P27181743	chr10:61143343-61143387	NM_009120:296	Sar1a	INSIDE	0.566	0.631	2216.17	1399.40	0.358	1667.68	596.47
A_68_P30680167	chr16:37384851-37384895	NM_001114611:172	Stxbp5l	INSIDE	0.566	0.629	1870.26	1176.79	0.356	1586.46	565.03
A_68_P26814406	chr9:108250276-108250320	NM_011678:137	Usp4	INSIDE	0.566	0.419	1705.18	714.12	0.237	1419.62	336.31
A_68_P32542578	chrX:92907030-92907074	NM_001034907:36	Zc3h12b	INSIDE	0.566	2.857	1730.47	4944.09	1.617	835.50	1351.21
A_68_P22953710	chr4:58956479-58956523	NM_001099323:1	Zkscan16	INSIDE	0.566	0.608	1084.88	660.06	0.344	862.70	296.98
A_68_P28091216	chr11:104330128-104330172	ENSMUST00000134266:-845		PROMOTER	0.566	0.399	3790.75	1511.63	0.226	3096.76	698.49
A_68_P25737283	chr8:28338782-28338826	NM_013462:1256	Adrb3	INSIDE	0.565	0.478	1126.79	539.00	0.270	883.04	238.86
A_68_P26885914	chr9:121748048-121748092	NM_028384:509	Ccdc13	INSIDE	0.565	0.632	920.03	581.07	0.357	657.55	234.52
A_68_P31252978	chr17:56098506-56098550	NM_028381:-81	Ccdc94	PROMOTER	0.565	0.506	1125.72	569.95	0.286	834.62	238.95
A_68_P27903934	chr11:70832798-70832842	NM_033562:-55	Derl2	DIVERGENT_PROMOTER	0.565	0.503	2204.32	1108.27	0.284	1714.27	486.74
A_68_P26612686	chr9:69609029-69609073	NM_022378:-303	Foxb1	PROMOTER	0.565	0.672	2272.22	1527.08	0.380	1816.04	689.95

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P22010766	chr3:27270872-27270916	NM_177330:622	Ghsr	INSIDE	0.565	0.694	2020.63	1402.78	0.392	1427.12	560.14
A_68_P21311215	chr2:69660694-69660738	NM_177784:290	Klhl23	INSIDE	0.565	0.647	2109.52	1363.94	0.365	1700.98	621.06
A_68_P22693714	chr4:3605437-3605481	NM_001111096:191	Lyn	INSIDE	0.565	0.542	1002.80	543.31	0.306	827.53	253.41
A_68_P22356952	chr3:97692829-97692873	NM_001039376:-220	Pde4dip	PROMOTER	0.565	0.581	1173.35	681.71	0.328	892.32	292.93
A_68_P23971131	chr5:108741769-108741813	NM_001081234:-153	Pigg	PROMOTER	0.565	0.577	1542.46	889.51	0.326	1240.48	403.92
A_68_P21604382	chr2:125548878-125548922	NM_199022:984	Shc4	INSIDE	0.565	0.409	1504.09	614.77	0.231	1178.89	272.42
A_68_P24542639	chr6:72566738-72566782	NM_009444:-18	Tgoln2	PROMOTER	0.565	0.570	1142.68	651.42	0.322	947.30	305.29
A_68_P25029683	chr7:30836003-30836047	NM_011748:391	Zfp14	INSIDE	0.565	0.643	1081.36	695.68	0.364	755.83	274.92
A_68_P32115177	chr19:41557970-41558016	ENSMUST00000067795:866		INSIDE	0.565	0.616	1560.04	960.34	0.348	1060.43	369.01
A_68_P23297491	chr4:129278370-129278414	NM_029748:442	2510006D16Rik	INSIDE	0.564	0.554	1089.87	604.22	0.313	906.89	283.60
A_68_P20286847	chr1:63493039-63493083	NM_001177600:583	Adam23	INSIDE	0.564	0.590	2294.50	1354.14	0.333	1842.08	612.75
A_68_P23284269	chr4:126921347-126921391	NM_030252:341	BC003266	INSIDE	0.564	0.460	1692.80	778.92	0.260	1393.23	361.55
A_68_P27277825	chr10:79076430-79076474	NM_198614:311	C2cd4c	INSIDE	0.564	0.342	2022.44	691.42	0.193	1722.39	331.93
A_68_P21799027	chr2:160935428-160935473	NM_173368:-658	Chd6	PROMOTER	0.564	0.682	1001.83	682.95	0.385	776.01	298.51
A_68_P25086655	chr7:51560012-51560056	NM_009131:2295	Clec11a	INSIDE	0.564	0.584	1693.26	988.26	0.329	1372.86	451.94
A_68_P24066887	chr5:125914212-125914256	NM_203319:184	Dhx37	INSIDE	0.564	0.504	2121.66	1068.58	0.284	1769.97	503.12
A_68_P20938879	chr1:193399292-193399336	NM_029766:99	Dtl	INSIDE	0.564	0.410	2542.52	1042.82	0.231	1970.82	455.87
A_68_P26804413	chr9:106558146-106558190	NM_001160353:272	Grm2	INSIDE	0.564	0.574	2025.33	1162.75	0.324	1662.37	538.64
A_68_P27095710	chr10:42303461-42303505	NM_152229:-88	Nr2e1	PROMOTER	0.564	0.594	1771.51	1053.13	0.335	1429.46	479.08
A_68_P31713386	chr18:53624258-53624302	NM_001033281:81	Prdm6	INSIDE	0.564	0.373	2439.14	909.74	0.210	1964.38	412.96
A_68_P31253055	chr17:56109896-56109940	NM_001159523:14	Shd	INSIDE	0.564	0.518	4610.58	2387.13	0.292	3559.17	1038.80
A_68_P23618267	chr5:38611613-38611657	NM_029162:33	Zbtb49	INSIDE	0.564	0.467	1488.70	695.63	0.264	1235.93	325.87
A_68_P27532961	chr10:126365502-126365546			Unknown	0.564	0.696	1833.29	1275.77	0.392	1719.39	674.83
A_68_P27932458	chr11:76308565-76308609	NM_198018:14335	Abr	INSIDE	0.563	0.513	1670.04	856.81	0.289	1335.96	385.79
A_68_P28032140	chr11:94189670-94189714	NM_146024:378	Ankrd40	INSIDE	0.563	0.532	4088.05	2175.64	0.299	2843.43	851.43
A_68_P21631052	chr2:130490403-130490447	NM_029832:-43	Ddrgk1	DIVERGENT_PROMOTER	0.563	0.664	1731.04	1148.78	0.374	1368.53	511.45
A_68_P31099383	chr17:24890123-24890167	NM_001012402:197	Hs3st6	INSIDE	0.563	0.630	1409.88	887.85	0.354	1160.29	411.09
A_68_P25656225	chr8:11557852-11557899	NM_011919:1810	Ing1	INSIDE	0.563	0.540	1067.19	576.73	0.304	871.63	265.32
A_68_P20391723	chr1:82288408-82288452	NM_010570:-416	Irs1	PROMOTER	0.563	0.412	1571.80	647.33	0.232	1306.74	303.13
A_68_P28513155	chr12:70269942-70269986	NM_001081406:164	Lrr1	INSIDE	0.563	0.646	1595.59	1030.61	0.364	1213.98	441.28
A_68_P22210465	chr3:67319575-67319619	NM_001164763:-151	Rarres1	PROMOTER	0.563	0.605	1333.46	806.95	0.341	1058.70	360.81
A_68_P29502937	chr14:30781713-30781757	NM_019979:169	Selk	INSIDE	0.563	0.654	2837.27	1854.71	0.368	2160.24	794.56
A_68_P28185710	chr11:120485805-120485849	NM_153056:490	Sirt7	INSIDE	0.563	0.544	1310.04	712.60	0.306	1028.17	314.88
A_68_P22917598	chr4:52452191-52452235	NM_008017:92	Smc2	INSIDE	0.563	0.530	1960.76	1039.04	0.298	1727.26	514.92
A_68_P27689370	chr11:32433541-32433585	NM_009288:297	Stk10	INSIDE	0.563	0.618	1245.10	768.86	0.348	942.19	327.51
A_68_P24118491	chr5:136387249-136387293	NM_018871:23241	Ywhag	INSIDE	0.563	2.731	1500.76	4098.78	1.538	1042.21	1602.46
A_68_P32957266	chr17:8477443-8477487	NM_018819:787	Brp44l	INSIDE	0.562	0.540	2045.56	1104.06	0.304	1646.50	499.84
A_68_P20829088	chr1:173610061-173610105	NM_007649:-2103	Cd48	PROMOTER	0.562	2.889	2481.68	7170.39	1.625	2263.70	3677.64
A_68_P24830594	chr6:127030212-127030256	NM_022657:7315	Fgf23	INSIDE	0.562	0.643	796.56	512.55	0.362	643.98	232.88
A_68_P28041927	chr11:95868155-95868199	NM_009951:-918	Igf2bp1	PROMOTER	0.562	0.548	986.48	540.10	0.308	926.11	284.97
A_68_P32252897	chrX:10295608-10295654	NM_001166635:1140	Mid1ip1	INSIDE	0.562	0.691	1207.34	834.01	0.388	552.43	214.53
A_68_P21842485	chr2:168426812-168426856	NM_001037178:321	Nfatc2	INSIDE	0.562	0.424	1492.40	632.27	0.238	1299.45	309.63
A_68_P23057181	chr4:82151702-82151757	NM_001113209:-517	Nfib	PROMOTER	0.562	0.645	1116.94	719.93	0.363	898.38	325.68
A_68_P28058441	chr11:98635083-98635127	NM_145434:1452	Nr1d1	INSIDE	0.562	0.495	1093.90	541.80	0.278	1028.08	286.08
A_68_P25377819	chr7:109384967-109385014	NM_145583:13403	Pgap2	INSIDE	0.562	2.859	888.88	2541.17	1.608	785.22	1262.72
A_68_P20029520	chr1:10983953-10983997	NM_029525:429	Prex2	INSIDE	0.562	0.439	1493.77	655.96	0.247	1230.28	303.83
A_68_P26588674	chr9:65477102-65477146	NM_028030:-1264	Rbpms2	PROMOTER	0.562	0.542	1527.94	828.87	0.305	1209.09	368.88
A_68_P22044439	chr3:33698918-33698962	NM_025978:-176	Ttc14	PROMOTER	0.562	0.275	2184.87	601.13	0.155	1810.25	279.75
A_68_P24002094	chr5:114581485-114581529	NM_011677:342	Ung	INSIDE	0.562	0.697	2466.04	1718.55	0.391	1766.12	691.36
A_68_P23237068	chr4:117559980-117560024	NM_033617:-68	Atp6v0b	PROMOTER	0.561	0.520	3287.93	1710.73	0.292	2579.57	752.50
A_68_P24142832	chr5:141180716-141180760	NM_172724:-238	Baat1	DIVERGENT_PROMOTER	0.561	0.612	2843.49	1739.02	0.343	2029.52	696.21

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P29941246	chr14:119254241-119254285	NM_001160099:91	Cldn10	INSIDE	0.561	0.580	1588.08	921.60	0.325	1242.28	404.29
A_68_P21823222	chr2:165151741-165151785	NM_207705:-9369	Elmo2	PROMOTER	0.561	0.563	2297.23	1293.88	0.316	1698.80	536.64
A_68_P25730814	chr8:27229164-27229208	NM_207659:510	Hook3	INSIDE	0.561	0.465	1832.79	852.16	0.261	1488.23	388.33
A_68_P30146826	chr15:37890566-37890610	NM_199476:222	Rrm2b	INSIDE	0.561	0.592	2331.50	1379.43	0.332	1642.59	545.08
A_68_P30489324	chr15:100883675-100883719	NM_011323:116995	Scn8a	DOWNSTREAM	0.561	0.627	1675.76	1050.43	0.352	1580.13	556.04
A_68_P28224317	chr12:8778225-8778269	NM_011519:45	Sdc1	INSIDE	0.561	0.563	2360.37	1329.96	0.316	1718.40	543.22
A_68_P27915644	chr11:72991108-72991152	NM_029564:546	Tax1bp3	INSIDE	0.561	0.614	1118.93	687.16	0.344	937.63	322.86
A_68_P30580619	chr16:18589104-18589148	NM_011532:-2064	Tbx1	PROMOTER	0.561	0.697	2396.69	1671.42	0.391	1860.59	727.67
A_68_P21070952	chr2:25118487-25118531	NM_175286:391	Tprn	INSIDE	0.561	0.472	2594.30	1223.22	0.264	1909.58	505.07
A_68_P25355274	chr7:105509904-105509948	NM_001168539:-88	Tsku	PROMOTER	0.561	0.488	1169.56	570.41	0.273	1020.35	279.06
A_68_P31403191	chr17:84585735-84585779	NM_001001806:1531	Zfp36l2	INSIDE	0.561	0.595	1047.30	623.28	0.334	877.89	293.28
A_68_P23204069	chr4:109723823-109723867			Unknown	0.561	0.482	2207.85	1065.21	0.271	1683.30	456.01
A_68_P24377801	chr6:38484955-38484999	NM_025363:116	1110001J03Rik	INSIDE	0.560	0.622	1455.55	905.08	0.348	1209.77	421.18
A_68_P31609276	chr18:33954463-33954507	NR_038151:-61	2410004N09Rik	PROMOTER	0.560	0.719	2316.79	1666.26	0.403	1838.05	739.95
A_68_P21081717	chr2:26865712-26865756	NM_029862:249	5930434B04Rik	INSIDE	0.560	0.488	1458.96	711.61	0.273	1037.33	283.46
A_68_P24618848	chr6:87863953-87863997	NM_173737:5	8430410A17Rik	INSIDE	0.560	0.378	2092.85	790.05	0.211	1739.85	367.76
A_68_P28181983	chr11:119908193-119908237	NM_001198787:-5119	Aatk	PROMOTER	0.560	0.701	2711.60	1901.38	0.393	2101.40	825.63
A_68_P21741662	chr2:150730240-150730284	NM_024465:205	Abhd12	INSIDE	0.560	0.552	1913.46	1055.45	0.309	1584.74	489.26
A_68_P25276874	chr7:89484048-89484092	NM_001190374:-133	Adamtsl3	PROMOTER	0.560	46.465	529.23	24590.75	26.006	626.01	16279.64
A_68_P21901918	chr2:179906691-179906735	NM_019822:420	Adrm1	INSIDE	0.560	0.711	1492.54	1061.72	0.399	1260.83	502.47
A_68_P24798990	chr6:120481585-120481629	NM_144815:-289	Cecr5	PROMOTER	0.560	0.325	1978.65	643.44	0.182	1646.51	299.76
A_68_P23979845	chr5:110877631-110877675	NM_001142642:-130	Fbrsl1	PROMOTER	0.560	0.631	2505.81	1581.38	0.354	1994.69	705.30
A_68_P22924772	chr4:53727484-53727528	NM_139309:453	Fktn	INSIDE	0.560	0.679	1666.83	1132.53	0.381	1370.51	521.66
A_68_P26683680	chr9:83341498-83341543	NM_029434:-6786	Lca5	PROMOTER	0.560	0.624	910.87	568.13	0.349	741.85	258.92
A_68_P22683294	chr3:157699823-157699867	NM_024194:178	Lrrc40	INSIDE	0.560	0.487	2499.03	1217.62	0.273	2043.10	557.29
A_68_P23946409	chr5:103854106-103854150	NM_011204:-82	Ptpn13	PROMOTER	0.560	0.619	1473.05	912.23	0.347	1290.53	447.50
A_68_P24156971	chr5:144288853-144288897	NM_009007:-13	Rac1	PROMOTER	0.560	0.666	2639.95	1758.58	0.373	1981.84	738.77
A_68_P24170389	chr5:147656737-147656781	NM_026864:112	Rasl11a	INSIDE	0.560	0.649	1181.89	767.18	0.364	1037.70	377.39
A_68_P27682716	chr11:31269467-31269511	NM_011491:573	Stc2	INSIDE	0.560	0.561	1058.09	594.10	0.314	903.97	284.24
A_68_P22728295	chr4:11083786-11083830	NM_001199105:221	Trp53inp1	INSIDE	0.560	0.563	1881.95	1060.08	0.316	1447.62	457.02
A_68_P21555162	chr2:116801525-116801569	ENSMUST00000083860:-7637		PROMOTER	0.560	0.521	1151.20	599.45	0.291	928.06	270.45
A_68_P23331579	chr4:135543347-135543391	NM_025411:-209	1110049F12Rik	PROMOTER	0.559	0.640	1505.82	963.38	0.358	1300.10	465.03
A_68_P23154898	chr4:101092046-101092090	NM_009647:-239	Ak4	PROMOTER	0.559	0.389	1620.81	630.52	0.218	1481.13	322.15
A_68_P27392329	chr10:99950462-99950506	NM_146009:-438	Cep290	DIVERGENT_PROMOTER	0.559	0.337	1814.92	610.94	0.188	1345.69	253.04
A_68_P30895376	chr16:78302422-78302466	NM_001025192:509	Cxadr	INSIDE	0.559	0.599	1035.41	619.77	0.334	734.45	245.67
A_68_P25952525	chr8:73063833-73063877	NM_007924:281	Ell	INSIDE	0.559	0.535	1118.59	598.08	0.299	918.35	274.41
A_68_P27541867	chr10:127962642-127962686	NM_011843:251	Esyt1	INSIDE	0.559	0.577	1870.60	1080.15	0.323	1422.16	459.21
A_68_P24326457	chr6:29383678-29383722	NM_001081185:548	Flnc	INSIDE	0.559	0.668	1801.03	1203.76	0.373	1262.17	471.32
A_68_P21572765	chr2:119853360-119853404	NM_001114637:164	Jmjd7	INSIDE	0.559	0.471	1169.44	550.26	0.263	993.44	261.09
A_68_P25423373	chr7:119369629-119369673	NM_001193305:301	Mical2	INSIDE	0.559	0.707	2118.24	1496.69	0.395	1671.64	660.13
A_68_P24119914	chr5:136674559-136674603	NM_025774:244	Prkrip1	INSIDE	0.559	0.609	2183.08	1330.26	0.341	1509.25	514.25
A_68_P26540098	chr9:56924586-56924630	NM_001110350:426	Sin3a	INSIDE	0.559	0.712	3459.83	2462.91	0.398	2827.68	1125.53
A_68_P21826274	chr2:165671183-165671231	NM_027230:38982	Zmynd8	INSIDE	0.559	4.337	1961.36	8505.97	2.425	1400.38	3396.47
A_68_P30977032	chr16:93683403-93683447	NM_173047:-39	Cbr3	PROMOTER	0.558	0.567	1827.85	1036.24	0.316	1438.18	454.79
A_68_P28143856	chr11:113613201-113613245	NM_001163346:-93	Cdc42ep4	PROMOTER	0.558	0.674	1217.12	820.91	0.376	970.52	364.96
A_68_P26505085	chr9:50507371-50507415	NM_178118:28697	Dixdc1	INSIDE	0.558	0.489	1050.32	513.12	0.273	769.66	209.88
A_68_P21727904	chr2:147870499-147870543	NM_010446:2185	Foxa2	INSIDE	0.558	0.632	2231.15	1409.17	0.353	1644.72	580.08
A_68_P25737190	chr8:28317205-28317249	NM_029674:-4207	Got1l1	PROMOTER	0.558	0.709	1356.61	961.52	0.396	1032.68	408.54
A_68_P28997649	chr13:44825063-44825107	NM_001205044:-1058	Jarid2	PROMOTER	0.558	0.532	2829.26	1504.07	0.297	2181.41	647.35
A_68_P29842694	chr14:99697586-99697630	NM_009769:-301	Klf5	PROMOTER	0.558	0.555	2008.47	1115.62	0.310	1623.46	502.74
A_68_P25016725	chr7:28115897-28115945	NM_001113549:2747	Ltbp4	INSIDE	0.558	0.616	1201.99	740.92	0.344	1039.46	357.39

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P30424508	chr15:89145163-89145207	NM_001081030:558	Sbf1	INSIDE	0.558	0.538	1198.03	644.62	0.300	1067.07	320.46
A_68_P24044263	chr5:121835304-121835348	NM_001163470:298	Trafd1	INSIDE	0.558	0.489	1698.87	830.23	0.273	1368.54	373.35
A_68_P26947989	chr10:12588953-12588997	NM_011682:-7441	Utrn	PROMOTER	0.558	0.531	974.37	517.69	0.296	848.90	251.55
A_68_P25954145	A_68_P25954145			Unknown	0.558	0.568	1583.85	899.80	0.317	1109.55	351.82
A_68_P27992494	chr11:86900082-86900126	NM_024262:175	1200011M11Rik	INSIDE	0.557	0.685	3633.35	2489.28	0.381	2646.03	1009.26
A_68_P21147278	chr2:38142391-38142435	NM_146122:492	Dennd1a	INSIDE	0.557	0.697	4186.41	2917.72	0.388	3094.62	1200.72
A_68_P30156152	chr15:39688848-39688892	NM_022722:146	Dpys	INSIDE	0.557	0.581	1804.16	1048.81	0.324	1202.43	389.35
A_68_P20834313	chr1:174563103-174563147	NM_026725:-19	Dusp23	PROMOTER	0.557	0.482	1550.12	747.21	0.268	1209.27	324.62
A_68_P28175187	chr11:118861087-118861131	NM_001030291:11607	Enpp7	DOWNSTREAM	0.557	0.558	1312.41	732.47	0.311	959.99	298.16
A_68_P25023220	chr7:29501806-29501850	NM_015796:20	Fbxo17	INSIDE	0.557	0.656	1623.49	1064.23	0.365	1443.82	527.31
A_68_P29484663	chr14:27852219-27852263	NM_134437:54	Il17rd	INSIDE	0.557	0.516	1253.38	646.71	0.287	1027.00	295.15
A_68_P20566309	chr1:123224172-123224218	NM_133748:145	Insig2	INSIDE	0.557	0.487	1336.67	651.27	0.272	1040.86	282.63
A_68_P21345534	chr2:75542163-75542207	NM_010902:514	Nfe2l2	INSIDE	0.557	0.483	2548.48	1229.88	0.269	2074.48	557.51
A_68_P25956587	chr8:73900036-73900080	NM_010150:5793	Nr2f6	INSIDE	0.557	0.568	1405.79	798.22	0.316	1202.23	380.34
A_68_P27265099	chr10:76424280-76424324	NM_021568:390	Pcbp3	INSIDE	0.557	0.670	1142.64	765.24	0.373	972.69	362.62
A_68_P27924766	chr11:75007358-75007402	NM_177708:-114	Rtn4rl1	DIVERGENT_PROMOTER	0.557	0.556	1115.18	619.93	0.310	883.17	273.44
A_68_P26454290	chr9:42072563-42072607	NM_172769:-201	Sc5d	PROMOTER	0.557	0.466	2173.31	1012.46	0.259	1775.26	460.30
A_68_P24046791	chr5:122286329-122286373	NM_008507:460	Sh2b3	INSIDE	0.557	0.520	1493.26	776.52	0.290	1281.16	371.15
A_68_P31097896	chr17:24664666-24664710	NM_001172113:195	Traf7	INSIDE	0.557	0.341	5166.04	1761.38	0.190	3885.73	738.42
A_68_P24397781	chr6:42299527-42299571	NM_011777:-278	Zyx	PROMOTER	0.557	0.595	988.78	588.11	0.331	793.73	262.99
A_68_P21710707	chr2:144993216-144993260	ENSMUST00000110007:-251		PROMOTER	0.557	0.439	1459.90	641.05	0.245	1295.40	316.87
A_68_P20861819	chr1:179726176-179726220	NM_007422:442	Adss	INSIDE	0.556	0.534	1026.39	548.56	0.297	842.72	250.47
A_68_P21073309	chr2:25463281-25463325	NM_001024616:664	B230208H17Rik	INSIDE	0.556	0.422	1283.25	541.75	0.235	1017.19	238.59
A_68_P26127081	chr8:106695023-106695067	NM_001141922:632	Bean1	INSIDE	0.556	0.638	1363.79	870.38	0.355	1289.77	458.06
A_68_P22449310	chr3:116126022-116126067	NM_001080818:906	Cdc14a	INSIDE	0.556	0.599	1344.64	805.42	0.333	1127.01	375.04
A_68_P21822538	chr2:165059682-165059726	NM_174988:533	Cdh22	INSIDE	0.556	0.576	2327.71	1341.58	0.320	1922.96	615.69
A_68_P26238593	chr8:125749038-125749082	NM_194444:320	Cdk10	INSIDE	0.556	0.520	1983.84	1032.21	0.289	1550.55	448.44
A_68_P22340672	chr3:94590209-94590253	NM_001037711:207	Cgn	INSIDE	0.556	0.730	1766.28	1288.82	0.406	1252.38	508.07
A_68_P25051005	chr7:36539482-36539526	NM_178704:-31	Dpy19l3	PROMOTER	0.556	0.541	2558.75	1384.64	0.301	2077.84	624.93
A_68_P27897957	chr11:69734148-69734192	NM_001166590:-38	Eif5a	PROMOTER	0.556	0.655	936.87	613.40	0.364	849.72	309.06
A_68_P26213863	chr8:121868494-121868539	NM_024219:79	Hsbp1	INSIDE	0.556	0.491	1489.62	730.74	0.273	1214.04	330.94
A_68_P29613305	chr14:55236808-55236852	NR_030457:-1208	Mir686	PROMOTER	0.556	0.656	1403.16	919.91	0.365	1204.35	439.34
A_68_P20877311	chr1:182627122-182627166	NM_013729:21	Mixl1	INSIDE	0.556	0.675	5597.45	3780.38	0.375	4215.78	1582.74
A_68_P24974337	chr7:13629455-13629499	NM_145819:10637	Mzf1	INSIDE	0.556	0.460	1369.40	629.44	0.255	1254.65	320.46
A_68_P23575729	chr5:31262539-31262583	NM_016703:174	Preb	INSIDE	0.556	0.435	1957.97	852.60	0.242	1574.30	381.42
A_68_P22405717	chr3:107136584-107136628	NM_001045807:-399	Rbm15	PROMOTER	0.556	0.481	1819.97	875.19	0.267	1356.02	362.69
A_68_P32113650	chr19:41280684-41280728	NM_011904:558	Tll2	INSIDE	0.556	0.416	2341.26	973.11	0.231	1880.05	434.34
A_68_P29730260	chr14:76244587-76244631	NM_009429:-454	Tpt1	PROMOTER	0.556	0.620	1882.04	1166.11	0.345	1509.21	519.98
A_68_P25615117	chr8:3676454-3676498	NM_025701:0	Trappc5	INSIDE	0.556	0.418	1651.13	689.43	0.232	1207.39	280.25
A_68_P27854524	chr11:62364466-62364510	NM_011664:-517	Ubb	PROMOTER	0.556	0.626	3728.27	2333.43	0.348	2821.54	981.17
A_68_P23548555	chr5:25211490-25211534	NM_020570:103	Xrcc2	INSIDE	0.556	0.450	1279.43	575.45	0.250	1054.18	263.46
A_68_P22283291	chr3:82932267-82932311	ENSMUST00000047876:880		INSIDE	0.556	0.432	2029.46	876.27	0.240	1548.71	372.00
A_68_P32054915	chr19:29880098-29880142	NM_172836:379	9930021J03Rik	INSIDE	0.555	0.614	866.77	532.58	0.341	733.85	250.22
A_68_P24172965	chr5:148116273-148116317	NM_007673:2531	Cdx2	INSIDE	0.555	0.566	1928.69	1091.83	0.314	1504.76	472.42
A_68_P28833516	chr13:13485759-13485803	NM_031999:111	Gpr137b	INSIDE	0.555	0.623	1968.81	1226.19	0.346	1665.85	575.57
A_68_P30424715	chr15:89185807-89185851	NM_178919:262	Lmf2	INSIDE	0.555	0.665	1547.05	1028.76	0.369	1238.97	457.63
A_68_P20799114	chr1:168169051-168169095	NM_175296:-197	Mael	PROMOTER	0.555	3.213	4234.87	13605.29	1.784	3466.50	6184.25
A_68_P31127302	chr17:29459217-29459261	NM_023734:3412	Pi16	INSIDE	0.555	2.465	2975.74	7336.30	1.369	1879.24	2572.35
A_68_P22774390	chr4:21616242-21616286	NM_001080771:-3154	Prdm13	PROMOTER	0.555	0.433	1791.33	775.75	0.240	1502.19	361.15
A_68_P23233186	chr4:116924691-116924735	NM_026837:119	Tmem53	INSIDE	0.555	0.523	1081.98	565.55	0.290	914.03	265.04
A_68_P31259988	chr17:57226985-57227029	NM_009451:199	Tubb4	INSIDE	0.555	0.642	1049.31	673.97	0.357	849.33	302.91

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P23694951	chr5:52862528-52862572			Unknown	0.555	0.485	2330.56	1131.04	0.269	1806.00	486.70
A_68_P26595472	chr9:66682802-66682846	NM_026674:-311	Aph1c	PROMOTER	0.554	0.564	2116.14	1193.05	0.312	1592.91	497.13
A_68_P28104944	chr11:106911768-106911812	NM_176850:81446	Bptf	INSIDE	0.554	2.532	46344.44	117337.80	1.402	36795.29	51603.19
A_68_P23222744	chr4:114659711-114659755	NM_025647:101	Cmpk1	INSIDE	0.554	0.469	2116.44	992.63	0.260	1720.59	446.81
A_68_P28737539	chr12:111516074-111516118	NR_002866:182	Dio3os	INSIDE	0.554	0.557	1383.04	769.67	0.308	1133.20	349.36
A_68_P22343254	chr3:95087394-95087438	NM_133858:560	Fam63a	INSIDE	0.554	0.511	1412.47	721.45	0.283	1056.22	298.82
A_68_P28751073	chr12:113827105-113827149	NM_198411:132	Inf2	INSIDE	0.554	0.528	1145.20	604.34	0.292	902.36	263.67
A_68_P24284102	chr6:21164876-21164920	NM_019697:-1210	Kcnd2	PROMOTER	0.554	0.595	1729.34	1028.65	0.329	1273.09	419.27
A_68_P20877313	chr1:182627309-182627353	NM_013729:-165	Mixl1	PROMOTER	0.554	0.623	3579.75	2230.22	0.345	2884.62	995.97
A_68_P24004044	chr5:114894084-114894128	NM_029956:-70	Mmab	DIVERGENT_PROMOTER	0.554	0.504	1070.43	539.18	0.279	929.38	259.14
A_68_P27041530	chr10:30522669-30522713	NM_172495:223	Ncoa7	INSIDE	0.554	0.548	1606.18	880.11	0.304	1306.02	396.82
A_68_P23176715	chr4:104782702-104782746	NM_178143:-221	Prkaa2	PROMOTER	0.554	0.429	2125.66	912.00	0.238	1625.92	386.73
A_68_P31259825	chr17:57198936-57198980	NM_025877:328	Slc25a23	INSIDE	0.554	0.488	2654.48	1296.22	0.271	2082.08	563.67
A_68_P32168786	chr19:50752601-50752645	NM_021377:480	Sorcs1	INSIDE	0.554	0.620	1509.19	935.50	0.343	1213.94	416.53
A_68_P25661253	chr8:12396004-12396049	NM_009233:508	Sox1	INSIDE	0.554	0.488	1936.47	945.71	0.271	1446.16	391.54
A_68_P24136159	chr5:140020492-140020536	NM_013702:663	Uncx	INSIDE	0.554	0.493	1501.07	740.30	0.273	1128.42	308.57
A_68_P25614206	chr8:3493424-3493468	NM_080461:309	Zfp358	INSIDE	0.554	0.352	2119.63	746.48	0.195	1681.69	327.95
A_68_P31497267	chr18:11997722-11997766	NM_001146287:-38	Cables1	PROMOTER	0.553	0.486	1665.49	808.73	0.268	1224.89	328.79
A_68_P27913316	chr11:72608989-72609033	NM_001024926:331	Cyb5d2	INSIDE	0.553	0.692	1555.18	1076.84	0.383	1307.64	500.27
A_68_P30478221	chr15:98927716-98927760	NM_176835:-2176	Dnajc22	DIVERGENT_PROMOTER	0.553	0.383	1523.30	583.61	0.212	1164.54	246.89
A_68_P23155326	chr4:101169630-101169674	NM_198412:400	Dnajc6	INSIDE	0.553	0.660	2483.52	1639.61	0.365	2019.88	737.18
A_68_P21010978	chr2:12340776-12340820	NM_024185:289	Fam188a	INSIDE	0.553	0.697	1174.00	817.77	0.385	958.38	369.45
A_68_P27284104	chr10:80040680-80040724	NM_078477:-661	Klf16	PROMOTER	0.553	0.607	2026.42	1230.08	0.336	1567.43	526.54
A_68_P23445965	chr5:3596035-3596079	NM_027777:-9	Pex1	PROMOTER	0.553	0.527	1240.26	653.58	0.291	1005.49	292.76
A_68_P24119438	chr5:136578137-136578181	NM_133914:18373	Rasa4	INSIDE	0.553	0.659	1416.44	932.98	0.364	1122.29	409.03
A_68_P28261128	chr12:15821694-15821738	NM_144551:1875	Trib2	INSIDE	0.553	0.685	3081.72	2110.61	0.379	2537.93	960.76
A_68_P22630562	chr3:148651256-148651304	ENSMUST00000098518:1000		INSIDE	0.553	0.455	1153.17	525.19	0.252	894.15	225.40
A_68_P31891632	chr18:85121550-85121594	NM_025969:-656	1700034H14Rik	PROMOTER	0.552	0.478	2856.82	1365.88	0.264	2229.58	588.18
A_68_P31112025	chr17:26853064-26853108	NM_029870:492	A930001N09Rik	INSIDE	0.552	0.575	2484.45	1428.84	0.317	2103.29	667.25
A_68_P32213516	chr19:58529694-58529738	NM_010279:-760	Gfra1	PROMOTER	0.552	0.699	3599.35	2514.57	0.386	2391.78	922.06
A_68_P24431596	chr6:49163809-49163853	NM_023670:1123	Igf2bp3	INSIDE	0.552	0.528	1902.95	1004.54	0.291	1562.22	455.06
A_68_P23120295	chr4:94645754-94645798	NM_177239:15	Mysm1	INSIDE	0.552	0.623	1198.81	746.32	0.344	1053.70	362.31
A_68_P30368650	chr15:79634238-79634282	NM_030689:879	Nptxr	INSIDE	0.552	0.707	1287.74	910.09	0.390	1115.47	435.02
A_68_P30346012	chr15:75920669-75920713	NM_144847:-247	Nrbp2	PROMOTER	0.552	0.670	1346.58	901.54	0.369	932.08	344.37
A_68_P27551119	chr11:3189697-3189741	NM_019574:-741	Patz1	PROMOTER	0.552	0.697	1944.77	1355.02	0.385	1623.76	625.05
A_68_P20633689	chr1:136391258-136391302	NM_145510:44	Rabif	INSIDE	0.552	0.449	1167.36	523.97	0.248	924.39	229.20
A_68_P27798062	chr11:52045287-52045331	NM_011543:-188	Skp1a	PROMOTER	0.552	0.536	1812.67	971.02	0.296	1514.98	448.31
A_68_P22446821	chr3:115710285-115710329	NM_023214:18	Slc30a7	INSIDE	0.552	0.621	1370.18	850.22	0.342	1049.51	359.32
A_68_P20411726	chr1:88255561-88255605	NR_002851:-2680	Snord82	PROMOTER	0.552	0.724	2936.10	2125.00	0.400	2155.77	861.95
A_68_P29733545	chr14:76814748-76814792	NM_207652:-857	Tsc22d1	PROMOTER	0.552	0.670	1552.87	1040.69	0.370	1208.06	446.93
A_68_P24155561	chr5:143997211-143997255	NM_177681:346	Zfp12	INSIDE	0.552	0.717	2810.31	2014.94	0.396	2164.43	857.11
A_68_P26660364	chr9:78463666-78463710	NM_153098:336	Cd109	INSIDE	0.551	0.484	2473.96	1196.74	0.267	2093.29	558.35
A_68_P31118681	chr17:27956946-27956990	NM_001033279:519	D17Wsu92e	INSIDE	0.551	0.485	2873.68	1393.55	0.267	2432.03	649.68
A_68_P24593936	chr6:83456719-83456763	NM_001162521:223	Dguok	INSIDE	0.551	0.637	858.23	546.91	0.351	760.83	267.37
A_68_P31418994	chr17:87154526-87154570	NM_010137:1345	Epas1	INSIDE	0.551	0.645	1176.05	758.34	0.356	976.78	347.35
A_68_P28221299	chr12:8305679-8305723	NM_013527:3060	Gdf7	INSIDE	0.551	0.562	1176.39	661.38	0.310	942.05	291.95
A_68_P25048708	chr7:36103274-36103318	NM_026181:163	Gpatch1	INSIDE	0.551	0.600	2849.90	1709.53	0.331	2327.19	769.70
A_68_P31425154	chr17:88197235-88197279	NM_199251:78	Kcnk12	INSIDE	0.551	0.642	1855.73	1190.91	0.354	1480.17	523.58
A_68_P31095211	chr17:24210441-24210485	NM_027008:-10	Kctd5	PROMOTER	0.551	0.582	2467.49	1437.18	0.321	1824.41	585.38
A_68_P21747681	chr2:151931454-151931498	NM_029688:11	Srxn1	INSIDE	0.551	0.690	2167.54	1495.96	0.380	1752.81	666.04
A_68_P23309106	chr4:131476303-131476347	NM_001201367:-1361	Tmem200b	PROMOTER	0.551	0.672	1491.79	1002.37	0.370	1377.04	509.77

						Sham group			TiO$_2$-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P30596854	chr16:22265994-22266038	NM_009186:-14	Tra2b	PROMOTER	0.551	0.416	2931.55	1220.49	0.230	2189.19	502.54
A_68_P27635753	chr11:21139469-21139513	NM_139061:599	Vps54	INSIDE	0.551	0.630	1069.12	673.57	0.347	883.52	306.69
A_68_P32134051	chr19:44808722-44808771			Unknown	0.551	2.986	1372.34	4098.20	1.645	901.26	1482.86
A_68_P27910205	chr11:72028532-72028576	NM_001163728:-85	4930563E22Rik	PROMOTER	0.550	0.471	1501.69	707.05	0.259	1237.94	320.34
A_68_P30811312	chr16:62846773-62846817	NM_026577:72	Arl13b	INSIDE	0.550	0.665	2678.06	1782.18	0.366	2119.09	775.27
A_68_P21703962	chr2:143688269-143688313	NM_009751:619	Bfsp1	INSIDE	0.550	0.546	3013.50	1646.23	0.301	2402.58	722.05
A_68_P24058180	chr5:124357134-124357178	NM_026603:-127	Denr	PROMOTER	0.550	0.502	3004.11	1508.81	0.276	2477.22	684.61
A_68_P29941731	chr14:119324409-119324453	NM_025943:-2041	Dzip1	PROMOTER	0.550	0.475	1629.32	774.21	0.261	1344.65	351.27
A_68_P20612315	chr1:132774907-132774951	NM_026976:12575	Faim3	INSIDE	0.550	0.439	1576.37	691.78	0.241	1307.67	315.70
A_68_P28727214	chr12:109544952-109544996	NM_001044380:495	Hhipl1	INSIDE	0.550	0.429	1893.69	812.73	0.236	1451.64	342.78
A_68_P25613343	chr8:3279377-3279421	NM_010568:219	Insr	INSIDE	0.550	0.481	1718.27	825.72	0.264	1383.28	365.34
A_68_P25098817	chr7:53652411-53652455	NM_001112739:566	Kcnc1	INSIDE	0.550	0.504	2277.86	1147.36	0.277	1965.29	544.59
A_68_P25016713	chr7:28114386-28114430	NM_001113549:4259	Ltbp4	INSIDE	0.550	0.724	1877.58	1359.86	0.398	1365.19	543.97
A_68_P30425255	chr15:89284136-89284180	NM_021921:-183	Mapk8ip2	PROMOTER	0.550	0.697	4044.32	2817.95	0.383	2992.20	1146.30
A_68_P24592786	chr6:83276392-83276436	NM_145571:382	Mobkl1b	INSIDE	0.550	0.506	1381.30	698.94	0.278	1160.57	322.90
A_68_P25090466	chr7:52241494-52241538	NM_019830:186	Prmt1	INSIDE	0.550	0.582	2394.80	1392.61	0.320	1757.31	561.92
A_68_P26630338	chr9:72772983-72773027	NM_028116:-452	Pygo1	PROMOTER	0.550	0.586	2539.61	1488.02	0.322	1916.71	617.62
A_68_P31253475	chr17:56176053-56176097	NM_013664:-75	Sh3gl1	DIVERGENT_PROMOTER	0.550	0.553	4830.53	2671.43	0.304	3637.50	1106.08
A_68_P25026345	chr7:30066535-30066579	NM_001082548:440	Spint2	INSIDE	0.550	0.718	1768.27	1268.84	0.395	1463.88	577.69
A_68_P24534825	chr6:71094013-71094057	NM_001033929:336	Thnsl2	INSIDE	0.550	0.529	2103.11	1112.05	0.291	1601.07	465.56
A_68_P22857437	chr4:40420294-40420338	NM_001166009:154	Tmem215	INSIDE	0.550	0.522	1267.86	662.26	0.287	1098.66	315.69
A_68_P27898020	chr11:69749025-69749069	NM_016875:-354	Ybx2	PROMOTER	0.550	0.566	2117.23	1197.87	0.311	1787.40	556.56
A_68_P30959877	chr16:90935364-90935408	NM_026502:-292	1110004E09Rik	PROMOTER	0.549	0.655	975.44	638.67	0.359	806.84	289.87
A_68_P21646220	chr2:133378597-133378641	NM_007553:-316	Bmp2	PROMOTER	0.549	0.608	1727.31	1050.49	0.334	1473.87	491.72
A_68_P31933965	chr19:6320530-6320574	NM_001033342:14096	Cdc42bpg	INSIDE	0.549	3.625	1485.09	5383.15	1.989	1314.89	2615.11
A_68_P20522333	chr1:111879695-111879739	NM_172853:-597	Cdh7	PROMOTER	0.549	0.625	2362.99	1475.73	0.343	1769.93	606.97
A_68_P28705225	chr12:105989571-105989615	NM_148948:570	Dicer1	INSIDE	0.549	0.404	1714.93	693.62	0.222	1382.82	307.15
A_68_P26406144	chr9:32348552-32348596	NM_008026:379	Fli1	INSIDE	0.549	0.569	917.17	522.06	0.312	752.94	235.12
A_68_P27282040	chr10:79723724-79723768	NM_010255:-33	Gamt	DIVERGENT_PROMOTER	0.549	0.456	3792.04	1728.04	0.250	2988.07	747.36
A_68_P23091882	chr4:88368088-88368132	NM_172871:302	Klhl9	INSIDE	0.549	0.575	1844.70	1060.45	0.316	1498.88	472.96
A_68_P26500006	chr9:49605230-49605274	NM_001081445:1922	Ncam1	INSIDE	0.549	0.306	2266.14	694.34	0.168	1697.68	285.48
A_68_P21565424	chr2:118503074-118503118	NM_001145854:115	Pak6	INSIDE	0.549	0.425	1545.02	657.06	0.233	1355.55	316.31
A_68_P26809843	chr9:107501498-107501542	NM_009153:6213	Sema3b	INSIDE	0.549	3.968	607.40	2409.97	2.178	440.27	958.74
A_68_P31019372	chr17:5840861-5840905	NM_025664:-497	Snx9	PROMOTER	0.549	0.626	1071.86	671.50	0.344	818.74	281.71
A_68_P20638618	chr1:137210111-137210155	NM_011590:182	Timm17a	INSIDE	0.549	0.528	2434.31	1285.29	0.290	1764.74	511.79
A_68_P21736744	chr2:149656175-149656219	NM_001085521:-322	Tmem90b	PROMOTER	0.549	0.414	1518.06	628.69	0.227	1125.00	255.93
A_68_P24427172	chr6:48389196-48389240	NM_001085415:5871	Zfp467	INSIDE	0.549	1.351	4264.31	5759.59	0.741	2680.08	1985.71
A_68_P28740680	chr12:112088415-112088460	NM_001199785:-51	Zfp839	DIVERGENT_PROMOTER	0.549	0.750	4590.79	3442.32	0.412	3358.40	1383.67
A_68_P23023123	chr4:74923898-74923942	NM_025849:270	3110001D03Rik	INSIDE	0.548	0.648	1123.40	728.35	0.355	848.05	301.35
A_68_P26888898	chr9:122261191-122261235	NM_026179:479	Abhd5	INSIDE	0.548	0.475	1220.49	580.11	0.260	1149.07	299.21
A_68_P26531723	chr9:55359728-55359772	NM_145615:300	Etfa	INSIDE	0.548	0.568	1555.05	882.77	0.311	1334.06	414.85
A_68_P28429306	chr12:52449562-52449606	NM_001015099:368	G2e3	INSIDE	0.548	0.644	1112.50	716.32	0.353	1006.48	355.44
A_68_P21129593	chr2:34609363-34609407	NM_025709:1368	Gapvd1	INSIDE	0.548	0.546	3536.90	1930.95	0.299	2825.39	844.86
A_68_P21147671	chr2:38210043-38210094	NM_010710:3241	Lhx2	INSIDE	0.548	0.563	946.02	532.52	0.308	580.27	178.99
A_68_P24981706	chr7:17061083-17061127	NM_008718:1025	Npas1	INSIDE	0.548	0.582	1004.12	584.56	0.319	874.17	279.13
A_68_P31306704	chr17:66868707-66868751	NM_024448:282	Rab12	INSIDE	0.548	0.368	2046.32	752.61	0.201	1460.20	294.13
A_68_P24992460	chr7:19868360-19868404	NM_001025364:-8065	Rtn2	PROMOTER	0.548	0.493	1960.99	966.53	0.270	1462.25	394.66
A_68_P31151613	chr17:34168502-34168546	NM_001077709:111	Slc39a7	INSIDE	0.548	0.588	1203.11	706.85	0.322	898.48	289.29
A_68_P28635988	chr12:92885896-92885940	NM_175367:138958	Ston2	INSIDE	0.548	2.984	964.38	2877.66	1.635	863.57	1412.37
A_68_P30251030	chr15:58765208-58765252	NM_175151:55	Tatdn1	INSIDE	0.548	0.598	1946.93	1163.77	0.327	1508.81	493.79
A_68_P23749880	chr5:64621862-64621906	NM_019636:70435	Tbc1d1	INSIDE	0.548	0.474	1482.14	702.26	0.260	1194.78	310.27

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P30385311	chr15:82730377-82730421	NR_027799:-1507	Tbrg3	PROMOTER	0.548	0.707	1452.20	1026.17	0.388	1282.99	497.26
A_68_P27902563	chr11:70578032-70578076	NM_177565:106	Zfp3	INSIDE	0.548	0.405	1453.52	587.98	0.222	1276.75	282.92
A_68_P31292451	chr17:64212897-64212941	ENSMUST00000050753:222		INSIDE	0.548	0.616	2031.27	1252.16	0.338	1684.70	568.61
A_68_P27085192	chr10:40403058-40403102	NM_177793:-7	9030224M15Rik	PROMOTER	0.547	0.682	1325.94	904.47	0.373	1157.92	431.89
A_68_P28751330	chr12:113858462-113858506	NM_007421:227	Adssl1	INSIDE	0.547	0.643	4984.36	3205.37	0.352	3561.95	1253.03
A_68_P30149944	chr15:38448175-38448219	NM_001102458:825	Azin1	INSIDE	0.547	0.721	6662.80	4806.06	0.394	5041.57	1987.79
A_68_P29292644	chr13:105607137-105607182	NM_026072:-126	Cwc27	DIVERGENT_PROMOTER	0.547	0.609	1368.52	833.90	0.333	1139.10	379.52
A_68_P20413588	chr1:88600253-88600297	NM_001172157:-104	Dis3l2	PROMOTER	0.547	0.626	3588.05	2247.88	0.343	2757.39	945.60
A_68_P29026629	chr13:49777484-49777528	NM_172015:8	Iars	INSIDE	0.547	0.646	1137.31	735.03	0.354	945.69	334.59
A_68_P24089926	chr5:130090512-130090556	NM_011846:446	Mmp17	INSIDE	0.547	0.421	1943.77	818.03	0.230	1667.85	383.78
A_68_P20352130	chr1:75121478-75121522	NM_029342:300	Nhej1	INSIDE	0.547	0.505	1453.54	733.90	0.276	1120.07	309.27
A_68_P25410004	chr7:116925392-116925436	NM_020610:-355	Nrip3	PROMOTER	0.547	0.676	1933.21	1307.24	0.370	1507.09	557.46
A_68_P30587017	chr16:20302514-20302558	NM_001005767:-101	Parl	PROMOTER	0.547	0.730	2179.68	1592.07	0.400	1745.38	697.47
A_68_P28112590	chr11:108204958-108205002	NM_011101:222	Prkca	INSIDE	0.547	0.716	1635.90	1170.74	0.391	1247.44	488.36
A_68_P28164528	chr11:117193656-117193700	NM_001113488:52	Septin9	INSIDE	0.547	0.472	1732.47	818.41	0.258	1274.35	329.23
A_68_P31969894	chr19:14672643-14672687	NM_011600:-191	Tle4	PROMOTER	0.547	0.448	1528.45	684.76	0.245	1323.42	324.57
A_68_P27513159	chr10:122634312-122634356	NM_027604:-355	Usp15	PROMOTER	0.547	0.569	1198.25	681.30	0.311	905.95	281.84
A_68_P24958144	chr7:7073964-7074008	NM_172738:201	Zfp954	INSIDE	0.547	0.594	2113.52	1255.26	0.325	1698.24	551.27
A_68_P28041229	chr11:95720981-95721025	NM_008081:55183	B4galnt2	DOWNSTREAM	0.546	0.659	908.26	598.24	0.360	803.74	289.06
A_68_P26199702	chr8:119445672-119445716	NM_028131:55	Cenpn	INSIDE	0.546	0.614	949.24	582.54	0.335	819.18	274.50
A_68_P25835333	chr8:47377718-47377762	NM_173789:2285	Helt	INSIDE	0.546	0.709	1376.17	975.11	0.387	1184.63	458.14
A_68_P28581705	chr12:82696134-82696178	NM_027213:-211	Med6	PROMOTER	0.546	3.552	7665.01	27224.48	1.939	4821.74	9348.28
A_68_P21076059	chr2:25915973-25916017	NM_001037098:31922	Nacc2	INSIDE	0.546	3.135	557.06	1746.57	1.712	472.85	809.35
A_68_P25021470	chr7:29157527-29157571	NM_001083912:133	Plekhg2	INSIDE	0.546	0.452	1942.28	876.99	0.246	1514.20	373.18
A_68_P21101101	chr2:29918413-29918457	NM_001204875:-3559	Set	PROMOTER	0.546	0.653	878.99	574.01	0.357	637.51	227.30
A_68_P28351013	chr12:35731615-35731659	NM_001014973:-224	Snx13	PROMOTER	0.546	0.624	967.64	604.04	0.341	954.36	325.42
A_68_P24056370	chr5:124023089-124023133	NM_029929:-86	Vps33a	PROMOTER	0.546	0.646	1251.04	808.41	0.353	1059.59	373.89
A_68_P22341850	chr3:94818782-94818826	NM_030074:356	Zfp687	INSIDE	0.546	0.581	1044.57	606.94	0.317	792.04	251.19
A_68_P23611143	chr5:37420486-37420530	ENSMUST00000165557:12377		DOWNSTREAM	0.546	0.522	1411.75	736.26	0.285	1149.64	327.25
A_68_P28680559	chr12:101437798-101437842	NM_009790:70	Calm1	INSIDE	0.545	0.438	1423.84	623.99	0.239	1086.39	259.37
A_68_P29038492	chr13:52625955-52625999	NM_001024474:229	Diras2	INSIDE	0.545	0.682	4342.23	2960.54	0.372	3238.56	1203.85
A_68_P28396957	chr12:45310575-45310620	NM_013760:458	Dnajb9	INSIDE	0.545	0.405	1667.74	675.83	0.221	1374.69	303.33
A_68_P25507036	chr7:134890617-134890661	NM_172748:350	Fbxl19	INSIDE	0.545	0.577	3130.41	1805.33	0.314	2168.27	681.06
A_68_P24830597	chr6:127030465-127030509	NM_022657:7567	Fgf23	INSIDE	0.545	0.659	3245.69	2139.62	0.359	2522.13	906.67
A_68_P25668519	chr8:13468177-13468227	NM_019521:26333	Gas6	INSIDE	0.545	2.755	986.63	2718.03	1.502	664.35	997.76
A_68_P23284717	chr4:127003796-127003840	NM_008126:2551	Gjb3	INSIDE	0.545	4.401	2507.42	11034.19	2.398	1882.09	4513.55
A_68_P21438061	chr2:93796206-93796250	NM_001145034:1029	Gm13889	INSIDE	0.545	0.646	3243.11	2093.86	0.352	2326.97	818.79
A_68_P30344599	chr15:75692883-75692927	NM_026960:136	Gsdmd	INSIDE	0.545	0.654	1225.36	800.98	0.356	892.64	317.78
A_68_P20725330	chr1:155033404-155033448	NM_008485:151	Lamc2	INSIDE	0.545	0.571	1269.63	725.03	0.311	1053.56	327.89
A_68_P27271615	chr10:77472561-77472605	NM_008826:-41	Pfkl	PROMOTER	0.545	0.580	1289.63	748.22	0.316	1077.71	340.70
A_68_P26825597	chr9:110646599-110646643	NM_001083935:-430	Pth1r	PROMOTER	0.545	0.686	2045.01	1402.42	0.374	1634.41	611.20
A_68_P26467468	chr9:44215837-44215881	NM_024266:62	Rps25	INSIDE	0.545	0.472	3137.36	1480.95	0.257	2248.34	578.92
A_68_P22149789	chr3:54589967-54590012	NM_019483:30486	Smad9	INSIDE	0.545	2.793	751.23	2098.47	1.523	693.79	1056.72
A_68_P26453528	chr9:41931891-41931935	NM_011436:460	Sorl1	INSIDE	0.545	0.463	1655.88	766.03	0.252	1376.90	347.07
A_68_P20261291	chr1:59030219-59030263	NM_172406:86	Trak2	INSIDE	0.545	0.467	2678.36	1252.08	0.255	2055.05	523.99
A_68_P23293641	chr4:128561860-128561904	NM_178110:499	Trim62	INSIDE	0.545	0.667	2352.63	1569.34	0.364	1936.20	703.94
A_68_P22955051	chr4:59202692-59202736	NM_011673:293	Ugcg	INSIDE	0.545	0.563	1620.86	912.76	0.307	1262.37	387.28
A_68_P26494154	chr9:48644306-48644350	NM_001033324:-278	Zbtb16	PROMOTER	0.545	0.533	1469.34	782.75	0.291	1137.61	330.51
A_68_P23694950	chr5:52862343-52862387			Unknown	0.545	0.575	1162.21	668.40	0.314	889.66	279.09
A_68_P21061191	chr2:22895186-22895230	NM_001077190:552	Abi1	INSIDE	0.544	0.528	1339.40	707.62	0.287	1188.33	341.57
A_68_P26128839	chr8:107033201-107033245	NM_180958:565	Ccdc79	INSIDE	0.544	0.619	1433.66	887.98	0.337	1088.20	366.73

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P21425958	chr2:91848432-91848476	NM_011957:15873	Creb3l1	INSIDE	0.544	0.461	1531.75	705.60	0.251	1151.80	288.78
A_68_P27487944	chr10:118305191-118305235	NM_001014390:747	Dyrk2	INSIDE	0.544	0.645	1276.23	823.73	0.351	1093.33	383.90
A_68_P24193751	chr5:151755711-151755755	NM_013823:551	Kl	INSIDE	0.544	0.537	1002.19	538.11	0.292	947.84	276.69
A_68_P20624276	chr1:134777196-134777240	NM_010732:287	Lrrn2	INSIDE	0.544	0.629	1327.89	835.28	0.342	1101.54	376.70
A_68_P22882728	chr4:45421725-45421769	NM_001009949:-108	Mcart1	PROMOTER	0.544	0.460	1645.80	756.44	0.250	1276.62	319.43
A_68_P24089919	chr5:130089703-130089747	NM_011846:-364	Mmp17	PROMOTER	0.544	0.649	3126.10	2027.88	0.353	2301.27	812.81
A_68_P22606646	chr3:144781460-144781506	NM_001162538:-70	Odf2l	PROMOTER	0.544	0.598	2282.71	1365.36	0.325	1816.47	590.70
A_68_P31381751	chr17:80606502-80606546	NM_001195485:121	Srsf7	INSIDE	0.544	0.617	1660.75	1024.34	0.335	1280.02	429.18
A_68_P31156002	chr17:34973346-34973390	NM_019442:480	Stk19	INSIDE	0.544	0.616	1454.28	895.82	0.335	1323.89	444.02
A_68_P27365510	chr10:94977758-94977802	NM_080560:-15	Ube2n	PROMOTER	0.544	0.448	1157.40	518.61	0.244	935.78	228.11
A_68_P26467843	chr9:44291481-44291525	ENSMUST00000136322:4642		DOWNSTREAM	0.544	0.674	1666.30	1123.51	0.367	1189.81	436.68
A_68_P24010683	chr5:116081567-116081611	NR_027810:237	1110006O24Rik	INSIDE	0.543	0.480	3967.39	1902.82	0.261	3024.88	788.20
A_68_P23332632	chr4:135762182-135762226	NM_001008232:-75	Asap3	PROMOTER	0.543	2.821	18055.88	50943.65	1.533	12634.63	19363.60
A_68_P30371083	chr15:80085473-80085517	NM_009716:-119	Atf4	PROMOTER	0.543	0.632	913.43	577.46	0.343	744.56	255.46
A_68_P31929038	chr19:5491024-5491068	NM_007687:592	Cfl1	INSIDE	0.543	0.647	1064.32	688.27	0.351	871.14	306.02
A_68_P22317612	chr3:88972806-88972850	NM_001163432:4102	Clk2	INSIDE	0.543	1.357	5688.68	7717.31	0.736	4168.93	3069.01
A_68_P32145760	chr19:46836584-46836628	NM_001102471:508	Cnnm2	INSIDE	0.543	0.449	2306.30	1035.74	0.244	1821.43	444.46
A_68_P25951443	chr8:72899164-72899208	NM_016685:1740	Comp	INSIDE	0.543	0.397	1681.33	668.26	0.216	1209.96	261.28
A_68_P26079750	chr8:97362477-97362521	NM_026452:182	Coq9	INSIDE	0.543	0.377	3531.86	1332.20	0.205	2767.06	566.52
A_68_P30511523	chr16:4679735-4679779	NM_030205:-36	Coro7	DIVERGENT_PROMOTER	0.543	0.679	1880.36	1276.46	0.369	1458.73	537.79
A_68_P29410629	chr14:13173646-13173690	NM_080433:4711	Fezf2	DOWNSTREAM	0.543	0.462	1147.86	529.98	0.250	1052.13	263.56
A_68_P30683214	chr16:37916363-37916407	NM_153394:-197	Gpr156	PROMOTER	0.543	0.654	962.33	629.66	0.355	758.05	269.48
A_68_P26017803	chr8:86566236-86566280	NM_016671:216	Il27ra	INSIDE	0.543	0.727	3520.60	2560.29	0.395	2614.92	1033.06
A_68_P20644038	chr1:138028419-138028463	NM_001039472:463	Kif21b	INSIDE	0.543	0.566	1200.58	679.11	0.307	1107.51	340.33
A_68_P32148154	chr19:47254136-47254180	NM_021360:849	Neurl1a	INSIDE	0.543	6.887	11150.18	76794.00	3.742	7444.01	27859.02
A_68_P29057299	chr13:55932917-55932961	NM_011097:-152	Pitx1	PROMOTER	0.543	0.491	1163.44	570.69	0.266	928.53	247.14
A_68_P23656662	chr5:45841524-45841568	NM_024236:-78	Qdpr	DIVERGENT_PROMOTER	0.543	0.446	1395.00	622.19	0.242	1152.90	279.07
A_68_P20557411	chr1:121401081-121401125	NM_022327:257	Ralb	INSIDE	0.543	0.592	3035.96	1797.70	0.322	2369.74	762.06
A_68_P31925255	chr19:4811527-4811571	NM_019869:86	Rbm14	INSIDE	0.543	0.553	1317.37	728.30	0.300	1027.16	308.37
A_68_P22165084	chr3:57539624-57539668	NM_011883:-341	Rnf13	PROMOTER	0.543	0.444	1615.48	717.98	0.241	1336.18	322.20
A_68_P31930504	chr19:5731477-5731521	NM_020491:223	Sssca1	INSIDE	0.543	0.578	1028.03	593.89	0.314	770.02	241.55
A_68_P30792107	chr16:58523074-58523118	NM_018784:329	St3gal6	INSIDE	0.543	0.578	1177.04	680.78	0.314	897.75	281.89
A_68_P20066611	chr1:19199816-19199872	NM_001025305:-2290	Tcfap2b	PROMOTER	0.543	0.645	1427.03	920.39	0.350	1101.28	385.88
A_68_P31121931	chr17:28478403-28478447	NM_001204156:8867	Tead3	INSIDE	0.543	0.478	1439.41	687.77	0.260	1169.74	303.73
A_68_P24136132	chr5:140016559-140016603	NM_013702:-3271	Uncx	PROMOTER	0.543	0.700	2479.04	1736.39	0.381	1900.50	723.36
A_68_P24638017	chr6:91235626-91235670			Unknown	0.543	0.687	1656.86	1137.58	0.373	1269.65	473.01
A_68_P25210209	chr7:77426428-77426472	AK148659:-1805		PROMOTER	0.543	0.619	1217.24	753.20	0.336	966.29	324.78
A_68_P25841618	chr8:48499216-48499260	ENSMUST00000074466:756		INSIDE	0.543	0.410	1619.11	663.44	0.222	1311.63	291.71
A_68_P24464804	chr6:54631784-54631828	NM_026629:41	2410066E13Rik	INSIDE	0.542	0.375	1375.53	515.97	0.203	1127.07	229.13
A_68_P23417005	chr4:151552435-151552479	NM_001146057:-7786	Acot7	PROMOTER	0.542	0.278	2371.44	659.43	0.151	1876.67	282.61
A_68_P28050942	chr11:97361786-97361830	NM_021493:50335	Arhgap23	INSIDE	0.542	0.664	2050.85	1360.95	0.359	1674.22	601.87
A_68_P30573854	chr16:17452586-17452630	NM_007764:529	Crkl	INSIDE	0.542	0.685	1684.53	1154.00	0.372	1284.92	477.48
A_68_P25502555	chr7:133991327-133991371	NM_010069:282	Doc2a	INSIDE	0.542	0.526	1156.49	608.46	0.285	965.39	275.48
A_68_P27677361	chr11:29924802-29924846	NM_146016:1209	Eml6	INSIDE	0.542	0.668	1041.82	695.84	0.362	987.53	357.17
A_68_P29309824	chr13:108949176-108949220	NM_028042:267	Ercc8	INSIDE	0.542	0.546	937.84	512.42	0.296	779.43	230.99
A_68_P23539565	chr5:23536003-23536047	NM_053090:477	Fam126a	INSIDE	0.542	0.540	2375.65	1283.56	0.293	1969.12	576.23
A_68_P25023289	chr7:29517672-29517716	NM_015796:15886	Fbxo17	INSIDE	0.542	0.613	1326.90	813.96	0.332	1094.32	363.66
A_68_P22299771	chr3:85691284-85691328	NM_177130:134	Glt28d2	INSIDE	0.542	0.544	1148.12	624.12	0.295	976.14	287.65
A_68_P26445379	chr9:40608906-40608950	NM_031165:-427	Hspa8	PROMOTER	0.542	0.499	1949.01	972.53	0.271	1501.36	406.35
A_68_P24322954	chr6:28782175-28782219	NM_138682:-449	Lrrc4	PROMOTER	0.542	0.515	1533.76	790.29	0.280	1204.87	336.76
A_68_P27560503	chr11:4847990-4848034	NM_010904:55	Nefh	INSIDE	0.542	0.436	2764.76	1204.94	0.236	2271.19	536.02

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P30498007	chr15:102301316-102301361	NM_001103165:276	Pcbp2	INSIDE	0.542	0.688	1724.37	1187.17	0.373	1255.17	468.11
A_68_P24994423	chr7:20214968-20215012	NM_009046:-203	Relb	PROMOTER	0.542	0.679	1367.16	927.81	0.368	1126.93	414.69
A_68_P20596468	chr1:129574040-129574084	NM_028135:536	Tmem163	INSIDE	0.542	0.553	1420.07	785.55	0.300	1096.41	328.69
A_68_P31335318	chr17:71966149-71966193	NM_175639:616	Wdr43	INSIDE	0.542	0.536	1731.96	927.84	0.290	1479.80	429.51
A_68_P30657579	chr16:33381453-33381497	NM_011749:614	Zfp148	INSIDE	0.542	0.588	1881.85	1107.05	0.319	1357.88	432.86
A_68_P20412466	chr1:88401070-88401114			Unknown	0.542	0.595	2556.51	1521.12	0.323	2060.87	664.88
A_68_P25457396	chr7:125387673-125387717	NR_027879:274	4930583K01Rik	INSIDE	0.541	0.431	2179.68	939.57	0.233	1564.34	364.96
A_68_P25737279	chr8:28338376-28338420	NM_013462:1662	Adrb3	INSIDE	0.541	0.720	4041.98	2911.20	0.389	2792.44	1087.61
A_68_P29342438	chr13:114584476-114584520	NM_172595:-217	Arl15	PROMOTER	0.541	0.581	1224.91	711.98	0.315	961.95	302.75
A_68_P26948226	chr10:12642736-12642780	NR_038027:167	B230208H11Rik	INSIDE	0.541	0.614	959.35	589.19	0.332	836.80	277.82
A_68_P31125919	chr17:29230688-29230732	NM_007669:-6	Cdkn1a	PROMOTER	0.541	0.612	2807.15	1719.38	0.331	2049.09	678.77
A_68_P23193625	chr4:107595986-107596030	NM_009949:186	Cpt2	INSIDE	0.541	0.570	1575.74	897.86	0.308	1261.84	388.93
A_68_P29681786	chr14:67486350-67486394	NM_009955:1065	Dpysl2	INSIDE	0.541	0.609	4537.04	2763.69	0.330	3389.91	1117.68
A_68_P30363918	chr15:78861120-78861164	NM_013847:-161	Gcat	PROMOTER	0.541	0.470	2274.42	1068.97	0.254	1734.85	441.01
A_68_P27189024	chr10:62485962-62486006	NM_001079824:613	Hnrnph3	INSIDE	0.541	0.692	2870.62	1986.57	0.375	2192.99	821.34
A_68_P24126843	chr5:138086478-138086522	NM_010571:442	Irs3	INSIDE	0.541	0.522	1114.03	581.40	0.282	1075.10	303.33
A_68_P24038700	chr5:120885515-120885559	NM_008499:3642	Lhx5	INSIDE	0.541	0.456	4240.57	1934.99	0.247	3343.32	825.08
A_68_P28071732	chr11:100931187-100931231	NM_013792:-199	Naglu	PROMOTER	0.541	0.389	1752.33	682.15	0.211	1435.44	302.28
A_68_P24818880	chr6:125082083-125082127	NM_138747:204	Nop2	INSIDE	0.541	0.519	4512.78	2343.53	0.281	3630.37	1020.18
A_68_P21473128	chr2:101637014-101637058	NM_001083810:828	Prr5l	INSIDE	0.541	0.708	2475.47	1753.79	0.383	1980.21	759.31
A_68_P24609765	chr6:86321486-86321530	NM_026506:-25	Snrpg	PROMOTER	0.541	0.561	980.67	550.01	0.304	827.07	251.16
A_68_P21585133	chr2:122060313-122060357	NM_146126:-240	Sord	PROMOTER	0.541	0.546	1617.85	884.11	0.296	1450.86	429.30
A_68_P27089728	chr10:41239688-41239732	NM_016898:405	Cd164	INSIDE	0.540	0.390	1355.81	529.30	0.211	1090.99	229.82
A_68_P31614001	chr18:34811328-34811372	NM_178347:40	Cdc23	INSIDE	0.540	0.692	2518.82	1742.23	0.373	1822.46	680.62
A_68_P32265724	chrX:12858330-12858374	NM_010028:205	Ddx3x	INSIDE	0.540	0.508	1080.21	548.94	0.274	445.91	122.29
A_68_P22869099	chr4:42963311-42963355	NM_019874:-2633	Dnajb5	PROMOTER	0.540	0.712	1323.06	941.75	0.384	1081.19	415.56
A_68_P24609728	chr6:86315617-86315661	NM_025591:-38	Fam136a	PROMOTER	0.540	0.717	3758.40	2694.67	0.387	2969.11	1150.06
A_68_P21132488	chr2:35112210-35112254	NM_001206367:354	Gsn	INSIDE	0.540	0.606	1346.80	816.75	0.328	1093.01	358.22
A_68_P21339410	chr2:74601035-74601079	NM_010467:20	Hoxd1	INSIDE	0.540	0.604	1186.35	716.54	0.326	957.69	312.34
A_68_P29717921	chr14:73909953-73909997	NM_026119:119	Med4	INSIDE	0.540	0.453	1921.04	869.75	0.244	1616.83	395.26
A_68_P32026208	chr19:24936124-24936168	NM_175013:186	Pgm5	INSIDE	0.540	0.581	1036.10	602.43	0.314	837.92	263.05
A_68_P21623005	chr2:128926868-128926912	NM_009086:159	Polr1b	INSIDE	0.540	0.619	1011.25	626.33	0.334	806.44	269.47
A_68_P21901044	chr2:179776594-179776638	NM_011969:491	Psma7	INSIDE	0.540	0.609	3878.26	2362.91	0.329	2914.69	958.39
A_68_P22405708	chr3:107135601-107135645	NM_001045807:585	Rbm15	INSIDE	0.540	0.544	1421.81	774.13	0.294	1190.38	349.86
A_68_P25761252	chr8:33119752-33119796	ENSMUST00000080782:-193		PROMOTER	0.540	0.572	2313.32	1322.48	0.309	1858.36	574.11
A_68_P26528458	chr9:54765158-54765202	NM_177351:84	Agphd1	INSIDE	0.539	0.449	1164.67	523.52	0.242	912.64	221.10
A_68_P28149796	chr11:114653639-114653683	NM_028055:3546	Btbd17	INSIDE	0.539	0.605	1012.98	612.71	0.326	895.07	292.07
A_68_P23196910	chr4:108292768-108292812	NM_177045:230	Cc2d1b	INSIDE	0.539	0.612	4166.43	2548.41	0.330	2976.81	981.07
A_68_P25265479	chr7:87377398-87377442	NM_011870:82	Cib1	INSIDE	0.539	0.608	4253.81	2587.49	0.328	3241.80	1062.18
A_68_P22305779	chr3:86724403-86724447	NM_001195496:382	Dclk2	INSIDE	0.539	0.310	2021.40	626.65	0.167	1718.49	286.96
A_68_P25609547	chr7:152025243-152025287	NM_008007:748	Fgf3	INSIDE	0.539	0.604	1651.95	997.23	0.325	1374.01	446.97
A_68_P25944668	chr8:71317470-71317515	NM_027590:-360	Ints10	PROMOTER	0.539	0.605	1118.93	677.13	0.326	919.07	299.85
A_68_P26022615	chr8:87436867-87436911	NM_019945:24364	Mast1	INSIDE	0.539	0.557	1579.59	879.45	0.300	1196.93	359.25
A_68_P30532723	chr16:8471005-8471050	NM_146247:122	Mettl22	INSIDE	0.539	0.587	1087.20	638.15	0.317	803.36	254.38
A_68_P20874690	chr1:182186271-182186316	NM_001128605:138	Psen2	INSIDE	0.539	0.630	2751.06	1733.59	0.340	2283.29	775.66
A_68_P31936308	chr19:6906036-6906086	NM_019924:9031	Rps6ka4	INSIDE	0.539	3.598	2399.74	8634.04	1.940	1578.13	3060.96
A_68_P27181840	chr10:61158435-61158479	NM_027912:195	Tysnd1	INSIDE	0.539	0.559	1478.70	826.44	0.301	1225.02	369.29
A_68_P25959007	chr8:74432656-74432700	NM_001166645:174	Zfp882	INSIDE	0.539	0.635	820.64	521.05	0.342	739.49	252.94
A_68_P30403119	chr15:85641848-85641892	NM_001164625:257	2210021J22Rik	INSIDE	0.538	0.540	1398.88	754.73	0.290	1111.34	322.74
A_68_P29443675	chr14:20643061-20643105	NM_026528:-37	2700060E02Rik	PROMOTER	0.538	0.615	1171.55	720.77	0.331	1111.87	368.15
A_68_P32054913	chr19:29879873-29879917	NM_172836:605	9930021J03Rik	INSIDE	0.538	0.475	2404.99	1143.19	0.256	1820.32	465.54

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P23595357	chr5:34959448-34959497	NM_001024458:43110	Add1	INSIDE	0.538	4.228	1353.64	5723.59	2.273	954.73	2170.37
A_68_P21866701	chr2:172764888-172764932	NM_007557:884	Bmp7	INSIDE	0.538	0.594	2080.97	1235.60	0.319	1501.23	479.30
A_68_P26137126	chr8:108502836-108502891	NM_027960:456	Dpep3	INSIDE	0.538	5.455	266.55	1454.01	2.936	209.99	616.48
A_68_P26001979	chr8:83403513-83403557	NM_021356:844	Gab1	INSIDE	0.538	0.401	1993.30	800.17	0.216	1390.58	300.27
A_68_P27235134	chr10:70844276-70844325	NM_027184:33760	Ipmk	INSIDE	0.538	4.305	163.15	702.31	2.317	208.29	482.53
A_68_P25494915	chr7:132634916-132634960	NM_026330:118	Nsmce1	INSIDE	0.538	0.678	2798.73	1897.41	0.365	2099.17	765.53
A_68_P26586478	chr9:65063416-65063460	NM_177460:942	Parp16	INSIDE	0.538	0.609	1142.28	695.48	0.328	1012.99	332.08
A_68_P23162218	chr4:102432046-102432090	NM_144906:-899	Sgip1	PROMOTER	0.538	0.433	1480.49	640.74	0.233	1296.96	301.71
A_68_P25195706	chr7:74904045-74904089	NM_183312:562	Synm	INSIDE	0.538	0.435	1667.21	724.89	0.234	1472.48	344.67
A_68_P22538543	chr3:132347141-132347185	NM_173032:55	Tbck	INSIDE	0.538	0.648	1433.46	928.75	0.348	1176.50	410.00
A_68_P26978748	chr10:18734800-18734844	NM_001166402:-3053	Tnfaip3	PROMOTER	0.538	0.417	3438.18	1432.36	0.224	2664.50	596.84
A_68_P24287932	chr6:21801985-21802029	NM_173007:509	Tspan12	INSIDE	0.538	0.517	2203.92	1138.52	0.278	1836.71	510.11
A_68_P24432033	chr6:49269637-49269686	NM_175098:310	Ccdc126	INSIDE	0.537	0.626	854.45	535.11	0.336	757.41	254.51
A_68_P25015864	chr7:27951357-27951401	NM_053208:443	Egln2	INSIDE	0.537	0.503	3145.81	1582.63	0.270	2313.69	625.17
A_68_P21229090	chr2:54288809-54288853	NM_173030:33	Galnt13	INSIDE	0.537	0.475	2104.72	998.70	0.255	1616.68	412.23
A_68_P32056973	chr19:30249514-30249558	NM_138595:372	Gldc	INSIDE	0.537	0.693	1365.76	946.23	0.372	1000.56	372.57
A_68_P31978257	chr19:16208260-16208304	NM_008139:962	Gnaq	INSIDE	0.537	0.350	1795.94	629.12	0.188	1381.92	260.20
A_68_P20510206	chr1:108656242-108656286	NM_027534:55	Kdsr	INSIDE	0.537	0.574	2879.18	1652.62	0.308	2172.45	670.18
A_68_P23985659	chr5:111846818-111846862	NM_001081235:-345	Mn1	PROMOTER	0.537	0.453	1403.31	635.91	0.243	1104.49	268.77
A_68_P21639373	chr2:132078980-132079024	NM_011045:-86	Pcna	DIVERGENT_PROMOTER	0.537	0.674	1327.11	894.74	0.362	1078.25	390.50
A_68_P26920793	chr10:7512764-7512808	NM_026141:95	Ppil4	INSIDE	0.537	0.520	1395.72	725.17	0.279	1023.24	285.45
A_68_P29578888	chr14:47504466-47504510	NM_001037221:1849	Samd4	INSIDE	0.537	0.459	2559.16	1174.53	0.246	2128.73	524.34
A_68_P27915806	chr11:73013237-73013281	NM_029031:275	Shpk	INSIDE	0.537	0.571	1243.69	710.72	0.307	961.60	295.21
A_68_P25016925	chr7:28146852-28146896	NM_001199235:32651	Spnb4	INSIDE	0.537	0.575	1653.97	950.83	0.309	1471.23	453.96
A_68_P27841686	chr11:60033953-60033997	NM_011480:132	Srebf1	INSIDE	0.537	0.480	1636.00	785.54	0.258	1292.43	333.03
A_68_P20302824	chr1:66515076-66515120	NM_175510:78	Unc80	INSIDE	0.537	0.442	2680.25	1183.87	0.237	2131.57	505.42
A_68_P26495379	chr9:48863756-48863800	NM_012039:93	Zw10	INSIDE	0.537	0.706	1299.77	917.03	0.379	1151.55	436.01
A_68_P30665013	chr16:34573097-34573141	ENSMUST00000114961:500		INSIDE	0.537	0.728	3479.74	2532.98	0.391	2622.93	1025.69
A_68_P32186047	chr19:54119811-54119855	NM_007417:161	Adra2a	INSIDE	0.536	0.587	3096.72	1818.20	0.315	2514.63	791.42
A_68_P22970308	chr4:63071362-63071406	NM_001045514:-6905	Akna	PROMOTER	0.536	0.613	1618.74	991.68	0.328	1251.62	410.78
A_68_P23897548	chr5:93473182-93473226	NM_175270:844	Ankrd56	INSIDE	0.536	0.504	2230.22	1123.66	0.270	1844.26	498.19
A_68_P21615857	chr2:127657373-127657417	NM_001113179:201	Bub1	INSIDE	0.536	0.610	1653.90	1008.38	0.327	1335.81	436.17
A_68_P26170766	chr8:114414003-114414047	NM_019950:20075	Chst5	INSIDE	0.536	0.485	2072.53	1004.22	0.260	1651.10	429.15
A_68_P21706947	chr2:144219117-144219161	NM_181417:24368	Csrp2bp	INSIDE	0.536	2.854	879.23	2509.04	1.530	714.56	1093.14
A_68_P30350021	chr15:76528223-76528267	NM_182805:1051	Gpt	INSIDE	0.536	0.499	2407.88	1201.20	0.267	1944.87	520.05
A_68_P28269097	chr12:17183053-17183097	NM_201531:620	Kcnf1	INSIDE	0.536	0.706	1723.04	1217.03	0.378	1194.79	452.14
A_68_P25954147	chr8:73321717-73321761	NM_199308:-5406	Mast3	PROMOTER	0.536	0.676	1483.89	1002.87	0.362	1063.48	384.95
A_68_P31734231	chr18:57292496-57292540	NM_001001979:-225	Megf10	PROMOTER	0.536	0.632	1758.89	1111.93	0.339	1408.68	477.32
A_68_P20593974	chr1:129101586-129101630	NM_145128:46	Mgat5	INSIDE	0.536	0.540	1337.71	722.43	0.290	1015.63	294.19
A_68_P20370459	chr1:78200539-78200583	NM_001159520:-6849	Pax3	PROMOTER	0.536	0.683	1263.90	862.82	0.366	1074.63	393.14
A_68_P31655262	chr18:42553965-42554009	NM_138945:-264	Pou4f3	PROMOTER	0.536	0.470	2878.95	1352.84	0.252	2437.99	614.19
A_68_P28549421	chr12:76697259-76697303	NM_012024:-93	Ppp2r5e	PROMOTER	0.536	0.576	3414.71	1966.81	0.309	2422.58	748.13
A_68_P25094132	chr7:52884421-52884465	NM_028544:1536	Rasip1	INSIDE	0.536	1.350	2985.70	4029.90	0.724	2220.03	1606.46
A_68_P23993053	chr5:113006095-113006139	NM_019982:89	Sez6l	INSIDE	0.536	0.541	3984.37	2155.95	0.290	3078.01	892.33
A_68_P23187158	chr4:106584284-106584328	NM_023672:232	Ssbp3	INSIDE	0.536	0.538	1632.94	877.89	0.288	1352.29	389.68
A_68_P25092468	chr7:52588927-52588971	NM_175130:202	Trpm4	INSIDE	0.536	0.543	2576.90	1399.29	0.291	1828.71	532.36
A_68_P25143365	chr7:63049393-63049437	NM_146190:-103	Tubgcp5	PROMOTER	0.536	1.392	4737.08	6594.67	0.747	3718.33	2776.19
A_68_P32363627	chrX:45610039-45610084	NM_028276:-49	Utp14a	PROMOTER	0.536	0.539	1200.53	647.27	0.289	404.71	116.99
A_68_P29113346	chr13:69137647-69137691	NM_153534:751	Adcy2	INSIDE	0.535	0.440	1345.71	592.01	0.236	1189.35	280.10
A_68_P30589273	chr16:20733395-20733439	NM_009893:217	Chrd	INSIDE	0.535	0.496	1500.39	744.75	0.265	1252.52	332.43
A_68_P21338549	chr2:74494232-74494276	NM_007967:3222	Evx2	INSIDE	0.535	0.346	2116.62	731.62	0.185	1745.05	322.58

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28707019	chr12:106271229-106271273	NM_028419:352	Glrx5	INSIDE	0.535	0.396	1445.97	572.75	0.212	1100.45	232.99
A_68_P20648919	chr1:138845800-138845844	NM_001159769:4385	Nr5a2	INSIDE	0.535	0.399	1742.35	696.01	0.214	1534.85	327.94
A_68_P31676055	chr18:46440555-46440599	NM_172627:-72	Pggt1b	PROMOTER	0.535	0.619	1297.61	802.79	0.331	1152.58	381.29
A_68_P24428257	chr6:48551937-48551981	NM_001079901:8077	Repin1	DOWNSTREAM	0.535	0.531	4169.93	2214.12	0.284	3189.15	905.31
A_68_P24043184	chr5:121654997-121655041	NM_011290:509	Rpl6	INSIDE	0.535	0.663	1199.86	795.04	0.354	982.68	348.03
A_68_P27282240	chr10:79755289-79755333	NM_009091:135	Rps15	INSIDE	0.535	0.667	1450.87	967.98	0.357	1121.97	400.75
A_68_P22342542	chr3:94965500-94965544	NM_011351:-2773	Sema6c	PROMOTER	0.535	0.571	1346.41	768.17	0.305	1051.43	320.68
A_68_P20886548	chr1:184339548-184339592	NM_173378:273	Trp53bp2	INSIDE	0.535	0.618	889.01	549.56	0.331	808.57	267.35
A_68_P25499299	chr7:133343490-133343534	NM_028816:410	Xpo6	INSIDE	0.535	0.735	3441.86	2530.75	0.394	2583.45	1016.96
A_68_P23255466	chr4:120887199-120887243	ENSMUST00000056635:469		INSIDE	0.535	0.471	1690.16	795.81	0.252	1419.38	357.76
A_68_P21224226	chr2:53051139-53051183	NM_022989:43	Arl6ip6	INSIDE	0.534	0.426	1242.49	529.75	0.228	1089.20	248.21
A_68_P23895411	chr5:93104067-93104111	NM_177230:65	Ccdc158	INSIDE	0.534	0.730	1930.12	1408.97	0.390	1535.13	598.00
A_68_P29134804	chr13:72766185-72766229	NR_030701:-194	D430050G20	DIVERGENT_PROMOTER	0.534	0.472	2227.09	1050.28	0.252	1665.29	419.72
A_68_P24735991	chr6:108779125-108779169	NM_138677:512	Edem1	INSIDE	0.534	0.594	884.04	524.77	0.317	706.55	224.11
A_68_P28530004	chr12:73172194-73172239	NM_181752:-238	Gpr135	PROMOTER	0.534	0.608	1217.10	740.47	0.325	1036.36	336.95
A_68_P22565463	chr3:137527117-137527161	NM_016750:-424	H2afz	PROMOTER	0.534	0.415	2737.64	1135.15	0.221	2273.51	503.52
A_68_P29054563	chr13:55463630-55463674	NM_025828:492	Lman2	INSIDE	0.534	0.582	2594.81	1511.19	0.311	1910.63	594.39
A_68_P30557333	chr16:13448464-13448508	NR_030549:-1129	Mir193b	PROMOTER	0.534	0.562	2408.52	1353.68	0.300	1803.85	541.31
A_68_P20449355	chr1:94370405-94370449	NM_024197:-91	Ndufa10	PROMOTER	0.534	0.626	889.06	556.74	0.334	644.07	215.30
A_68_P26388504	chr9:29219516-29219560	NM_172290:551176	Ntm	INSIDE	0.534	0.666	1955.15	1303.07	0.356	1485.82	528.84
A_68_P28863266	chr13:19714869-19714913	NM_016687:-153	Sfrp4	DIVERGENT_PROMOTER	0.534	0.699	1695.05	1184.97	0.373	1424.99	531.78
A_68_P32185502	chr19:54019941-54019985	NM_019658:597	Shoc2	INSIDE	0.534	0.645	1907.01	1229.57	0.344	1454.47	500.38
A_68_P31943153	chr19:8787770-8787814	NM_008577:595	Slc3a2	INSIDE	0.534	0.676	1585.38	1072.11	0.361	1172.38	423.18
A_68_P26580558	chr9:64027298-64027342	NM_183316:217	Snapc5	INSIDE	0.534	0.572	2819.00	1612.87	0.305	2279.26	696.29
A_68_P31919099	chr19:3767561-3767605	NM_001167884:162	Suv420h1	INSIDE	0.534	0.520	1448.19	752.98	0.278	1192.43	331.36
A_68_P20444771	chr1:93699116-93699160	NM_007855:1085	Twist2	INSIDE	0.534	0.530	1369.72	726.43	0.283	1052.66	298.32
A_68_P28931385	chr13:32894778-32894822	NM_030215:902	Wrnip1	INSIDE	0.534	0.472	1235.22	583.52	0.252	899.07	226.98
A_68_P26595475	chr9:66683088-66683132	NM_026674:-597	Aph1c	PROMOTER	0.533	0.569	3058.67	1739.29	0.303	2286.37	693.61
A_68_P29246781	chr13:97313402-97313446	NM_001164222:735	Col4a3bp	INSIDE	0.533	0.540	2701.59	1460.20	0.288	2053.29	591.26
A_68_P25362942	chr7:106775190-106775234	NM_001195529:401	Gm4980	INSIDE	0.533	0.469	1476.70	691.87	0.250	1077.85	269.29
A_68_P25473609	chr7:128536673-128536717	NM_001081327:885	Hs3st2	INSIDE	0.533	0.527	1665.04	877.49	0.281	1382.91	388.38
A_68_P27950599	chr11:79525184-79525228	NR_029579:-264	Mir193	PROMOTER	0.533	0.346	2199.70	761.37	0.184	1904.29	351.12
A_68_P20640025	chr1:137429239-137429283	NM_173437:52672	Nav1	INSIDE	0.533	2.979	2700.63	8045.90	1.589	1960.85	3116.36
A_68_P30146831	chr15:37891066-37891112	NM_199476:-278	Rrm2b	PROMOTER	0.533	0.634	998.11	632.36	0.338	902.89	304.89
A_68_P26844288	chr9:114277438-114277482	NM_019922:22370	Crtap	DOWNSTREAM	0.532	0.503	1497.39	753.86	0.268	1268.14	339.71
A_68_P23336251	chr4:136392310-136392354	NM_010142:-482	Ephb2	PROMOTER	0.532	0.641	1804.03	1156.03	0.341	1498.37	510.35
A_68_P20720547	chr1:154247487-154247531	NM_177756:512	Glt25d2	INSIDE	0.532	0.630	1331.51	838.96	0.335	937.45	314.34
A_68_P28071796	chr11:100941137-100941181	NM_010475:1434	Hsd17b1	INSIDE	0.532	0.657	1392.13	915.02	0.350	1086.16	379.97
A_68_P30925477	chr16:84774396-84774440	NM_023844:51	Jam2	INSIDE	0.532	0.733	2998.51	2199.19	0.391	2229.88	870.81
A_68_P20510205	chr1:108656151-108656195	NM_027534:147	Kdsr	INSIDE	0.532	0.685	1556.75	1066.07	0.364	1233.63	449.37
A_68_P28032110	chr11:94183065-94183109	NM_026313:139	Luc7l3	INSIDE	0.532	0.714	1852.21	1323.37	0.380	1152.22	438.26
A_68_P30424873	chr15:89209271-89209315	NM_001013022:393	Odf3b	INSIDE	0.532	0.701	5150.98	3609.14	0.373	3802.05	1416.55
A_68_P30961690	chr16:91226016-91226061	NM_016967:244	Olig2	INSIDE	0.532	0.696	1090.68	758.73	0.370	925.55	342.54
A_68_P22467630	chr3:119485493-119485539	NM_019550:790	Ptbp2	INSIDE	0.532	0.711	1604.82	1140.42	0.378	1134.49	428.65
A_68_P27942192	chr11:78059616-78059660	NM_009143:391	Sdf2	INSIDE	0.532	0.569	1964.93	1117.66	0.303	1486.96	450.02
A_68_P21760344	chr2:154233694-154233738	NM_009228:104	Snta1	INSIDE	0.532	0.555	1883.34	1044.62	0.295	1697.06	500.75
A_68_P22049390	chr3:34549137-34549181	NM_011443:232	Sox2	INSIDE	0.532	0.527	2314.83	1219.76	0.280	1864.55	522.61
A_68_P27995863	chr11:87551226-87551270	NM_009296:182	Supt4h1	INSIDE	0.532	0.552	1604.92	885.25	0.293	1244.19	364.88
A_68_P25352336	chr7:104937141-104937185	ENSMUST00000172423:112		INSIDE	0.532	0.417	2664.85	1110.47	0.222	2289.28	507.92
A_68_P20411732	chr1:88256159-88256203	NR_015507:32	C130036L24Rik	INSIDE	0.531	0.584	2833.67	1653.54	0.310	2282.19	706.71
A_68_P28187624	chr11:120794237-120794281	NM_027745:-72	Ccdc57	PROMOTER	0.531	0.630	979.24	616.72	0.334	694.21	232.19

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26127989	chr8:106864528-106864572	NM_024217:57	Cmtm3	INSIDE	0.531	3.567	2705.88	9651.50	1.893	1636.22	3097.11
A_68_P20266463	chr1:59970586-59970630	NM_001037725:759	Fam117b	INSIDE	0.531	0.741	2514.61	1862.46	0.393	2202.29	865.86
A_68_P23590782	chr5:34064726-34064770	NM_001163216:-206	Fgfr3	PROMOTER	0.531	0.689	1161.14	800.35	0.366	854.02	312.68
A_68_P29543501	chr14:37948355-37948400	NM_001199122:-52	Ghitm	PROMOTER	0.531	0.660	1103.99	728.97	0.351	924.81	324.34
A_68_P30575507	chr16:17759672-17759716	NM_145479:-19	Klhl22	PROMOTER	0.531	0.600	3488.89	2093.91	0.319	2907.37	926.01
A_68_P23279071	chr4:125932970-125933014	NM_001145970:571	Mtap7d1	INSIDE	0.531	0.416	3133.26	1304.23	0.221	2249.58	497.33
A_68_P20611337	chr1:132612275-132612319	NM_001162416:-1143	Pfkfb2	PROMOTER	0.531	0.423	1200.60	507.44	0.225	1033.62	232.06
A_68_P29094157	chr13:63664712-63664756	NM_008957:2094	Ptch1	INSIDE	0.531	0.641	1748.04	1119.74	0.340	1306.15	444.22
A_68_P27278803	chr10:79229502-79229546	NM_144528:142	Rnf126	INSIDE	0.531	0.634	2469.59	1565.00	0.337	1791.62	602.94
A_68_P27332529	chr10:89148969-89149013	NM_198021:40	Scyl2	INSIDE	0.531	0.697	1423.12	991.24	0.370	1195.74	441.94
A_68_P24120067	chr5:136707928-136707972	NM_018825:12823	Sh2b2	INSIDE	0.531	2.580	2576.89	6648.62	1.370	1811.15	2481.20
A_68_P25952345	chr8:73033987-73034031	NM_019883:258	Uba52	INSIDE	0.531	0.523	1817.14	951.17	0.278	1421.48	395.29
A_68_P31255137	chr17:56443079-56443123	NM_001111078:-635	Uhrf1	PROMOTER	0.531	0.361	2256.96	815.72	0.192	1682.86	323.24
A_68_P26884795	chr9:121578529-121578573	NM_011703:26717	Vipr1	INSIDE	0.531	0.618	2321.23	1433.59	0.328	1719.39	563.48
A_68_P32133761	chr19:44758930-44758974	ENSMUST00000166501:10813		DOWNSTREAM	0.531	0.470	2258.10	1060.93	0.249	1733.64	432.31
A_68_P24091170	chr5:130384460-130384504	NM_026916:73	4930579G22Rik	INSIDE	0.530	0.567	2042.86	1157.47	0.300	1718.06	515.90
A_68_P31849682	chr18:78013054-78013098	NM_007505:570	Atp5a1	INSIDE	0.530	0.666	6049.71	4029.27	0.353	4937.87	1742.18
A_68_P26486118	chr9:47338069-47338113	NM_001025600:-344	Cadm1	PROMOTER	0.530	0.478	1112.89	532.05	0.253	837.34	212.03
A_68_P28776179	chr12:119081965-119082009	NM_146040:-347	Cdca7l	PROMOTER	0.530	0.596	922.78	549.92	0.316	763.66	241.31
A_68_P23541889	chr5:23950730-23950774	NM_023229:301	Fastk	INSIDE	0.530	0.581	1987.04	1153.56	0.308	1611.98	495.89
A_68_P30347360	chr15:76124857-76124901	NM_001195537:15	Gm10345	INSIDE	0.530	0.563	1041.93	586.88	0.299	872.91	260.61
A_68_P30500796	chr15:102765447-102765491	NM_010463:-1815	Hoxc12	PROMOTER	0.530	0.579	1629.59	944.23	0.307	1508.98	463.54
A_68_P26716008	chr9:90008880-90008924	NM_001039147:756	Morf4l1	INSIDE	0.530	0.675	5682.17	3835.14	0.358	4100.41	1466.62
A_68_P29001574	chr13:45485076-45485120	NM_153789:-12	Mylip	PROMOTER	0.530	0.531	1866.41	991.57	0.281	1653.44	465.34
A_68_P25353895	chr7:105259944-105259988	NM_008663:8037	Myo7a	INSIDE	0.530	0.700	1793.40	1255.01	0.371	1483.63	550.32
A_68_P20632581	chr1:136195963-136196007	NM_001144855:33521	Ppfia4	INSIDE	0.530	0.643	2492.75	1602.60	0.341	1852.97	631.25
A_68_P25553144	chr7:142729766-142729810	NM_011212:282	Ptpre	INSIDE	0.530	0.582	1821.22	1059.71	0.308	1581.80	487.82
A_68_P32773804	chrX:155693758-155693802	NM_148945:-271	Rps6ka3	PROMOTER	0.530	3.452	4698.70	16218.21	1.829	2372.12	4339.42
A_68_P20354344	chr1:75476279-75476323	NM_177056:194	Tmem198	INSIDE	0.530	0.438	2068.17	905.45	0.232	1589.86	369.02
A_68_P23594734	chr5:34856584-34856628	NM_139064:22	Tnip2	INSIDE	0.530	0.519	2578.87	1339.05	0.275	2021.01	555.90
A_68_P22341859	chr3:94819900-94819945	NM_030074:-762	Zfp687	PROMOTER	0.530	0.544	1255.30	682.68	0.288	1007.23	290.23
A_68_P30476331	chr15:98593814-98593858	NM_007478:-287	Arf3	PROMOTER	0.529	0.434	1932.01	839.28	0.230	1535.45	352.93
A_68_P24330599	chr6:30125667-30125711	NR_038124:-934	BB283400	DIVERGENT_PROMOTER	0.529	0.471	1364.52	642.08	0.249	1005.33	250.05
A_68_P29449134	chr14:21613118-21613162	NM_001039138:170	Camk2g	INSIDE	0.529	0.294	1853.08	544.01	0.155	1427.08	221.52
A_68_P30135998	chr15:35867761-35867805	NM_053071:219	Cox6c	INSIDE	0.529	0.432	1432.50	618.45	0.229	1182.85	270.29
A_68_P24138259	chr5:140384979-140385023	NM_175522:1104	Elfn1	INSIDE	0.529	0.635	1341.42	851.77	0.336	1017.60	341.66
A_68_P28152627	chr11:115158906-115158950	NM_178035:-68	Fads6	DIVERGENT_PROMOTER	0.529	0.592	1506.01	892.06	0.313	1283.10	402.22
A_68_P22071617	chr3:38787100-38787144	NM_183221:1261	Fat4	INSIDE	0.529	0.639	1698.34	1084.82	0.338	1263.31	426.53
A_68_P27973307	chr11:83567440-83567484	NM_145432:324	Heatr6	INSIDE	0.529	0.647	1670.46	1080.41	0.342	1291.74	441.55
A_68_P31259697	chr17:57171063-57171108	NM_010613:-155	Khsrp	PROMOTER	0.529	0.585	1395.41	816.58	0.310	1094.26	338.73
A_68_P28192099	chr11:121563822-121563866	NM_144797:104	Metrnl	INSIDE	0.529	0.553	1960.77	1085.19	0.293	1643.80	481.06
A_68_P23536414	chr5:22940038-22940082	NM_026984:-186	Mll5	PROMOTER	0.529	0.407	1445.13	587.67	0.215	1076.97	231.55
A_68_P20188963	chr1:43503219-43503263	NM_010879:645	Nck2	INSIDE	0.529	0.657	2062.99	1356.04	0.347	1601.98	556.67
A_68_P31415146	chr17:86568164-86568208	NM_011104:1062	Prkce	INSIDE	0.529	0.635	1508.75	957.50	0.336	1104.97	370.74
A_68_P27503751	chr10:120912576-120912620	NM_138956:708	Rassf3	INSIDE	0.529	0.636	2735.34	1740.44	0.337	2085.38	702.08
A_68_P27833616	chr11:58751821-58751865	NM_022423:566	Rnf187	INSIDE	0.529	0.642	846.79	543.99	0.340	674.29	229.19
A_68_P24120068	chr5:136708025-136708069	NM_018825:12727	Sh2b2	INSIDE	0.529	2.946	1957.15	5765.04	1.560	1345.02	2097.57
A_68_P26394906	chr9:30234770-30234814	NM_028874:-121	Snx19	PROMOTER	0.529	0.634	2493.71	1580.00	0.335	2136.38	716.08
A_68_P23590340	chr5:34000396-34000440	NM_026698:63	Tmem129	INSIDE	0.529	0.552	1864.36	1029.78	0.292	1445.13	422.26
A_68_P29531327	chr14:35487897-35487941	NM_001004436:805	Wapal	INSIDE	0.529	0.629	1321.86	831.18	0.333	1027.48	341.99
A_68_P25269627	chr7:88137961-88138005	NM_178707:-587	Zfp592	PROMOTER	0.529	0.475	1775.37	842.83	0.251	1519.33	381.72

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25604019	chr7:151165292-151165337			Unknown	0.529	0.434	1469.68	637.78	0.230	1170.38	268.85
A_68_P29613142	chr14:55203593-55203649	NM_028890:21125	4931414P19Rik	INSIDE	0.528	3.177	531.23	1687.54	1.678	473.37	794.39
A_68_P27571287	chr11:6963887-6963931	NM_009622:417	Adcy1	INSIDE	0.528	0.561	1086.20	609.81	0.296	937.42	277.72
A_68_P28195051	chr12:3427564-3427608	NM_172421:703	Asxl2	INSIDE	0.528	0.694	1675.94	1162.81	0.367	1311.65	480.87
A_68_P30378500	chr15:81416070-81416114	NM_177821:-551	Ep300	PROMOTER	0.528	0.676	1310.47	885.42	0.357	1049.19	374.23
A_68_P28493246	chr12:66067167-66067211	NM_177805:460	Fam179b	INSIDE	0.528	0.648	1451.03	940.29	0.342	1111.93	380.15
A_68_P21339408	chr2:74600811-74600855	NM_010467:-204	Hoxd1	PROMOTER	0.528	0.558	2033.10	1134.00	0.295	1600.30	471.32
A_68_P21010259	chr2:12223211-12223256	NM_001001309:314	Itga8	INSIDE	0.528	0.686	1837.42	1260.25	0.362	1435.62	519.59
A_68_P26082839	chr8:97877231-97877275	NM_008609:1016	Mmp15	INSIDE	0.528	0.638	884.76	564.61	0.337	719.94	242.36
A_68_P25501810	chr7:133839074-133839118	NM_029420:201	Slx1b	INSIDE	0.528	0.651	1914.41	1247.04	0.344	1490.69	512.50
A_68_P26504540	chr9:50412429-50412473	NM_013897:445	Timm8b	INSIDE	0.528	0.635	957.49	607.85	0.335	808.13	270.70
A_68_P27290791	chr10:81063724-81063768	NM_053254:-101	Tle6	DIVERGENT_PROMOTER	0.528	0.588	1477.87	869.72	0.311	1247.37	387.83
A_68_P25184109	chr7:72838329-72838373	NM_026795:48	Tm2d3	INSIDE	0.528	0.507	2105.01	1066.45	0.268	1576.93	421.87
A_68_P25405561	chr7:116154611-116154655	NM_021885:239	Tub	INSIDE	0.528	0.428	1254.12	536.30	0.226	1062.98	240.08
A_68_P31157814	chr17:35272332-35272376	NM_057171:168	Bag6	INSIDE	0.527	0.550	1620.34	891.65	0.290	1254.70	363.55
A_68_P21040894	chr2:18612064-18612108	NM_001001334:-8562	BC061194	PROMOTER	0.527	0.636	879.57	559.69	0.335	756.60	253.70
A_68_P21612763	chr2:127161943-127161987	NM_010090:70	Dusp2	INSIDE	0.527	0.415	1381.84	573.89	0.219	1181.19	258.47
A_68_P21113207	chr2:31938899-31938943	NM_175511:305	Fam78a	INSIDE	0.527	0.442	3151.64	1393.05	0.233	2489.87	579.90
A_68_P31254845	chr17:56395400-56395444	NM_010192:-793	Fem1a	PROMOTER	0.527	0.490	1685.22	825.45	0.258	1313.88	338.91
A_68_P27950592	chr11:79524502-79524546	NR_029579:-946	Mir193	PROMOTER	0.527	0.481	2598.95	1250.46	0.253	1890.95	479.02
A_68_P30137684	chr15:36212197-36212241	NM_013923:684	Rnf19a	INSIDE	0.527	0.559	1358.96	759.71	0.295	1087.80	320.36
A_68_P29288687	chr13:104899925-104899970	NM_144838:78	Sgtb	INSIDE	0.527	0.658	3487.76	2296.13	0.347	2668.97	926.00
A_68_P23072588	chr4:84851180-84851224	NM_019535:-157	Sh3gl2	PROMOTER	0.527	0.624	863.04	538.62	0.329	831.01	273.33
A_68_P28744028	chr12:112667836-112667880	NM_028807:12218	1200009I06Rik	INSIDE	0.526	0.649	1883.15	1222.35	0.341	1429.66	488.04
A_68_P20265717	chr1:59820840-59820884	NM_007561:-618	Bmpr2	PROMOTER	0.526	0.467	1127.96	526.30	0.245	983.90	241.53
A_68_P28187625	chr11:120794313-120794357	NM_027745:-148	Ccdc57	PROMOTER	0.526	0.484	1751.38	848.39	0.255	1263.67	321.70
A_68_P30508954	chr16:4213021-4213065	NM_001025432:362	Crebbp	INSIDE	0.526	0.674	2557.64	1725.06	0.355	2017.28	715.64
A_68_P23203773	chr4:109655219-109655263	NM_172296:4611	Dmrta2	INSIDE	0.526	0.569	1057.83	601.95	0.299	879.38	263.17
A_68_P23317815	chr4:133036401-133036445	NM_175307:375	Fam46b	INSIDE	0.526	0.695	1689.50	1174.35	0.366	1246.47	455.87
A_68_P27783947	chr11:49447973-49448018	NM_008029:24815	Flt4	INSIDE	0.526	1.367	3184.53	4353.73	0.719	2326.58	1673.18
A_68_P28614430	chr12:88488238-88488282	NM_010363:-407	Gstz1	PROMOTER	0.526	0.678	1114.53	755.34	0.356	977.63	348.19
A_68_P20567331	chr1:123424359-123424403	NM_010483:662	Htr5b	INSIDE	0.526	0.452	1275.69	576.62	0.238	1193.13	283.71
A_68_P25044855	chr7:35438249-35438293	NM_146188:-410	Kctd15	PROMOTER	0.526	0.476	1339.92	638.08	0.250	1162.42	291.04
A_68_P23006655	chr4:70196033-70196077	NM_172694:-92	Megf9	PROMOTER	0.526	0.513	1080.16	554.51	0.270	939.24	253.74
A_68_P25261460	chr7:86649666-86649710	NR_029818:-461	Mir9-3	PROMOTER	0.526	0.659	866.11	571.20	0.347	708.77	245.94
A_68_P25261269	chr7:86610660-86610704	NM_017462:477	Polg	INSIDE	0.526	0.352	2361.12	829.94	0.185	1736.33	321.23
A_68_P22350096	chr3:96397949-96397993	NM_027241:111	Polr3gl	INSIDE	0.526	0.538	2987.97	1608.27	0.283	1981.79	561.16
A_68_P24980582	chr7:16858850-16858896	NM_001136270:169	Prr24	INSIDE	0.526	3.083	7046.42	21723.01	1.620	4740.82	7681.36
A_68_P26044795	chr8:91567813-91567857	NM_021390:227	Sall1	INSIDE	0.526	0.330	1868.36	616.44	0.173	1602.95	277.95
A_68_P21900712	chr2:179711703-179711747	NR_033782:167	4921531C22Rik	INSIDE	0.525	0.563	1067.86	601.46	0.296	855.19	253.06
A_68_P20395062	chr1:82836520-82836565	NM_010472:485	Agfg1	INSIDE	0.525	0.473	2355.63	1115.29	0.248	2053.78	510.21
A_68_P32260255	chrX:11655059-11655115	NM_029510:2593	Bcor	INSIDE	0.525	0.556	1059.70	589.72	0.292	446.82	130.49
A_68_P21777898	chr2:157391806-157391850	NM_016916:269	Blcap	INSIDE	0.525	0.533	1132.85	603.97	0.280	971.06	271.87
A_68_P23366008	chr4:141349558-141349602	NM_015733:54	Casp9	INSIDE	0.525	3.292	6717.58	22113.85	1.728	4665.93	8061.83
A_68_P28071818	chr11:100943909-100943954	NM_027896:-7	Coasy	PROMOTER	0.525	0.618	1182.11	730.56	0.324	784.20	254.46
A_68_P22889573	chr4:46614584-46614628	NM_001164804:195	Coro2a	INSIDE	0.525	0.541	1659.55	897.98	0.284	1346.16	382.59
A_68_P31157715	chr17:35258104-35258148	NM_009975:266	Csnk2b	INSIDE	0.525	0.671	2018.35	1355.21	0.353	1461.97	515.49
A_68_P21570231	chr2:119372809-119372853	NM_172857:533	Exd1	INSIDE	0.525	0.591	1897.79	1122.21	0.310	1620.11	502.83
A_68_P23227295	chr4:115690207-115690251	NM_010173:279	Faah	INSIDE	0.525	0.549	2199.10	1207.29	0.288	2005.15	577.49
A_68_P29702362	chr14:70999309-70999353	NM_194345:312	Fam160b2	INSIDE	0.525	0.359	1598.94	574.24	0.188	1237.15	233.10
A_68_P27357060	chr10:93499035-93499079	NM_053072:311	Fgd6	INSIDE	0.525	0.653	1340.98	875.59	0.343	1185.84	406.51

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P21812431	chr2:163264311-163264355	NM_144891:130	Gdap1l1	INSIDE	0.525	0.540	1278.39	690.65	0.283	1056.04	299.37
A_68_P22348232	chr3:96025442-96025486	NM_178214:421	Hist2h2be	INSIDE	0.525	0.634	1337.54	848.64	0.333	1018.16	339.35
A_68_P22190746	chr3:63099501-63099545	NM_008604:-271	Mme	PROMOTER	0.525	0.555	3999.99	2220.29	0.292	3196.57	931.94
A_68_P23365306	chr4:141219776-141219820	NM_001033150:232	Plekhm2	INSIDE	0.525	0.343	1595.14	546.53	0.180	1260.13	226.86
A_68_P22350868	chr3:96531418-96531462	NM_028925:-78	Polr3c	DIVERGENT_PROMOTER	0.525	0.567	1474.70	835.95	0.297	1356.25	403.34
A_68_P25090667	chr7:52271089-52271133	NM_001008422:509	Scaf1	INSIDE	0.525	0.597	935.41	558.13	0.313	703.40	220.26
A_68_P21623519	chr2:129024601-129024645	NM_001159593:114	Slc20a1	INSIDE	0.525	0.599	2687.80	1610.63	0.314	1991.40	625.96
A_68_P21330519	chr2:73111290-73111334	NM_001005343:1330	Sp9	INSIDE	0.525	0.451	1831.50	826.07	0.237	1456.82	345.17
A_68_P24097663	chr5:131782424-131782475	NM_145218:943	Wbscr17	INSIDE	0.525	0.541	947.64	512.44	0.284	790.04	224.30
A_68_P29662310	chr14:64225813-64225857	NM_173393:468	Xkr6	INSIDE	0.525	0.541	2910.96	1575.77	0.284	2322.28	659.56
A_68_P30386394	chr15:82887167-82887211	AK139602:182019		INSIDE	0.525	0.460	1550.68	712.93	0.241	1176.77	284.14
A_68_P28833742	chr13:12794705-12794749	ENSMUST00000104944:98		INSIDE	0.525	0.564	1525.15	860.01	0.296	1349.65	399.67
A_68_P26595470	chr9:66682593-66682637	NM_026674:-101	Aph1c	PROMOTER	0.524	0.575	3493.70	2008.35	0.301	2816.28	848.41
A_68_P23295723	chr4:128916179-128916223	NM_001033189:9487	C77080	INSIDE	0.524	0.532	3414.15	1816.75	0.279	2652.26	739.66
A_68_P20442008	chr1:93262992-93263036	NM_173395:8	Fam132b	INSIDE	0.524	0.623	3507.65	2185.83	0.326	2714.21	885.50
A_68_P24466585	chr6:54942609-54942653	NM_026637:231	Ggct	INSIDE	0.524	0.482	1086.83	523.50	0.252	916.67	231.24
A_68_P30511777	chr16:4726653-4726697	NM_001136066:314	Hmox2	INSIDE	0.524	0.514	2757.78	1417.92	0.269	2341.07	630.63
A_68_P23600187	chr5:35731282-35731326	NM_010445:-461	Hmx1	PROMOTER	0.524	0.522	1697.52	886.83	0.274	1428.06	390.66
A_68_P22698894	chr4:4719763-4719807	NM_177730:669	Impad1	INSIDE	0.524	0.687	1867.04	1283.49	0.360	1425.36	513.73
A_68_P24325222	chr6:29162054-29162098	NM_011829:195	Impdh1	INSIDE	0.524	0.560	2574.26	1441.17	0.293	1716.21	503.33
A_68_P20354542	chr1:75501748-75501792	NM_178884:1257	Obsl1	INSIDE	0.524	0.390	2008.01	782.44	0.204	1542.57	314.94
A_68_P30386866	chr15:82979570-82979614	NM_178627:174	Poldip3	INSIDE	0.524	0.447	1219.72	545.34	0.234	986.78	231.29
A_68_P31302581	chr17:66121665-66121709	NM_133685:406	Rab31	INSIDE	0.524	0.714	2274.34	1623.87	0.374	1834.79	687.09
A_68_P27283982	chr10:80023920-80023964	NM_025852:363	Rexo1	INSIDE	0.524	0.385	2003.75	771.99	0.202	1626.95	328.65
A_68_P23468799	chr5:8623093-8623137	NM_198620:-162	Rundc3b	PROMOTER	0.524	0.551	1394.30	768.90	0.289	1118.35	323.01
A_68_P31254208	chr17:56288089-56288133	NM_001130456:-8344	Sema6b	PROMOTER	0.524	2.602	6117.85	15916.37	1.362	4071.00	5545.04
A_68_P26667556	chr9:79915402-79915446	NM_146003:715	Senp6	INSIDE	0.524	0.580	1184.12	686.23	0.303	1003.97	304.68
A_68_P21476827	chr2:102241389-102241433	NM_020267:-353	Trim44	PROMOTER	0.524	0.700	1758.05	1230.21	0.366	1369.47	501.80
A_68_P29531321	chr14:35487082-35487126	NM_001004436:-9	Wapal	PROMOTER	0.524	0.495	3713.31	1839.03	0.259	3076.43	798.07
A_68_P28818475	chr13:9763163-9763207	NM_001199141:1376	Zmynd11	INSIDE	0.524	0.567	1210.13	686.07	0.297	1053.98	313.34
A_68_P28743061	chr12:112512577-112512621	NM_033603:3277	Amn	INSIDE	0.523	0.681	3901.04	2654.67	0.356	2858.10	1018.09
A_68_P20377068	chr1:79668401-79668445	NM_183027:125	Ap1s3	INSIDE	0.523	0.705	2389.03	1683.13	0.369	1803.25	665.03
A_68_P26521203	chr9:53344856-53344900	NM_007499:-102	Atm	DIVERGENT_PROMOTER	0.523	0.480	1954.94	938.10	0.251	1532.71	384.40
A_68_P27386037	chr10:98726254-98726298	NM_026268:412	Dusp6	INSIDE	0.523	0.555	1184.29	657.03	0.290	1010.52	292.97
A_68_P29161996	chr13:78302959-78303003	NM_001163419:455030	Fam172a	INSIDE	0.523	0.708	1326.64	938.85	0.370	1070.86	396.19
A_68_P31100623	chr17:25097367-25097411	NM_198937:180	Hn1l	INSIDE	0.523	0.461	1873.12	863.53	0.241	1688.36	406.87
A_68_P31344183	chr17:73457385-73457429	NM_001081071:82	Lclat1	INSIDE	0.523	0.321	1799.39	577.36	0.168	1490.87	250.21
A_68_P29162323	chr13:78342968-78343012	NM_010151:-4747	Nr2f1	PROMOTER	0.523	0.627	1214.20	761.07	0.328	1068.19	350.34
A_68_P30423566	chr15:88991488-88991534	NM_001159521:12770	Plxnb2	INSIDE	0.523	3.344	930.56	3111.62	1.748	714.34	1248.70
A_68_P24980575	chr7:16858057-16858101	NM_001136270:963	Prr24	INSIDE	0.523	0.678	1582.48	1072.73	0.354	1159.31	410.80
A_68_P22659976	chr3:153636770-153636814	NM_001081263:393	Slc44a5	INSIDE	0.523	0.537	1862.95	1001.08	0.281	1449.80	407.80
A_68_P30656968	chr16:33251336-33251380	NM_080557:-183	Snx4	PROMOTER	0.523	0.611	1409.78	860.70	0.320	1120.48	358.00
A_68_P23916493	chr5:98596245-98596289			Unknown	0.523	0.637	1222.64	779.36	0.333	1036.38	345.34
A_68_P21741660	chr2:150730004-150730048	NM_024465:441	Abhd12	INSIDE	0.522	0.663	3093.69	2050.35	0.346	2373.54	821.67
A_68_P25700848	chr8:18846199-18846243	NM_026792:-58	Agpat5	PROMOTER	0.522	0.509	1102.65	561.01	0.265	892.11	236.84
A_68_P31933382	chr19:6241388-6241441	NM_194348:-253	Atg2a	DIVERGENT_PROMOTER	0.522	0.641	1685.53	1081.01	0.335	1362.54	456.31
A_68_P28924024	chr13:31712368-31712412	NM_010225:-5294	Foxf2	PROMOTER	0.522	0.634	1177.27	746.26	0.331	925.39	306.28
A_68_P23250459	chr4:119960018-119960062	NM_194060:-174	Foxo6	PROMOTER	0.522	0.507	6242.18	3163.84	0.264	4501.15	1190.08
A_68_P22791944	chr4:25726907-25726951	NM_010243:222	Fut9	INSIDE	0.522	0.746	3942.61	2941.31	0.389	3012.64	1172.89
A_68_P28158433	chr11:116142782-116142826	NM_010254:552	Galr2	INSIDE	0.522	0.699	1461.04	1020.97	0.365	1225.86	447.11
A_68_P31731707	chr18:56868451-56868495	NM_010721:1006	Lmnb1	INSIDE	0.522	0.653	1130.13	737.47	0.340	888.28	302.36

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P21099810	chr2:29702001-29702045	NR_029838:-775	Mir219-2	PROMOTER	0.522	0.532	1726.86	918.25	0.277	1250.61	346.80
A_68_P32132944	chr19:44629890-44629934	NM_026061:-7	Ndufb8	DIVERGENT_PROMOTER	0.522	0.648	876.50	568.25	0.338	721.40	244.16
A_68_P31207972	chr17:46766049-46766093	NM_175168:383	Ptk7	INSIDE	0.522	0.489	3103.20	1518.78	0.255	2376.47	606.87
A_68_P26630975	chr9:72892792-72892836	NM_023635:143	Rab27a	INSIDE	0.522	0.587	2110.75	1239.23	0.307	1765.63	541.52
A_68_P28172264	chr11:118430533-118430577	NM_001024931:340332	Rbfox3	INSIDE	0.522	0.513	1315.00	674.32	0.268	984.46	263.47
A_68_P22392368	chr3:104442587-104442631	NM_009196:18	Slc16a1	INSIDE	0.522	0.566	1703.49	964.24	0.296	1295.31	382.87
A_68_P31247136	chr17:54437767-54437811	NM_022025:571	Slc5a7	INSIDE	0.522	0.671	1318.86	885.17	0.351	1023.01	358.71
A_68_P28778756	chr12:119539812-119539856	NM_001166385:79	Sp4	INSIDE	0.522	0.452	1511.26	683.41	0.236	1125.00	265.51
A_68_P20596472	chr1:129574599-129574643	NM_028135:-22	Tmem163	PROMOTER	0.522	0.693	1917.07	1328.71	0.362	1445.26	522.72
A_68_P20349750	chr1:74708445-74708489	NM_001014974:139	Ttll4	INSIDE	0.522	0.412	2042.66	842.41	0.215	1604.77	345.34
A_68_P26345603	chr9:20935690-20935734	NM_001205312:7	Tyk2	INSIDE	0.522	0.447	1299.32	581.22	0.234	950.51	222.05
A_68_P20599491	chr1:130140934-130140978	NM_026390:199	Ubxn4	INSIDE	0.522	0.677	2087.79	1413.90	0.353	1703.00	601.59
A_68_P21617369	chr2:127952159-127952203	NM_009754:407	Bcl2l11	INSIDE	0.521	0.528	2129.39	1124.93	0.275	1695.44	466.84
A_68_P27684135	chr11:31572000-31572044	NM_001024919:-160	Bod1	PROMOTER	0.521	0.500	1403.15	701.95	0.261	1110.76	289.66
A_68_P23470689	chr5:8997395-8997439	NM_023733:-270	Crot	PROMOTER	0.521	0.541	1008.41	545.45	0.282	794.17	223.71
A_68_P22324269	chr3:90068935-90068979	NM_201407:-1499	Dennd4b	PROMOTER	0.521	0.551	995.76	548.92	0.287	937.25	269.07
A_68_P33003690	chr1_random:342987-343031	NM_177389:-95	Mia3	PROMOTER	0.521	0.536	3386.71	1814.67	0.279	2521.96	703.67
A_68_P28457818	chr12:57714241-57714285	NM_008701:9	Nkx2-9	INSIDE	0.521	0.542	1256.19	680.95	0.283	992.38	280.45
A_68_P24984095	chr7:17530028-17530072	NM_001099636:20	Pnmal2	INSIDE	0.521	0.651	1539.60	1001.72	0.339	1231.81	417.29
A_68_P21784240	chr2:158492976-158493020	NM_001159662:128	Ppp1r16b	INSIDE	0.521	0.498	1902.05	946.70	0.259	1560.31	404.36
A_68_P28035861	chr11:94840510-94840554	NM_009161:-2891	Sgca	PROMOTER	0.521	0.655	892.65	584.79	0.341	755.20	257.88
A_68_P31836526	chr18:75526561-75526605	NM_001042660:-436	Smad7	PROMOTER	0.521	0.462	2780.33	1284.39	0.241	2151.86	517.83
A_68_P24328151	chr6:29686313-29686357	NM_176996:838	Smo	INSIDE	0.521	0.490	1382.36	677.01	0.255	1119.40	285.82
A_68_P25034254	chr7:31741889-31741933	NM_011680:-88	Usf2	PROMOTER	0.521	0.456	1801.66	821.91	0.238	1564.91	372.27
A_68_P23440547	chr4:155148630-155148674	NM_147776:18	Vwa1	INSIDE	0.521	0.662	2450.19	1622.79	0.345	1828.98	630.97
A_68_P28931377	chr13:32893930-32893974	NM_030215:54	Wrnip1	INSIDE	0.521	0.400	1803.71	721.31	0.208	1417.83	295.59
A_68_P27279427	chr10:79337379-79337423	NM_001170935:-21	BC005764	DIVERGENT_PROMOTER	0.520	0.697	3505.25	2441.76	0.362	2603.48	942.18
A_68_P30371303	chr15:80118250-80118294	NM_001044308:605	Cacna1i	INSIDE	0.520	0.557	1719.51	957.94	0.290	1356.02	392.85
A_68_P31374516	chr17:79336106-79336150	NM_001024806:282	Cebpz	INSIDE	0.520	0.672	1013.10	681.20	0.350	885.58	309.93
A_68_P23792212	chr5:72895290-72895334	NM_016869:135	Corin	INSIDE	0.520	0.496	1492.72	739.71	0.258	1165.66	300.32
A_68_P20600403	chr1:130313627-130313671	NM_177445:345	Dars	INSIDE	0.520	0.421	1579.20	664.11	0.219	1326.39	289.93
A_68_P25009058	chr7:26004203-26004247	NM_207677:654	Dedd2	INSIDE	0.520	0.672	3997.66	2685.31	0.349	2861.04	998.56
A_68_P30963516	chr16:91547641-91547685	NM_008338:324	Ifngr2	INSIDE	0.520	0.638	1030.78	658.13	0.332	884.86	293.86
A_68_P27533648	chr10:126479103-126479147	NM_010792:137	Mettl1	INSIDE	0.520	0.627	2175.66	1364.15	0.326	1711.38	558.10
A_68_P31151560	chr17:34162324-34162368	NR_029800:-309	Mir219-1	PROMOTER	0.520	0.563	2440.44	1374.98	0.293	1678.09	491.25
A_68_P29589360	chr14:49282109-49282153	NM_144841:417	Otx2	INSIDE	0.520	0.524	1009.66	528.59	0.272	850.24	231.39
A_68_P28107252	chr11:107331040-107331084	NM_145823:972	Pitpnc1	INSIDE	0.520	0.607	2393.36	1453.50	0.316	1967.44	621.57
A_68_P22518620	chr3:128902934-128902978	NM_001042504:115	Pitx2	INSIDE	0.520	0.691	2387.47	1650.08	0.359	1963.44	705.65
A_68_P23417945	chr4:151687256-151687300	NM_001033489:5456	Rnf207	INSIDE	0.520	0.527	1833.26	965.97	0.274	1332.43	365.40
A_68_P31930772	chr19:5770953-5770997	NM_023912:427	Scyl1	INSIDE	0.520	0.655	1920.96	1257.37	0.340	1369.97	466.12
A_68_P30979311	chr16:94084490-94084534	NM_011377:-992	Sim2	PROMOTER	0.520	0.552	1013.62	559.29	0.287	862.01	247.44
A_68_P30001154	chr15:8586390-8586434	NM_148938:74395	Slc1a3	INSIDE	0.520	4.194	624.39	2618.46	2.182	622.94	1359.41
A_68_P27162285	chr10:57514583-57514627	NM_020561:255	Smpdl3a	INSIDE	0.520	0.534	1247.20	665.50	0.277	986.73	273.53
A_68_P29477470	chr14:26276881-26276925	NM_183208:-1768	Zmiz1	PROMOTER	0.520	0.358	1595.70	571.13	0.186	1111.08	206.81
A_68_P23291908	chr4:128262900-128262946	NM_177758:24420	Zscan20	INSIDE	0.520	3.081	1828.81	5635.01	1.601	1362.16	2181.09
A_68_P31161374	chr17:36002854-36002898	NM_001146710:-196	2310014H01Rik	PROMOTER	0.519	0.538	1848.47	994.37	0.279	1230.22	343.55
A_68_P26822982	chr9:110207662-110207706	NM_001081381:-11	2610002I17Rik	PROMOTER	0.519	0.491	1155.40	567.39	0.255	918.98	234.03
A_68_P26749722	chr9:96790253-96790298	NM_153420:-434	Acpl2	PROMOTER	0.519	0.510	1346.84	687.13	0.265	990.00	261.93
A_68_P22202887	chr3:65762326-65762370	NM_019937:-201	Ccnl1	PROMOTER	0.519	0.591	1278.90	756.02	0.307	1053.73	323.14
A_68_P31567781	chr18:25913080-25913124	NM_001146292:-618	Celf4	PROMOTER	0.519	0.678	1334.73	904.99	0.352	1199.85	422.05
A_68_P31065305	chr17:15517994-15518045	NM_007865:-5232	Dll1	PROMOTER	0.519	0.519	1623.07	842.03	0.269	1325.33	356.95

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P23363642	chr4:140924465-140924509	NM_001085513:352	Fam131c	INSIDE	0.519	0.558	2287.61	1275.69	0.289	1791.64	518.35
A_68_P23973156	chr5:109058413-109058457	NM_153569:324	Gak	INSIDE	0.519	0.606	4363.22	2646.10	0.315	3148.67	991.30
A_68_P23591962	chr5:34325727-34325771	NM_001033458:-374	Gm1673	PROMOTER	0.519	0.579	1267.64	734.52	0.301	1019.87	306.96
A_68_P29048047	chr13:54287555-54287599	NM_008286:79	Hrh2	INSIDE	0.519	0.549	1330.37	730.23	0.285	1098.78	313.18
A_68_P20240337	chr1:55144375-55144419	NM_010477:380	Hspd1	INSIDE	0.519	0.594	2443.80	1450.86	0.308	2004.29	617.99
A_68_P23298314	chr4:129418594-129418638	NM_011317:910	Khdrbs1	INSIDE	0.519	0.525	1377.45	723.44	0.273	1242.32	338.57
A_68_P20905055	chr1:187941024-187941068	NM_146106:143	Lyplal1	INSIDE	0.519	0.471	2071.17	974.55	0.244	1586.16	387.40
A_68_P21345533	chr2:75542035-75542079	NM_010902:642	Nfe2l2	INSIDE	0.519	0.523	1396.72	730.30	0.271	1119.48	303.92
A_68_P27804893	chr11:53276844-53276888	NM_027917:6160	Shroom1	INSIDE	0.519	0.595	906.20	539.18	0.309	811.85	250.84
A_68_P20962671	chr2:3392446-3392492	NM_022724:-210	Suv39h2	PROMOTER	0.519	0.521	984.43	513.13	0.270	782.82	211.70
A_68_P28099381	chr11:105927583-105927627	NM_027346:184	Taco1	INSIDE	0.519	0.617	2035.81	1255.81	0.320	1585.00	507.13
A_68_P23254146	chr4:120624021-120624065	NM_001005788:264	Zfp69	INSIDE	0.519	0.454	1515.26	688.54	0.236	1260.87	297.48
A_68_P23331982	chr4:135638026-135638070	ENSMUST00000121307:-7161		PROMOTER	0.519	0.644	1097.24	707.11	0.334	951.27	318.09
A_68_P22885561	chr4:45896280-45896324	NM_028788:34484	1300002K09Rik	INSIDE	0.518	3.420	921.96	3153.51	1.773	691.69	1226.57
A_68_P29746359	chr14:78936378-78936422	NM_001164503:267	Akap11	INSIDE	0.518	0.603	1770.61	1066.91	0.312	1508.62	471.03
A_68_P25954403	chr8:73362971-73363015	NM_027560:627	Arrdc2	INSIDE	0.518	0.524	1499.61	785.72	0.272	1276.75	346.77
A_68_P28115682	chr11:108781991-108782035	NM_015732:350	Axin2	INSIDE	0.518	0.453	2557.17	1159.25	0.235	2215.46	520.00
A_68_P24157330	chr5:144383580-144383624	NM_011182:287	Cyth3	INSIDE	0.518	0.607	2619.29	1588.92	0.314	2100.62	659.94
A_68_P20827300	chr1:173259326-173259370	NM_001128609:73	Dedd	INSIDE	0.518	0.364	1930.26	703.37	0.189	1665.09	314.02
A_68_P32219658	chr19:59543743-59543787	NM_010132:10585	Emx2	DOWNSTREAM	0.518	0.571	989.70	564.72	0.295	803.68	237.39
A_68_P28771929	chr12:118392739-118392783	NR_033538:-3018	Gm10421	PROMOTER	0.518	0.513	1032.45	529.89	0.266	691.08	183.88
A_68_P24126242	chr5:137972085-137972129	NM_010312:2351	Gnb2	INSIDE	0.518	0.587	1855.41	1088.88	0.304	1489.16	453.02
A_68_P26213861	chr8:121868279-121868323	NM_024219:-137	Hsbp1	PROMOTER	0.518	0.441	1227.41	541.85	0.229	953.94	218.26
A_68_P26022686	chr8:87447681-87447725	NM_019945:13550	Mast1	INSIDE	0.518	2.821	2382.49	6719.96	1.461	1713.15	2503.61
A_68_P28037998	chr11:95171463-95171507	NM_001195003:76	Myst2	INSIDE	0.518	0.604	1913.35	1155.83	0.313	1555.98	487.26
A_68_P26075129	chr8:96561318-96561362	NM_001093757:243	Ogfod1	INSIDE	0.518	0.721	2131.22	1536.21	0.373	1534.30	572.41
A_68_P32957129	chr17:8534343-8534387	NM_178774:761	Prr18	INSIDE	0.518	0.626	1114.38	697.44	0.324	1032.46	334.91
A_68_P21629881	chr2:130276040-130276084	NM_001163688:49	Ptpra	INSIDE	0.518	0.626	5416.56	3392.06	0.324	3935.00	1275.44
A_68_P31311916	chr17:67703103-67703147	NM_008984:675	Ptprm	INSIDE	0.518	0.531	1401.92	744.02	0.275	1148.81	315.56
A_68_P26628115	chr9:72339784-72339828	NM_009359:-43	Tex9	PROMOTER	0.518	0.579	922.11	534.25	0.300	796.02	239.04
A_68_P27942254	chr11:78075324-78075368	NM_001002004:91	2610507B11Rik	INSIDE	0.517	0.572	1212.73	693.61	0.296	959.54	283.96
A_68_P22775538	chr4:21858442-21858486	NM_175234:-8	6230409E13Rik	PROMOTER	0.517	0.568	1159.15	658.86	0.294	1039.90	305.84
A_68_P21564754	chr2:118375138-118375182	NM_138313:254	Bmf	INSIDE	0.517	0.639	7210.45	4606.30	0.330	5323.14	1756.68
A_68_P26816838	chr9:108728469-108728513	NM_080437:-160	Celsr3	PROMOTER	0.517	0.409	3585.13	1465.05	0.211	2717.36	574.18
A_68_P20293011	chr1:64579120-64579164	NM_001037726:-235	Creb1	PROMOTER	0.517	0.564	3850.61	2170.53	0.291	2688.19	783.60
A_68_P25025638	chr7:29940590-29940634	NM_001146023:617	Fam98c	INSIDE	0.517	0.684	3093.74	2114.94	0.353	2326.73	822.15
A_68_P27973894	chr11:83664886-83664930	NM_009330:538	Hnf1b	INSIDE	0.517	0.656	2460.11	1613.38	0.339	1948.79	660.51
A_68_P25596369	chr7:149846534-149846578	NM_001122736:384	Igf2	INSIDE	0.517	0.596	1727.31	1029.74	0.308	1472.01	453.38
A_68_P20947552	chr1:194979319-194979363	NM_016851:35	Irf6	INSIDE	0.517	0.616	967.79	596.45	0.319	873.62	278.55
A_68_P25599905	chr7:150482316-150482360	NR_001461:114	Kcnq1ot1	INSIDE	0.517	1.366	7091.04	9685.35	0.707	4961.85	3505.79
A_68_P32119292	chr19:42222487-42222531	NM_183195:630	Marveld1	INSIDE	0.517	0.737	5617.74	4142.62	0.381	4129.04	1574.01
A_68_P30557335	chr16:13448659-13448703	NR_030549:-935	Mir193b	PROMOTER	0.517	0.585	3380.12	1976.05	0.302	2588.96	782.22
A_68_P26522115	chr9:53513955-53513999	NM_175562:361	Rab39	INSIDE	0.517	0.736	2541.23	1870.45	0.380	2054.21	781.16
A_68_P28531916	chr12:73509185-73509229	NM_153457:720	Rtn1	INSIDE	0.517	0.679	1209.17	820.57	0.351	909.19	319.29
A_68_P27896512	chr11:69494853-69494903	NM_030702:594	Senp3	INSIDE	0.517	0.570	1478.72	843.10	0.295	1087.25	320.45
A_68_P27091227	chr10:41530014-41530058	NM_001162908:-343	Sesn1	DIVERGENT_PROMOTER	0.517	0.586	1123.65	658.05	0.303	858.74	260.18
A_68_P26706484	chr9:87634686-87634730	NM_023814:-8613	Tbx18	PROMOTER	0.517	0.338	1611.29	544.04	0.175	1292.66	225.65
A_68_P27332827	chr10:89208343-89208387	NM_029166:629	Uhrf1bp1l	INSIDE	0.517	0.602	2053.76	1236.54	0.311	1498.78	466.31
A_68_P24818153	chr6:124958879-124958923	NM_175557:-922	Zfp384	PROMOTER	0.517	0.505	1347.18	679.78	0.261	1055.62	275.37
A_68_P26038371	chr8:90485107-90485151	NM_033327:-1634	Zfp423	PROMOTER	0.517	0.517	1355.59	700.29	0.267	1180.36	315.23
A_68_P21041406	chr2:18689012-18689056	ENSMUST00000119424:8424		DOWNSTREAM	0.517	0.612	2252.81	1378.47	0.316	1719.65	544.06

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P23547918	chr5:25035180-25035225	NR_027388:-633	1700096K18Rik	PROMOTER	0.516	0.509	1014.77	516.90	0.263	909.77	239.35
A_68_P30725228	chr16:45159441-45159485	NM_026402:521	Atg3	INSIDE	0.516	0.405	1313.07	532.40	0.209	1403.01	293.47
A_68_P22202886	chr3:65762239-65762283	NM_019937:-113	Ccnl1	PROMOTER	0.516	0.713	1822.10	1298.53	0.368	1502.71	552.31
A_68_P27101048	chr10:43299118-43299162	NM_009846:166	Cd24a	INSIDE	0.516	0.599	2997.47	1794.56	0.309	2305.45	711.81
A_68_P22520449	chr3:129236571-129236615	NM_130450:1289	Elovl6	INSIDE	0.516	0.523	1307.01	683.74	0.270	1073.46	289.89
A_68_P21768928	chr2:155834064-155834108	NM_025516:226	Ergic3	INSIDE	0.516	0.475	2318.92	1100.41	0.245	1700.86	416.77
A_68_P25596372	chr7:149846899-149846943	NM_001122736:20	Igf2	INSIDE	0.516	0.713	1993.94	1421.96	0.368	1828.72	673.07
A_68_P31613845	chr18:34784223-34784267	NM_001166407:-33	Kif20a	PROMOTER	0.516	0.651	951.51	619.24	0.336	714.48	239.96
A_68_P23088447	chr4:87678387-87678431	NM_027326:903	Mllt3	INSIDE	0.516	0.708	2138.29	1514.01	0.365	1765.23	645.04
A_68_P29982188	chr15:5093945-5093989	NM_001013367:106	Prkaa1	INSIDE	0.516	0.276	2168.50	598.03	0.142	1691.22	240.81
A_68_P24061766	chr5:124981229-124981273	NM_021430:150	Rilpl1	INSIDE	0.516	0.406	1536.95	624.37	0.210	1115.47	233.86
A_68_P30970267	chr16:92606200-92606244	NM_001111023:91351	Runx1	INSIDE	0.516	1.408	3130.00	4407.72	0.726	2354.96	1709.68
A_68_P26700014	chr9:86465671-86465715	NM_001145968:33	Rwdd2a	INSIDE	0.516	0.585	4142.67	2424.58	0.302	3140.75	949.10
A_68_P21621499	chr2:128643821-128643865	NM_028248:-196	Tmem87b	PROMOTER	0.516	0.683	1950.87	1332.09	0.352	1528.32	538.48
A_68_P30125732	chr15:33617536-33617580	NM_001085421:80	Tspyl5	INSIDE	0.516	0.643	818.41	525.87	0.331	724.43	240.09
A_68_P31403203	chr17:84587080-84587124	NM_001001806:185	Zfp36l2	INSIDE	0.516	0.305	2182.82	664.69	0.157	1708.21	268.44
A_68_P28725238	chr12:109244329-109244373	NM_001079883:-2726	Bcl11b	PROMOTER	0.515	0.644	1347.74	868.21	0.332	1134.29	376.64
A_68_P26233347	chr8:124956923-124956967	NM_007806:-104	Cyba	PROMOTER	0.515	0.547	1100.64	602.03	0.282	904.73	255.00
A_68_P24880219	chr6:137703098-137703142	NM_172733:23	Dera	INSIDE	0.515	0.390	1596.78	622.99	0.201	1310.11	263.15
A_68_P21111665	chr2:31702261-31702305	NM_178887:-757	Fibcd1	PROMOTER	0.515	0.479	2368.72	1135.18	0.247	1803.38	445.06
A_68_P25411259	chr7:117161867-117161911	NM_181517:-50	Ipo7	PROMOTER	0.515	0.552	949.56	524.16	0.284	874.94	248.56
A_68_P30018898	chr15:11835366-11835410	NM_001039181:41	Npr3	INSIDE	0.515	0.443	2915.23	1291.08	0.228	2417.64	551.50
A_68_P21707654	chr2:144353449-144353493	NM_029763:-10	Polr3f	DIVERGENT_PROMOTER	0.515	0.383	3800.11	1457.21	0.197	3178.40	627.48
A_68_P23269524	chr4:124336535-124336579	NM_011141:1668	Pou3f1	INSIDE	0.515	0.447	1919.96	858.72	0.230	1485.26	341.83
A_68_P28698040	chr12:104770943-104770987	NM_028980:190	Ppp4r4	INSIDE	0.515	0.546	2406.01	1314.29	0.281	1969.38	553.65
A_68_P28611531	chr12:88019465-88019515	NM_177354:-159	Vash1	PROMOTER	0.515	0.684	1095.39	748.84	0.352	803.68	282.97
A_68_P20565673	chr1:123074631-123074675	AK045543:90602		INSIDE	0.515	0.568	1014.34	575.87	0.292	733.95	214.68
A_68_P23404035	chr4:149422780-149422824	ENSMUST00000134236:-319		PROMOTER	0.515	0.517	1437.99	743.77	0.266	1136.85	302.59
A_68_P25677407	chr8:14911603-14911647	NM_001037736:-92	Arhgef10	PROMOTER	0.514	0.531	2007.66	1065.07	0.273	1585.43	432.17
A_68_P28725020	chr12:109218453-109218497	NM_001079883:23150	Bcl11b	INSIDE	0.514	0.522	1741.54	909.57	0.269	1359.26	365.23
A_68_P27309451	chr10:85061404-85061448	NM_001017525:271	Btbd11	INSIDE	0.514	0.434	2082.85	903.63	0.223	1569.36	349.73
A_68_P21762930	chr2:154718365-154718409	NM_026030:256	Eif2s2	INSIDE	0.514	0.404	1515.20	611.42	0.208	1128.13	234.09
A_68_P29660085	chr14:63864436-63864480	NM_008092:-361	Gata4	PROMOTER	0.514	0.597	1016.09	606.78	0.307	842.41	258.44
A_68_P29503210	chr14:30821909-30821953	NM_019583:152	Il17rb	INSIDE	0.514	0.416	2050.39	853.93	0.214	1709.47	366.18
A_68_P31220014	chr17:49072235-49072279	NM_027452:350	Lrfn2	INSIDE	0.514	0.570	1560.05	889.24	0.293	1206.37	353.68
A_68_P21576250	chr2:120434989-120435033	NM_025657:41	Lrrc57	INSIDE	0.514	0.469	1152.32	540.37	0.241	995.00	239.74
A_68_P21550150	chr2:115888204-115888259	NM_001159569:2126	Meis2	INSIDE	0.514	0.495	1260.07	624.13	0.255	1004.28	255.89
A_68_P20353933	chr1:75419052-75419096	NM_001085370:36890	Speg	INSIDE	0.514	0.669	3596.88	2407.46	0.344	2505.44	862.47
A_68_P21395951	chr2:84877360-84877404	NM_001136081:-225	Ssrp1	PROMOTER	0.514	0.739	3665.82	2709.21	0.380	2642.53	1004.21
A_68_P31655787	chr18:42671213-42671257	NM_001039474:94	Tcerg1	INSIDE	0.514	0.558	2278.01	1270.94	0.287	1850.43	530.33
A_68_P27290579	chr10:81033785-81033829	NM_019725:-4470	Tle2	PROMOTER	0.514	0.602	3634.26	2189.17	0.310	2801.37	867.32
A_68_P24049902	chr5:122804456-122804500	NM_019780:57	Vps29	INSIDE	0.514	0.688	2582.45	1776.29	0.353	1990.30	703.43
A_68_P23692831	chr5:52506869-52506913	AK076709:-1661		PROMOTER	0.514	0.542	2493.95	1351.59	0.279	2230.71	621.46
A_68_P25653638	chr8:11187989-11188033	ENSMUST00000151014:256		INSIDE	0.514	0.539	1477.14	796.28	0.277	1199.82	332.17
A_68_P26883803	chr9:121403379-121403423	NM_031161:1407	Cck	INSIDE	0.513	0.743	2674.70	1987.12	0.381	1869.53	711.97
A_68_P28752829	chr12:114067223-114067267	NM_028023:356	Cdca4	INSIDE	0.513	0.670	3014.77	2019.46	0.344	2247.10	772.13
A_68_P31928721	chr19:5447928-5447972	NM_010235:253	Fosl1	INSIDE	0.513	0.555	2362.33	1312.03	0.285	1703.15	485.09
A_68_P27765087	chr11:45757827-45757871	NM_028185:589	Lsm11	INSIDE	0.513	0.548	1017.78	557.34	0.281	781.41	219.55
A_68_P24946857	chr7:3644688-3644732	NM_029934:417	Mboat7	INSIDE	0.513	0.400	1815.75	726.91	0.206	1469.67	302.04
A_68_P26821062	chr9:109834457-109834501	NM_001205331:201	Mtap4	INSIDE	0.513	0.548	2387.42	1308.77	0.281	1888.78	530.86
A_68_P26261063	chr8:129588776-129588820	NM_001122850:843	Pard3	INSIDE	0.513	0.555	1085.47	602.93	0.285	750.86	213.86

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P21752418	chr2:152841222-152841266	NM_178939:-125	Pdrg1	PROMOTER	0.513	0.656	1014.82	665.35	0.336	837.41	281.53
A_68_P21867219	chr2:172847604-172847648	NM_019547:224	Rbm38	INSIDE	0.513	0.711	1925.78	1370.09	0.365	1461.18	532.79
A_68_P29073064	chr13:58503963-58504007	NM_001168248:27	Rmi1	INSIDE	0.513	0.455	2328.87	1060.36	0.233	1774.24	414.23
A_68_P25408484	chr7:116662619-116662663	NM_011975:-68	Rpl27a	PROMOTER	0.513	0.618	1778.81	1099.42	0.317	1300.08	411.92
A_68_P27989555	chr11:86358098-86358142	NM_001114334:189	Rps6kb1	INSIDE	0.513	0.518	1411.96	731.79	0.266	1152.60	306.25
A_68_P25507651	chr7:134985781-134985825	NM_009294:481	Stx4a	INSIDE	0.513	0.509	1031.52	524.89	0.261	745.01	194.56
A_68_P28048726	chr11:96976651-96976695	NM_019507:-27	Tbx21	PROMOTER	0.513	0.478	1637.70	783.49	0.246	1353.46	332.43
A_68_P21084619	chr2:27281633-27281677	NM_009500:691	Vav2	INSIDE	0.513	0.596	2520.63	1502.35	0.306	1744.29	533.62
A_68_P27212532	chr10:67010792-67010836	NM_001005419:889	Ado	INSIDE	0.512	0.635	858.81	545.74	0.325	664.71	216.20
A_68_P27897126	chr11:69609386-69609430	NM_009601:31	Chrnb1	INSIDE	0.512	0.661	1292.68	854.96	0.338	1008.82	341.48
A_68_P32143334	chr19:46413011-46413055	NM_001164290:118	Cuedc2	INSIDE	0.512	0.469	1230.91	577.32	0.240	1008.01	241.88
A_68_P31160531	chr17:35837972-35838016	NM_001198833:-459	Ddr1	PROMOTER	0.512	0.598	2415.69	1445.06	0.306	1771.13	542.49
A_68_P27445215	chr10:110182553-110182597	NM_178609:54	E2f7	INSIDE	0.512	0.436	1420.39	619.06	0.223	1097.74	244.80
A_68_P30446023	chr15:93105424-93105468	NM_001033275:69	Gxylt1	INSIDE	0.512	0.475	1298.36	616.26	0.243	1064.07	258.39
A_68_P24798577	chr6:120413598-120413642	NM_008359:406	Il17ra	INSIDE	0.512	0.712	1682.85	1198.87	0.365	1554.18	566.60
A_68_P24990858	chr7:19589997-19590041	NM_178757:605	Irf2bp1	INSIDE	0.512	0.649	4180.13	2712.88	0.332	3243.74	1076.99
A_68_P31158190	chr17:35332751-35332795	NM_008518:1321	Ltb	INSIDE	0.512	0.484	1166.87	564.21	0.248	895.35	221.65
A_68_P29443159	chr14:20570751-20570795	NM_008695:294	Nid2	INSIDE	0.512	0.519	1191.32	618.11	0.266	971.94	258.12
A_68_P27638836	chr11:21893026-21893070	NM_011023:8606	Otx1	DOWNSTREAM	0.512	0.605	1749.74	1058.92	0.310	1436.46	444.96
A_68_P24907678	chr6:142912941-142912985	NM_011374:10	St8sia1	INSIDE	0.512	4.197	2260.30	9487.15	2.149	1804.81	3878.40
A_68_P24114328	chr5:135499558-135499602	NM_016801:139	Stx1a	INSIDE	0.512	0.650	1259.02	818.09	0.333	1013.75	337.49
A_68_P28042483	chr11:95985716-95985760	NM_172799:-9361	Ttll6	PROMOTER	0.512	0.665	958.90	637.64	0.341	944.08	321.73
A_68_P31215625	chr17:48179041-48179085	AK007241:-3819		PROMOTER	0.512	0.729	1847.15	1346.97	0.373	1533.05	572.26
A_68_P27835624	chr11:59040902-59040946	NM_001130408:740	Arf1	INSIDE	0.511	0.617	2545.03	1569.28	0.315	1884.92	593.33
A_68_P21646218	chr2:133378320-133378364	NM_007553:-592	Bmp2	PROMOTER	0.511	0.700	1924.24	1346.76	0.357	1606.86	574.39
A_68_P28279804	chr12:21292173-21292217	NM_018813:37	Cpsf3	INSIDE	0.511	0.635	852.53	541.29	0.325	694.88	225.55
A_68_P22288630	chr3:83844564-83844615	NM_172681:-506	D930015E06Rik	PROMOTER	0.511	0.600	1416.59	850.62	0.307	1108.94	340.37
A_68_P31333824	chr17:71660558-71660602	NM_145158:-275	Emilin2	PROMOTER	0.511	0.673	2729.26	1836.49	0.344	2302.06	791.75
A_68_P30801798	chr16:60605990-60606034	NM_007938:-655	Epha6	PROMOTER	0.511	0.467	1476.39	689.57	0.239	1364.89	325.79
A_68_P25273844	chr7:88908139-88908183	NM_025997:322	Fam103a1	INSIDE	0.511	0.550	982.21	539.94	0.281	705.12	198.12
A_68_P29034749	chr13:51942380-51942424	NM_011817:359	Gadd45g	INSIDE	0.511	0.623	1565.13	975.81	0.318	1087.34	346.26
A_68_P22864172	chr4:41702487-41702531	NM_016658:383	Galt	INSIDE	0.511	0.631	2104.90	1329.09	0.323	1595.48	515.14
A_68_P26458693	chr9:42751946-42751990	NM_175481:486	Grik4	INSIDE	0.511	1.462	9798.38	14322.62	0.747	6431.69	4805.55
A_68_P26020946	chr8:87180770-87180814	NM_010499:5959	Ier2	DOWNSTREAM	0.511	0.431	2241.58	965.52	0.220	1678.43	369.65
A_68_P30506990	chr16:3884336-3884380	NM_029090:-260	Nat15	PROMOTER	0.511	0.549	2044.21	1122.05	0.281	1551.00	435.45
A_68_P31622630	chr18:36357100-36357144	NM_001167891:-308	Nrg2	PROMOTER	0.511	0.452	1860.39	840.59	0.231	1443.43	333.15
A_68_P27835027	chr11:58949650-58949694	NM_001171512:205	Obscn	INSIDE	0.511	0.537	1404.96	753.92	0.274	1265.11	346.76
A_68_P25368681	chr7:107756005-107756054	NM_001163663:-70	Rab6	PROMOTER	0.511	0.514	1615.80	830.53	0.263	1380.20	362.52
A_68_P30350127	chr15:76540848-76540892	NM_058214:119	Recql4	INSIDE	0.511	0.668	1775.08	1186.16	0.342	1352.78	462.13
A_68_P30377736	chr15:81230239-81230283	NM_133726:-136	St13	DIVERGENT_PROMOTER	0.511	0.636	1652.89	1051.20	0.325	1243.42	404.08
A_68_P24951866	chr7:5013371-5013415	NM_001205231:-352	U2af2	PROMOTER	0.511	0.525	1150.93	604.71	0.268	918.34	246.56
A_68_P25411817	chr7:117265589-117265633	NM_009516:38	Wee1	INSIDE	0.511	0.375	1760.24	660.82	0.192	1550.17	297.36
A_68_P31615538	chr18:35091084-35091128	NM_144866:551	Etf1	INSIDE	0.510	0.632	2002.13	1264.58	0.322	1498.30	482.38
A_68_P25023288	chr7:29517538-29517582	NM_015796:15752	Fbxo17	INSIDE	0.510	0.588	912.14	536.30	0.300	817.40	245.08
A_68_P30630410	chr16:28445868-28445912	NM_183064:-577	Fgf12	PROMOTER	0.510	0.707	2576.61	1821.60	0.360	1966.69	708.89
A_68_P21345229	chr2:75497988-75498032	NR_033513:664	Gm6793	INSIDE	0.510	0.486	2613.81	1269.29	0.248	2037.51	504.86
A_68_P20897165	chr1:186556818-186556862	NM_008250:-468	Hlx	PROMOTER	0.510	0.627	1028.58	644.62	0.320	926.83	296.27
A_68_P24609843	chr6:86338939-86338994	NM_025823:8178	Pcyox1	INSIDE	0.510	3.848	666.54	2564.55	1.963	552.45	1084.53
A_68_P28269480	chr12:17273418-17273462	NM_027959:40	Pdia6	INSIDE	0.510	0.651	2058.29	1340.09	0.332	1785.25	592.77
A_68_P31295068	chr17:64681131-64681175	NM_001025309:71	Pja2	INSIDE	0.510	0.442	2533.20	1119.03	0.225	2101.75	473.18
A_68_P20642552	chr1:137815854-137815898	NM_019645:-275	Pkp1	PROMOTER	0.510	0.611	2166.92	1323.26	0.311	1704.79	530.71

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P30396225	chr15:84511839-84511883	NM_146061:433	Prr5	INSIDE	0.510	0.501	2069.43	1036.24	0.255	1674.23	427.60
A_68_P24591678	chr6:83092414-83092458	NM_009106:5359	Rtkn	INSIDE	0.510	0.544	1362.14	740.92	0.277	1054.37	292.49
A_68_P27138498	chr10:52410952-52410996	NM_178675:668	Slc35f1	INSIDE	0.510	0.542	982.61	532.30	0.277	855.59	236.59
A_68_P25618383	chr8:4677621-4677665	ENSMUST00000058918:723		INSIDE	0.510	0.714	3232.09	2306.85	0.364	2311.63	842.24
A_68_P32202582	chr19:56797590-56797634	NM_007419:751	Adrb1	INSIDE	0.509	0.519	1228.43	637.95	0.265	789.68	208.88
A_68_P28593178	chr12:84861329-84861374	NM_030246:-64	Dcaf4	PROMOTER	0.509	0.659	1175.40	774.41	0.336	951.78	319.41
A_68_P20612316	chr1:132774985-132775029	NM_026976:12653	Faim3	INSIDE	0.509	0.366	1452.22	531.65	0.186	1143.31	213.05
A_68_P21486778	chr2:103867915-103867959	NM_020593:-19	Fbxo3	PROMOTER	0.509	0.500	1250.65	625.27	0.254	1039.88	264.62
A_68_P24728933	chr6:107479987-107480031	NM_008516:289	Lrrn1	INSIDE	0.509	0.571	2352.89	1344.39	0.291	1889.07	549.00
A_68_P21199929	chr2:48804619-48804663	NR_033442:147	Orc4	INSIDE	0.509	0.697	1869.92	1302.45	0.354	1442.42	511.04
A_68_P21142145	chr2:37298992-37299036	NM_001033960:-8759	Rabgap1	PROMOTER	0.509	0.687	1727.49	1186.17	0.349	1324.23	462.48
A_68_P21780568	chr2:157854743-157854787	NM_027434:235	Rprd1b	INSIDE	0.509	0.595	2441.06	1452.79	0.303	1892.12	573.15
A_68_P23344730	chr4:137806358-137806402	NM_001099631:55	Sh2d5	INSIDE	0.509	0.413	2445.43	1010.44	0.210	1774.98	373.19
A_68_P31412112	chr17:86086622-86086666	NM_011380:950	Six2	INSIDE	0.509	0.627	1292.35	809.94	0.319	1152.84	367.85
A_68_P22956443	chr4:59450910-59450954	NM_001163288:573	Susd1	INSIDE	0.509	0.730	6056.34	4421.95	0.372	4740.52	1762.26
A_68_P30510785	chr16:4558716-4558760	NM_031182:982	Tcfap4	INSIDE	0.509	0.429	2293.06	983.82	0.218	1732.25	378.00
A_68_P24114264	chr5:135485504-135485548	NR_033794:201	Abhd11	INSIDE	0.508	0.669	1282.03	857.73	0.340	938.05	318.73
A_68_P29977061	chr15:3945633-3945677	NM_145930:98	AW549877	INSIDE	0.508	0.642	2560.84	1643.83	0.326	2170.23	708.28
A_68_P25586435	chr7:148246749-148246793	NM_177897:-402	B4galnt4	PROMOTER	0.508	0.609	864.20	526.70	0.309	774.20	239.57
A_68_P25094601	chr7:52962152-52962196	NM_016974:1558	Dbp	INSIDE	0.508	0.503	1957.27	984.22	0.255	1589.42	405.91
A_68_P22317567	chr3:88963692-88963736	NM_008227:365	Hcn3	INSIDE	0.508	0.589	1460.91	861.08	0.299	1216.82	364.27
A_68_P31217293	chr17:48549071-48549115	NM_001110832:53	Nfya	INSIDE	0.508	0.742	5210.63	3868.13	0.377	3695.38	1394.35
A_68_P26345766	chr9:20969493-20969537	NM_183408:-643	Pde4a	PROMOTER	0.508	0.715	1602.54	1145.24	0.363	1262.67	458.37
A_68_P30346951	chr15:76060156-76060200	NM_201385:-251	Plec	PROMOTER	0.508	0.478	1602.64	765.41	0.242	1309.91	317.54
A_68_P25581338	chr7:147130178-147130222	NM_009482:446	Utf1	INSIDE	0.508	0.603	1427.31	861.20	0.306	1137.09	348.46
A_68_P26038381	chr8:90486316-90486360	NM_033327:-2844	Zfp423	PROMOTER	0.508	0.687	1521.67	1045.01	0.349	1154.13	402.49
A_68_P30388925	chr15:83357441-83357485	NM_007546:171	Bik	INSIDE	0.507	0.664	1048.29	695.80	0.337	851.32	286.62
A_68_P30486705	chr15:100445276-100445320	NM_011873:-794	Dazap2	PROMOTER	0.507	0.408	1286.53	524.76	0.207	1011.88	209.35
A_68_P24868564	chr6:135683145-135683189	NM_008171:440363	Grin2b	INSIDE	0.507	4.190	1333.07	5585.51	2.125	917.72	1950.39
A_68_P22311357	chr3:87827642-87827686	NM_022031:3769	Hapln2	INSIDE	0.507	0.621	1291.59	802.02	0.315	1091.23	343.72
A_68_P20799115	chr1:168169115-168169174	NM_175296:-269	Mael	PROMOTER	0.507	5.741	186.23	1069.13	2.909	135.52	394.29
A_68_P31139421	chr17:31523560-31523605	NM_001163748:404	Pde9a	INSIDE	0.507	0.698	1798.13	1254.35	0.354	1297.10	459.05
A_68_P24995081	chr7:20334787-20334831	NM_008990:114	Pvrl2	INSIDE	0.507	0.647	2243.68	1452.11	0.328	1670.83	547.76
A_68_P26948616	chr10:12728440-12728484	NM_175102:207	Sf3b5	INSIDE	0.507	0.432	2366.77	1022.64	0.219	1933.08	423.55
A_68_P27923087	chr11:74709868-74709912	NM_197943:692	Sgsm2	INSIDE	0.507	0.520	1107.95	576.24	0.264	894.69	236.03
A_68_P27848102	chr11:61191658-61191702	NM_026183:-103	Slc47a1	PROMOTER	0.507	1.406	3890.51	5468.60	0.713	3248.35	2315.81
A_68_P32036080	chr19:26680365-26680409	NM_011416:737	Smarca2	INSIDE	0.507	0.571	1200.32	685.53	0.290	959.91	278.16
A_68_P27256923	chr10:74980993-74981047	NM_026095:234	Snrpd3	INSIDE	0.507	0.481	1409.53	678.13	0.244	1050.05	256.07
A_68_P31152609	chr17:34324546-34324590	NM_001161730:68	Tap1	INSIDE	0.507	0.532	2606.50	1387.87	0.270	2083.49	562.90
A_68_P26459754	chr9:42924375-42924419	NM_001034863:257	Tmem136	INSIDE	0.507	0.585	906.18	530.44	0.297	705.80	209.28
A_68_P28936501	chr13:34169775-34169819	NM_009450:81	Tubb2a	INSIDE	0.507	0.539	1638.25	882.70	0.273	1315.64	359.39
A_68_P26805304	chr9:106724237-106724281	NM_001015507:-48	Vprbp	PROMOTER	0.507	0.710	1469.79	1043.29	0.360	1103.93	397.48
A_68_P26871701	chr9:119231116-119231160	ENSMUST00000128880:302		INSIDE	0.507	0.626	878.26	549.98	0.317	674.69	214.02
A_68_P24541218	chr6:72297585-72297629	NM_026696:296	0610030E20Rik	INSIDE	0.506	0.640	1200.57	768.92	0.324	976.07	316.47
A_68_P25581585	chr7:147164519-147164563	NM_001033465:114	6430531B16Rik	INSIDE	0.506	0.590	1228.92	724.51	0.298	839.09	250.14
A_68_P20239575	chr1:54982981-54983025	NM_001081433:229	Ankrd44	INSIDE	0.506	0.502	1728.21	868.19	0.254	1361.37	345.90
A_68_P31776706	chr18:64820510-64820554	NM_001001488:122	Atp8b1	INSIDE	0.506	0.644	1484.65	956.16	0.326	1323.99	431.07
A_68_P29682516	chr14:67627743-67627787	NM_009761:-50	Bnip3l	PROMOTER	0.506	0.648	1485.99	962.27	0.328	1149.10	376.56
A_68_P24225087	chr6:8209485-8209529	NR_033518:219	Gm16039	INSIDE	0.506	0.565	2212.07	1250.54	0.286	1747.95	500.35
A_68_P29856566	chr14:102128766-102128810	NM_201529:-356	Lmo7	PROMOTER	0.506	0.395	1807.39	714.19	0.200	1485.16	296.82
A_68_P25957673	chr8:74115916-74115960	NM_025396:-144	Pgls	PROMOTER	0.506	0.377	3086.45	1162.11	0.191	2465.23	470.05

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P20053922	chr1:16095556-16095600	NM_133832:-384	Rdh10	DIVERGENT_PROMOTER	0.506	0.546	1711.47	933.66	0.276	1379.27	380.66
A_68_P22286849	chr3:83570700-83570744	NM_009144:480	Sfrp2	INSIDE	0.506	0.704	2903.66	2044.40	0.357	2270.81	809.60
A_68_P25618723	chr8:4779387-4779431	NM_011369:126	Shcbp1	INSIDE	0.506	0.369	1739.58	641.96	0.187	1489.84	278.05
A_68_P29070326	chr13:58009122-58009166	NM_001166464:549	Spock1	INSIDE	0.506	0.524	1246.19	653.13	0.265	1059.14	280.90
A_68_P25724849	chr8:26128143-26128187	NM_027194:482	Tm2d2	INSIDE	0.506	0.472	1720.20	811.15	0.239	1345.00	321.23
A_68_P28078649	chr11:102146096-102146140	NM_028076:-156	Tmub2	PROMOTER	0.506	0.657	1328.67	872.90	0.332	1108.92	368.39
A_68_P28751782	chr12:113917645-113917689	NM_001100460:616	Zbtb42	INSIDE	0.506	0.733	2166.76	1587.69	0.371	1635.97	606.63
A_68_P32565206	chrX:98893365-98893413	ENSMUST00000073812:-6199		PROMOTER	0.506	3.208	1355.34	4347.84	1.625	589.21	957.26
A_68_P20153981	chr1:37486651-37486695	NM_198006:276	6330578E17Rik	INSIDE	0.505	0.626	2263.79	1417.08	0.316	1818.64	575.33
A_68_P24800464	chr6:120772369-120772413	NM_007510:313	Atp6v1e1	INSIDE	0.505	0.573	2045.06	1172.60	0.289	1552.76	449.45
A_68_P20351100	chr1:74939365-74939409	NM_021541:323	Cryba2	INSIDE	0.505	0.611	960.87	587.30	0.309	797.41	246.27
A_68_P28067421	chr11:100181597-100181641	NM_011508:309	Eif1	INSIDE	0.505	0.388	2398.67	929.51	0.196	1907.61	373.50
A_68_P27784888	chr11:49608283-49608327	NM_013529:648	Gfpt2	INSIDE	0.505	0.482	1537.48	740.55	0.243	1337.59	325.21
A_68_P27270904	chr10:77364916-77364963	NM_145152:342	Lrrc3	INSIDE	0.505	0.572	1069.92	612.22	0.289	833.59	240.67
A_68_P22771645	chr4:20705806-20705850	NM_172987:-13	Nkain3	PROMOTER	0.505	3.486	10184.38	35497.85	1.759	7168.92	12613.22
A_68_P31627037	chr18:37303374-37303418	NM_001003672:-226	Pcdhac2	PROMOTER	0.505	0.615	1109.08	682.28	0.311	974.39	302.66
A_68_P30397302	chr15:84685989-84686033	NM_001081166:549	Phf21b	INSIDE	0.505	0.526	1246.85	655.29	0.265	978.96	259.70
A_68_P24770497	chr6:115311740-115311784	NM_001127330:524	Pparg	INSIDE	0.505	0.586	2380.61	1394.49	0.296	1937.70	573.60
A_68_P24591254	chr6:83020596-83020640	NM_009392:-399	Tlx2	DIVERGENT_PROMOTER	0.505	0.608	3648.78	2219.56	0.307	2681.41	823.38
A_68_P26052838	chr8:92871596-92871645	NM_172913:531	Tox3	INSIDE	0.505	0.698	2166.30	1512.29	0.353	1706.60	601.80
A_68_P25948612	chr8:72426018-72426066	NM_032004:-71	Tssk6	PROMOTER	0.505	0.627	991.05	621.52	0.317	751.56	238.08
A_68_P31962486	chr19:12869204-12869248	NR_024093:1387	U05342	INSIDE	0.505	0.456	2112.45	964.22	0.230	1734.61	399.72
A_68_P26924746	chr10:8238018-8238062	NM_177387:583	Ust	INSIDE	0.505	0.612	1224.44	749.46	0.309	964.32	297.83
A_68_P22164435	chr3:57379593-57379637	NM_133784:184	Wwtr1	INSIDE	0.505	0.490	1214.79	595.55	0.248	1018.93	252.32
A_68_P29102452	chr13:65343492-65343545			Unknown	0.505	5.486	5160.80	28310.35	2.769	3648.61	10102.47
A_68_P26397643	chr9:30729700-30729744	NM_001024139:315	Adamts15	INSIDE	0.504	0.569	1883.97	1072.40	0.287	1442.49	414.02
A_68_P31253494	chr17:56179975-56180019	NM_013733:158	Chaf1a	INSIDE	0.504	0.505	1012.57	511.72	0.255	732.23	186.66
A_68_P24372701	chr6:37391699-37391743	NM_178661:428	Creb3l2	INSIDE	0.504	0.562	1416.80	796.68	0.283	1123.79	318.38
A_68_P25505455	chr7:134536637-134536681	NM_198011:477	E430018J23Rik	INSIDE	0.504	0.521	993.18	517.43	0.263	860.95	226.19
A_68_P22308548	chr3:87329844-87329888	NM_001083318:367	Etv3	INSIDE	0.504	0.497	1438.35	715.39	0.251	1087.17	272.68
A_68_P26134825	chr8:108129199-108129243	NM_001081241:92	Fam65a	INSIDE	0.504	0.463	4343.91	2010.93	0.233	3434.23	801.16
A_68_P23591965	chr5:34325967-34326011	NM_001033458:-134	Gm1673	PROMOTER	0.504	0.467	1675.98	783.04	0.235	1339.29	315.28
A_68_P20875108	chr1:182261016-182261060	NR_003623:-358	Gm5069	PROMOTER	0.504	0.427	2698.69	1151.73	0.215	2106.15	453.33
A_68_P20875111	chr1:182261385-182261429	NR_003623:-726	Gm5069	PROMOTER	0.504	0.628	1635.64	1027.29	0.317	1228.47	389.23
A_68_P27279732	chr10:79383697-79383741	NM_053244:4003	Kiss1r	INSIDE	0.504	0.690	2161.99	1492.60	0.348	1683.69	586.03
A_68_P29689081	chr14:68702832-68702876	NM_010910:914	Nefl	INSIDE	0.504	0.601	1916.37	1151.87	0.303	1448.18	438.39
A_68_P31167786	chr17:37334030-37334074	NM_001011518:859	Olfr94	INSIDE	0.504	0.627	1326.07	831.18	0.316	1130.14	356.97
A_68_P23433034	chr4:154009287-154009331	NM_001177995:1674	Prdm16	INSIDE	0.504	0.539	2032.43	1095.75	0.271	1647.95	447.39
A_68_P31108918	chr17:26340491-26340535	NM_001081069:606	Rgs11	INSIDE	0.504	0.612	1512.53	925.60	0.309	1224.05	377.86
A_68_P21580974	chr2:121275109-121275153	NM_011354:167	Serf2	INSIDE	0.504	0.508	1930.91	981.26	0.256	1715.70	439.52
A_68_P22169679	chr3:58496414-58496458	NM_009174:-126	Siah2	PROMOTER	0.504	0.590	905.23	534.20	0.297	801.03	238.01
A_68_P21623514	chr2:129024077-129024121	NM_001159593:-410	Slc20a1	PROMOTER	0.504	0.576	2595.13	1495.79	0.291	1903.21	553.12
A_68_P27673276	chr11:29072349-29072395	NM_134034:-534	Smek2	PROMOTER	0.504	0.498	1991.74	991.42	0.251	1411.18	353.74
A_68_P28520017	chr12:71447587-71447631	NM_001110202:993	Trim9	INSIDE	0.504	0.429	1306.83	560.48	0.216	1053.01	227.62
A_68_P24054162	chr5:123593214-123593258	ENSMUST00000056053:271		INSIDE	0.504	0.726	1843.26	1337.78	0.366	1568.19	573.43
A_68_P33012178	chr9_random:57139-57183	NR_027950:2468	4930526I15Rik	DOWNSTREAM	0.503	0.409	1912.33	781.62	0.206	1501.20	308.77
A_68_P31096791	chr17:24489119-24489163	NM_001039581:150	Abca3	INSIDE	0.503	0.575	1359.48	781.13	0.289	1045.09	302.20
A_68_P21111659	chr2:31701359-31701403	NM_178887:145	Fibcd1	INSIDE	0.503	0.479	1794.74	859.85	0.241	1531.96	369.25
A_68_P30479788	chr15:99200288-99200332	NM_011711:587	Fmnl3	INSIDE	0.503	0.512	1140.24	583.70	0.258	798.12	205.64
A_68_P24904452	chr6:142363210-142363254	NM_145572:58397	Gys2	DOWNSTREAM	0.503	0.413	1462.01	604.36	0.208	1226.68	255.18
A_68_P23970077	chr5:108494745-108494789	NM_013827:6	Mtf2	INSIDE	0.503	0.472	1575.18	743.09	0.237	1182.80	280.55

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25522280	chr7:137690501-137690545	NM_001162855:373	Nsmce4a	INSIDE	0.503	0.564	2401.25	1353.98	0.284	1791.02	508.46
A_68_P21818227	chr2:164323199-164323243	NM_133779:196	Pigt	INSIDE	0.503	0.627	1939.02	1216.47	0.315	1421.70	448.25
A_68_P20782631	chr1:165242518-165242562	NM_011127:1241	Prrx1	INSIDE	0.503	0.648	2463.38	1597.12	0.326	1983.37	647.09
A_68_P27630331	chr11:20101120-20101164	NM_008996:-462	Rab1	PROMOTER	0.503	0.633	1313.60	830.93	0.318	915.64	291.46
A_68_P26803653	chr9:106379642-106379686	NM_145620:25	Rrp9	INSIDE	0.503	0.511	1815.86	927.42	0.257	1356.06	348.63
A_68_P28137823	chr11:112643047-112643091	NM_011448:-455	Sox9	PROMOTER	0.503	0.674	943.84	635.97	0.339	792.57	268.85
A_68_P21935172	chr3:9004150-9004194	NM_001025263:343	Tpd52	INSIDE	0.503	0.587	3003.09	1762.66	0.295	2286.45	674.61
A_68_P30388854	chr15:83341412-83341456	NM_178869:-97	Ttll1	PROMOTER	0.503	0.526	2594.20	1364.28	0.264	1902.91	502.95
A_68_P23865423	chr5:87233404-87233448	NM_177680:-88	Ythdc1	PROMOTER	0.503	0.719	1949.41	1400.99	0.362	1550.02	560.57
A_68_P21121521	chr2:33286475-33286519	NM_001085507:348	Zbtb34	INSIDE	0.503	0.511	1156.35	591.23	0.257	874.47	224.73
A_68_P31758245	chr18:61696023-61696067	NM_177828:146	Arhgef37	INSIDE	0.502	0.570	3424.01	1951.50	0.286	2888.38	826.87
A_68_P29737459	chr14:77436746-77436790	NM_175369:190	Ccdc122	INSIDE	0.502	0.696	1125.01	783.27	0.350	1001.93	350.47
A_68_P31620296	chr18:35989257-35989301	NM_133687:-193	Cxxc5	PROMOTER	0.502	0.421	1309.01	550.85	0.211	1045.22	221.00
A_68_P21761231	chr2:154395665-154395709	NM_007891:-98	E2f1	PROMOTER	0.502	0.342	2061.10	704.35	0.172	1604.47	275.25
A_68_P21727918	chr2:147872154-147872201	NM_010446:528	Foxa2	INSIDE	0.502	0.593	1016.49	602.73	0.298	746.00	222.03
A_68_P23573357	chr5:30891361-30891405	NM_010608:840	Kcnk3	INSIDE	0.502	0.581	1413.66	821.28	0.292	1082.69	315.65
A_68_P27901340	chr11:70376701-70376745	NM_001045959:340	Mink1	INSIDE	0.502	0.542	3265.26	1769.89	0.272	2467.73	671.72
A_68_P23905255	chr5:96638963-96639007	NM_001039084:-149	Mrpl1	PROMOTER	0.502	0.715	1586.70	1133.80	0.359	1245.38	446.86
A_68_P21495913	chr2:105509959-105510003	NR_002867:507	Pax6os1	INSIDE	0.502	0.575	1299.46	747.59	0.289	1042.77	301.29
A_68_P23354494	chr4:139389036-139389081	NM_011039:-175	Pax7	PROMOTER	0.502	0.643	1596.62	1027.05	0.323	1247.57	402.67
A_68_P30979318	chr16:94085768-94085812	NM_011377:286	Sim2	INSIDE	0.502	0.551	1614.65	889.06	0.276	1302.63	360.09
A_68_P23541735	chr5:23931232-23931276	NM_009207:205	Slc4a2	INSIDE	0.502	0.591	1220.94	721.48	0.297	1048.39	311.24
A_68_P24090829	chr5:130293530-130293574	NR_003681:-6884	Snora15	PROMOTER	0.502	0.646	1032.41	666.54	0.324	844.36	273.80
A_68_P20352744	chr1:75216331-75216375	NM_009447:-524	Tuba4a	PROMOTER	0.502	0.657	1219.81	801.55	0.330	938.84	309.65
A_68_P26356133	chr9:23028290-23028334	NM_028472:793	Bmper	INSIDE	0.501	0.718	4984.49	3577.87	0.360	3648.44	1311.63
A_68_P26821951	chr9:110003563-110003607	NM_133347:14502	Dhx30	INSIDE	0.501	0.497	1054.41	524.01	0.249	862.41	214.92
A_68_P21565607	chr2:118528199-118528243	NM_001081971:1479	Gm1337	INSIDE	0.501	0.573	2083.12	1193.66	0.287	1618.38	464.29
A_68_P20285212	chr1:63160117-63160161	NM_001081436:703	Ino80d	INSIDE	0.501	0.624	979.00	610.57	0.312	833.36	260.19
A_68_P25512275	chr7:135883649-135883693	NM_145955:273	Mcmbp	INSIDE	0.501	0.600	1175.55	705.52	0.300	1019.38	306.24
A_68_P20620659	chr1:134213013-134213057	NM_001195025:333	Nuak2	INSIDE	0.501	0.617	1276.45	786.99	0.309	1170.21	361.54
A_68_P26245546	chr8:126957920-126957964	NM_171824:-106	Pgbd5	PROMOTER	0.501	0.410	1437.98	590.23	0.206	1129.08	232.08
A_68_P29568494	chr14:45608721-45608765	NM_008964:957	Ptger2	INSIDE	0.501	0.520	2224.91	1156.07	0.260	1586.01	412.60
A_68_P25351155	chr7:104728838-104728882	NM_001081267:455	Rsf1	INSIDE	0.501	0.578	2138.36	1236.69	0.290	1872.34	542.59
A_68_P20596471	chr1:129574483-129574527	NM_028135:94	Tmem163	INSIDE	0.501	0.699	1868.43	1306.48	0.350	1589.87	557.18
A_68_P31675570	chr18:46358067-46358111	NM_001170855:384	Trim36	INSIDE	0.501	0.620	1180.61	732.54	0.311	987.23	306.77
A_68_P26486122	chr9:47338579-47338623	NM_001025600:166	Cadm1	INSIDE	0.500	0.506	1109.75	561.40	0.253	835.76	211.30
A_68_P23415140	chr4:151236795-151236839	NM_001081557:-939	Camta1	PROMOTER	0.500	0.631	1044.21	659.27	0.316	825.57	260.62
A_68_P30362466	chr15:78632748-78632792	NM_130859:702	Card10	INSIDE	0.500	0.581	1544.53	897.58	0.290	1268.59	368.48
A_68_P20601161	chr1:130487885-130487929	NM_009911:970	Cxcr4	INSIDE	0.500	0.419	2586.95	1084.96	0.210	1983.28	415.54
A_68_P24793349	chr6:119430121-119430165	NM_133940:457	Fbxl14	INSIDE	0.500	0.443	1249.63	553.10	0.221	952.77	211.01
A_68_P29717289	chr14:73784847-73784891	NM_008410:210	Itm2b	INSIDE	0.500	0.645	1090.62	703.48	0.323	962.78	310.73
A_68_P21571250	chr2:119568776-119568820	NM_146125:726	Itpka	INSIDE	0.500	0.466	1121.11	522.59	0.233	939.45	218.97
A_68_P21666831	chr2:136940212-136940256	NM_013822:2022	Jag1	INSIDE	0.500	0.531	1250.72	663.64	0.265	875.80	232.27
A_68_P27285906	chr10:80317819-80317863	NM_025349:114	Lsm7	INSIDE	0.500	0.562	964.30	541.89	0.281	725.20	203.91
A_68_P29142608	chr13:73984841-73984885	NM_028186:217	Nkd2	INSIDE	0.500	0.591	1343.61	794.71	0.296	1034.83	306.07
A_68_P22522614	chr3:129581824-129581868	NM_183423:-2255	Pla2g12a	PROMOTER	0.500	1.369	3800.75	5201.39	0.684	2739.15	1873.33
A_68_P30475880	chr15:98507518-98507562	NM_172612:352	Rnd1	INSIDE	0.500	0.509	2553.07	1299.78	0.255	2075.69	528.77
A_68_P29050859	chr13:54795572-54795616	NR_027395:-273	Rnf44	DIVERGENT_PROMOTER	0.500	0.552	2845.53	1571.61	0.276	2362.35	652.97
A_68_P27259390	chr10:75384205-75384249	NM_001161853:133	Smarcb1	INSIDE	0.500	0.330	1647.38	542.89	0.165	1498.10	246.72
A_68_P27851931	chr11:61890435-61890479	NM_001029936:-142	Specc1	PROMOTER	0.500	3.261	4090.40	13339.98	1.631	2596.31	4235.81
A_68_P20937460	chr1:193149822-193149866	NM_025864:1	Tmem206	INSIDE	0.500	0.606	936.75	567.97	0.303	746.32	226.24

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31771008	chr18:63851869-63851913	NM_016792:123	Txnl1	INSIDE	0.500	0.624	967.36	604.02	0.312	795.19	248.03
A_68_P28729922	chr12:110031214-110031258	NM_009537:-284	Yy1	PROMOTER	0.500	0.706	3619.11	2555.48	0.353	2766.67	976.39
A_68_P25241764	chr7:82926889-82926933	AK049415:-9978		PROMOTER	0.500	0.667	4412.53	2944.48	0.334	3362.99	1121.56
A_68_P20935795	chr1:192849358-192849402	NR_027298:151	A230020J21Rik	INSIDE	0.499	0.543	1577.88	856.18	0.271	1289.41	348.96
A_68_P28567750	chr12:80231609-80231653	NM_009705:-144	Arg2	PROMOTER	0.499	0.548	1062.12	582.11	0.273	855.37	233.72
A_68_P27677359	chr11:29924618-29924662	NM_146016:1393	Eml6	INSIDE	0.499	0.668	1041.80	695.63	0.333	875.65	291.61
A_68_P24674232	chr6:97567208-97567252	NM_145148:421	Frmd4b	INSIDE	0.499	0.668	1871.75	1250.40	0.333	1258.95	419.73
A_68_P26319145	chr9:14556214-14556258	NM_010242:330	Fut4	INSIDE	0.499	0.513	1155.82	592.86	0.256	969.65	248.00
A_68_P25021899	chr7:29221970-29222015	NM_022024:-473	Gmfg	DIVERGENT_PROMOTER	0.499	0.618	1029.93	636.38	0.308	901.62	277.76
A_68_P28077066	chr11:101887900-101887944	NM_007863:347	Mpp3	INSIDE	0.499	0.653	1395.17	911.44	0.326	1050.26	342.28
A_68_P29237525	chr13:95645453-95645497	NM_011021:-107	Otp	PROMOTER	0.499	0.567	1406.86	797.81	0.283	1267.55	358.50
A_68_P26016104	chr8:86223190-86223234	NM_177262:-134	Pkn1	PROMOTER	0.499	0.574	1098.93	630.83	0.286	899.64	257.49
A_68_P24061289	chr5:124890348-124890392	NM_030241:432	Setd8	INSIDE	0.499	0.534	4435.36	2367.73	0.266	3424.01	912.46
A_68_P29116719	chr13:69750004-69750048	NM_175283:315	Srd5a1	INSIDE	0.499	0.542	2348.08	1273.45	0.270	1991.53	538.44
A_68_P27560196	chr11:4795414-4795458	NM_172438:91	Thoc5	INSIDE	0.499	0.703	1912.31	1344.39	0.351	1524.05	534.85
A_68_P29438120	chr14:19159804-19159848	NM_009455:4532	Ube2e1	INSIDE	0.499	1.438	13529.53	19455.29	0.718	9696.69	6961.56
A_68_P28567992	chr12:80273136-80273180	NM_016800:287	Vti1b	INSIDE	0.499	0.647	2254.18	1459.04	0.323	1866.96	602.41
A_68_P27926186	chr11:75268311-75268355	NM_138950:-113	Wdr81	DIVERGENT_PROMOTER	0.499	0.685	1489.05	1019.78	0.341	1045.26	356.93
A_68_P27083332	chr10:40022071-40022115	NM_009665:-98	Amd1	PROMOTER	0.498	0.615	1393.29	856.67	0.306	1096.09	335.78
A_68_P26426474	chr9:36533941-36533985	NM_007691:281	Chek1	INSIDE	0.498	0.617	2866.35	1769.95	0.308	2181.68	671.28
A_68_P24600279	chr6:84535601-84535645	NM_175475:8182	Cyp26b1	INSIDE	0.498	0.661	845.60	559.03	0.329	781.39	257.13
A_68_P26224705	chr8:123653054-123653101	NM_008024:1493	Foxl1	INSIDE	0.498	0.652	1045.68	681.81	0.325	798.27	259.20
A_68_P23964040	chr5:107354969-107355013	NM_177873:-81	Hfm1	PROMOTER	0.498	0.639	2141.64	1367.76	0.318	1834.41	583.29
A_68_P32095557	chr19:37509810-37509854	NM_008245:502	Hhex	INSIDE	0.498	0.365	2104.86	768.63	0.182	1796.54	326.42
A_68_P32051826	chr19:29325786-29325831	NM_001048177:-509	Jak2	PROMOTER	0.498	0.408	2178.12	887.94	0.203	1962.57	398.06
A_68_P28161570	chr11:116704403-116704447	NM_033398:339	Jmjd6	INSIDE	0.498	0.734	2270.11	1665.81	0.366	1630.54	596.14
A_68_P26022975	chr8:87504092-87504136	NM_008416:-1467	Junb	PROMOTER	0.498	0.681	1146.44	780.67	0.339	1015.43	344.21
A_68_P24990613	chr7:19542978-19543022	NM_001029877:31764	Nova2	INSIDE	0.498	0.658	1894.30	1246.22	0.328	1379.28	452.06
A_68_P26766650	chr9:99775559-99775603	NM_011440:1009	Sox14	INSIDE	0.498	0.698	1933.57	1350.29	0.348	1542.75	536.85
A_68_P28740640	chr12:112082039-112082083	NM_011973:-2911	Stk30	DIVERGENT_PROMOTER	0.498	0.699	1298.54	908.06	0.348	1025.62	356.89
A_68_P21962519	chr3:16083394-16083438	NM_001145919:234	Ythdf3	INSIDE	0.498	0.479	1491.03	713.64	0.238	1208.42	287.88
A_68_P31260731	A_68_P31260731			Unknown	0.498	0.513	1531.13	785.43	0.256	1222.57	312.56
A_68_P25890690	chr8:59819837-59819881	ENSMUST00000132988:8944		DOWNSTREAM	0.498	0.632	1163.87	735.94	0.315	1070.31	337.23
A_68_P21044872	chr2:19352911-19352955	ENSMUST00000137714:678		INSIDE	0.498	0.581	1296.24	752.53	0.289	1028.10	297.09
A_68_P26235838	chr8:125299671-125299715	NM_144932:288	Acsf3	INSIDE	0.497	0.634	879.09	557.22	0.315	751.30	236.47
A_68_P31862682	chr18:80347987-80348031	NM_175028:213	Adnp2	INSIDE	0.497	0.641	6326.56	4058.41	0.319	4988.63	1590.41
A_68_P29270037	chr13:101545636-101545680	NM_021886:196	Cenph	INSIDE	0.497	0.482	1991.03	959.10	0.239	1613.78	386.23
A_68_P23247367	chr4:119487484-119487528	NM_010657:224	Hivep3	INSIDE	0.497	0.581	1776.78	1032.20	0.289	1394.74	403.02
A_68_P26682081	chr9:83040074-83040118	NM_026122:118	Hmgn3	INSIDE	0.497	0.640	1373.14	879.38	0.318	1083.76	344.67
A_68_P20735832	chr1:156945633-156945677	NM_010500:1112	Ier5	INSIDE	0.497	0.656	1503.64	986.31	0.326	1275.79	415.95
A_68_P25737017	chr8:28284572-28284616	NM_001080813:524	Rab11fip1	INSIDE	0.497	0.587	4001.98	2348.08	0.291	3137.30	914.17
A_68_P24536421	chr6:71389996-71390040	NM_024288:613	Rmnd5a	INSIDE	0.497	0.495	2162.93	1071.61	0.246	1714.27	422.27
A_68_P30596855	chr16:22266102-22266148	NM_009186:-122	Tra2b	PROMOTER	0.497	0.469	1763.69	826.70	0.233	1298.29	302.60
A_68_P26816565	chr9:108686233-108686277	ENSMUST00000035219:128		INSIDE	0.497	0.542	1993.23	1079.69	0.269	1531.95	412.37
A_68_P32070030	chr19:32464044-32464088	NR_033198:361	2700046G09Rik	INSIDE	0.496	0.679	1243.17	844.35	0.337	1071.11	361.03
A_68_P28612732	chr12:88224969-88225013	NM_145836:774	6430527G18Rik	INSIDE	0.496	0.516	1454.63	750.69	0.256	1240.20	317.14
A_68_P31464038	chr18:4635009-4635053	NM_001081963:104	9430020K01Rik	INSIDE	0.496	0.512	3171.82	1624.49	0.254	2380.57	605.03
A_68_P29387299	chr14:8835518-8835562	NM_025341:125	Abhd6	INSIDE	0.496	0.496	1829.45	908.22	0.246	1383.90	341.01
A_68_P31541315	chr18:20904732-20904776	NM_019737:151	B4galt6	INSIDE	0.496	0.483	3673.30	1774.40	0.239	2711.68	649.15
A_68_P22874559	chr4:43970296-43970340	NM_027450:-255	Glipr2	PROMOTER	0.496	0.559	1771.03	989.51	0.277	1386.07	383.78
A_68_P23441153	chr4:155243478-155243522	NM_024472:49	Gltpd1	INSIDE	0.496	0.652	897.42	585.11	0.323	694.65	224.60

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P29026628	chr13:49777406-49777450	NM_172015:-70	Iars	PROMOTER	0.496	0.548	1193.14	653.29	0.272	896.64	243.65
A_68_P27271936	chr10:77532518-77532562	NM_015790:428	Icosl	INSIDE	0.496	0.466	1122.48	522.87	0.231	925.33	213.67
A_68_P21816596	chr2:163993800-163993844	NM_008435:3027	Kcns1	INSIDE	0.496	0.552	1509.46	833.12	0.274	1233.01	337.56
A_68_P27994973	chr11:87405603-87405647	NM_133215:-94	Mtmr4	PROMOTER	0.496	1.489	5235.41	7798.09	0.739	3633.11	2683.93
A_68_P20590467	chr1:128389351-128389395	NM_172484:132	Nckap5	INSIDE	0.496	0.592	1414.93	837.30	0.293	1179.18	346.01
A_68_P32760557	chrX:152059508-152059553	NM_001093750:-1660	Ptchd1	PROMOTER	0.496	0.613	1047.90	641.91	0.304	410.56	124.87
A_68_P30485731	chr15:100253716-100253768	NM_008732:-256	Slc11a2	PROMOTER	0.496	0.653	1447.85	944.76	0.324	1067.65	345.79
A_68_P31058944	chr17:14416346-14416390	NM_022315:-144	Smoc2	PROMOTER	0.496	0.549	1622.83	891.43	0.272	1123.03	305.84
A_68_P29107216	chr13:67161978-67162022	NM_001166218:106	Zfp712	INSIDE	0.496	0.614	1579.81	969.42	0.304	1241.60	378.03
A_68_P29961926	chr14:122873265-122873309	NM_009574:-1319	Zic2	DIVERGENT_PROMOTER	0.496	0.613	2803.90	1718.23	0.304	2119.16	644.41
A_68_P21127430	chr2:34262482-34262526	ENSMUST00000147337:-198		PROMOTER	0.496	0.536	2465.42	1321.60	0.266	2199.96	585.52
A_68_P21127432	chr2:34262730-34262774	ENSMUST00000147337:50		INSIDE	0.496	0.618	1482.75	916.35	0.306	1120.34	343.31
A_68_P30394508	chr15:84237151-84237195	NM_001163145:40355	1810041L15Rik	INSIDE	0.495	3.611	5381.34	19431.95	1.786	3483.19	6219.70
A_68_P21421625	chr2:91105340-91105384	NM_001166024:91	Arfgap2	INSIDE	0.495	0.604	1291.45	779.89	0.299	948.79	283.61
A_68_P33008888	chr12:21117412-21117456	NM_001004364:-182	Asap2	PROMOTER	0.495	0.624	2182.03	1360.53	0.309	1852.20	572.08
A_68_P25458767	chr7:125676796-125676840	NM_009940:9	Coq7	INSIDE	0.495	0.687	1716.01	1179.57	0.340	1340.19	455.98
A_68_P27696175	chr11:33580643-33580689	NM_001190885:162919	Kcnip1	INSIDE	0.495	0.672	1483.55	996.39	0.333	1260.53	419.36
A_68_P30018903	chr15:11836061-11836105	NM_001039181:-653	Npr3	PROMOTER	0.495	0.722	1765.01	1275.08	0.357	1463.43	523.00
A_68_P25050419	chr7:36432218-36432262	NM_019746:261	Pdcd5	INSIDE	0.495	0.524	1773.00	928.48	0.259	1469.40	381.18
A_68_P29388217	chr14:9005728-9005772	NM_024221:-244	Pdhb	PROMOTER	0.495	0.695	1410.05	979.64	0.344	1176.69	404.65
A_68_P23610088	chr5:37260189-37260233	NM_172994:402	Ppp2r2c	INSIDE	0.495	0.675	1768.04	1193.35	0.334	1317.65	440.50
A_68_P22319356	chr3:89234182-89234226	NM_026869:-554	Pygo2	PROMOTER	0.495	0.461	1171.65	540.19	0.228	971.62	221.59
A_68_P25953808	chr8:73279185-73279229	NM_001166399:629	Rab3a	INSIDE	0.495	0.628	1646.81	1034.74	0.311	1179.88	367.20
A_68_P32036081	chr19:26680484-26680528	NM_011416:857	Smarca2	INSIDE	0.495	0.463	1318.06	610.05	0.229	1232.79	282.36
A_68_P30374040	chr15:80542264-80542308	NM_144812:544	Tnrc6b	INSIDE	0.495	0.647	2328.40	1505.81	0.320	1688.43	540.25
A_68_P32260636	chrX:11712923-11712967	NM_001168321:24537	Bcor	INSIDE	0.494	0.527	1614.31	851.15	0.261	660.37	172.06
A_68_P25948527	chr8:72412099-72412143	NM_026818:-829	Cilp2	PROMOTER	0.494	0.726	1619.68	1176.51	0.359	1040.00	372.95
A_68_P32121150	chr19:42506930-42506974	NM_145123:-679	Crtac1	PROMOTER	0.494	0.601	1071.34	643.49	0.297	792.14	235.11
A_68_P24047549	chr5:122398855-122398899	NM_007804:98958	Cux2	INSIDE	0.494	0.424	1593.28	674.77	0.209	1301.92	272.49
A_68_P32030085	chr19:25580326-25580370	NM_015826:153	Dmrt1	INSIDE	0.494	0.668	1249.14	833.98	0.330	999.07	329.54
A_68_P29515525	chr14:32898520-32898564	NM_001047433:309	Dph3	INSIDE	0.494	0.402	2249.71	905.32	0.199	1744.50	347.04
A_68_P22149458	chr3:54539187-54539231	NM_001163570:78	Exosc8	INSIDE	0.494	0.560	2287.99	1281.08	0.276	1736.72	479.98
A_68_P30487413	chr15:100559897-100559941	NM_001161767:-111	Galnt6	PROMOTER	0.494	0.518	2203.93	1142.41	0.256	1760.26	450.33
A_68_P27973306	chr11:83567372-83567416	NM_145432:256	Heatr6	INSIDE	0.494	0.358	1511.56	541.48	0.177	1255.91	222.24
A_68_P31938325	chr19:7240713-7240757	NM_134147:109477	Macrod1	INSIDE	0.494	0.601	1881.54	1131.71	0.297	1393.49	413.83
A_68_P27926234	chr11:75275864-75275908	NR_029739:-1331	Mir22	PROMOTER	0.494	0.502	1393.46	699.44	0.248	1145.59	284.29
A_68_P21600380	chr2:124949503-124949547	NM_001162417:-128	Myef2	PROMOTER	0.494	0.465	1835.58	853.12	0.229	1450.53	332.74
A_68_P31923511	chr19:4510848-4510892	NM_001162946:399	Pcx	INSIDE	0.494	0.652	1093.31	712.58	0.322	931.84	299.86
A_68_P20163206	chr1:39044427-39044471	NM_026850:-210	Pdcl3	PROMOTER	0.494	0.423	3066.50	1298.39	0.209	2276.08	476.23
A_68_P25093636	chr7:52781291-52781335	NM_008654:326	Ppp1r15a	INSIDE	0.494	0.592	1683.46	996.36	0.292	1416.98	414.25
A_68_P28118795	chr11:109335066-109335110	NM_001029842:-178	Slc16a6	PROMOTER	0.494	0.603	1130.37	681.16	0.298	940.74	280.31
A_68_P21765289	chr2:155212485-155212529	NM_178111:4915	Trp53inp2	INSIDE	0.494	1.369	3149.57	4313.11	0.677	2137.30	1446.26
A_68_P21622285	chr2:128793081-128793125	NM_178404:-35	Zc3h6	PROMOTER	0.494	0.506	1903.96	964.00	0.250	1312.20	328.14
A_68_P24130914	chr5:139060935-139060979	NM_001044747:15	Zfp68	INSIDE	0.494	0.723	1924.95	1391.16	0.357	1499.59	535.79
A_68_P27255927	chr10:74779785-74779829	NM_009630:119	Adora2a	INSIDE	0.493	0.672	1237.39	831.22	0.331	943.47	312.53
A_68_P22520456	chr3:129237236-129237280	NM_130450:1955	Elovl6	INSIDE	0.493	0.615	1443.86	888.58	0.303	1109.90	336.77
A_68_P21115862	chr2:32390731-32390776	NM_153560:-125	Fam102a	PROMOTER	0.493	0.363	1535.39	557.81	0.179	1201.38	215.36
A_68_P26421597	chr9:35075221-35075265	NM_194257:110	Fam118b	INSIDE	0.493	0.560	1163.26	651.81	0.276	933.09	257.77
A_68_P24133859	chr5:139625867-139625911	NM_001081265:-288	Heatr2	PROMOTER	0.493	3.006	10901.91	32770.22	1.481	6902.72	10221.18
A_68_P26228503	chr8:124254738-124254782	NM_020605:302	Jph3	INSIDE	0.493	0.662	4592.01	3037.78	0.326	3475.80	1132.46
A_68_P25098820	chr7:53652793-53652837	NM_001112739:948	Kcnc1	INSIDE	0.493	0.725	2334.88	1692.51	0.357	1771.71	633.10

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P23192856	chr4:107476288-107476332	NM_001080926:1447	Lrp8	INSIDE	0.493	0.692	1614.87	1117.23	0.341	1128.58	385.27
A_68_P22056222	chr3:35899243-35899287	NM_023644:336	Mccc1	INSIDE	0.493	0.460	1174.19	539.96	0.227	919.31	208.37
A_68_P21495956	chr2:105515369-105515413	NM_013627:-1211	Pax6	DIVERGENT_PROMOTER	0.493	0.451	1145.93	516.28	0.222	925.68	205.79
A_68_P22345831	chr3:95622735-95622779	NM_001081293:120	Rprd2	INSIDE	0.493	0.687	2580.20	1771.66	0.339	1837.65	622.59
A_68_P22030179	chr3:30692442-30692486	NM_027016:667	Sec62	INSIDE	0.493	0.596	2371.11	1413.16	0.294	1916.45	563.10
A_68_P29023537	chr13:49242028-49242072	NM_029361:1333	Wnk2	INSIDE	0.493	0.553	1026.73	567.95	0.273	760.28	207.34
A_68_P30686477	chr16:38522888-38522932	NM_024273:-163	4930455C21Rik	PROMOTER	0.492	0.730	1769.00	1292.00	0.359	1288.50	462.83
A_68_P20331601	chr1:71603829-71603873	NM_026195:121	Atic	INSIDE	0.492	0.572	1087.42	622.15	0.282	942.67	265.52
A_68_P25275162	chr7:89137615-89137659	NM_007562:-451	Bnc1	PROMOTER	0.492	0.655	901.73	590.46	0.322	598.73	192.80
A_68_P29134764	chr13:72761714-72761758	NR_030701:4276	D430050G20	INSIDE	0.492	0.716	1701.25	1217.58	0.352	1327.54	467.01
A_68_P31677411	chr18:46685323-46685367	NM_173423:281	Fem1c	INSIDE	0.492	0.694	3789.43	2629.76	0.341	2702.09	922.10
A_68_P23796638	chr5:73648010-73648054	NM_028194:-175	Fryl	PROMOTER	0.492	0.432	1338.67	578.04	0.212	1027.83	218.19
A_68_P24519506	chr6:66986584-66986628	NM_007836:795	Gadd45a	INSIDE	0.492	0.572	3227.80	1846.34	0.282	2687.87	756.64
A_68_P23927130	chr5:100406931-100406976	NM_001077265:1004	Hnrnpd	INSIDE	0.492	0.521	1374.29	715.84	0.256	1040.83	266.89
A_68_P28041918	chr11:95867212-95867256	NM_009951:24	Igf2bp1	INSIDE	0.492	0.525	1538.94	807.91	0.258	1191.60	307.57
A_68_P29612545	chr14:55082897-55082941	NM_022993:-65	Lrp10	PROMOTER	0.492	0.465	1962.67	912.81	0.229	1527.36	349.52
A_68_P22303239	chr3:86351242-86351286	NM_011839:941	Mab21l2	INSIDE	0.492	0.598	1614.71	964.91	0.294	1195.95	351.85
A_68_P29237593	chr13:95652973-95653017	NM_011021:7413	Otp	INSIDE	0.492	0.526	1211.10	636.50	0.259	1074.15	277.83
A_68_P29057276	chr13:55930039-55930083	NM_011097:2726	Pitx1	INSIDE	0.492	0.714	2090.57	1493.64	0.352	1604.25	564.22
A_68_P30476735	chr15:98661367-98661411	NM_016781:551	Prkag1	INSIDE	0.492	0.550	1437.00	789.77	0.270	1160.60	313.62
A_68_P31108119	chr17:26204737-26204781	NM_001162868:1364	Rab11fip3	INSIDE	0.492	0.685	1720.41	1179.28	0.337	1446.61	487.65
A_68_P26805685	chr9:106788200-106788244	NM_175402:1109	Rbm15b	INSIDE	0.492	0.598	1088.56	651.41	0.294	830.57	244.54
A_68_P31924875	chr19:4756268-4756312	NM_025717:-234	Rbm4b	PROMOTER	0.492	0.689	1893.55	1304.09	0.339	1588.78	538.28
A_68_P22336825	chr3:93324681-93324725	NM_016740:285	S100a11	INSIDE	0.492	0.475	1116.92	529.99	0.234	890.27	208.04
A_68_P30489277	chr15:100877902-100877949	NM_011323:111224	Scn8a	DOWNSTREAM	0.492	0.572	1566.30	896.17	0.281	1222.01	343.79
A_68_P26983369	chr10:19569958-19570002	NM_029529:1285	Slc35d3	INSIDE	0.492	0.503	1367.23	688.20	0.248	1009.08	249.76
A_68_P21092715	chr2:28555096-28555140	NM_027283:53	1700026L06Rik	INSIDE	0.491	0.650	1138.32	739.99	0.319	940.14	300.02
A_68_P21566798	chr2:118728254-118728298	NM_001045523:926	Bahd1	INSIDE	0.491	0.615	1793.63	1103.81	0.302	1414.19	427.61
A_68_P30588523	chr16:20619843-20619887	NM_028420:1487	Camk2n2	INSIDE	0.491	1.360	5028.18	6836.13	0.667	3604.50	2405.53
A_68_P21075528	chr2:25838113-25838157	NM_001115076:668	Camsap1	INSIDE	0.491	0.707	3109.82	2199.19	0.347	2264.66	786.34
A_68_P21107277	chr2:31008194-31008238	NM_178760:381	Gpr107	INSIDE	0.491	0.521	1101.55	573.61	0.256	929.38	237.79
A_68_P27258887	chr10:75299960-75300008	NM_010361:-2358	Gstt2	PROMOTER	0.491	0.664	1469.45	975.94	0.326	1161.91	379.01
A_68_P22348231	chr3:96025351-96025395	NM_178214:329	Hist2h2be	INSIDE	0.491	0.348	2059.56	717.03	0.171	1615.94	276.38
A_68_P23637425	chr5:42155503-42155547	NM_007524:-65	Nkx3-2	PROMOTER	0.491	0.530	2223.40	1178.35	0.260	1664.94	432.94
A_68_P26816178	chr9:108595255-108595302	NM_008924:805	Prkar2a	INSIDE	0.491	0.645	804.21	518.88	0.317	700.23	222.05
A_68_P21707834	chr2:144381520-144381564	NM_019787:-470	Sec23b	DIVERGENT_PROMOTER	0.491	0.524	1561.14	817.77	0.257	1207.69	310.56
A_68_P24950723	chr7:4781645-4781689	NM_172737:14632	Shisa7	INSIDE	0.491	2.830	3360.14	9507.66	1.390	2245.47	3120.90
A_68_P21330529	chr2:73112421-73112465	NM_001005343:2460	Sp9	INSIDE	0.491	0.660	3662.17	2418.17	0.324	2776.38	899.26
A_68_P31932352	chr19:6047496-6047540	NM_001164709:374	Syvn1	INSIDE	0.491	0.502	1959.48	983.17	0.246	1510.55	372.35
A_68_P22323355	chr3:89883388-89883433	NM_022314:6795	Tpm3	INSIDE	0.491	0.404	1330.90	537.16	0.198	1163.31	230.75
A_68_P29143150	chr13:74074924-74074968	NM_027182:269	Trip13	INSIDE	0.491	0.462	3704.86	1709.81	0.227	2739.37	620.89
A_68_P30356630	chr15:77759323-77759367	NM_019913:80	Txn2	INSIDE	0.491	0.516	1660.39	857.00	0.253	1292.87	327.33
A_68_P20509920	chr1:108609243-108609287	NM_009741:1603	Bcl2	INSIDE	0.490	0.662	1171.34	775.04	0.324	952.90	308.93
A_68_P21611440	chr2:126896255-126896304	NM_026678:-113	Blvra	PROMOTER	0.490	0.663	2615.34	1733.34	0.325	2058.76	669.03
A_68_P31373928	chr17:79234991-79235035	NM_181649:157	Ccdc75	INSIDE	0.490	0.608	1355.91	823.81	0.297	1059.03	314.99
A_68_P31022580	chr17:6986963-6987007	NM_009510:145	Ezr	INSIDE	0.490	0.450	1493.85	671.80	0.220	1262.16	277.97
A_68_P23269775	chr4:124377958-124378002	NM_010213:38	Fhl3	INSIDE	0.490	0.538	2623.76	1410.84	0.263	2064.18	543.47
A_68_P26084323	chr8:98157470-98157514	NM_030198:34	Gins3	INSIDE	0.490	0.644	1796.46	1157.20	0.316	1431.88	452.09
A_68_P25150561	chr7:64642517-64642562	NR_033504:-102	Gm9962	DIVERGENT_PROMOTER	0.490	0.449	1807.40	810.77	0.220	1425.00	313.44
A_68_P28118150	chr11:109224474-109224518	NM_010303:389	Gna13	INSIDE	0.490	0.588	2640.98	1552.30	0.288	2010.43	579.54
A_68_P21093572	chr2:28695445-28695489	NM_001166033:414	Gtf3c4	INSIDE	0.490	0.542	1010.39	547.18	0.265	800.93	212.35

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P21044976	chr2:19367626-19367673	NM_018809:360	Ptf1a	INSIDE	0.490	0.656	1479.15	970.04	0.321	1286.41	413.57
A_68_P28683724	chr12:101963187-101963231	NM_153587:30	Rps6ka5	INSIDE	0.490	0.480	2493.49	1195.92	0.235	2088.58	491.28
A_68_P23212280	chr4:111392824-111392869	NM_026470:232	Spata6	INSIDE	0.490	0.438	1747.77	766.17	0.215	1483.13	318.46
A_68_P22385237	chr3:103084452-103084496	NM_001079830:1259	Trim33	INSIDE	0.490	0.698	2203.17	1538.33	0.342	1451.29	496.79
A_68_P24830747	chr6:127059111-127059169	NM_177003:430	9630033F20Rik	INSIDE	0.489	0.628	1497.81	940.76	0.307	1301.40	399.40
A_68_P27560708	chr11:4887125-4887169	NM_007454:239	Ap1b1	INSIDE	0.489	0.697	4765.26	3323.48	0.341	3644.17	1241.86
A_68_P30472484	chr15:97835084-97835128	NM_001113515:49	Col2a1	INSIDE	0.489	0.643	1403.13	901.75	0.315	1122.06	352.90
A_68_P30366491	chr15:79271911-79271956	NM_013767:554	Csnk1e	INSIDE	0.489	0.636	1677.27	1067.49	0.311	1333.40	414.71
A_68_P28493835	chr12:66176402-66176461	NM_178912:-161	Fancm	DIVERGENT_PROMOTER	0.489	0.558	1182.85	659.90	0.273	861.92	235.30
A_68_P29996501	chr15:7762967-7763011	NM_010275:1978	Gdnf	INSIDE	0.489	0.364	2461.17	895.06	0.178	1707.36	303.57
A_68_P32090698	chr19:36628741-36628785	NM_001163471:-366	Hectd2	PROMOTER	0.489	0.595	2248.85	1337.14	0.291	1664.63	483.79
A_68_P22388053	chr3:103594655-103594699	NM_010432:522	Hipk1	INSIDE	0.489	0.652	2358.97	1538.21	0.319	1716.38	546.89
A_68_P27804084	chr11:53114187-53114231	NM_008300:-227	Hspa4	PROMOTER	0.489	0.540	1122.90	606.22	0.264	1038.25	274.20
A_68_P22934418	chr4:55543459-55543503	NM_010637:1867	Klf4	INSIDE	0.489	0.538	1611.10	867.00	0.263	1261.18	332.22
A_68_P27482565	chr10:117147534-117147578	NM_010786:216	Mdm2	INSIDE	0.489	0.534	1301.76	695.21	0.261	1130.71	295.02
A_68_P29075352	chr13:58908396-58908440	NM_001025074:-775	Ntrk2	PROMOTER	0.489	0.659	2536.05	1670.02	0.322	1999.16	644.05
A_68_P22393108	chr3:104584185-104584229	NM_027982:233	Ppm1j	INSIDE	0.489	0.626	2432.93	1522.23	0.306	1881.45	575.45
A_68_P24877028	chr6:137201005-137201049	NM_001164401:207	Ptpro	INSIDE	0.489	0.607	2148.51	1304.75	0.297	1693.93	502.81
A_68_P23328515	chr4:134990204-134990248	NM_022980:-506	Rcan3	PROMOTER	0.489	0.703	1738.96	1222.08	0.344	1410.08	484.53
A_68_P20304095	chr1:66747574-66747618	NM_025683:130	Rpe	INSIDE	0.489	0.364	2463.11	897.32	0.178	2142.67	381.80
A_68_P21106251	chr2:30822965-30823009	NM_144884:452	Tor1a	INSIDE	0.489	0.476	3023.40	1439.48	0.233	2264.47	527.50
A_68_P24791281	chr6:119057478-119057522	NM_001159533:707	Cacna1c	INSIDE	0.488	0.454	2298.28	1042.53	0.221	1910.78	423.18
A_68_P25533789	chr7:139508721-139508765	NM_029935:96	Chst15	INSIDE	0.488	0.580	1655.12	959.62	0.283	1350.92	382.53
A_68_P24619080	chr6:87930668-87930712	NM_198622:786	H1fx	INSIDE	0.488	0.604	2033.85	1228.42	0.295	1860.91	548.16
A_68_P22388054	chr3:103594799-103594843	NM_010432:378	Hipk1	INSIDE	0.488	0.404	2251.66	909.39	0.197	1777.28	350.43
A_68_P29515925	chr14:32978942-32978986	NM_019744:-13	Ncoa4	PROMOTER	0.488	0.384	1559.27	598.63	0.188	1418.60	266.00
A_68_P31625587	chr18:36904013-36904057	NM_010885:168	Ndufa2	INSIDE	0.488	0.706	2629.35	1855.44	0.344	1958.35	674.10
A_68_P20259229	chr1:58561716-58561760	NM_001025378:-3478	Orc2	PROMOTER	0.488	0.613	1220.41	748.30	0.299	1036.45	310.21
A_68_P21580767	chr2:121239698-121239742	NM_007952:83	Pdia3	INSIDE	0.488	0.464	1856.14	861.06	0.226	1526.10	345.63
A_68_P27630335	chr11:20101626-20101670	NM_008996:44	Rab1	INSIDE	0.488	0.626	976.58	611.62	0.306	867.42	265.32
A_68_P28194541	chr12:3309848-3309892	NM_016676:99	Rab10	INSIDE	0.488	0.569	2174.95	1238.12	0.278	1733.52	481.18
A_68_P28280595	chr12:21423493-21423537	NM_011739:-217	Ywhaq	PROMOTER	0.488	0.524	1861.72	976.25	0.256	1439.01	368.48
A_68_P21115063	chr2:32237069-32237113	NM_198001:345	1110008P14Rik	INSIDE	0.487	0.635	813.33	516.47	0.309	625.13	193.40
A_68_P21632193	chr2:130732022-130732066	NR_015523:88	A730017L22Rik	INSIDE	0.487	0.448	1208.61	540.95	0.218	986.16	214.80
A_68_P25090210	chr7:52184875-52184919	NM_001077264:-36	Ap2a1	PROMOTER	0.487	0.497	1125.86	559.74	0.242	850.21	205.95
A_68_P26834222	chr9:112137879-112137923	NM_001177619:-555	Arpp21	PROMOTER	0.487	0.497	1421.06	705.74	0.242	1267.75	306.45
A_68_P31065259	chr17:15512604-15512648	NM_007865:161	Dll1	INSIDE	0.487	0.468	1288.39	603.05	0.228	926.33	211.00
A_68_P31156012	chr17:34974444-34974488	NM_001163770:503	Dom3z	INSIDE	0.487	0.622	1713.07	1065.59	0.303	1350.94	409.64
A_68_P25020569	chr7:28964516-28964561	NM_010092:26	Dyrk1b	INSIDE	0.487	0.644	954.38	614.76	0.314	868.98	272.77
A_68_P32219573	chr19:59534086-59534130	NM_010132:929	Emx2	INSIDE	0.487	0.383	1447.80	554.09	0.186	1176.86	219.13
A_68_P31112795	chr17:26986945-26986989	NM_008700:-8456	Nkx2-5	PROMOTER	0.487	0.596	1721.05	1025.00	0.290	1291.32	374.77
A_68_P21911590	chr2:181335967-181336011	NM_133701:-35	Prpf6	DIVERGENT_PROMOTER	0.487	0.665	1374.26	913.55	0.324	983.56	318.63
A_68_P21105567	chr2:30701245-30701289	NM_009116:380	Prrx2	INSIDE	0.487	0.536	1063.78	569.84	0.261	841.23	219.68
A_68_P31207970	chr17:46765913-46765957	NM_175168:519	Ptk7	INSIDE	0.487	0.587	1359.07	797.16	0.286	1009.10	288.38
A_68_P27911821	chr11:72302535-72302580	NM_153060:849	Spns2	INSIDE	0.487	0.643	1352.13	869.12	0.313	1065.32	333.18
A_68_P28881306	chr13:23515429-23515473	NM_013924:285	Abt1	INSIDE	0.486	0.501	1304.49	654.11	0.244	1021.46	249.03
A_68_P28002760	chr11:88725701-88725745	NM_001042541:178	Akap1	INSIDE	0.486	0.621	1989.26	1234.52	0.302	1676.77	505.57
A_68_P27843668	chr11:60351780-60351824	NM_172943:618	Alkbh5	INSIDE	0.486	0.593	2332.94	1383.25	0.288	1880.47	541.65
A_68_P27750956	chr11:43342693-43342737	NM_001045530:429	Ccnjl	INSIDE	0.486	0.645	2025.15	1305.63	0.313	1622.45	508.59
A_68_P32099207	chr19:38129688-38129732	NM_001164362:179	Cep55	INSIDE	0.486	0.558	1634.87	912.57	0.271	1289.73	349.94
A_68_P26001978	chr8:83403405-83403452	NM_021356:950	Gab1	INSIDE	0.486	0.502	1639.93	822.60	0.244	1281.09	312.36

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P29034751	chr13:51942528-51942572	NM_011817:507	Gadd45g	INSIDE	0.486	1.416	11702.50	16567.28	0.689	8042.87	5539.15
A_68_P24864116	chr6:134847884-134847928	NM_001167695:-73	Gpr19	PROMOTER	0.486	0.427	1300.51	555.03	0.207	1069.51	221.73
A_68_P24038672	chr5:120882014-120882058	NM_008499:142	Lhx5	INSIDE	0.486	0.436	1538.10	670.10	0.212	1325.14	280.69
A_68_P31934085	chr19:6341468-6341512	NM_009006:241	Map4k2	INSIDE	0.486	0.671	1478.67	992.70	0.326	1237.50	403.43
A_68_P21839459	chr2:167924216-167924266	NM_021409:17737	Pard6b	INSIDE	0.486	3.416	584.47	1996.35	1.659	535.97	889.17
A_68_P27647502	chr11:23670649-23670693	NM_009044:300	Rel	INSIDE	0.486	0.652	2102.83	1371.24	0.317	1788.84	566.53
A_68_P28988729	chr13:43266743-43266787	NM_025935:-36	Tbc1d7	PROMOTER	0.486	0.678	1334.18	905.10	0.330	1075.69	354.84
A_68_P27273027	chr10:77707175-77707219	NM_001081055:191	Trappc10	INSIDE	0.486	0.604	988.87	596.80	0.293	877.04	257.23
A_68_P28599061	chr12:85911065-85911109	NM_007701:285	Vsx2	INSIDE	0.486	0.611	1566.71	957.78	0.297	1357.31	403.32
A_68_P30481998	chr15:99556153-99556197	NM_183256:126	2310016M24Rik	INSIDE	0.485	0.664	2354.99	1564.25	0.322	1729.37	556.70
A_68_P28187623	chr11:120794145-120794189	NM_027745:20	Ccdc57	INSIDE	0.485	0.666	1253.90	834.77	0.323	1006.35	324.87
A_68_P30895372	chr16:78302001-78302045	NM_001025192:87	Cxadr	INSIDE	0.485	0.644	1640.50	1056.16	0.312	1285.44	401.09
A_68_P28036958	chr11:95006743-95006787	NM_007867:351	Dlx4	INSIDE	0.485	0.688	4489.99	3088.20	0.334	3238.82	1080.56
A_68_P23395155	chr4:147932643-147932687	NM_016699:129	Exosc10	INSIDE	0.485	0.586	886.56	519.22	0.284	766.71	217.58
A_68_P25369176	chr7:107855309-107855353	NM_178764:115	Fam168a	INSIDE	0.485	0.525	1320.02	693.27	0.255	1090.90	278.11
A_68_P27077934	chr10:39089328-39089372	NM_001122892:-254	Fyn	PROMOTER	0.485	1.459	9707.23	14159.60	0.708	6682.81	4732.36
A_68_P21929617	chr3:7612894-7612938	NM_008371:511	Il7	INSIDE	0.485	0.523	1153.86	603.00	0.254	1067.39	270.70
A_68_P21812066	chr2:163201241-163201292	NM_021566:22443	Jph2	INSIDE	0.485	1.413	1545.63	2183.51	0.685	1222.47	837.03
A_68_P22139474	chr3:52845318-52845362	NM_175386:-128	Lhfp	PROMOTER	0.485	0.698	2128.02	1485.84	0.339	1611.47	545.91
A_68_P24816270	chr6:124613220-124613264	NM_145130:121	Lpcat3	INSIDE	0.485	0.680	2281.06	1550.91	0.330	1601.01	528.04
A_68_P23361560	chr4:140566716-140566760	NM_008546:187	Mfap2	INSIDE	0.485	0.496	1156.20	573.98	0.241	893.26	214.88
A_68_P29613301	chr14:55236421-55236465	NR_030457:-820	Mir686	PROMOTER	0.485	0.633	1569.75	994.38	0.307	1231.88	378.47
A_68_P25021608	chr7:29178020-29178064	NM_019458:28	Paf1	INSIDE	0.485	0.602	1810.55	1090.50	0.292	1319.52	385.55
A_68_P27288652	chr10:80755895-80755939	NM_001146687:200	Pip5k1c	INSIDE	0.485	0.427	2716.23	1159.04	0.207	2212.44	458.22
A_68_P25183345	chr7:72672251-72672295			Unknown	0.485	0.748	4782.02	3578.94	0.363	3972.57	1441.72
A_68_P26548608	chr9:58402565-58402609	ENSMUST00000098676:-19		PROMOTER	0.485	0.413	1333.16	550.07	0.200	1058.15	211.61
A_68_P27787100	chr11:49988573-49988624	NM_026543:246	3010026O09Rik	INSIDE	0.484	0.595	1168.90	695.64	0.288	776.36	223.67
A_68_P31158465	chr17:35373569-35373613	NM_023179:50	Atp6v1g2	INSIDE	0.484	0.727	2241.25	1630.25	0.352	1591.45	560.35
A_68_P28109102	chr11:107655644-107655688	NM_019431:112	Cacng4	INSIDE	0.484	0.556	1788.57	994.28	0.269	1320.97	355.36
A_68_P25565281	chr7:144514141-144514185	NM_001113414:-8034	Ebf3	PROMOTER	0.484	0.643	1717.13	1103.61	0.311	1446.85	449.80
A_68_P24115511	chr5:135726586-135726630	NM_010246:309	Fzd9	INSIDE	0.484	0.470	2130.42	1001.81	0.227	1662.56	378.18
A_68_P28452661	chr12:56701135-56701179	NM_020287:1253	Insm2	INSIDE	0.484	0.448	1892.63	848.42	0.217	1554.72	336.97
A_68_P23328805	chr4:135050806-135050850	NM_028995:-409	Nipal3	DIVERGENT_PROMOTER	0.484	0.603	1098.79	663.09	0.292	856.25	249.85
A_68_P31311921	chr17:67703645-67703689	NM_008984:133	Ptprm	INSIDE	0.484	0.637	1627.31	1036.43	0.308	1495.69	461.41
A_68_P22281783	chr3:82680573-82680617	NM_001146328:-189	Rbm46	PROMOTER	0.484	1.399	1858.55	2600.42	0.678	1455.68	986.26
A_68_P21835385	chr2:167247037-167247081	NM_148929:-162	Slc9a8	PROMOTER	0.484	0.664	1773.84	1178.65	0.321	1353.62	435.08
A_68_P30544457	chr16:10785415-10785459	NM_009896:193	Socs1	INSIDE	0.484	0.417	2700.03	1126.63	0.202	2124.78	428.99
A_68_P24006041	chr5:115224674-115224718	NR_027872:296	4930515G01Rik	INSIDE	0.483	0.522	1829.39	954.87	0.252	1493.79	376.31
A_68_P30337992	chr15:74394645-74394689	NM_174991:48041	Bai1	INSIDE	0.483	0.665	1714.56	1140.18	0.321	1333.96	428.37
A_68_P26790786	chr9:104164871-104164915	NM_001163026:368	Dnajc13	INSIDE	0.483	0.425	1834.27	778.78	0.205	1387.67	284.86
A_68_P23597968	chr5:35399719-35399763	NM_172708:8	Dok7	INSIDE	0.483	0.725	1681.12	1218.03	0.350	1334.37	466.66
A_68_P20634005	chr1:136453383-136453427	NM_152895:-3350	Kdm5b	DIVERGENT_PROMOTER	0.483	0.595	1761.01	1048.22	0.287	1387.93	398.75
A_68_P24979588	chr7:16683856-16683900	NM_025898:-113	Napa	PROMOTER	0.483	0.549	1638.19	898.82	0.265	1405.09	372.68
A_68_P30397310	chr15:84686778-84686823	NM_001081166:-241	Phf21b	PROMOTER	0.483	0.691	3869.34	2672.26	0.334	2983.60	995.79
A_68_P30497693	chr15:102235932-102235976	NM_013672:-792	Sp1	PROMOTER	0.483	0.563	1706.22	960.11	0.272	1277.79	347.43
A_68_P22538542	chr3:132347071-132347115	NM_173032:-15	Tbck	DIVERGENT_PROMOTER	0.483	0.530	2348.87	1245.55	0.256	1857.29	475.36
A_68_P26140912	chr8:109207098-109207142	NM_173037:153	Tmco7	INSIDE	0.483	0.570	1022.10	582.28	0.275	966.40	266.05
A_68_P31151137	chr17:34077801-34077845	NM_020603:155	Wdr46	INSIDE	0.483	0.707	1352.91	956.04	0.341	1024.41	349.80
A_68_P30762456	chr16:52453372-52453416	NM_009655:-284	Alcam	PROMOTER	0.482	0.403	1841.83	741.46	0.194	1337.84	259.65
A_68_P23281852	chr4:126430875-126430919	NM_133886:-117	AU040320	PROMOTER	0.482	0.570	2215.34	1261.74	0.275	1570.02	431.24
A_68_P29530302	chr14:35315095-35315147	NM_009758:612	Bmpr1a	INSIDE	0.482	0.599	1221.79	731.81	0.289	1077.15	310.83

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26825042	chr9:110559281-110559325	NM_028312:296	Ccdc12	INSIDE	0.482	0.617	2313.78	1428.18	0.297	1753.97	521.53
A_68_P21762928	chr2:154718164-154718208	NM_026030:456	Eif2s2	INSIDE	0.482	0.521	3504.72	1826.80	0.251	2641.39	663.62
A_68_P25394534	chr7:112959304-112959348	NM_025301:275	Mrpl17	INSIDE	0.482	0.653	1215.91	794.16	0.315	937.64	295.07
A_68_P27921011	chr11:74336607-74336651	NM_001015046:67032	Rap1gap2	INSIDE	0.482	0.673	3342.51	2250.51	0.324	2475.59	802.64
A_68_P22312701	chr3:88044948-88044992	NM_021375:13636	Rhbg	DOWNSTREAM	0.482	0.400	1768.14	707.26	0.193	1340.77	258.59
A_68_P30377732	chr15:81229723-81229767	NM_133726:380	St13	INSIDE	0.482	0.642	1394.93	895.13	0.309	1246.24	385.22
A_68_P23316765	chr4:132833435-132833480	NM_025667:248	Tmem222	INSIDE	0.482	0.581	2523.92	1466.58	0.280	2020.68	566.19
A_68_P22145981	chr3:53959830-53959874	NM_016984:-173	Trpc4	PROMOTER	0.482	0.592	1367.19	808.74	0.285	1112.73	317.09
A_68_P29256601	chr13:99032893-99032937	NM_178918:33	Utp15	INSIDE	0.482	0.569	2426.49	1380.02	0.274	1982.66	543.99
A_68_P27095961	chr10:42351968-42352012	ENSMUST00000144806:48347		INSIDE	0.482	0.711	1303.14	927.00	0.343	1092.05	374.44
A_68_P28450732	chr12:56225370-56225414	NM_001100116:-122	1700047I17Rik2	PROMOTER	0.481	0.695	1744.69	1213.31	0.334	1633.27	545.84
A_68_P27282598	chr10:79804958-79805002	NM_001113548:6211	Adamtsl5	INSIDE	0.481	0.428	1589.39	680.46	0.206	1199.97	247.28
A_68_P27171935	chr10:59465906-59465950	NM_025514:-68	Anapc16	DIVERGENT_PROMOTER	0.481	0.501	2530.57	1266.60	0.241	2123.48	510.99
A_68_P20455320	chr1:95297981-95298025	NM_207031:27530	Ano7	INSIDE	0.481	0.652	1115.64	727.50	0.313	903.76	283.23
A_68_P24798783	chr6:120443507-120443551	NM_033567:297	Cecr6	INSIDE	0.481	0.454	2166.85	982.79	0.218	1678.62	366.17
A_68_P22861616	chr4:41261724-41261768	NM_026893:188	Dcaf12	INSIDE	0.481	0.699	1489.47	1040.41	0.336	1226.08	411.88
A_68_P30746980	chr16:49699315-49699359	NM_028680:-70	Ift57	PROMOTER	0.481	0.699	3152.72	2204.33	0.336	2447.18	822.39
A_68_P20938882	chr1:193399613-193399657	NM_178632:22	Ints7	INSIDE	0.481	0.496	1494.60	741.54	0.239	1079.60	257.53
A_68_P20806524	chr1:169619169-169619217	NM_033652:-496	Lmx1a	PROMOTER	0.481	0.492	1224.37	602.89	0.237	1036.42	245.71
A_68_P21614450	chr2:127413402-127413446	NM_029963:263	Mrps5	INSIDE	0.481	0.702	1575.99	1106.42	0.337	1167.14	393.86
A_68_P20164271	chr1:39251178-39251222	NM_008719:84	Npas2	INSIDE	0.481	0.378	2295.88	868.81	0.182	1697.49	309.03
A_68_P26268778	chr8:130882433-130882477	NM_008737:-518	Nrp1	PROMOTER	0.481	0.712	1356.25	965.21	0.342	1017.05	347.82
A_68_P21706649	chr2:144157501-144157545	NM_152947:-424	Ovol2	PROMOTER	0.481	0.484	1533.54	742.41	0.233	1176.65	273.94
A_68_P28458266	chr12:57793635-57793679	NM_011041:-2969	Pax9	PROMOTER	0.481	0.582	1359.23	791.15	0.280	1150.77	322.38
A_68_P28549419	chr12:76697049-76697093	NM_012024:117	Ppp2r5e	INSIDE	0.481	0.664	5537.38	3677.83	0.319	3978.85	1271.15
A_68_P31108130	chr17:26205973-26206017	NM_001162868:128	Rab11fip3	INSIDE	0.481	0.682	2004.10	1366.87	0.328	1539.18	505.40
A_68_P29011800	chr13:47218349-47218393	NM_146042:282	Rnf144b	INSIDE	0.481	0.690	1064.79	735.20	0.332	727.15	241.26
A_68_P25507247	chr7:134920536-134920580	NM_178029:-344	Setd1a	PROMOTER	0.481	0.341	3262.41	1113.63	0.164	2654.59	435.65
A_68_P20878657	chr1:182873054-182873098	NM_144794:428	Tmem63a	INSIDE	0.481	0.689	1123.22	773.44	0.331	846.78	280.24
A_68_P24431874	chr6:49213690-49213734	NM_198102:339	Tra2a	INSIDE	0.481	0.437	2489.43	1086.95	0.210	1956.38	410.72
A_68_P23339580	chr4:136944275-136944319	ENSMUST00000078305:-6911		PROMOTER	0.481	0.401	1933.98	775.16	0.193	1422.75	274.21
A_68_P20140038	chr1:34735220-34735264	ENSMUST00000159326:210		INSIDE	0.481	0.573	1164.49	667.48	0.276	931.28	256.86
A_68_P25677406	chr8:14911525-14911569	NM_001037736:-170	Arhgef10	PROMOTER	0.480	0.642	1548.94	993.75	0.308	1391.38	428.63
A_68_P25948511	chr8:72409941-72409985	NM_026818:1329	Cilp2	INSIDE	0.480	0.526	1118.11	587.97	0.253	865.18	218.55
A_68_P30230393	chr15:54944017-54944061	NM_145470:1	Deptor	INSIDE	0.480	0.550	2257.27	1242.03	0.264	1758.95	464.63
A_68_P26467019	chr9:44135043-44135087	NM_007875:137	Dpagt1	INSIDE	0.480	0.539	1362.77	734.99	0.259	1126.21	291.65
A_68_P28186830	chr11:120657372-120657416	NM_026824:315	Dus1l	INSIDE	0.480	0.659	2813.60	1854.72	0.316	2222.26	702.91
A_68_P20456054	chr1:95408480-95408524	NM_145519:-178	Farp2	PROMOTER	0.480	0.465	1324.72	616.09	0.223	1060.35	236.71
A_68_P32140226	chr19:45817015-45817059	NM_001166361:338	Fgf8	INSIDE	0.480	0.537	1065.37	572.62	0.258	836.27	215.78
A_68_P26374353	chr9:26962841-26962885	NM_023277:144	Jam3	INSIDE	0.480	0.597	940.40	561.62	0.287	786.31	225.60
A_68_P30575506	chr16:17759553-17759597	NM_145479:-139	Klhl22	PROMOTER	0.480	0.679	1589.70	1079.12	0.326	1274.65	415.05
A_68_P25015935	chr7:27963726-27963770	NR_037283:-2636	Mir3101	PROMOTER	0.480	0.709	1802.20	1277.94	0.341	1472.34	501.47
A_68_P20184671	chr1:42754188-42754232	NM_008900:220	Pou3f3	INSIDE	0.480	0.646	959.00	619.22	0.310	929.95	288.27
A_68_P29094168	chr13:63665973-63666017	NM_008957:834	Ptch1	INSIDE	0.480	0.677	1363.51	922.75	0.325	1064.54	345.90
A_68_P30578596	chr16:18249157-18249201	NM_001080999:203	Trmt2a	INSIDE	0.480	0.671	1791.48	1202.58	0.322	1420.71	457.65
A_68_P28072252	chr11:101017412-101017456	NM_134028:237	Tubg2	INSIDE	0.480	0.569	1803.32	1026.03	0.273	1412.35	385.83
A_68_P21579349	chr2:120996373-120996418	NM_178889:490	Zscan29	INSIDE	0.480	0.666	1797.60	1197.59	0.320	1294.63	413.66
A_68_P25007467	chr7:25729309-25729353			Unknown	0.480	0.547	2520.07	1379.55	0.263	1841.60	483.62
A_68_P28976947	chr13:41345064-41345108	NM_001135577:-126	BC024659	PROMOTER	0.479	0.526	2012.27	1059.02	0.252	1435.63	361.73
A_68_P31152223	chr17:34257573-34257617	NR_037970:-749	Brd2	PROMOTER	0.479	0.648	2483.84	1609.22	0.310	1780.17	552.63
A_68_P23448645	chr5:4104155-4104199	NM_020010:521	Cyp51	INSIDE	0.479	0.667	1310.96	874.53	0.319	1029.64	328.77

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28576810	chr12:81744684-81744728	NM_007951:142	Erh	INSIDE	0.479	0.739	3291.02	2433.20	0.354	2654.68	939.45
A_68_P31876066	chr18:82575283-82575327	NM_008082:865	Galr1	INSIDE	0.479	0.483	2065.44	997.01	0.231	1600.25	370.27
A_68_P23165464	chr4:102986645-102986689	NM_025909:216	Oma1	INSIDE	0.479	0.613	996.25	610.96	0.294	859.86	252.48
A_68_P25666157	chr8:13105151-13105195	NM_178708:171	Pcid2	INSIDE	0.479	0.530	1273.97	675.04	0.254	1099.59	279.25
A_68_P25614335	chr8:3515288-3515332	NM_001122818:-73	Pnpla6	PROMOTER	0.479	0.619	2298.49	1423.24	0.297	1726.09	512.10
A_68_P28059432	chr11:98798988-98799032	NM_001177302:-21	Rara	PROMOTER	0.479	0.604	1672.00	1009.06	0.289	1168.93	337.96
A_68_P32599603	chrX:108577244-108577288	NM_025949:74288	Rps6ka6	INSIDE	0.479	0.559	1003.25	560.77	0.268	437.18	117.08
A_68_P22286850	chr3:83570771-83570815	NM_009144:550	Sfrp2	INSIDE	0.479	0.595	1282.53	762.50	0.285	914.27	260.51
A_68_P28344354	chr12:34642575-34642619	NM_011658:61	Twist1	INSIDE	0.479	0.582	2241.59	1305.33	0.279	1874.20	522.72
A_68_P30471849	chr15:97739034-97739078	NM_009504:-329	Vdr	PROMOTER	0.479	0.585	1964.43	1148.28	0.280	1583.43	443.33
A_68_P31149741	chr17:33766122-33766166	NM_026712:108	Zfp414	INSIDE	0.479	0.612	906.13	554.98	0.294	758.17	222.56
A_68_P24037871	chr5:120752306-120752350			Unknown	0.479	0.679	1497.79	1017.36	0.326	1161.83	378.34
A_68_P29672920	chr14:65962654-65962698	AK028094:17509		DOWNSTREAM	0.479	0.494	1747.19	863.93	0.237	1355.93	321.23
A_68_P20447498	chr1:94077040-94077084	AK155250:-144		PROMOTER	0.479	0.560	2293.44	1283.74	0.268	1734.42	464.74
A_68_P27958467	chr11:80965329-80965373	NM_007384:1055	Accn1	INSIDE	0.478	0.656	1189.57	779.90	0.313	1067.78	334.62
A_68_P30673619	chr16:36072197-36072241	NM_001159422:-9142	Ccdc58	PROMOTER	0.478	0.554	1163.45	644.47	0.265	915.06	242.18
A_68_P28732710	chr12:110691897-110691941	NM_001190703:254	Dlk1	INSIDE	0.478	0.502	2056.95	1033.52	0.240	1542.30	370.33
A_68_P29631501	chr14:58694549-58694593	NM_013518:3048	Fgf9	INSIDE	0.478	0.378	1966.29	743.61	0.181	1526.29	276.13
A_68_P29034755	chr13:51943120-51943164	NM_011817:1099	Gadd45g	INSIDE	0.478	0.402	1902.56	765.41	0.192	1503.63	288.92
A_68_P20644872	chr1:138156299-138156343	NM_001101516:1130	Gpr25	INSIDE	0.478	0.513	1269.17	650.55	0.245	954.00	233.70
A_68_P27280641	chr10:79516441-79516485	NM_001037741:-319	Gpx4	PROMOTER	0.478	0.502	2844.34	1428.39	0.240	1949.29	468.24
A_68_P26526554	chr9:54434551-54434595	NM_029573:255	Idh3a	INSIDE	0.478	0.328	1901.35	623.56	0.157	1481.35	232.28
A_68_P31622626	chr18:36356438-36356482	NM_001167891:354	Nrg2	INSIDE	0.478	0.582	1174.01	683.70	0.279	994.54	277.10
A_68_P31303253	chr17:66234412-66234456	NM_001198949:-171	Ralbp1	PROMOTER	0.478	0.647	1063.99	688.12	0.309	889.87	274.93
A_68_P26316371	chr9:14080770-14080814	NM_030261:48	Sesn3	INSIDE	0.478	0.559	1900.92	1061.75	0.267	1585.58	423.54
A_68_P31487968	chr18:10030044-10030088	NM_001038589:81	Usp14	INSIDE	0.478	0.718	2964.47	2127.98	0.343	2212.20	758.69
A_68_P26494989	chr9:48793954-48794001	NM_175482:488	Usp28	INSIDE	0.478	0.544	958.06	521.24	0.260	769.11	199.94
A_68_P29961944	chr14:122875451-122875495	NM_009574:867	Zic2	INSIDE	0.478	0.595	2523.21	1501.09	0.284	1988.30	565.48
A_68_P26448727	chr9:41184693-41184737	AK081773:-5916		PROMOTER	0.478	0.417	2003.36	836.30	0.200	1502.34	300.04
A_68_P26074974	chr8:96535812-96535856	NM_011787:706	Amfr	INSIDE	0.477	0.589	2100.45	1236.68	0.281	1586.27	445.93
A_68_P31058439	chr17:14340006-14340050	NM_172826:810	Dact2	INSIDE	0.477	0.524	1451.59	760.53	0.250	1301.74	325.01
A_68_P23227292	chr4:115689902-115689946	NM_010173:583	Faah	INSIDE	0.477	0.496	1430.53	709.23	0.236	1154.19	272.86
A_68_P21485377	chr2:103601079-103601123	NM_153126:307	Nat10	INSIDE	0.477	0.590	1023.16	603.68	0.281	767.63	216.03
A_68_P29275477	chr13:102537731-102537775	NM_001077495:420	Pik3r1	INSIDE	0.477	0.489	1109.14	542.56	0.233	910.65	212.37
A_68_P21813660	chr2:163484302-163484346	NM_001164053:131	Pkig	INSIDE	0.477	0.560	986.37	552.78	0.267	905.78	242.04
A_68_P27841324	chr11:59989338-59989382	NM_001037764:35777	Rai1	INSIDE	0.477	0.623	1199.73	746.89	0.297	978.58	290.76
A_68_P22165085	chr3:57539702-57539746	NM_011883:-263	Rnf13	PROMOTER	0.477	0.526	2000.56	1052.59	0.251	1715.08	430.87
A_68_P27877798	chr11:66340379-66340423	NM_001034874:-772	Shisa6	PROMOTER	0.477	0.563	2271.08	1279.17	0.269	1743.23	468.57
A_68_P28671225	chr12:99866511-99866555	NM_178914:139	Spata7	INSIDE	0.477	0.714	2053.80	1466.08	0.341	1525.59	519.84
A_68_P29856116	chr14:102053116-102053160	NM_016723:-45	Uchl3	PROMOTER	0.477	0.678	1252.29	848.85	0.323	1035.20	334.63
A_68_P28694455	chr12:104187509-104187553	NM_001081017:462	Unc79	INSIDE	0.477	0.648	1703.01	1103.15	0.309	1328.01	409.98
A_68_P30141816	chr15:36937216-36937260	NM_026521:-81	Zfp706	PROMOTER	0.477	0.588	2500.93	1471.67	0.281	1874.31	526.37
A_68_P27083323	chr10:40020837-40020881	NM_007444:1134	Amd2	INSIDE	0.476	0.678	1594.46	1081.77	0.323	1282.78	414.38
A_68_P24115153	chr5:135663286-135663330	NM_011714:116	Baz1b	INSIDE	0.476	0.659	1057.98	697.28	0.314	927.00	290.73
A_68_P27272488	chr10:77632611-77632655	NM_138601:-119	D10Jhu81e	PROMOTER	0.476	0.523	1479.67	774.53	0.249	1114.96	277.98
A_68_P21603036	chr2:125331219-125331263	NM_007993:934	Fbn1	INSIDE	0.476	0.657	935.55	614.36	0.313	779.93	243.78
A_68_P31422103	chr17:87665170-87665214	NM_139295:95	Mcfd2	INSIDE	0.476	0.560	4201.84	2354.54	0.267	2989.83	797.80
A_68_P29453022	chr14:22318726-22318770	NM_001205241:-243	Myst4	PROMOTER	0.476	0.652	2715.22	1769.97	0.310	2259.17	700.97
A_68_P22872799	chr4:43644616-43644660	NM_173788:-168	Npr2	PROMOTER	0.476	1.511	3992.20	6032.33	0.719	2609.02	1875.02
A_68_P24950541	chr7:4744529-4744573	NM_009081:-16	Rpl28	DIVERGENT_PROMOTER	0.476	0.725	1844.12	1336.34	0.345	1373.30	474.08
A_68_P20191089	chr1:43884192-43884236	NM_026430:339	Uxs1	INSIDE	0.476	0.662	867.69	574.69	0.315	768.64	242.48

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P24760554	chr6:113574432-113574476	NM_009507:440	Vhl	INSIDE	0.476	0.671	2660.19	1784.19	0.319	2034.11	649.02
A_68_P22964960	chr4:62186324-62186371	NM_177607:-55	4933430I17Rik	DIVERGENT_PROMOTER	0.475	0.529	1219.13	644.59	0.251	848.41	212.90
A_68_P30459963	chr15:95621546-95621590	NM_175344:295	Ano6	INSIDE	0.475	0.516	2300.58	1186.50	0.245	1680.35	411.74
A_68_P29144944	chr13:74346071-74346115	NM_177333:56	Exoc3	INSIDE	0.475	0.623	3066.97	1910.91	0.296	2497.47	739.39
A_68_P31106388	chr17:25946298-25946342	NM_001164225:291	Fbxl16	INSIDE	0.475	0.688	1554.55	1069.98	0.327	1248.05	407.99
A_68_P20826007	chr1:172995883-172995927	NM_010188:-6370	Fcgr3	PROMOTER	0.475	0.324	7844.01	2538.94	0.154	6645.24	1021.34
A_68_P28137853	chr11:112646459-112646503	NM_011448:2957	Sox9	INSIDE	0.475	0.635	5799.83	3681.65	0.302	4110.70	1239.86
A_68_P24459344	chr6:53769514-53769558	NM_025817:1283	Tril	INSIDE	0.475	1.411	4056.02	5722.18	0.670	2907.24	1947.23
A_68_P21115067	chr2:32237497-32237541	NM_198001:-83	1110008P14Rik	PROMOTER	0.474	0.452	3164.68	1431.07	0.215	2248.98	482.49
A_68_P25539028	chr7:140316412-140316456	NM_009980:-1268	Ctbp2	PROMOTER	0.474	0.420	1352.64	568.73	0.199	1173.11	233.91
A_68_P24533914	chr6:70907055-70907100	NM_001101464:478	Foxi3	INSIDE	0.474	0.616	1034.28	637.53	0.292	821.83	240.22
A_68_P32117486	chr19:41921651-41921695	NM_177603:950	Frat2	INSIDE	0.474	0.525	2050.18	1075.58	0.249	1582.09	393.70
A_68_P25350314	chr7:104548897-104548941	NM_024220:406	Ndufc2	INSIDE	0.474	0.708	1873.10	1326.63	0.336	1456.45	488.82
A_68_P20961506	chr2:3200909-3200953	NM_008708:-629	Nmt2	PROMOTER	0.474	0.537	1726.64	927.27	0.255	1287.86	328.03
A_68_P30422878	chr15:88898359-88898403	NM_001002005:8225	Panx2	INSIDE	0.474	2.966	1936.80	5744.91	1.406	1405.19	1975.56
A_68_P24123993	chr5:137463233-137463277	NM_011962:366	Plod3	INSIDE	0.474	0.553	1095.74	606.16	0.262	781.43	204.85
A_68_P24462649	chr6:54277015-54277059	NM_030024:31	Prr15	INSIDE	0.474	0.460	1777.85	817.43	0.218	1426.55	311.18
A_68_P31024853	chr17:7374468-7374512	NM_011299:27	Rps6ka2	INSIDE	0.474	0.528	1322.33	697.66	0.250	1141.11	285.31
A_68_P31857881	chr18:79305640-79305684	NM_053099:468	Setbp1	INSIDE	0.474	0.628	5152.73	3235.64	0.298	3688.43	1097.86
A_68_P27750513	chr11:43247484-43247528	NM_148673:274	Slu7	INSIDE	0.474	0.604	1473.17	889.54	0.286	1210.37	346.10
A_68_P31104790	chr17:25707537-25707581	NM_011447:73	Sox8	INSIDE	0.474	0.513	1839.25	943.00	0.243	1423.75	346.34
A_68_P31930506	chr19:5731655-5731699	NM_020491:45	Sssca1	INSIDE	0.474	0.485	2931.98	1423.06	0.230	2146.46	493.78
A_68_P26431942	chr9:37464709-37464753	NM_025289:167	Tbrg1	INSIDE	0.474	0.558	919.30	513.02	0.265	693.35	183.39
A_68_P29508103	chr14:31638633-31638679	NM_028839:-123	Tmem110	PROMOTER	0.474	0.641	1383.44	886.42	0.304	1115.78	338.92
A_68_P24327619	chr6:29559522-29559566	NM_177296:63	Tnpo3	INSIDE	0.474	0.545	1375.40	749.19	0.258	1119.01	289.03
A_68_P31156341	chr17:35031034-35031078	NM_198886:-447	Zbtb12	PROMOTER	0.474	0.628	960.50	602.87	0.297	786.37	233.74
A_68_P22691831	chr4:3158152-3158196			Unknown	0.474	0.444	1492.57	662.67	0.210	1442.86	303.53
A_68_P21840494	chr2:168106782-168106826	ENSMUST00000109191:-172		PROMOTER	0.474	0.613	4148.95	2543.21	0.291	3278.74	952.99
A_68_P24541217	chr6:72297432-72297476	NM_026696:144	0610030E20Rik	INSIDE	0.473	0.544	1173.35	638.12	0.257	961.45	247.19
A_68_P32053384	chr19:29596371-29596418	NR_015567:83	A930007I19Rik	INSIDE	0.473	0.570	972.26	554.23	0.269	784.74	211.41
A_68_P28836401	chr13:14047360-14047404	NM_178640:442	B3galnt2	INSIDE	0.473	0.498	1672.03	833.04	0.236	1311.99	308.99
A_68_P28962018	chr13:38750527-38750572	NM_025380:348	Eef1e1	INSIDE	0.473	0.529	1293.25	684.71	0.250	1003.15	251.03
A_68_P25957748	chr8:74126235-74126279	NM_001166213:4712	Fam129c	INSIDE	0.473	0.476	1866.23	888.43	0.225	1409.07	317.59
A_68_P30642670	chr16:30599886-30599930	NM_177632:100	Fam43a	INSIDE	0.473	0.614	2985.20	1833.32	0.291	2009.95	584.06
A_68_P23145500	chr4:99317555-99317599	NM_010425:-5413	Foxd3	PROMOTER	0.473	0.624	2532.12	1581.00	0.295	1875.23	553.52
A_68_P26000510	chr8:83135226-83135270	NM_001167898:311	Frem3	INSIDE	0.473	0.687	1682.60	1156.70	0.325	1417.04	460.90
A_68_P26346365	chr9:21092135-21092179	NM_145416:257	Kri1	INSIDE	0.473	0.659	1141.12	752.12	0.312	934.66	291.63
A_68_P20961508	chr2:3201225-3201269	NM_008708:-313	Nmt2	PROMOTER	0.473	0.732	2027.47	1483.22	0.346	1469.18	508.10
A_68_P25435754	chr7:121559761-121559805	NM_011055:1015	Pde3b	INSIDE	0.473	0.659	838.96	553.00	0.312	774.19	241.19
A_68_P30979597	chr16:94347042-94347086	NM_011377:261560	Sim2	INSIDE	0.473	0.532	2893.16	1538.32	0.251	2255.31	566.90
A_68_P23576135	chr5:31350810-31350854	NM_177870:-380	Slc5a6	PROMOTER	0.473	0.577	1275.52	735.41	0.273	903.48	246.57
A_68_P28168286	chr11:117830189-117830233	NM_007707:470	Socs3	INSIDE	0.473	0.485	1355.41	657.76	0.230	1091.57	250.74
A_68_P30380080	chr15:81690283-81690327	NM_020507:-1548	Tob2	PROMOTER	0.473	0.481	2092.30	1006.96	0.228	1728.62	393.52
A_68_P21075774	chr2:25877393-25877437	NM_133835:-134	Ubac1	PROMOTER	0.473	0.587	929.27	545.17	0.277	735.12	203.83
A_68_P21084623	chr2:27282256-27282300	NM_009500:67	Vav2	INSIDE	0.473	0.558	3145.39	1754.33	0.264	2375.05	626.26
A_68_P25075288	chr7:48157851-48157898	NM_021387:3227	Vstm2b	INSIDE	0.473	0.630	1247.51	786.47	0.298	905.97	270.08
A_68_P24974125	chr7:13594994-13595038	NM_001024699:133	Zbtb45	INSIDE	0.473	1.355	3694.32	5006.44	0.640	2654.12	1699.85
A_68_P26403090	chr9:31840408-31840452			Unknown	0.473	0.376	1630.61	613.81	0.178	1260.21	224.50
A_68_P22129173	chr3:51144733-51144777	ENSMUST00000135496:-174		PROMOTER	0.473	0.675	4449.62	3001.69	0.319	3463.98	1104.51
A_68_P23222740	chr4:114659326-114659370	NM_025647:485	Cmpk1	INSIDE	0.472	0.487	1647.80	802.03	0.230	1205.52	276.76
A_68_P31951138	chr19:10599754-10599798	NM_001164272:43	Cpsf7	INSIDE	0.472	0.479	1594.89	764.44	0.226	1409.44	319.07

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31157714	chr17:35257967-35258011	NM_009975:404	Csnk2b	INSIDE	0.472	0.713	1646.62	1174.39	0.336	1354.79	455.74
A_68_P21317590	chr2:70956135-70956179	NM_028593:46	Cybrd1	INSIDE	0.472	0.418	3059.45	1277.99	0.197	2248.01	443.31
A_68_P26016157	chr8:86239183-86239227	NM_197982:129	Ddx39	INSIDE	0.472	0.548	2210.33	1210.20	0.259	1900.00	491.19
A_68_P28419964	chr12:50485980-50486024	NM_008241:2009	Foxg1	INSIDE	0.472	0.553	2152.69	1189.94	0.261	1712.87	446.76
A_68_P25892523	chr8:60131751-60131795	NM_001167981:80	Galnt7	INSIDE	0.472	0.557	2676.26	1490.97	0.263	2155.19	566.67
A_68_P24449395	chr6:52195431-52195475	NR_015348:211	Hoxa11as	INSIDE	0.472	0.477	1110.75	529.39	0.225	889.37	200.15
A_68_P20739614	chr1:157590081-157590125	NM_010712:-945	Lhx4	PROMOTER	0.472	0.703	5881.13	4136.58	0.332	4653.92	1546.13
A_68_P27286341	chr10:80380635-80380679	NM_010722:334	Lmnb2	INSIDE	0.472	0.487	1673.95	814.70	0.230	1361.95	312.94
A_68_P31934035	chr19:6335704-6335748	NM_001168490:688	Men1	INSIDE	0.472	0.386	3461.25	1336.00	0.182	2378.54	432.94
A_68_P26144743	chr8:109948649-109948693	NM_026277:268	Nob1	INSIDE	0.472	0.543	964.11	523.06	0.256	858.72	220.12
A_68_P31640473	chr18:39648559-39648603	NM_008173:-1681	Nr3c1	PROMOTER	0.472	1.405	4421.18	6213.11	0.664	3063.80	2033.46
A_68_P26343622	chr9:20531703-20531748	NM_173777:933	Olfm2	INSIDE	0.472	0.370	2747.40	1015.49	0.174	2246.34	391.89
A_68_P30961944	chr16:91270214-91270258	NM_016968:223	Olig1	INSIDE	0.472	0.457	1283.92	587.13	0.216	1004.69	216.65
A_68_P31627038	chr18:37303465-37303509	NM_001003672:-136	Pcdhac2	PROMOTER	0.472	0.722	1640.17	1184.88	0.341	1425.13	486.14
A_68_P31985662	chr19:17468432-17468476	NM_019437:-78	Rfk	PROMOTER	0.472	0.417	3102.35	1293.67	0.197	2617.78	514.97
A_68_P22030177	chr3:30692267-30692311	NM_027016:491	Sec62	INSIDE	0.472	0.442	1312.52	580.65	0.209	1143.66	239.01
A_68_P28261127	chr12:15821624-15821668	NM_144551:1945	Trib2	INSIDE	0.472	0.419	2338.01	980.55	0.198	1791.67	354.29
A_68_P26372145	chr9:26541609-26541653	ENSMUST00000067362:195		INSIDE	0.472	0.604	2151.66	1300.39	0.285	1704.51	486.61
A_68_P29531802	chr14:35582497-35582541	ENSMUST00000143244:9106		INSIDE	0.472	0.620	2418.52	1498.84	0.293	1839.47	538.37
A_68_P24056049	chr5:123958827-123958871	NM_198611:-1620	B3gnt4	PROMOTER	0.471	0.661	2449.16	1620.11	0.312	2061.15	642.77
A_68_P27788009	chr11:50139294-50139338	NM_001110499:-141	Canx	PROMOTER	0.471	0.466	1378.00	642.66	0.220	1091.46	239.59
A_68_P30459325	chr15:95485192-95485236	NM_207533:-12	Dbx2	PROMOTER	0.471	0.699	1706.24	1192.21	0.329	1140.96	375.23
A_68_P32129171	chr19:43954139-43954183	NM_028029:32722	Dnmbp	INSIDE	0.471	0.428	3182.83	1361.88	0.201	2210.38	445.27
A_68_P21629726	chr2:130250214-130250258	NM_001114541:141	Fam113a	INSIDE	0.471	0.515	1386.82	714.78	0.243	1080.77	262.17
A_68_P30642673	chr16:30600225-30600275	NM_177632:442	Fam43a	INSIDE	0.471	0.502	1239.68	621.77	0.236	1011.07	239.09
A_68_P24793341	chr6:119429106-119429150	NM_133940:-557	Fbxl14	PROMOTER	0.471	1.354	3221.50	4360.39	0.638	2446.36	1561.18
A_68_P31063013	chr17:15115758-15115802	NM_001123367:-4	Gm3417	DIVERGENT_PROMOTER	0.471	0.517	1851.68	957.30	0.243	1691.50	411.68
A_68_P32095558	chr19:37509889-37509933	NM_008245:580	Hhex	INSIDE	0.471	0.509	1751.67	892.45	0.240	1582.63	379.54
A_68_P20832394	chr1:174256462-174256506	NM_008429:2910	Kcnj9	INSIDE	0.471	0.702	1531.96	1075.27	0.330	1106.62	365.65
A_68_P24038701	chr5:120885606-120885650	NM_008499:3734	Lhx5	INSIDE	0.471	0.399	2019.20	806.60	0.188	1501.33	282.27
A_68_P24764866	chr6:114232993-114233037	NM_178703:386	Slc6a1	INSIDE	0.471	0.533	1506.24	803.05	0.251	1206.57	302.85
A_68_P29937483	chr14:118635646-118635690	NM_177753:584	Sox21	INSIDE	0.471	0.649	2099.79	1362.56	0.305	1634.50	499.23
A_68_P29292646	chr13:105607347-105607391	NM_026075:50	Srek1ip1	INSIDE	0.471	0.441	1745.54	769.69	0.208	1192.85	247.69
A_68_P24164951	chr5:145993056-145993100	NM_028298:451	Zfp655	INSIDE	0.471	0.556	1210.41	672.50	0.262	1057.89	277.07
A_68_P24154098	chr5:143690981-143691026			Unknown	0.471	0.660	855.55	565.07	0.311	747.35	232.27
A_68_P28607942	chr12:87423668-87423712	NM_001199843:180	1700019E19Rik	INSIDE	0.470	0.595	2058.51	1224.67	0.280	1637.92	458.01
A_68_P20504209	chr1:107560642-107560686	NM_029349:227	2310035C23Rik	INSIDE	0.470	0.554	1750.35	969.90	0.260	1233.58	320.97
A_68_P28656381	chr12:96933833-96933877	NM_201518:3419	Flrt2	INSIDE	0.470	0.524	1366.33	715.37	0.246	1140.47	280.64
A_68_P22892660	chr4:47105120-47105164	NM_172693:318	Galnt12	INSIDE	0.470	0.618	991.77	612.74	0.290	756.44	219.62
A_68_P26622300	chr9:71333407-71333451	NM_001164793:-663	Grinl1a	PROMOTER	0.470	0.558	1220.55	681.52	0.262	1050.40	275.48
A_68_P28271880	chr12:17697825-17697869	NM_016677:227	Hpcal1	INSIDE	0.470	0.636	900.56	572.63	0.299	796.02	238.04
A_68_P22404200	chr3:106904965-106905010	NM_008417:503	Kcna2	INSIDE	0.470	0.491	1476.98	725.75	0.231	1028.24	237.46
A_68_P31130474	chr17:30026534-30026578	NM_001081160:-1729	Mdga1	PROMOTER	0.470	0.578	1314.33	759.29	0.271	1054.23	286.10
A_68_P28301679	chr12:27099772-27099816	NM_001081977:327	Rnf144a	INSIDE	0.470	0.623	3090.85	1926.55	0.293	2339.86	685.71
A_68_P20945779	chr1:194661281-194661325	NM_001177794:16639	Sertad4	DOWNSTREAM	0.470	0.428	1399.41	598.48	0.201	1143.28	229.72
A_68_P27165511	chr10:58276497-58276541	NM_172788:412	Sh3rf3	INSIDE	0.470	0.573	1509.66	865.21	0.270	1204.93	324.88
A_68_P21101533	chr2:29989110-29989161	NM_146252:-255	Tbc1d13	DIVERGENT_PROMOTER	0.470	0.705	1526.27	1075.63	0.331	1120.23	370.66
A_68_P25004262	chr7:25101544-25101588	NM_001199321:119	Zfp94	INSIDE	0.470	0.719	2015.64	1448.31	0.338	1391.49	470.18
A_68_P21421302	chr2:91042978-91043022	NM_007387:-68	Acp2	DIVERGENT_PROMOTER	0.469	0.553	1544.97	853.77	0.259	1194.36	309.42
A_68_P24674230	chr6:97567022-97567066	NM_145148:607	Frmd4b	INSIDE	0.469	0.572	1018.31	582.90	0.268	869.90	233.50
A_68_P24992976	chr7:19967388-19967432	NR_030759:-4581	Mir343	PROMOTER	0.469	0.538	1121.89	603.12	0.252	935.90	236.16

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P24051803	chr5:123158016-123158060	NM_011026:473	P2rx4	INSIDE	0.469	0.538	1178.68	634.53	0.252	925.97	233.59
A_68_P27109366	chr10:44786725-44786769	NM_011156:-273	Prep	PROMOTER	0.469	0.630	1146.19	722.10	0.295	977.61	288.59
A_68_P24137873	chr5:140302698-140302742	NM_025604:77	Psmg3	INSIDE	0.469	0.585	1517.65	888.49	0.275	1208.26	331.73
A_68_P26260677	chr8:129494964-129495008	NM_172762:-7	Rbm34	PROMOTER	0.469	0.470	1410.04	663.32	0.221	1205.66	266.11
A_68_P30152564	chr15:39028639-39028683	NM_053271:-1217	Rims2	PROMOTER	0.469	0.685	1621.62	1110.15	0.321	1135.29	364.41
A_68_P26044784	chr8:91566566-91566616	NM_021390:1471	Sall1	INSIDE	0.469	0.628	1205.93	756.78	0.294	986.55	290.39
A_68_P32340125	chrX:39264784-39264828	NM_001033422:272	Thoc2	INSIDE	0.469	1.577	6527.99	10294.78	0.740	2716.10	2010.36
A_68_P27850821	chr11:61668019-61668063	NM_013881:554	Ulk2	INSIDE	0.469	0.615	921.91	566.85	0.289	894.06	258.08
A_68_P20778493	chr1:164501104-164501148	NM_016796:168	Vamp4	INSIDE	0.469	0.563	2489.20	1400.49	0.264	2284.57	602.27
A_68_P27589657	chr11:11016303-11016347	NM_177033:2306	Vwc2	INSIDE	0.469	0.643	1224.08	786.97	0.302	1031.46	311.26
A_68_P21388692	chr2:83484476-83484520	NM_026934:-236	Zc3h15	PROMOTER	0.469	0.602	1674.83	1008.09	0.282	1220.88	344.55
A_68_P25504797	chr7:134398221-134398265	NM_177362:10203	Zfp771	INSIDE	0.469	0.439	1289.62	566.25	0.206	989.47	203.64
A_68_P20192515	chr1:44159202-44159246	NM_029368:9	1700029F09Rik	INSIDE	0.468	0.483	1667.14	805.58	0.226	1423.63	321.98
A_68_P24449865	chr6:52264311-52264355	NR_038163:494	5730457N03Rik	INSIDE	0.468	0.442	1882.45	831.31	0.207	1404.11	290.39
A_68_P28612719	chr12:88223642-88223689	NM_145836:2099	6430527G18Rik	INSIDE	0.468	0.594	1052.63	625.27	0.278	853.20	237.12
A_68_P31369877	chr17:78600790-78600834	NM_015800:1225	Crim1	INSIDE	0.468	0.707	1646.14	1163.88	0.331	1227.24	406.36
A_68_P26240286	chr8:126038854-126038898	NM_001170976:479	Dbndd1	INSIDE	0.468	0.633	1393.98	881.80	0.296	1074.10	317.89
A_68_P24602877	chr6:85019040-85019084	NM_177077:445	Exoc6b	INSIDE	0.468	0.490	1377.13	674.50	0.229	1065.92	244.36
A_68_P24620285	chr6:88140131-88140179	NM_008090:-8503	Gata2	PROMOTER	0.468	0.648	2131.57	1381.31	0.303	1653.83	501.27
A_68_P26586064	chr9:64989806-64989850	NM_008988:833	Igdcc3	INSIDE	0.468	0.560	1358.97	761.54	0.262	1042.01	273.08
A_68_P32142233	chr19:46210854-46210898	NM_008852:11939	Pitx3	INSIDE	0.468	0.469	2790.16	1308.54	0.219	2201.20	483.12
A_68_P22169681	chr3:58496575-58496620	NM_009174:-287	Siah2	PROMOTER	0.468	0.542	1220.30	661.62	0.254	847.22	215.09
A_68_P31924555	chr19:4712589-4712633	NM_021287:1388	Spnb3	INSIDE	0.468	0.565	1249.14	706.20	0.265	1019.90	270.06
A_68_P27628921	chr11:19825017-19825061	NM_033523:594	Spred2	INSIDE	0.468	0.469	4522.81	2122.40	0.220	3561.26	781.88
A_68_P31320371	chr17:69186413-69186457	NM_001206661:-41	Tmem200c	PROMOTER	0.468	0.599	1833.77	1098.41	0.281	1413.42	396.60
A_68_P22382659	chr3:102539232-102539276	NM_027533:562	Tspan2	INSIDE	0.468	0.485	3086.63	1495.77	0.227	2452.08	556.29
A_68_P23955157	A_68_P23955157			Unknown	0.468	4.729	398.85	1886.19	2.212	309.92	685.44
A_68_P24787430	chr6:118512210-118512259	NM_001081112:40	Ankrd26	INSIDE	0.467	0.595	2127.73	1265.26	0.277	1523.83	422.85
A_68_P32260572	chrX:11705418-11705462	NM_001168321:32041	Bcor	INSIDE	0.467	0.572	1644.76	940.80	0.267	615.99	164.54
A_68_P28175448	chr11:118902325-118902369	NM_013926:-119	Cbx8	PROMOTER	0.467	0.643	2083.81	1339.54	0.300	1467.55	440.81
A_68_P29627745	chr14:58017455-58017499	NM_030004:-156	Cryl1	PROMOTER	0.467	0.497	1504.53	747.01	0.232	1267.21	293.90
A_68_P26807068	chr9:107095792-107095844	NM_153413:38422	Dock3	INSIDE	0.467	5.465	905.88	4950.49	2.550	696.03	1774.54
A_68_P26585436	chr9:64880684-64880728	NM_028906:442	Dpp8	INSIDE	0.467	0.699	1563.21	1093.18	0.326	1063.72	347.30
A_68_P24658386	chr6:94650061-94650105	NM_008377:57	Lrig1	INSIDE	0.467	0.722	2034.01	1468.57	0.337	1755.80	592.25
A_68_P24377897	chr6:38501394-38501438	NM_001170849:-27	Luc7l2	PROMOTER	0.467	0.536	2359.55	1265.25	0.250	2165.71	541.85
A_68_P27922356	chr11:74584498-74584542	NM_026197:156	Mettl16	INSIDE	0.467	0.541	1514.82	819.63	0.253	1039.96	263.00
A_68_P21501839	chr2:106535501-106535545	NM_029837:-235	Mpped2	PROMOTER	0.467	0.609	1671.72	1017.64	0.284	1385.85	394.21
A_68_P22339050	chr3:94247442-94247486	NM_030116:207	Mrpl9	INSIDE	0.467	0.706	2630.32	1858.27	0.330	2047.71	676.03
A_68_P23281848	chr4:126430490-126430534	NM_011986:161	Ncdn	INSIDE	0.467	0.557	1957.44	1090.81	0.260	1608.46	418.21
A_68_P28875777	chr13:22099045-22099089	NM_019429:2544	Prss16	INSIDE	0.467	0.536	1015.41	544.28	0.250	861.09	215.62
A_68_P30778981	chr16:56037605-56037649	NM_029092:261	Rg9mtd1	INSIDE	0.467	0.420	1245.39	522.66	0.196	997.37	195.53
A_68_P24054149	chr5:123591328-123591372	NM_175092:-8712	Rhof	PROMOTER	0.467	0.477	1636.68	781.23	0.223	1258.59	280.63
A_68_P27045330	chr10:31328554-31328598	NM_001146349:955	Rnf217	INSIDE	0.467	0.463	2002.46	926.91	0.216	1624.02	351.12
A_68_P32234209	chrX:5977910-5977954	NM_001040459:670	Shroom4	INSIDE	0.467	1.426	3548.57	5061.29	0.666	1349.60	899.01
A_68_P25661257	chr8:12396498-12396542	NM_009233:1002	Sox1	INSIDE	0.467	0.699	2548.57	1781.43	0.326	1820.57	594.08
A_68_P28033247	chr11:94347425-94347469	NM_144827:-822	Spata20	PROMOTER	0.467	0.635	896.09	569.16	0.297	743.17	220.44
A_68_P31093747	chr17:23944056-23944100	NM_175229:3925	Srrm2	INSIDE	0.467	1.416	1224.30	1733.34	0.661	1023.49	676.73
A_68_P24104838	chr5:133017511-133017555	NM_177047:681	Auts2	INSIDE	0.466	0.677	1020.42	690.35	0.315	838.88	264.39
A_68_P21077003	chr2:26057606-26057650	NM_001039653:4448	Lhx3	INSIDE	0.466	0.441	2104.38	927.16	0.205	1689.06	346.69
A_68_P25279966	chr7:90018157-90018201	NM_175366:2336	Mex3b	INSIDE	0.466	0.598	945.76	565.74	0.279	699.85	195.23
A_68_P25948617	chr8:72426740-72426784	NM_023312:-305	Ndufa13	PROMOTER	0.466	0.541	1871.68	1012.20	0.252	1402.86	353.32

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31988616	chr19:17911313-17911358	NM_001190483:787	Pcsk5	INSIDE	0.466	0.599	1225.76	734.57	0.279	1047.43	292.23
A_68_P30447264	chr15:93331165-93331209	NM_001033217:95136	Prickle1	INSIDE	0.466	1.561	2699.48	4212.75	0.727	2023.69	1470.26
A_68_P20353660	chr1:75381669-75381713	NM_001085370:-494	Speg	PROMOTER	0.466	1.573	5132.50	8074.70	0.733	3395.55	2488.68
A_68_P27855417	chr11:62545135-62545179	NM_133208:-2561	Zfp287	PROMOTER	0.466	0.701	1194.57	837.43	0.327	992.98	324.31
A_68_P24155794	chr5:144031725-144031769	NM_017467:-45	Zfp316	PROMOTER	0.466	0.561	1936.11	1086.82	0.262	1548.00	404.81
A_68_P24973048	chr7:13388705-13388749	NM_026046:15483	Zfp329	DOWNSTREAM	0.466	0.697	1307.60	911.89	0.325	1083.63	351.86
A_68_P25021520	chr7:29164259-29164303	NM_011756:-33	Zfp36	PROMOTER	0.466	0.666	1620.87	1079.14	0.310	1331.10	413.27
A_68_P24010682	chr5:116081413-116081457	NR_027810:391	1110006O24Rik	INSIDE	0.465	0.585	1981.41	1158.76	0.272	1367.20	372.10
A_68_P22402613	chr3:106525217-106525262	NM_001039488:640	4933421E11Rik	INSIDE	0.465	0.674	3373.51	2272.66	0.313	2582.86	808.30
A_68_P20252945	chr1:57463017-57463061	NM_001081181:-353	9430016H08Rik	PROMOTER	0.465	0.573	1971.74	1129.97	0.266	1549.91	413.03
A_68_P28175797	chr11:118951776-118951826	NM_007625:-4249	Cbx4	PROMOTER	0.465	0.712	1396.94	995.03	0.332	1080.57	358.28
A_68_P27643749	chr11:22890683-22890727	NM_009837:112	Cct4	INSIDE	0.465	0.693	1394.15	966.78	0.322	1140.92	367.52
A_68_P20849636	chr1:177622240-177622284	NM_021350:-3778	Chml	PROMOTER	0.465	0.700	3019.19	2114.39	0.325	2048.46	666.65
A_68_P27259221	chr10:75356293-75356337	NM_024440:172	Derl3	INSIDE	0.465	0.597	1430.30	854.16	0.278	1172.62	325.43
A_68_P23609675	chr5:37187966-37188010	NM_026242:5	Mrfap1	INSIDE	0.465	0.470	1789.03	840.97	0.219	1560.60	341.40
A_68_P30883587	chr16:76293685-76293730	NM_173440:79587	Nrip1	INSIDE	0.465	1.378	2289.28	3155.19	0.640	1674.90	1072.31
A_68_P28269482	chr12:17273597-17273641	NM_027959:218	Pdia6	INSIDE	0.465	0.497	1277.94	634.88	0.231	976.51	225.42
A_68_P32071923	chr19:32831726-32831770	NM_008960:-318	Pten	PROMOTER	0.465	0.486	2005.36	974.46	0.226	1531.13	345.72
A_68_P32070012	chr19:32462008-32462052	NM_144792:914	Sgms1	INSIDE	0.465	0.636	2021.00	1284.89	0.295	1504.70	444.42
A_68_P30475041	chr15:98364232-98364276	NR_034052:-7364	Snora2b	PROMOTER	0.465	0.582	4763.06	2773.17	0.271	3439.02	931.88
A_68_P22393610	chr3:104667906-104667950	NM_153091:-70	St7l	DIVERGENT_PROMOTER	0.465	0.373	1659.75	618.42	0.173	1471.45	254.75
A_68_P21265453	chr2:61494424-61494471	NM_001164071:63294	Tank	DOWNSTREAM	0.465	0.591	1437.71	849.42	0.275	955.14	262.41
A_68_P30510672	chr16:4541712-4541756	NM_031182:17986	Tcfap4	DOWNSTREAM	0.465	0.579	1939.95	1122.57	0.269	1486.61	399.77
A_68_P27842504	chr11:60166452-60166496	NM_001039092:-67	Tom1l2	DIVERGENT_PROMOTER	0.465	0.454	1311.65	595.13	0.211	1114.16	234.83
A_68_P24459354	chr6:53770780-53770824	NM_025817:17	Tril	INSIDE	0.465	0.507	1818.07	922.10	0.236	1314.72	310.32
A_68_P20444769	chr1:93698784-93698828	NM_007855:753	Twist2	INSIDE	0.465	0.527	1498.21	789.11	0.245	1092.66	267.35
A_68_P28710685	chr12:106923369-106923413	NM_029654:61	Atg2b	INSIDE	0.464	0.489	1650.17	807.24	0.227	1234.84	280.45
A_68_P25951452	chr8:72900302-72900346	NM_016685:2878	Comp	INSIDE	0.464	0.556	1257.80	699.23	0.258	989.21	255.21
A_68_P20827968	chr1:173368006-173368050	NM_172647:337	F11r	INSIDE	0.464	0.415	2052.28	852.34	0.193	1636.65	315.13
A_68_P24129310	chr5:138635652-138635696	NM_177878:133	Mblac1	INSIDE	0.464	0.517	1585.64	819.11	0.239	1251.92	299.75
A_68_P23226097	chr4:115511687-115511731	NM_021461:-142	Mknk1	PROMOTER	0.464	0.598	2361.22	1413.00	0.278	1767.09	490.40
A_68_P27137647	chr10:52137521-52137565	NM_030250:190	Nus1	INSIDE	0.464	0.651	5850.61	3808.45	0.302	4439.83	1339.71
A_68_P27567708	chr11:6192040-6192084	NM_010956:463	Ogdh	INSIDE	0.464	0.572	2473.11	1415.47	0.265	2093.52	555.48
A_68_P31062916	chr17:15097920-15097964	NM_024250:295	Phf10	INSIDE	0.464	0.653	6295.84	4112.61	0.303	4914.93	1490.71
A_68_P21110351	chr2:31491732-31491776	NM_001123362:-3802	Prdm12	PROMOTER	0.464	0.703	1657.37	1165.20	0.326	1360.18	443.40
A_68_P20740065	chr1:157659643-157659687	NM_001024945:365	Qsox1	INSIDE	0.464	0.440	2015.71	886.96	0.204	1703.67	348.10
A_68_P23269837	chr4:124386139-124386183	NM_029157:-5944	Sf3a3	PROMOTER	0.464	0.728	3183.11	2317.38	0.338	2323.93	785.44
A_68_P26477291	chr9:45821396-45821440	NM_027498:516	Sik3	INSIDE	0.464	0.484	1634.85	790.55	0.225	1437.46	322.78
A_68_P31774240	chr18:64425610-64425654	NM_009182:11620	St8sia3	INSIDE	0.464	0.426	2867.14	1221.38	0.198	2108.09	416.43
A_68_P21070912	chr2:25110973-25111017	NM_177344:36	Tmem203	INSIDE	0.464	0.493	1972.73	973.27	0.229	1573.11	360.21
A_68_P28003255	chr11:88860965-88861009	NM_009546:270	Trim25	INSIDE	0.464	0.654	1701.70	1112.18	0.304	1229.69	373.28
A_68_P30499185	chr15:102523620-102523664			Unknown	0.464	0.651	1422.68	926.64	0.302	1174.67	354.81
A_68_P28755052	chr12:114394756-114394800	NM_134041:147	4930427A07Rik	INSIDE	0.463	0.324	1702.21	551.06	0.150	1313.65	196.77
A_68_P21773772	chr2:156688598-156688643	NR_015591:61	5430405H02Rik	INSIDE	0.463	0.535	1153.63	617.68	0.248	995.21	246.50
A_68_P31406130	chr17:85075448-85075492	NM_031884:6793	Abcg5	INSIDE	0.463	0.464	1145.15	530.85	0.215	984.79	211.54
A_68_P26017291	chr8:86479163-86479209	NM_024184:-406	Asf1b	PROMOTER	0.463	0.562	1330.21	747.39	0.260	1026.62	267.35
A_68_P24951853	chr7:5011977-5012021	NM_146178:3671	Ccdc106	INSIDE	0.463	0.432	1382.32	596.92	0.200	1177.84	235.28
A_68_P27795131	chr11:51464219-51464263	NR_027958:-215	D930048N14Rik	PROMOTER	0.463	0.509	1038.22	528.74	0.236	791.80	186.73
A_68_P29651209	chr14:62267312-62267356	NR_028264:33876	Dleu2	INSIDE	0.463	0.361	2229.34	804.10	0.167	1935.60	322.97
A_68_P23342688	chr4:137469440-137469484	NM_199307:51311	Ece1	INSIDE	0.463	0.548	1427.71	781.82	0.253	1358.60	344.25
A_68_P30501631	chr15:102865426-102865470	NM_013553:623	Hoxc4	INSIDE	0.463	0.569	2610.99	1486.39	0.264	1955.37	515.30

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31930561	chr19:5742058-5742102	NM_008520:1177	Ltbp3	INSIDE	0.463	0.603	951.02	573.22	0.279	751.16	209.65
A_68_P25581948	chr7:147233969-147234013	NM_010836:997	Msx3	INSIDE	0.463	0.570	1680.05	957.30	0.264	1210.76	319.27
A_68_P23310402	chr4:131700231-131700275	NM_013622:149	Oprd1	INSIDE	0.463	0.397	2616.83	1037.78	0.183	2323.33	426.26
A_68_P31029178	chr17:8995181-8995225	NM_011866:593	Pde10a	INSIDE	0.463	0.718	1523.98	1094.69	0.333	1280.21	425.82
A_68_P30650142	chr16:31933808-31933852	NM_172822:-106	Pigz	PROMOTER	0.463	0.582	1865.83	1086.52	0.270	1336.72	360.78
A_68_P23374047	chr4:142802126-142802170	NM_001081355:464	Prdm2	INSIDE	0.463	0.452	2303.49	1040.16	0.209	1772.34	370.54
A_68_P20023926	chr1:9738516-9738560	NM_173443:-75	Vcpip1	PROMOTER	0.463	0.472	1517.67	716.53	0.219	1190.45	260.22
A_68_P21017265	chr2:13496059-13496103	NM_011701:143	Vim	INSIDE	0.463	0.494	1039.25	512.94	0.228	894.88	204.34
A_68_P28072948	chr11:101126562-101126606	NM_175638:4704	Wnk4	INSIDE	0.463	0.619	977.66	605.58	0.287	880.52	252.40
A_68_P24864290	chr6:134877311-134877355	NR_037955:-1777	1190002F15Rik	PROMOTER	0.462	0.538	992.32	533.45	0.248	857.11	212.84
A_68_P30382913	chr15:82176419-82176463	NM_026914:-35	1500032L24Rik	PROMOTER	0.462	0.645	963.38	621.00	0.298	704.86	209.96
A_68_P23931758	chr5:101275769-101275813	NM_172715:543	Agpat9	INSIDE	0.462	0.479	1329.45	636.65	0.221	1183.39	261.82
A_68_P21760474	chr2:154262689-154262733	NM_009823:491	Cbfa2t2	INSIDE	0.462	0.638	1453.33	927.53	0.295	1239.88	365.91
A_68_P26505265	chr9:50536331-50536375	NM_178118:-263	Dixdc1	PROMOTER	0.462	0.709	1369.82	971.01	0.327	1114.03	364.82
A_68_P23527834	chr5:21290784-21290828	NM_009584:177	Dnajc2	INSIDE	0.462	0.621	2982.31	1851.15	0.287	2410.18	690.52
A_68_P31418995	chr17:87154659-87154703	NM_010137:1477	Epas1	INSIDE	0.462	0.551	1253.17	690.84	0.255	983.82	250.56
A_68_P25596355	chr7:149844923-149844967	NM_010514:-235	Igf2	DIVERGENT_PROMOTER	0.462	0.591	1490.03	880.28	0.273	1202.79	328.42
A_68_P30575512	chr16:17760349-17760393	NM_145479:657	Klhl22	INSIDE	0.462	0.607	1018.38	618.37	0.280	861.84	241.62
A_68_P24449267	chr6:52180763-52180807	NR_029912:-620	Mir196b	PROMOTER	0.462	0.517	1553.06	802.41	0.239	1186.13	283.41
A_68_P28987053	chr13:43011826-43011870	NM_001005740:206899	Phactr1	INSIDE	0.462	0.574	1020.04	585.88	0.265	896.87	237.93
A_68_P25957206	chr8:74031971-74032015	NM_032398:3676	Plvap	INSIDE	0.462	0.617	1776.78	1096.06	0.285	1370.90	390.45
A_68_P24995079	chr7:20334543-20334587	NM_008990:358	Pvrl2	INSIDE	0.462	0.691	1180.67	815.86	0.319	933.98	298.01
A_68_P20038592	chr1:12981645-12981695	NM_172841:-454	Slco5a1	PROMOTER	0.462	0.568	965.89	548.33	0.262	832.08	218.07
A_68_P22342446	chr3:94944251-94944296	NM_027206:2009	Tnfaip8l2	INSIDE	0.462	3.566	1855.17	6614.92	1.649	1356.31	2235.99
A_68_P28573970	chr12:81233412-81233456	NR_033514:397	2310015A10Rik	INSIDE	0.461	0.637	1584.81	1008.89	0.293	1205.71	353.78
A_68_P25265480	chr7:87377466-87377510	NM_011870:14	Cib1	INSIDE	0.461	0.745	3446.33	2567.13	0.344	2908.06	999.31
A_68_P31150248	chr17:33855451-33855495	NM_145486:143	Marchf2	INSIDE	0.461	0.518	1175.41	608.38	0.239	1107.68	264.24
A_68_P31411711	chr17:86014433-86014477	NR_038085:3282	Six3os1	INSIDE	0.461	0.645	1685.01	1087.39	0.297	1367.96	406.57
A_68_P22336405	chr3:93249236-93249280	NM_001163098:3007	Tchh	INSIDE	0.461	0.638	1908.11	1216.85	0.294	1482.56	435.74
A_68_P30534541	chr16:8831297-8831343	NM_001081400:1128	1810013L24Rik	INSIDE	0.460	0.671	952.04	638.54	0.309	786.53	242.84
A_68_P27894430	chr11:69154065-69154109	NR_027827:-184	A030009H04Rik	PROMOTER	0.460	0.634	885.96	561.45	0.291	805.19	234.60
A_68_P22058283	chr3:36374398-36374443	NM_009673:389	Anxa5	INSIDE	0.460	0.527	1028.66	542.16	0.243	753.08	182.64
A_68_P33016567	chr7:3424267-3424311	NM_133183:-1134	Cacng6	PROMOTER	0.460	0.707	1435.58	1015.24	0.325	1202.52	391.28
A_68_P26346391	chr9:21095271-21095315	NM_009878:361	Cdkn2d	INSIDE	0.460	0.729	2772.31	2022.37	0.336	2033.06	682.14
A_68_P25416680	chr7:118172636-118172680	NM_009431:194	Ctr9	INSIDE	0.460	0.650	2433.92	1581.60	0.299	1903.35	569.24
A_68_P26893206	chr9:123022552-123022596	NM_001081188:226	Exosc7	INSIDE	0.460	0.574	1057.47	606.69	0.264	795.13	209.92
A_68_P22149457	chr3:54539042-54539086	NM_001163570:222	Exosc8	INSIDE	0.460	0.630	1649.62	1039.92	0.290	1283.20	372.50
A_68_P24084080	chr5:129107459-129107503	NM_175284:500	Fzd10	INSIDE	0.460	0.627	951.34	596.55	0.289	832.58	240.41
A_68_P28989503	chr13:43398780-43398824	NM_001033399:739	Gfod1	INSIDE	0.460	0.576	954.66	549.71	0.265	777.04	205.71
A_68_P22767952	chr4:19968906-19968950	NM_010281:-270	Ggh	PROMOTER	0.460	0.505	1565.98	790.84	0.232	1284.93	298.32
A_68_P21339129	chr2:74565400-74565445	NM_010469:5388	Hoxd4	INSIDE	0.460	0.542	1058.17	574.00	0.250	952.19	237.60
A_68_P27956333	chr11:80593206-80593250	NM_177390:299	Myo1d	INSIDE	0.460	0.582	1144.28	666.42	0.268	911.42	244.25
A_68_P22129479	chr3:51212850-51212894	NM_025523:5	Ndufc1	INSIDE	0.460	0.562	1329.95	747.02	0.258	1022.55	264.13
A_68_P24981705	chr7:17060954-17060998	NM_008718:1153	Npas1	INSIDE	0.460	0.485	3392.34	1645.38	0.223	2717.13	606.84
A_68_P26640630	chr9:74711042-74711086	NM_008262:1337	Onecut1	INSIDE	0.460	0.364	1579.97	575.84	0.167	1299.53	217.67
A_68_P29480406	chr14:26722448-26722492	NM_207229:-91	Plac9	PROMOTER	0.460	0.565	3136.69	1773.15	0.260	2624.34	681.90
A_68_P24991720	chr7:19734447-19734491	NM_026111:77	Qpctl	INSIDE	0.460	0.398	1844.63	734.75	0.183	1385.49	253.69
A_68_P27540138	chr10:127650212-127650256	NM_025716:-1384	Spryd4	PROMOTER	0.460	0.631	1205.34	761.02	0.290	963.34	279.75
A_68_P30350971	chr15:76701517-76701566	NM_001007568:324	Zfp251	INSIDE	0.460	0.482	1470.61	708.58	0.222	1068.10	236.65
A_68_P30345601	chr15:75865270-75865314	ENSMUST00000100531:25794		INSIDE	0.460	1.432	1031.41	1477.28	0.659	983.97	648.22
A_68_P31936460	chr19:6930124-6930168	NM_001081291:2555	Ccdc88b	INSIDE	0.459	0.654	2669.86	1745.79	0.300	2085.51	626.56

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31619631	chr18:35862603-35862647	NM_029669:174	Dnajc18	INSIDE	0.459	0.616	1100.69	677.79	0.283	794.98	224.68
A_68_P22311355	chr3:87827371-87827415	NM_022031:4041	Hapln2	INSIDE	0.459	0.567	2341.18	1326.68	0.260	1900.76	493.92
A_68_P23349538	chr4:138631686-138631730	NM_021358:-1004	Htr6	PROMOTER	0.459	0.532	1016.76	540.52	0.244	826.12	201.40
A_68_P31601053	chr18:32227655-32227699	NM_173441:289	Iws1	INSIDE	0.459	0.618	1034.83	640.04	0.284	873.82	248.01
A_68_P20739566	chr1:157584400-157584444	NM_010712:4735	Lhx4	INSIDE	0.459	0.420	2129.12	894.97	0.193	1586.13	306.27
A_68_P30423403	chr15:88970637-88970681	NM_013871:475	Mapk12	INSIDE	0.459	0.565	1890.77	1067.54	0.259	1426.09	369.87
A_68_P31934033	chr19:6335488-6335532	NM_001168490:472	Men1	INSIDE	0.459	0.544	2134.24	1160.38	0.250	1686.74	421.39
A_68_P30295270	chr15:66800532-66800576	NM_008681:649	Ndrg1	INSIDE	0.459	0.395	1964.70	775.97	0.181	1550.23	280.93
A_68_P22558741	chr3:136333499-136333554	NM_008913:-207	Ppp3ca	PROMOTER	0.459	3.774	706.40	2666.24	1.734	568.58	985.80
A_68_P25962573	chr8:75247186-75247230	NM_001113248:22	Sin3b	INSIDE	0.459	0.500	3570.22	1785.07	0.230	2824.00	648.27
A_68_P20599492	chr1:130141015-130141059	NM_026390:279	Ubxn4	INSIDE	0.459	0.650	4640.72	3016.78	0.299	3399.53	1014.81
A_68_P22727922	chr4:11003062-11003106	NM_001085493:267	2310030N02Rik	INSIDE	0.458	0.608	1158.70	704.54	0.279	1073.45	299.16
A_68_P22346423	chr3:95733097-95733141	NM_023210:-61	Anp32e	PROMOTER	0.458	0.579	1126.65	652.73	0.265	910.30	241.52
A_68_P26345696	chr9:20954248-20954292	NM_016742:80	Cdc37	INSIDE	0.458	0.666	1284.61	855.41	0.305	942.60	287.57
A_68_P27176094	chr10:60149519-60149563	NM_023370:9698	Cdh23	INSIDE	0.458	0.684	2090.96	1430.59	0.313	1654.88	518.23
A_68_P22071613	chr3:38786725-38786769	NM_183221:885	Fat4	INSIDE	0.458	0.447	1492.68	666.98	0.205	1218.04	249.52
A_68_P29531954	chr14:35633533-35633577	NM_008166:233	Grid1	INSIDE	0.458	0.386	1652.93	637.33	0.177	1325.29	234.11
A_68_P25511565	chr7:135754795-135754839	NM_178641:-62	Inpp5f	PROMOTER	0.458	1.619	4253.80	6888.80	0.741	2914.50	2160.59
A_68_P21495934	chr2:105512616-105512660	NR_002867:-2151	Pax6os1	DIVERGENT_PROMOTER	0.458	0.519	1891.55	980.89	0.238	1399.98	332.81
A_68_P28041052	chr11:95692092-95692136	NM_153104:6301	Phospho1	INSIDE	0.458	0.647	1197.54	774.64	0.296	953.21	282.31
A_68_P23239474	chr4:117963100-117963144	NM_011213:880	Ptprf	INSIDE	0.458	0.464	2532.80	1174.08	0.212	1971.67	418.30
A_68_P27924763	chr11:75006899-75006943	NM_177708:-574	Rtn4rl1	DIVERGENT_PROMOTER	0.458	0.689	3535.73	2436.76	0.316	2509.06	792.08
A_68_P23195471	chr4:108000991-108001035	NM_027250:256	2010305A19Rik	INSIDE	0.457	0.734	5938.42	4356.88	0.336	4483.10	1504.40
A_68_P31864632	chr18:80665927-80665971	NM_026295:458	Ctdp1	INSIDE	0.457	0.543	2390.19	1297.01	0.248	1893.54	469.66
A_68_P20831244	chr1:174078454-174078498	NM_153555:331	Dcaf8	INSIDE	0.457	0.637	1517.09	966.18	0.291	1265.46	368.01
A_68_P30672033	chr16:35768842-35768886	NM_153550:578	Dirc2	INSIDE	0.457	0.605	1297.65	785.52	0.277	1184.21	327.64
A_68_P22407676	chr3:107434272-107434316	NM_153563:334	Fam40a	INSIDE	0.457	0.655	836.35	548.10	0.299	731.28	218.93
A_68_P24533907	chr6:70906387-70906431	NM_001101464:-191	Foxi3	PROMOTER	0.457	0.683	5098.82	3483.92	0.313	3316.49	1036.53
A_68_P30503777	chr15:103196605-103196649	NM_010577:553	Itga5	INSIDE	0.457	0.686	1752.04	1201.09	0.314	1377.01	431.76
A_68_P23156636	chr4:101390083-101390127	NM_010704:93	Lepr	INSIDE	0.457	0.542	1020.14	552.64	0.247	822.63	203.49
A_68_P24424404	chr6:47763266-47763310	NR_030485:-9637	Mir704	PROMOTER	0.457	0.621	1463.61	908.59	0.284	1072.58	304.09
A_68_P30369725	chr15:79844779-79844823	NM_011057:438	Pdgfb	INSIDE	0.457	0.450	1476.58	664.16	0.206	1097.39	225.69
A_68_P28741728	chr12:112276886-112276930	NM_198023:-1100	Rcor1	PROMOTER	0.457	0.494	1409.67	696.75	0.226	1096.84	247.53
A_68_P29700849	chr14:70750941-70750985	NM_001135152:-2722	Slc39a14	PROMOTER	0.457	0.737	2377.00	1752.80	0.337	1666.45	561.36
A_68_P26578203	chr9:63605811-63605855	NM_016769:-31	Smad3	PROMOTER	0.457	0.727	3276.63	2383.28	0.332	2138.08	710.59
A_68_P23395556	chr4:148000439-148000483	NM_001003898:645	Tardbp	INSIDE	0.457	0.400	1581.02	632.18	0.183	1092.36	199.45
A_68_P21266443	chr2:61650440-61650484	NM_009322:7953	Tbr1	INSIDE	0.457	0.568	1269.99	721.43	0.260	934.88	242.89
A_68_P32709178	chrX:139116482-139116526	NM_001199360:236	Tmem164	INSIDE	0.457	1.485	2611.94	3879.23	0.678	1209.09	820.00
A_68_P22324425	chr3:90097634-90097678	AK015985:249		INSIDE	0.457	0.629	1415.22	890.87	0.288	1161.57	334.38
A_68_P21755516	chr2:153356263-153356307	NM_001134300:-577	8430427H17Rik	PROMOTER	0.456	0.516	1139.99	587.97	0.235	889.87	209.24
A_68_P30646211	chr16:31200561-31200605	NM_030138:742	Acap2	INSIDE	0.456	0.483	2455.17	1186.49	0.220	1973.96	434.60
A_68_P25954408	chr8:73363586-73363630	NM_027560:11	Arrdc2	INSIDE	0.456	0.684	1297.47	887.59	0.312	956.10	298.18
A_68_P21094142	chr2:28771352-28771396	NM_019446:567	Barhl1	INSIDE	0.456	0.532	2671.45	1421.37	0.243	1808.28	438.59
A_68_P26402553	chr9:31721424-31721468	NM_013800:-576	Barx2	PROMOTER	0.456	0.621	2599.53	1613.81	0.283	2212.96	626.13
A_68_P31947333	chr19:9973849-9973893	NM_016692:153	Incenp	INSIDE	0.456	0.477	1230.50	586.85	0.218	1017.30	221.28
A_68_P21614869	chr2:127481863-127481907	NM_001171187:547	Mal	INSIDE	0.456	0.626	1145.91	717.62	0.286	964.41	275.64
A_68_P31126966	chr17:29400812-29400856	NM_026845:82	Ppil1	INSIDE	0.456	0.638	856.35	546.57	0.291	691.51	201.38
A_68_P24983572	chr7:17428015-17428059	NM_178900:-377	Prkd2	PROMOTER	0.456	0.494	2352.31	1161.71	0.225	1719.73	387.17
A_68_P24617030	chr6:87540705-87540749	NM_021381:-31	Prokr1	PROMOTER	0.456	0.625	3507.50	2192.63	0.285	2620.70	747.45
A_68_P21740962	chr2:150612685-150612729	NM_153781:175	Pygb	INSIDE	0.456	0.406	1854.77	752.86	0.185	1403.78	259.68
A_68_P25378793	chr7:109590580-109590624	NM_009103:394	Rrm1	INSIDE	0.456	0.540	6626.39	3578.50	0.246	4678.80	1151.19

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26809364	chr9:107437458-107437502	NM_019704:1205	Tmem115	INSIDE	0.456	0.565	1452.86	820.34	0.258	1061.04	273.42
A_68_P27836025	chr11:59103487-59103531	NM_009522:745	Wnt3a	INSIDE	0.456	0.276	2543.26	702.85	0.126	2027.03	255.69
A_68_P26342513	chr9:20264224-20264268	NM_011753:358	Zfp26	INSIDE	0.456	0.465	1580.60	735.40	0.212	1286.51	272.85
A_68_P27534361	chr10:126607747-126607791	NM_027739:4882	B4galnt1	INSIDE	0.455	0.603	1381.62	833.06	0.274	1141.31	312.97
A_68_P28959954	chr13:38438568-38438612	NM_007556:1006	Bmp6	INSIDE	0.455	0.672	2248.38	1510.00	0.306	1846.10	564.08
A_68_P31144187	chr17:32326072-32326116	NM_001033163:314	Ephx3	INSIDE	0.455	0.659	856.19	564.20	0.300	710.80	212.91
A_68_P30988901	chr16:95923763-95923807	NM_011809:-229	Ets2	PROMOTER	0.455	0.704	1608.77	1131.97	0.320	1315.41	421.38
A_68_P32117993	chr19:42007635-42007679	NM_001164561:148	Exosc1	INSIDE	0.455	0.493	1540.43	759.64	0.225	1328.72	298.39
A_68_P28540453	chr12:75008595-75008639	NM_010431:-237	Hif1a	PROMOTER	0.455	0.537	1693.26	909.27	0.244	1303.66	318.38
A_68_P30348596	chr15:76307956-76308000	NM_008296:104	Hsf1	INSIDE	0.455	0.471	2542.92	1197.92	0.214	2038.31	437.16
A_68_P24117359	chr5:136164594-136164638	NM_008898:-467	Por	PROMOTER	0.455	0.638	1615.63	1031.25	0.291	1284.71	373.31
A_68_P21101128	chr2:29921642-29921686	NM_001204875:-329	Set	PROMOTER	0.455	1.532	2617.19	4010.37	0.697	1966.23	1369.69
A_68_P30574557	chr16:17576828-17576872	NM_144852:-86	Slc7a4	PROMOTER	0.455	0.647	1637.39	1060.01	0.295	1311.48	386.28
A_68_P27294068	chr10:82322231-82322275	NM_001042514:-833	Txnrd1	PROMOTER	0.455	0.527	1103.64	581.49	0.240	897.92	215.07
A_68_P24974109	chr7:13593102-13593146	NM_001024699:2025	Zbtb45	INSIDE	0.455	4.787	1387.92	6643.87	2.179	1483.31	3232.05
A_68_P24128899	chr5:138558291-138558335	NM_001044703:180	Zscan21	INSIDE	0.455	0.563	2698.96	1520.41	0.256	2005.35	514.03
A_68_P32537730	chrX:91423475-91423519			Unknown	0.455	0.381	2836.08	1079.72	0.173	1399.97	242.55
A_68_P23339579	chr4:136944180-136944224	ENSMUST00000078305:-7005		PROMOTER	0.455	0.576	2205.65	1269.81	0.262	1709.42	448.02
A_68_P20714686	chr1:153275868-153275912	NM_026876:113	1190005F20Rik	INSIDE	0.454	0.485	2219.62	1075.83	0.220	1708.71	376.26
A_68_P28566337	chr12:79962384-79962437	NM_023721:215	Atp6v1d	INSIDE	0.454	0.573	1049.72	601.31	0.260	785.99	204.55
A_68_P21425372	chr2:91762936-91762980	NM_007699:613	Chrm4	INSIDE	0.454	0.711	1921.16	1365.93	0.323	1516.66	489.31
A_68_P26170772	chr8:114414651-114414695	NM_019950:19427	Chst5	INSIDE	0.454	1.456	1248.02	1817.02	0.660	1085.04	716.47
A_68_P22614659	chr3:146113265-146113309	NM_028836:-170	Ctbs	PROMOTER	0.454	0.492	1523.72	748.91	0.223	1212.16	270.64
A_68_P26135758	chr8:108282379-108282423	NM_027469:107	Gfod2	INSIDE	0.454	0.610	1234.17	753.37	0.277	938.18	259.84
A_68_P23329301	chr4:135126386-135126430	NM_001013756:3127	Grhl3	INSIDE	0.454	0.536	1452.22	779.08	0.243	1232.79	300.01
A_68_P28382007	chr12:41750810-41750854	NM_053122:156	Immp2l	INSIDE	0.454	0.572	2021.80	1155.65	0.260	1681.86	436.50
A_68_P32029540	chr19:25484871-25484921	NM_181404:173205	Kank1	INSIDE	0.454	3.394	1099.41	3731.11	1.542	863.42	1331.51
A_68_P27285553	chr10:80260510-80260554	NM_023900:839	Plekhj1	INSIDE	0.454	0.603	2912.80	1757.28	0.274	2105.75	576.33
A_68_P24126056	chr5:137943558-137943602	NM_028753:77	Pop7	INSIDE	0.454	0.587	983.88	578.02	0.267	845.07	225.53
A_68_P21637466	chr2:131735690-131735734	NM_011170:49	Prnp	INSIDE	0.454	0.529	1511.50	800.01	0.240	1246.66	299.47
A_68_P28190286	chr11:121249176-121249220	NM_139147:367	Rab40b	INSIDE	0.454	0.532	1436.73	764.37	0.242	1136.18	274.43
A_68_P27968801	chr11:82684323-82684367	NM_001164570:-98	Rffl	PROMOTER	0.454	0.455	1610.47	732.36	0.207	1231.36	254.43
A_68_P21820737	chr2:164786214-164786258	NM_020333:-7251	Slc12a5	PROMOTER	0.454	0.449	1368.56	615.03	0.204	1130.89	230.65
A_68_P30507721	chr16:4003615-4003659	NM_177472:-1956	Slx4	PROMOTER	0.454	0.362	1657.73	600.28	0.164	1289.18	211.83
A_68_P21101536	chr2:29989398-29989442	NM_146252:30	Tbc1d13	INSIDE	0.454	0.639	1289.64	824.39	0.290	948.16	275.09
A_68_P27083334	chr10:40022291-40022335	NM_009665:-318	Amd1	PROMOTER	0.453	0.540	1626.28	877.98	0.245	1254.26	306.87
A_68_P30641650	chr16:30388204-30388248	NM_001128094:390	Atp13a3	INSIDE	0.453	0.669	2570.18	1719.18	0.303	1876.88	568.63
A_68_P30589167	chr16:20716459-20716503	NM_009900:229	Clcn2	INSIDE	0.453	0.662	2648.65	1752.21	0.299	2376.23	711.54
A_68_P31330088	chr17:71012118-71012162	NM_001128181:101054	Dlgap1	INSIDE	0.453	1.496	2328.12	3482.04	0.678	1758.63	1192.07
A_68_P30180493	chr15:44259134-44259178	NM_175009:-500	Eny2	PROMOTER	0.453	0.422	1473.45	621.13	0.191	1181.77	225.44
A_68_P28120311	chr11:109583661-109583705	NM_153782:-112	Fam20a	PROMOTER	0.453	0.419	1787.46	748.26	0.190	1397.89	265.27
A_68_P29410630	chr14:13173724-13173771	NM_080433:4632	Fezf2	DOWNSTREAM	0.453	0.655	1059.17	693.65	0.296	846.28	250.92
A_68_P31863131	chr18:80433374-80433418	NM_001136181:10445	Hsbp1l1	INSIDE	0.453	0.493	1290.37	635.51	0.223	987.13	220.39
A_68_P24905346	chr6:142519942-142519986	NM_008428:-88	Kcnj8	PROMOTER	0.453	0.725	1854.73	1345.34	0.328	1478.94	485.44
A_68_P31516117	chr18:15308896-15308940	NM_134112:1037	Kctd1	INSIDE	0.453	0.679	1313.21	891.68	0.307	1025.35	315.20
A_68_P26716009	chr9:90009071-90009118	NM_001039147:564	Morf4l1	INSIDE	0.453	0.666	964.42	642.65	0.302	718.09	216.88
A_68_P22317892	chr3:89018127-89018171	NM_001161824:109	Mtx1	INSIDE	0.453	0.623	1854.34	1155.55	0.282	1487.06	419.54
A_68_P30961940	chr16:91269862-91269906	NM_016968:-129	Olig1	PROMOTER	0.453	0.521	1364.64	711.16	0.236	1158.15	273.66
A_68_P22878366	chr4:44676950-44676994	NM_008782:46340	Pax5	INSIDE	0.453	0.427	2104.81	898.28	0.193	1633.81	316.01
A_68_P26345767	chr9:20969656-20969700	NM_183408:-479	Pde4a	PROMOTER	0.453	0.615	2161.01	1329.88	0.279	1648.17	459.14
A_68_P28197877	chr12:3960273-3960317	NM_008895:5344	Pomc	INSIDE	0.453	0.503	2050.65	1031.25	0.228	1527.45	347.64

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28738223	chr12:111685895-111685939	NM_001135001:528	Ppp2r5c	INSIDE	0.453	0.484	1922.49	930.95	0.219	1473.75	323.19
A_68_P28186389	chr11:120582623-120582667	NM_133223:-137	Rac3	PROMOTER	0.453	0.512	2079.93	1065.18	0.232	1557.23	361.05
A_68_P22958420	chr4:59819277-59819321	NM_172468:777	Snx30	INSIDE	0.453	0.594	1284.35	762.54	0.269	988.56	265.67
A_68_P26717019	chr9:90165367-90165411	NM_194334:219	Tbc1d2b	INSIDE	0.453	0.582	1498.80	872.68	0.264	1262.42	332.92
A_68_P20052698	chr1:15795876-15795920	NM_009352:160	Terf1	INSIDE	0.453	0.461	1961.90	903.56	0.209	1491.05	311.09
A_68_P29569510	chr14:45839181-45839225	NM_172597:-133	Txndc16	DIVERGENT_PROMOTER	0.453	0.628	1068.30	671.23	0.284	530.92	150.99
A_68_P23400518	chr4:148800981-148801025	NM_022022:-262	Ube4b	PROMOTER	0.453	0.412	1376.42	567.31	0.187	1115.89	208.26
A_68_P26158468	chr8:112217560-112217604	NM_028018:-388	2400003C14Rik	PROMOTER	0.452	0.537	1559.31	838.02	0.243	1307.15	317.74
A_68_P29086263	chr13:60704015-60704059	NM_134062:465	Dapk1	INSIDE	0.452	0.621	1345.19	834.79	0.281	1021.44	286.60
A_68_P20351170	chr1:74947336-74947380	NR_029876:-63	Mir375	PROMOTER	0.452	0.411	2496.18	1026.47	0.186	2081.25	386.55
A_68_P26224549	chr8:123632350-123632394	NM_001166482:-93	Mthfsd	DIVERGENT_PROMOTER	0.452	0.640	1591.65	1018.46	0.289	1282.58	371.18
A_68_P27280977	chr10:79565295-79565339	NM_183426:131	Sbno2	INSIDE	0.452	0.463	3369.65	1558.55	0.209	2384.72	498.98
A_68_P26084862	chr8:98240139-98240183	NM_001035123:348	Setd6	INSIDE	0.452	0.669	1856.95	1242.26	0.303	1431.39	433.21
A_68_P26142250	chr8:109460044-109460088	NM_009229:417	Sntb2	INSIDE	0.452	0.514	1474.45	758.31	0.233	1244.93	289.51
A_68_P27542562	chr10:128106343-128106387	NM_173733:4610	Suox	DOWNSTREAM	0.452	0.510	1549.51	790.34	0.231	1277.90	294.62
A_68_P24994892	chr7:20301207-20301251	NM_001109748:-450	Tomm40	PROMOTER	0.452	0.561	1535.10	861.57	0.254	1205.67	305.93
A_68_P21579905	chr2:121097022-121097066	NM_013735:78	Trp53bp1	INSIDE	0.452	0.566	2441.59	1381.63	0.256	2012.26	514.89
A_68_P21092313	chr2:28496774-28496818	NM_022887:34	Tsc1	INSIDE	0.452	0.459	1582.59	726.76	0.208	1399.56	290.56
A_68_P24002095	chr5:114581570-114581614	NM_011677:428	Ung	INSIDE	0.452	0.669	1632.59	1092.65	0.303	1191.18	360.56
A_68_P24992403	chr7:19857732-19857776	NM_009499:-551	Vasp	PROMOTER	0.452	0.450	2584.13	1162.00	0.203	1938.30	393.84
A_68_P31402642	chr17:84495931-84495975	AK043195:-259		PROMOTER	0.452	0.713	1365.11	972.77	0.322	1076.71	347.05
A_68_P26003886	chr8:83866274-83866319	ENSMUST00000172167:-158		PROMOTER	0.452	0.633	1575.62	997.33	0.286	1059.28	302.99
A_68_P25527991	chr7:138506051-138506095	NM_026655:140	2310057M21Rik	INSIDE	0.451	0.559	1087.60	607.53	0.252	826.45	208.07
A_68_P30150546	chr15:38591825-38591869	NM_025494:188	Atp6v1c1	INSIDE	0.451	0.473	1277.36	604.40	0.213	1026.16	218.75
A_68_P22893293	chr4:47221194-47221238	NM_009928:333	Col15a1	INSIDE	0.451	0.710	7261.14	5151.80	0.320	5222.86	1672.20
A_68_P23278939	chr4:125911753-125911803	NM_001145970:21785	Mtap7d1	INSIDE	0.451	3.465	1273.29	4411.55	1.561	1031.98	1610.84
A_68_P31632701	chr18:38371127-38371171	NM_029357:-1732	Pcdh1	PROMOTER	0.451	0.621	1033.23	641.43	0.280	816.26	228.68
A_68_P25394039	chr7:112885744-112885788	NM_133951:133	Rrp8	INSIDE	0.451	0.447	1606.94	718.98	0.202	1312.88	264.64
A_68_P23482832	chr5:12383399-12383443	NM_028882:255	Sema3d	INSIDE	0.451	0.596	900.43	536.53	0.269	755.21	202.92
A_68_P29581357	chr14:47896981-47897025	NM_080843:185	Socs4	INSIDE	0.451	0.405	1761.55	714.21	0.183	1369.28	250.22
A_68_P21017268	chr2:13496366-13496411	NM_011701:451	Vim	INSIDE	0.451	0.547	1184.67	647.92	0.247	982.22	242.37
A_68_P27269570	chr10:77127215-77127259			Unknown	0.451	3.138	1643.33	5156.80	1.414	1093.83	1546.98
A_68_P27268621	chr10:76978260-76978304	NM_133998:276	1810008A18Rik	INSIDE	0.450	0.667	4574.43	3053.04	0.301	3239.55	973.60
A_68_P26217968	chr8:122638484-122638528	NM_001163762:455	6430548M08Rik	INSIDE	0.450	0.479	1376.07	658.56	0.216	1101.84	237.56
A_68_P21732682	chr2:148700871-148700915	NM_009976:312	Cst3	INSIDE	0.450	0.434	1634.82	709.94	0.196	1360.69	266.14
A_68_P22592456	chr3:142428233-142428277	NM_145546:44	Gtf2b	INSIDE	0.450	0.642	847.40	544.06	0.289	819.62	236.77
A_68_P28269095	chr12:17182821-17182865	NM_201531:852	Kcnf1	INSIDE	0.450	0.449	1330.17	597.50	0.202	1061.87	214.59
A_68_P28748127	chr12:113382080-113382124	NM_001097621:-2316	Kif26a	PROMOTER	0.450	0.280	1974.31	553.61	0.126	1580.17	199.56
A_68_P27262214	chr10:75931729-75931773	NM_019434:35	Mcm3ap	INSIDE	0.450	0.287	2471.94	708.97	0.129	1970.94	254.13
A_68_P20413379	chr1:88566390-88566434	NM_010933:736	Nppc	INSIDE	0.450	0.533	1446.19	770.17	0.240	1313.60	314.67
A_68_P23354457	chr4:139384411-139384455	NM_011039:4451	Pax7	INSIDE	0.450	0.584	995.36	581.26	0.263	732.20	192.58
A_68_P28451629	chr12:56499790-56499834	NM_011968:1	Psma6	INSIDE	0.450	0.659	975.07	642.35	0.297	837.49	248.53
A_68_P22215786	chr3:68297563-68297607	NR_036665:-530	Schip1	PROMOTER	0.450	0.428	3152.94	1348.73	0.193	2472.58	476.28
A_68_P25957540	chr8:74093690-74093734	NM_011977:887	Slc27a1	INSIDE	0.450	0.570	1188.11	677.45	0.257	973.27	249.67
A_68_P31924553	chr19:4712434-4712478	NM_021287:1234	Spnb3	INSIDE	0.450	0.671	1349.97	905.28	0.302	1028.50	310.31
A_68_P30512951	chr16:4964673-4964717	NM_028301:-364	Anks3	PROMOTER	0.449	0.465	1447.41	672.81	0.209	1062.93	221.98
A_68_P20350882	chr1:74902485-74902529	NM_009872:904	Cdk5r2	INSIDE	0.449	0.526	1585.72	834.75	0.236	1345.40	317.89
A_68_P25501141	chr7:133709739-133709783	NM_146200:120	Eif3c	INSIDE	0.449	0.584	3014.82	1759.84	0.262	2498.26	654.79
A_68_P23363149	chr4:140847557-140847601	NM_010139:-9576	Epha2	PROMOTER	0.449	0.512	2369.62	1212.75	0.230	2188.99	503.54
A_68_P21717106	chr2:146048812-146048856	NM_016889:1102	Insm1	INSIDE	0.449	0.614	980.36	601.66	0.275	894.71	246.48
A_68_P29240038	chr13:96095444-96095488	NR_035461:-5068	Mir1940	PROMOTER	0.449	0.288	2883.13	830.94	0.129	1613.99	208.88

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28071861	chr11:100948728-100948772	NM_001159384:147	Mlx	INSIDE	0.449	0.677	2486.91	1683.29	0.304	1903.81	578.81
A_68_P32143069	chr19:46379412-46379456	NM_019408:-750	Nfkb2	PROMOTER	0.449	0.447	2686.41	1201.59	0.201	2112.99	424.67
A_68_P27940753	chr11:77797545-77797589	NM_174852:1249	Phf12	INSIDE	0.449	0.475	1363.64	647.40	0.213	995.82	212.38
A_68_P26011763	chr8:85387565-85387609	NM_177378:332	Rnf150	INSIDE	0.449	0.656	2195.76	1439.35	0.294	1638.72	482.49
A_68_P27924778	chr11:75008653-75008697	NM_177708:1180	Rtn4rl1	INSIDE	0.449	0.669	1853.26	1239.36	0.300	1264.66	379.64
A_68_P25957549	chr8:74094641-74094686	NM_011977:1838	Slc27a1	INSIDE	0.449	0.487	1901.62	925.32	0.218	1411.90	308.25
A_68_P28189252	chr11:121066090-121066134	NM_025402:-150	1110031I02Rik	DIVERGENT_PROMOTER	0.448	0.729	3435.64	2503.65	0.326	2421.51	789.79
A_68_P25376021	chr7:109054423-109054467	NM_025605:94	2400001E08Rik	INSIDE	0.448	0.552	1499.79	827.77	0.247	1242.59	307.04
A_68_P31624569	chr18:36720617-36720661	NM_175375:382	Ankhd1	INSIDE	0.448	0.678	2049.77	1388.83	0.303	1603.52	486.33
A_68_P22291860	chr3:84387008-84387052	NM_001081093:-483	Arfip1	PROMOTER	0.448	0.631	1815.87	1146.56	0.283	1516.57	428.80
A_68_P21904962	chr2:180333066-180333110	NM_009936:162	Col9a3	INSIDE	0.448	0.686	2689.73	1844.72	0.307	2069.64	636.14
A_68_P30677440	chr16:36828175-36828219	NM_001113401:149	Eaf2	INSIDE	0.448	0.380	1847.89	702.56	0.170	1422.12	242.02
A_68_P24674231	chr6:97567120-97567164	NM_145148:509	Frmd4b	INSIDE	0.448	0.560	5348.50	2992.85	0.251	3784.83	949.10
A_68_P20432928	chr1:91819533-91819577	NM_010262:8197	Gbx2	DOWNSTREAM	0.448	0.565	3982.53	2251.11	0.253	3110.31	787.09
A_68_P28067614	chr11:100217488-100217532	NM_010404:-55	Hap1	PROMOTER	0.448	0.575	1133.08	651.98	0.258	869.63	224.19
A_68_P28831963	chr13:12488087-12488132	NM_144835:468	Heatr1	INSIDE	0.448	0.645	1517.25	978.13	0.289	1224.65	353.51
A_68_P28107584	chr11:107408339-107408383	NM_198298:-913	Helz	PROMOTER	0.448	0.609	1674.35	1019.42	0.273	1294.31	353.21
A_68_P27924565	chr11:74979765-74979809	NM_001098203:1868	Hic1	INSIDE	0.448	0.469	1230.09	577.15	0.210	904.45	189.90
A_68_P21902326	chr2:179960119-179960164	NM_001081171:423	Lama5	INSIDE	0.448	0.542	1267.02	686.26	0.243	999.45	242.55
A_68_P27281304	chr10:79613780-79613824	NM_021565:2768	Midn	INSIDE	0.448	0.690	3230.35	2229.42	0.309	2156.27	667.21
A_68_P30559115	chr16:13819208-13819252	NM_010946:-139	Ntan1	PROMOTER	0.448	0.613	2042.89	1252.94	0.275	1488.62	409.32
A_68_P30402716	chr15:85566360-85566404	NM_011144:177	Ppara	INSIDE	0.448	0.641	1474.90	945.52	0.287	1247.55	358.42
A_68_P30576622	chr16:17927537-17927581	NM_153150:754	Slc25a1	INSIDE	0.448	0.688	2021.54	1390.20	0.308	1549.55	477.85
A_68_P24034078	chr5:120130938-120130982	NM_011535:10283	Tbx3	INSIDE	0.448	0.550	1811.26	996.52	0.247	1513.80	373.50
A_68_P22749335	chr4:15193708-15193752	NM_181401:764	Tmem64	INSIDE	0.448	0.676	1452.89	982.25	0.303	1103.47	334.06
A_68_P20405966	chr1:84835679-84835723	NM_133975:179	Trip12	INSIDE	0.448	0.673	1931.43	1299.19	0.301	1759.24	530.16
A_68_P31102173	chr17:25325952-25325996	NM_001197024:630	Unkl	INSIDE	0.448	1.411	4361.39	6154.12	0.632	2988.51	1887.80
A_68_P30245925	chr15:57908333-57908377	NM_001042438:-310	Zhx1	PROMOTER	0.448	0.556	4504.29	2502.28	0.249	3468.84	863.28
A_68_P31075497	chr17:18047147-18047191	ENSMUST00000054871:22353		INSIDE	0.448	0.614	1242.77	763.11	0.275	1007.40	277.12
A_68_P32206524	chr19:57388995-57389039	ENSMUST00000111524:385		INSIDE	0.448	0.509	1524.90	775.46	0.228	1236.17	281.55
A_68_P25286562	chr7:91234889-91234933	NM_030728:105	9930013L23Rik	INSIDE	0.447	0.527	1669.55	879.18	0.235	1386.10	326.40
A_68_P24248435	chr6:13627675-13627719	NM_175312:270	B630005N14Rik	INSIDE	0.447	0.495	3160.95	1563.50	0.221	2444.29	540.72
A_68_P21428540	chr2:92274280-92274324	NM_009963:-76	Cry2	PROMOTER	0.447	0.485	2280.66	1106.33	0.217	1641.36	355.74
A_68_P29287622	chr13:104710157-104710201	NM_001005868:416	Erbb2ip	INSIDE	0.447	0.588	906.33	532.94	0.263	751.27	197.52
A_68_P22149452	chr3:54538552-54538602	NM_001163570:710	Exosc8	INSIDE	0.447	0.611	1174.63	717.56	0.273	917.47	250.67
A_68_P25273836	chr7:88907300-88907346	NM_025997:-516	Fam103a1	PROMOTER	0.447	0.581	1321.11	767.84	0.260	919.68	239.14
A_68_P25960243	chr8:74743668-74743712	NM_026455:62	Fam32a	INSIDE	0.447	0.668	1673.26	1117.32	0.299	1291.04	385.48
A_68_P25151575	chr7:64847050-64847094	NM_008071:530	Gabrb3	INSIDE	0.447	0.689	3099.78	2136.00	0.308	2431.03	748.86
A_68_P21766452	chr2:155418422-155418466	NM_008180:-2	Gss	PROMOTER	0.447	0.552	1662.28	917.93	0.247	1326.07	327.25
A_68_P27788210	chr11:50191797-50191841	NM_021510:598	Hnrnph1	INSIDE	0.447	0.742	2420.16	1794.73	0.332	1721.94	571.11
A_68_P29187684	chr13:83884882-83884926	NR_029545:6486	Mir9-2	DOWNSTREAM	0.447	0.594	1137.36	675.25	0.265	980.16	260.10
A_68_P21038062	chr2:17979342-17979387	NM_010804:2467	Mllt10	INSIDE	0.447	0.488	2359.60	1151.21	0.218	1771.60	386.70
A_68_P30961643	chr16:91220441-91220485	NM_016967:-5332	Olig2	PROMOTER	0.447	0.632	1232.36	778.97	0.283	856.94	242.19
A_68_P28107295	chr11:107340618-107340662	NM_025894:-201	Psmd12	DIVERGENT_PROMOTER	0.447	0.554	2323.51	1288.02	0.248	1839.94	456.38
A_68_P28164253	chr11:117151685-117151737	NM_001113487:24151	Septin9	INSIDE	0.447	4.153	316.04	1312.54	1.858	334.15	620.91
A_68_P28585118	chr12:83270099-83270143	NM_001167983:-882	Sipa1l1	PROMOTER	0.447	0.569	2305.16	1312.09	0.255	1793.11	456.73
A_68_P28549762	chr12:76770236-76770280	NM_028203:266	Wdr89	INSIDE	0.447	0.735	2446.61	1797.08	0.328	1847.07	606.24
A_68_P31879113	chr18:83078968-83079012	NM_183033:-1280	Zfp516	PROMOTER	0.447	1.389	7263.72	10088.54	0.621	4919.39	3053.47
A_68_P31159054	chr17:35496374-35496419	M19687:92581		INSIDE	0.447	0.631	1620.29	1021.71	0.282	1269.53	357.71
A_68_P24973681	chr7:13513425-13513470	NM_029809:683	2310014L17Rik	INSIDE	0.446	0.693	1574.98	1091.79	0.309	1150.74	355.56
A_68_P30378498	chr15:81415923-81415967	NM_177821:-699	Ep300	PROMOTER	0.446	0.582	2195.96	1278.50	0.260	1852.88	481.32

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P23416730	chr4:151506015-151506059	NM_019585:-3002	Espn	PROMOTER	0.446	0.720	3184.73	2291.50	0.321	2404.06	771.46
A_68_P28043444	chr11:96145749-96145793	NM_010461:2552	Hoxb8	INSIDE	0.446	0.539	3451.12	1861.77	0.241	2677.95	644.60
A_68_P28041910	chr11:95866408-95866452	NM_009951:828	Igf2bp1	INSIDE	0.446	0.728	1676.59	1220.03	0.325	1247.96	405.26
A_68_P28033523	chr11:94382882-94382926	NM_170671:-88	Mycbpap	PROMOTER	0.446	0.536	1774.96	951.92	0.239	1290.63	308.88
A_68_P22063505	chr3:37318090-37318134	NM_153561:400	Nudt6	INSIDE	0.446	0.595	1766.22	1050.41	0.265	1459.60	387.04
A_68_P31985663	chr19:17468572-17468616	NM_019437:62	Rfk	INSIDE	0.446	0.493	2174.07	1070.79	0.219	1675.67	367.73
A_68_P31024851	chr17:7374165-7374209	NM_011299:-277	Rps6ka2	PROMOTER	0.446	0.713	3137.62	2236.78	0.318	2286.50	726.99
A_68_P30370943	chr15:80064789-80064834	NM_178719:302	Smcr7l	INSIDE	0.446	0.655	1700.27	1113.63	0.292	1248.21	364.91
A_68_P24114432	chr5:135517814-135517858	NM_016801:18395	Stx1a	INSIDE	0.446	1.396	2378.55	3320.29	0.623	1640.68	1022.52
A_68_P22552061	chr3:135101698-135101742	NM_025356:-2	Ube2d3	DIVERGENT_PROMOTER	0.446	0.590	1701.83	1003.69	0.263	1466.57	385.37
A_68_P28078911	chr11:102180801-102180845	NM_011551:-412	Ubtf	PROMOTER	0.446	0.652	1379.17	898.69	0.291	1087.62	316.34
A_68_P28034315	chr11:94538289-94538333	NM_145828:497	Xylt2	INSIDE	0.446	0.588	3266.40	1920.22	0.262	2479.69	650.03
A_68_P23562834	chr5:28785352-28785396	NR_015562:-8149	9530036O11Rik	PROMOTER	0.445	0.664	5162.24	3429.44	0.296	3919.25	1159.80
A_68_P24792873	chr6:119339010-119339056	NM_197985:28469	Adipor2	INSIDE	0.445	0.561	2349.05	1317.51	0.249	1921.58	479.31
A_68_P28185536	chr11:120459969-120460013	NM_001038230:145	Anapc11	INSIDE	0.445	0.675	1691.06	1141.57	0.300	1408.93	423.21
A_68_P23332634	chr4:135762412-135762456	NM_001008232:155	Asap3	INSIDE	0.445	1.456	5422.86	7897.83	0.649	3741.92	2426.99
A_68_P23513995	chr5:18733341-18733385	NM_001170746:499	Magi2	INSIDE	0.445	0.584	1843.20	1076.15	0.260	1232.77	320.52
A_68_P23006649	chr4:70195250-70195294	NM_172694:690	Megf9	INSIDE	0.445	0.493	1476.67	728.09	0.220	1292.16	283.64
A_68_P32016082	chr19:23215759-23215803	NR_035423:-8140	Mir1192	PROMOTER	0.445	0.468	2544.85	1192.17	0.209	2104.26	438.85
A_68_P21820019	chr2:164658808-164658852	NM_001082974:266	Neurl2	INSIDE	0.445	0.576	2329.81	1342.62	0.256	1695.38	434.57
A_68_P24052509	chr5:123299880-123299924	NM_030564:-294	Rnf34	PROMOTER	0.445	0.663	969.86	643.23	0.295	778.82	230.07
A_68_P27936387	chr11:77029678-77029722	NM_177710:-226	Ssh2	PROMOTER	0.445	0.529	1386.73	733.42	0.235	1221.69	287.33
A_68_P20346773	chr1:74144944-74144988	NM_027884:26055	Tns1	INSIDE	0.445	0.456	1362.03	621.17	0.203	1054.48	213.78
A_68_P29672993	chr14:65977836-65977880	NM_199029:346	Zfp395	INSIDE	0.445	0.659	1259.26	829.55	0.293	1109.18	325.14
A_68_P25504739	chr7:134387875-134387919	NM_177362:-143	Zfp771	PROMOTER	0.445	0.593	1789.04	1060.87	0.264	1419.08	374.74
A_68_P27081279	chr10:39618779-39618823	NR_033628:244	AA474331	INSIDE	0.444	0.601	1486.98	893.63	0.267	1342.12	357.96
A_68_P25354923	chr7:105457417-105457461	NM_025408:599	Acer3	INSIDE	0.444	0.693	1705.31	1181.82	0.308	1299.88	399.96
A_68_P21907441	chr2:180701664-180701708	NM_001177707:-243	Arfgap1	PROMOTER	0.444	0.549	1007.37	552.64	0.244	750.71	182.98
A_68_P29856056	chr14:102039512-102039556	NM_001033132:154	Commd6	INSIDE	0.444	0.524	2094.58	1098.22	0.233	1458.91	339.78
A_68_P22609959	chr3:145313007-145313055	NM_010516:-81	Cyr61	PROMOTER	0.444	0.515	1021.54	525.69	0.229	776.44	177.50
A_68_P29747596	chr14:79132794-79132838	NM_001081336:-7920	Dgkh	PROMOTER	0.444	0.562	3136.63	1762.77	0.250	2305.16	575.59
A_68_P31286837	chr17:63229431-63229475	NM_010109:1214	Efna5	INSIDE	0.444	0.545	1056.23	575.46	0.242	786.12	190.15
A_68_P20825994	chr1:172994223-172994267	NM_010188:-4710	Fcgr3	PROMOTER	0.444	3.466	22821.82	79103.15	1.540	15614.41	24042.33
A_68_P31985484	chr19:17430865-17430909	NM_173442:271	Gcnt1	INSIDE	0.444	0.580	1236.59	717.45	0.258	1024.58	263.86
A_68_P21331222	chr2:73224458-73224502	NM_001190297:-25	Gpr155	PROMOTER	0.444	0.566	4010.01	2269.44	0.251	3134.06	787.82
A_68_P28882355	chr13:23673495-23673539	NM_175654:46	Hist1h4d	INSIDE	0.444	0.577	1228.26	708.59	0.256	898.56	230.00
A_68_P27862273	chr11:63732747-63732791	NM_018805:3018	Hs3st3b1	INSIDE	0.444	0.489	1102.67	539.65	0.217	913.95	198.59
A_68_P31516121	chr18:15309314-15309358	NM_134112:619	Kctd1	INSIDE	0.444	0.498	1951.11	971.09	0.221	1433.41	316.92
A_68_P21339749	chr2:74664060-74664104	NM_016804:214	Mtx2	INSIDE	0.444	0.467	1450.60	677.58	0.208	1291.15	268.03
A_68_P27536453	chr10:126971246-126971290	NM_183297:347	Nxph4	INSIDE	0.444	0.595	1610.34	957.72	0.264	1084.93	286.51
A_68_P22778520	chr4:22416842-22416887	NM_008899:-1586	Pou3f2	PROMOTER	0.444	0.539	1130.02	609.17	0.240	929.50	222.69
A_68_P23317226	chr4:132925776-132925820	NM_016981:112	Slc9a1	INSIDE	0.444	0.553	2591.34	1434.14	0.246	2238.00	549.81
A_68_P31118766	chr17:27976996-27977040	NM_011432:-13	Snrpc	PROMOTER	0.444	0.525	2298.67	1206.29	0.233	1889.17	439.82
A_68_P27044450	chr10:31165279-31165323	NM_009413:427	Tpd52l1	INSIDE	0.444	1.523	2312.79	3521.38	0.675	1632.74	1102.72
A_68_P30255505	chr15:59479171-59479215	NM_144549:-1016	Trib1	PROMOTER	0.444	0.602	942.82	567.58	0.267	726.19	193.97
A_68_P31722243	chr18:55147517-55147561	NM_175751:2296	Zfp608	INSIDE	0.444	0.413	1266.85	523.68	0.184	982.38	180.48
A_68_P32259782	chrX:11583929-11583973			Unknown	0.444	0.697	2404.83	1676.41	0.309	963.03	297.75
A_68_P21747319	chr2:151874059-151874103			Unknown	0.444	0.608	1098.52	668.35	0.270	908.39	245.48
A_68_P25671550	chr8:13975017-13975061	NM_173744:-261	2610019F03Rik	PROMOTER	0.443	0.550	1658.24	911.69	0.244	1268.81	309.06
A_68_P30958537	chr16:90727677-90727721	NM_025642:-82	2610039C10Rik	PROMOTER	0.443	0.419	2239.70	938.37	0.186	1728.55	320.74
A_68_P25267240	chr7:87679859-87679903	NM_007550:4	Blm	INSIDE	0.443	0.388	2732.14	1061.30	0.172	2245.55	386.81

						Sham group			TiO$_2$-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P23202006	chr4:109338923-109338967	NM_007671:-967	Cdkn2c	PROMOTER	0.443	0.593	1474.25	874.55	0.263	1226.01	322.23
A_68_P21566329	chr2:118640037-118640081	NM_026412:320	D2Ertd750e	INSIDE	0.443	1.588	15642.42	24845.41	0.703	10913.54	7672.78
A_68_P23363150	chr4:140847720-140847764	NM_010139:-9412	Epha2	PROMOTER	0.443	0.548	1558.73	853.96	0.243	1193.32	289.60
A_68_P25371474	chr7:108256833-108256877	NM_001146010:-434	Fchsd2	PROMOTER	0.443	0.409	1624.10	664.34	0.181	1226.50	222.45
A_68_P22030513	chr3:30755322-30755366	NM_001134385:473	Gpr160	INSIDE	0.443	0.555	2154.68	1195.23	0.246	1568.11	385.21
A_68_P20193921	chr1:44608865-44608909	NM_028450:371	Gulp1	INSIDE	0.443	0.456	2276.31	1037.24	0.202	1793.04	362.10
A_68_P27452133	chr10:111409980-111410024	NM_178610:252	Krr1	INSIDE	0.443	0.542	1265.23	685.94	0.240	884.31	212.47
A_68_P27154483	chr10:55835222-55835266	NM_001163833:8522	Msl3l2	INSIDE	0.443	0.444	1207.43	535.66	0.197	935.63	184.04
A_68_P22220270	chr3:69121308-69121352	NM_178726:491	Ppm1l	INSIDE	0.443	0.526	1482.27	779.49	0.233	1208.68	281.64
A_68_P27080344	chr10:39452278-39452323	NM_011264:335	Rev3l	INSIDE	0.443	0.567	1488.42	844.16	0.251	1117.16	280.88
A_68_P28974163	chr13:40823956-40824000	NM_001122948:1834	Tcfap2a	INSIDE	0.443	1.386	4339.19	6013.21	0.614	3160.68	1941.24
A_68_P31092956	chr17:23810793-23810838	NM_001008425:-78	Thoc6	PROMOTER	0.443	0.613	2258.70	1383.83	0.271	1685.84	457.61
A_68_P24164945	chr5:145992341-145992385	NM_001083958:-221	Zfp655	PROMOTER	0.443	0.599	1108.91	664.54	0.265	960.77	255.03
A_68_P30496553	chr15:102034646-102034690	NM_153194:-4029	Zfp740	PROMOTER	0.443	0.497	1135.27	564.41	0.220	894.13	196.99
A_68_P31215566	chr17:48168538-48168582	AK007241:6683		DOWNSTREAM	0.443	0.665	2308.10	1533.89	0.294	1577.82	464.11
A_68_P24686656	chr6:99472685-99472732	ENSMUST00000155466:144083		INSIDE	0.443	0.584	1226.42	715.75	0.259	909.21	235.18
A_68_P26135030	chr8:108160451-108160495	NM_181322:35	Ctcf	INSIDE	0.442	0.615	1113.39	684.51	0.271	911.29	247.39
A_68_P22305771	chr3:86723508-86723553	NM_001195496:1276	Dclk2	INSIDE	0.442	0.524	1049.98	550.62	0.232	924.09	214.13
A_68_P30600196	chr16:22858132-22858176	NM_001190804:237	Dnajb11	INSIDE	0.442	0.462	1650.30	763.25	0.204	1246.41	254.85
A_68_P26761641	chr9:98887034-98887078	NM_001122851:265	Faim	INSIDE	0.442	0.599	2072.05	1241.28	0.265	1863.64	493.75
A_68_P30589002	chr16:20693547-20693591	NM_133778:-1561	Fam131a	PROMOTER	0.442	1.654	4680.12	7740.39	0.730	3109.04	2270.27
A_68_P25609911	chr7:152081721-152081765	NM_008003:-694	Fgf15	PROMOTER	0.442	0.444	1253.54	556.52	0.196	989.14	193.93
A_68_P21116904	chr2:32549583-32549627	NM_010236:91	Fpgs	INSIDE	0.442	0.533	2061.20	1098.37	0.236	1755.02	413.65
A_68_P21565618	chr2:118529436-118529480	NM_001081971:241	Gm1337	INSIDE	0.442	0.518	1582.95	819.92	0.229	1202.22	275.24
A_68_P26847148	chr9:114842896-114842940	NM_175380:187	Gpd1l	INSIDE	0.442	0.646	1884.94	1217.44	0.285	1483.66	423.46
A_68_P28679268	chr12:101203451-101203495	NM_001164426:764	Kcnk13	INSIDE	0.442	0.736	2083.21	1532.32	0.325	1587.95	516.39
A_68_P26075899	chr8:96703109-96703153	NM_013602:142	Mt1	INSIDE	0.442	0.498	1026.81	511.41	0.220	911.68	200.51
A_68_P27282471	chr10:79786234-79786278	NM_008793:5962	Pcsk4	INSIDE	0.442	0.580	1614.05	936.13	0.257	1117.69	286.72
A_68_P21432195	chr2:92885557-92885608	NM_001177536:719	Prdm11	INSIDE	0.442	0.339	1532.01	519.27	0.150	1208.33	180.83
A_68_P26522114	chr9:53513817-53513861	NM_175562:499	Rab39	INSIDE	0.442	0.703	1514.20	1064.49	0.311	1219.90	379.01
A_68_P26948618	chr10:12728670-12728714	NM_175102:437	Sf3b5	INSIDE	0.442	0.533	2051.96	1092.68	0.235	1666.12	391.82
A_68_P28578875	chr12:82127694-82127738	NM_001146217:-78	Smoc1	PROMOTER	0.442	0.664	1497.68	994.72	0.294	1107.58	325.50
A_68_P26157753	chr8:112089724-112089768	NM_175646:-139	Txnl4b	DIVERGENT_PROMOTER	0.442	0.496	1241.52	615.33	0.219	986.23	215.99
A_68_P26232972	chr8:124900602-124900646	NM_001029993:109	Zc3h18	INSIDE	0.442	0.388	1718.34	666.76	0.171	1401.42	240.18
A_68_P27892698	chr11:68853700-68853744	NM_011496:-5422	Aurkb	PROMOTER	0.441	0.655	3670.83	2403.87	0.289	2532.99	730.83
A_68_P21516613	chr2:109517788-109517832	NM_001048139:1757	Bdnf	INSIDE	0.441	0.689	1157.11	797.50	0.304	929.69	282.59
A_68_P20600404	chr1:130313816-130313860	NM_177445:155	Dars	INSIDE	0.441	0.641	3398.23	2177.34	0.283	2341.08	662.18
A_68_P28100238	chr11:106078606-106078650	NM_028074:389	Ddx42	INSIDE	0.441	0.655	2883.28	1887.26	0.288	2163.76	624.04
A_68_P22318234	chr3:89070459-89070503	NM_026767:7	Dpm3	INSIDE	0.441	0.535	2096.22	1121.85	0.236	1553.58	366.66
A_68_P29699028	chr14:70478715-70478759	NM_018781:1485	Egr3	INSIDE	0.441	0.563	1355.65	763.34	0.248	993.42	246.71
A_68_P32227328	chr19:60887531-60887575	NM_001167829:80	Fam45a	INSIDE	0.441	0.501	1986.74	995.16	0.221	1578.45	348.66
A_68_P28530000	chr12:73171697-73171741	NM_181752:260	Gpr135	INSIDE	0.441	0.671	2296.17	1540.35	0.296	1759.27	519.91
A_68_P23332336	chr4:135703661-135703706	NM_008321:3947	Id3	DOWNSTREAM	0.441	0.505	1280.31	646.71	0.223	1010.68	225.39
A_68_P29616406	chr14:55733544-55733588	NM_177049:2206	Jph4	INSIDE	0.441	3.348	6057.86	20283.42	1.476	3752.85	5537.91
A_68_P23252895	chr4:120403760-120403804	NM_001081142:15999	Kcnq4	INSIDE	0.441	0.574	2018.15	1158.73	0.253	1578.47	399.81
A_68_P26343617	chr9:20530951-20530995	NM_173777:1686	Olfm2	INSIDE	0.441	0.539	1137.97	613.48	0.238	820.60	195.07
A_68_P24995078	chr7:20334418-20334462	NM_008990:482	Pvrl2	INSIDE	0.441	1.457	4703.29	6852.41	0.643	2952.10	1897.15
A_68_P31753490	chr18:60934321-60934365	NM_020600:93	Rps14	INSIDE	0.441	0.608	1030.88	626.42	0.268	766.85	205.72
A_68_P22286848	chr3:83570629-83570673	NM_009144:408	Sfrp2	INSIDE	0.441	0.580	3003.67	1742.06	0.256	2242.65	574.07
A_68_P31844546	chr18:77098668-77098712	NM_001109743:3547	Skor2	INSIDE	0.441	0.418	1625.46	679.48	0.185	1476.19	272.42
A_68_P27911317	chr11:72225169-72225213	NM_177776:25	Smtnl2	INSIDE	0.441	0.403	1735.43	698.68	0.177	1513.33	268.61

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27952008	chr11:79806189-79806233	NM_001163018:-397	Suz12	PROMOTER	0.441	0.572	915.55	524.12	0.252	779.33	196.59
A_68_P24057205	chr5:124170298-124170343	NM_027494:733	Zcchc8	INSIDE	0.441	0.346	2295.83	793.54	0.153	1866.38	284.69
A_68_P27968102	chr11:82578176-82578220	NM_025884:352	Zfp830	INSIDE	0.441	0.519	2850.36	1480.36	0.229	2169.05	496.36
A_68_P28350341	chr12:35592101-35592145	AK087563:-473		PROMOTER	0.441	0.654	1190.26	778.82	0.288	991.15	285.89
A_68_P27933172	chr11:76437300-76437344	ENSMUST00000155035:-1506		PROMOTER	0.441	0.624	2294.18	1431.63	0.276	1953.66	538.24
A_68_P31159056	chr17:35496669-35496713	M19687:92875		INSIDE	0.441	0.623	826.04	514.46	0.274	691.50	189.79
A_68_P27942255	chr11:78075391-78075435	NM_001002004:157	2610507B11Rik	INSIDE	0.440	0.526	2629.67	1382.05	0.231	1924.66	445.41
A_68_P30473516	chr15:97998981-97999025	NM_177716:766	AI836003	INSIDE	0.440	0.387	1924.31	743.77	0.170	1490.62	253.52
A_68_P27843675	chr11:60352579-60352623	NM_172943:1416	Alkbh5	INSIDE	0.440	0.495	1031.61	510.70	0.218	768.43	167.25
A_68_P26254625	chr8:128434525-128434569	NM_145608:197	BC021891	INSIDE	0.440	0.440	1331.18	586.11	0.194	1002.52	194.30
A_68_P27553119	chr11:3549485-3549529	NM_198162:-9196	Morc2a	PROMOTER	0.440	0.401	2147.12	860.50	0.176	1708.81	301.18
A_68_P30550105	chr16:11984315-11984359	NM_001174086:131	Shisa9	INSIDE	0.440	0.578	2001.15	1155.68	0.254	1514.02	385.06
A_68_P31930503	chr19:5731362-5731406	NM_020491:337	Sssca1	INSIDE	0.440	0.723	2204.80	1595.08	0.318	1671.91	531.85
A_68_P30476411	chr15:98608721-98608765	NM_011718:-161	Wnt10b	PROMOTER	0.440	0.662	1704.65	1127.74	0.291	1299.68	378.15
A_68_P20960102	chr1:197067849-197067893			Unknown	0.440	0.630	1025.93	645.86	0.277	798.20	221.16
A_68_P27646750	chr11:23533697-23533742	NM_027860:-88	0610010F05Rik	PROMOTER	0.439	0.620	1612.47	1000.42	0.272	1363.85	371.50
A_68_P30481999	chr15:99556228-99556272	NM_183256:202	2310016M24Rik	INSIDE	0.439	0.660	1722.97	1137.77	0.290	1309.47	379.55
A_68_P30686473	chr16:38522456-38522500	NM_024273:269	4930455C21Rik	INSIDE	0.439	0.485	1655.14	803.08	0.213	1287.88	274.02
A_68_P23293919	chr4:128602230-128602274	NM_172875:37409	Adc	DOWNSTREAM	0.439	0.704	1371.14	965.02	0.309	1094.55	338.56
A_68_P23230003	chr4:116269931-116269975	NR_029450:283	C530005A16Rik	INSIDE	0.439	0.628	1343.00	843.05	0.276	1099.52	303.25
A_68_P23439688	chr4:154998849-154998893	NM_007661:-107	Cdk11b	PROMOTER	0.439	0.482	1142.17	550.31	0.212	905.93	191.67
A_68_P30589275	chr16:20733601-20733645	NM_009893:423	Chrd	INSIDE	0.439	0.591	1890.77	1118.12	0.260	1433.01	372.01
A_68_P29047196	chr13:54150905-54150949	NM_010076:101	Drd1a	INSIDE	0.439	0.594	3805.06	2258.45	0.261	3019.15	786.63
A_68_P28072730	chr11:101087587-101087631	NM_007970:156	Ezh1	INSIDE	0.439	0.537	2728.69	1465.05	0.235	2056.54	484.28
A_68_P21903068	chr2:180069255-180069300	NM_008093:107	Gata5	INSIDE	0.439	0.542	1319.22	715.58	0.238	976.06	232.35
A_68_P27043768	chr10:31033252-31033296	NM_027168:64	Hddc2	INSIDE	0.439	0.610	1176.36	717.39	0.267	887.91	237.48
A_68_P24818962	chr6:125095826-125095870	NM_001039669:580	Iffo1	INSIDE	0.439	0.591	2255.04	1333.38	0.260	1958.61	508.31
A_68_P25010078	chr7:26165068-26165112	NM_001039507:10035	Lipe	INSIDE	0.439	0.459	1245.19	571.35	0.201	898.86	181.09
A_68_P22823553	chr4:32887074-32887124	NM_175364:-135	Lyrm2	PROMOTER	0.439	0.454	1133.03	514.86	0.200	944.85	188.67
A_68_P28197875	chr12:3960097-3960141	NM_008895:5168	Pomc	INSIDE	0.439	0.486	1905.28	926.48	0.213	1632.12	348.09
A_68_P24604720	chr6:85324839-85324883	NM_001003955:-232	Rab11fip5	PROMOTER	0.439	0.719	1662.08	1194.98	0.316	1279.46	404.09
A_68_P31412092	chr17:86084426-86084470	NM_011380:3146	Six2	INSIDE	0.439	0.648	2333.49	1511.04	0.284	1636.79	465.01
A_68_P22339767	chr3:94386067-94386111	NM_029721:536	Snx27	INSIDE	0.439	0.611	6243.91	3812.84	0.268	4648.40	1244.74
A_68_P31092987	chr17:23814347-23814391	NM_001161746:48	Tnfrsf12a	INSIDE	0.439	0.568	2157.24	1224.67	0.249	1778.86	443.64
A_68_P20858591	chr1:179189274-179189318	ENSMUST00000111159:-962		PROMOTER	0.439	0.645	1469.59	948.05	0.283	1227.30	347.22
A_68_P22029171	chr3:30494182-30494226	NM_029690:4588	Arpm1	DOWNSTREAM	0.438	0.628	1590.38	999.46	0.275	1188.76	327.46
A_68_P22822455	chr4:32702059-32702108	NM_001122978:-364	Casp8ap2	PROMOTER	0.438	0.588	1196.61	703.15	0.257	1015.33	261.36
A_68_P27171637	chr10:59414321-59414365	NM_029083:176	Ddit4	INSIDE	0.438	0.426	1369.55	584.01	0.187	1046.06	195.23
A_68_P28083893	chr11:103060694-103060738	NM_001077698:28265	Fmnl1	DOWNSTREAM	0.438	0.515	2513.03	1294.04	0.225	1828.85	412.35
A_68_P25766299	chr8:33994276-33994320	NM_001177589:66200	Gm3985	DOWNSTREAM	0.438	0.680	2856.05	1940.82	0.298	2150.00	640.63
A_68_P24186280	chr5:150438607-150438651	NM_013559:262	Hsph1	INSIDE	0.438	0.698	2606.55	1819.58	0.306	2104.52	643.74
A_68_P24326992	chr6:29457810-29457854	NM_001029985:120	Kcp	INSIDE	0.438	0.734	2819.38	2068.58	0.321	2183.45	700.91
A_68_P25256092	chr7:85723225-85723269	NM_008746:-522	Ntrk3	PROMOTER	0.438	0.647	1011.10	654.18	0.283	766.67	217.27
A_68_P26282995	chr9:6168715-6168768	NM_027924:130	Pdgfd	INSIDE	0.438	0.570	1318.34	751.53	0.250	1144.98	285.94
A_68_P21322066	chr2:71711031-71711075	NM_172665:-276	Pdk1	PROMOTER	0.438	0.474	2335.40	1106.96	0.207	1733.94	359.64
A_68_P28987052	chr13:43011760-43011804	NM_001005740:206833	Phactr1	INSIDE	0.438	0.656	2490.44	1634.25	0.287	2091.09	601.14
A_68_P23351037	chr4:138866350-138866394	NM_145384:243	Pqlc2	INSIDE	0.438	0.452	1914.53	864.68	0.198	1516.22	299.80
A_68_P30118688	chr15:32175071-32175115	NM_009154:525	Sema5a	INSIDE	0.438	0.645	1312.52	846.02	0.283	1106.30	312.62
A_68_P22324142	chr3:90052208-90052252	NM_013901:117	Slc39a1	INSIDE	0.438	0.508	1286.91	654.27	0.223	1118.40	248.91
A_68_P30572941	chr16:17276967-17277011	NM_177473:596	Tmem191c	INSIDE	0.438	0.513	1018.12	522.72	0.225	875.56	197.04
A_68_P32118291	chr19:42056116-42056160	NM_145500:-114	Ubtd1	DIVERGENT_PROMOTER	0.438	0.640	2745.78	1757.67	0.281	2175.59	610.50

						Sham group			TiO$_2$-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31092275	chr17:23684173-23684217	NM_001033496:16999	Zfp213	DOWNSTREAM	0.438	0.694	1466.01	1017.79	0.304	1135.55	345.69
A_68_P20893091	chr1:185857997-185858041	NM_028516:-141	1700056E22Rik	DIVERGENT_PROMOTER	0.437	0.657	861.33	565.99	0.287	713.63	205.10
A_68_P20148960	chr1:36604078-36604122	NM_026241:-54	Ankrd39	PROMOTER	0.437	0.390	1415.38	551.80	0.170	1034.18	176.20
A_68_P25022917	chr7:29415899-29415943	NM_175319:114	C330005M16Rik	INSIDE	0.437	0.520	1440.02	748.27	0.227	1222.21	277.84
A_68_P28175804	chr11:118952556-118952600	NM_007625:-5027	Cbx4	PROMOTER	0.437	0.467	1441.59	672.56	0.204	1179.66	240.53
A_68_P25011515	chr7:26503925-26503969	NM_028771:126	Ccdc97	INSIDE	0.437	0.397	2050.70	813.70	0.173	1600.72	277.58
A_68_P23527832	chr5:21290509-21290553	NM_009584:453	Dnajc2	INSIDE	0.437	0.671	1741.11	1167.70	0.293	1419.28	415.80
A_68_P21339241	chr2:74578701-74578745	NM_010468:28673	Hoxd3	INSIDE	0.437	0.593	1239.05	734.25	0.259	898.72	232.99
A_68_P28377236	chr12:40949170-40949214	NM_013562:584	Ifrd1	INSIDE	0.437	0.528	1354.55	715.20	0.231	1160.77	267.99
A_68_P24828020	chr6:126595162-126595206	NM_010595:635	Kcna1	INSIDE	0.437	0.607	1548.56	939.63	0.265	1216.48	322.52
A_68_P23006657	chr4:70196174-70196218	NM_172694:-234	Megf9	PROMOTER	0.437	0.589	1971.72	1161.27	0.257	1607.21	413.20
A_68_P30575818	chr16:17807580-17807624	NM_153790:10228	Scarf2	INSIDE	0.437	0.702	1450.27	1018.03	0.306	1203.90	368.91
A_68_P32218217	chr19:59335443-59335487	NM_172523:97	Slc18a2	INSIDE	0.437	0.375	1951.34	730.94	0.164	1600.79	261.74
A_68_P31791992	chr18:67624679-67624723	NM_144867:198	Slmo1	INSIDE	0.437	0.430	1964.17	844.63	0.188	1581.87	297.14
A_68_P26239286	chr8:125857009-125857053	NM_172287:418	Spire2	INSIDE	0.437	0.417	2644.30	1103.38	0.182	2061.87	376.19
A_68_P31213636	chr17:47825672-47825716	NM_001164729:-359	Tomm6	DIVERGENT_PROMOTER	0.437	0.614	1449.34	889.49	0.268	1090.21	292.12
A_68_P23200903	chr4:109079476-109079520	NM_153392:-206	Ttc39a	PROMOTER	0.437	0.469	1459.99	684.90	0.205	1153.72	236.25
A_68_P24469550	chr6:55401858-55401902	NM_001025372:-93	Adcyap1r1	PROMOTER	0.436	0.548	2826.73	1548.02	0.239	2086.40	498.17
A_68_P25273840	chr7:88907783-88907827	NM_025997:-34	Fam103a1	PROMOTER	0.436	0.587	1312.42	770.10	0.256	1072.47	274.12
A_68_P25950855	chr8:72807002-72807046	NM_001146153:127	Homer3	INSIDE	0.436	0.610	3020.53	1843.68	0.266	2430.86	647.54
A_68_P25098706	chr7:53632477-53632521	NM_010866:655	Myod1	INSIDE	0.436	0.656	3452.43	2263.98	0.286	2667.74	762.17
A_68_P26203093	chr8:120022311-120022355	NM_172285:142	Plcg2	INSIDE	0.436	0.441	1297.85	572.58	0.192	1146.51	220.34
A_68_P32958525	chr17:8627413-8627457	NM_009309:147	T	INSIDE	0.436	0.669	1899.94	1271.80	0.292	1570.06	458.17
A_68_P23164319	chr4:102786672-102786716	NM_146254:210	Wdr78	INSIDE	0.436	0.438	2729.97	1196.26	0.191	2013.77	384.95
A_68_P21053766	chr2:21063512-21063556	ENSMUST00000137984:47		INSIDE	0.436	0.617	4598.39	2836.91	0.269	3394.23	913.08
A_68_P24464806	chr6:54631922-54631966	NM_026629:179	2410066E13Rik	INSIDE	0.435	0.525	1947.35	1021.62	0.228	1774.77	404.87
A_68_P31108560	chr17:26276183-26276227	NM_001159598:574	Axin1	INSIDE	0.435	1.451	8023.27	11640.05	0.632	5667.44	3580.60
A_68_P23210413	chr4:111087417-111087472	NM_026279:-166	Bend5	PROMOTER	0.435	0.554	1649.22	913.64	0.241	1311.55	315.76
A_68_P30588530	chr16:20620757-20620801	NM_028420:573	Camk2n2	INSIDE	0.435	0.471	2118.12	998.07	0.205	1663.51	341.23
A_68_P27364532	chr10:94786282-94786326	NM_009950:427	Cradd	INSIDE	0.435	0.404	1815.26	733.87	0.176	1427.80	251.19
A_68_P32026410	chr19:24971751-24971795	NM_008022:4027	Foxd4	DOWNSTREAM	0.435	0.395	1349.91	532.92	0.172	1103.84	189.46
A_68_P24466829	chr6:54988330-54988374	NM_180678:358	Gars	INSIDE	0.435	0.550	2430.92	1338.08	0.239	1941.61	464.96
A_68_P24449064	chr6:52156622-52156666	NM_010454:1979	Hoxa6	INSIDE	0.435	0.491	1095.46	538.22	0.214	920.02	196.71
A_68_P29508896	chr14:31764964-31765008	NM_011849:313	Nek4	INSIDE	0.435	0.666	1633.10	1088.41	0.290	1378.71	399.28
A_68_P28426163	chr12:51750413-51750457	NM_008858:-224	Prkd1	PROMOTER	0.435	0.452	1637.89	740.09	0.197	1377.70	270.95
A_68_P22129914	chr3:51288525-51288569	NM_016858:659	Rab33b	INSIDE	0.435	0.480	2286.28	1096.36	0.208	1743.88	363.60
A_68_P20901342	chr1:187278951-187278995	NM_001033286:246	Slc30a10	INSIDE	0.435	0.414	1573.57	650.90	0.180	1299.23	233.87
A_68_P30016102	chr15:11329112-11329156	NM_033074:279	Tars	INSIDE	0.435	1.477	2294.80	3389.60	0.643	1792.16	1152.62
A_68_P20552784	chr1:120524752-120524796	NM_023755:253	Tcfcp2l1	INSIDE	0.435	0.553	1832.94	1014.46	0.241	1488.49	358.16
A_68_P22413525	chr3:108394707-108394751	NM_181400:533	Wdr47	INSIDE	0.435	0.486	2053.26	997.28	0.211	1599.90	338.04
A_68_P27306493	chr10:84565965-84566009	NM_001013028:615	AI597468	INSIDE	0.434	0.556	1941.87	1079.40	0.241	1589.97	383.45
A_68_P30476325	chr15:98593156-98593200	NM_007478:371	Arf3	INSIDE	0.434	0.661	4392.11	2903.33	0.287	3220.23	924.08
A_68_P21580444	chr2:121181215-121181259	NM_009897:-3140	Ckmt1	DIVERGENT_PROMOTER	0.434	0.461	1306.01	601.82	0.200	1063.72	212.59
A_68_P21904963	chr2:180333140-180333184	NM_009936:236	Col9a3	INSIDE	0.434	0.609	2667.80	1625.38	0.264	2106.33	556.86
A_68_P29515526	chr14:32898628-32898679	NM_001047433:198	Dph3	INSIDE	0.434	0.537	1318.22	708.39	0.233	1040.87	242.91
A_68_P30373739	chr15:80502384-80502428	NM_145986:130	Fam83f	INSIDE	0.434	0.643	1311.34	843.82	0.279	1111.32	310.20
A_68_P26025053	chr8:88016777-88016821	NM_173866:283	Gpt2	INSIDE	0.434	0.679	1680.35	1140.21	0.294	1320.66	388.62
A_68_P26622303	chr9:71333818-71333862	NM_178602:-50	Grinl1a	PROMOTER	0.434	0.403	2113.33	851.67	0.175	1713.63	299.51
A_68_P28279800	chr12:21291772-21291816	NM_008403:304	Itgb1bp1	INSIDE	0.434	0.300	1716.13	514.83	0.130	1348.71	175.47
A_68_P27924627	chr11:74987037-74987081	NR_029546:-125	Mir132	PROMOTER	0.434	0.692	2353.48	1629.06	0.300	1962.89	589.02
A_68_P31866349	chr18:80910082-80910126	NM_001164110:-294	Nfatc1	PROMOTER	0.434	0.568	2641.35	1501.07	0.247	2097.65	517.57

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P22220267	chr3:69120847-69120891	NM_178726:29	Ppm1l	INSIDE	0.434	0.545	2515.36	1370.78	0.236	1904.22	450.07
A_68_P22341989	chr3:94846418-94846462	NM_008951:27	Psmd4	INSIDE	0.434	0.561	1911.42	1072.31	0.243	1493.72	363.34
A_68_P21557415	chr2:117168712-117168756	NM_011246:-121	Rasgrp1	PROMOTER	0.434	0.597	1661.08	991.78	0.259	1394.04	361.06
A_68_P26344897	chr9:20781232-20781276	NM_010333:-17	S1pr2	PROMOTER	0.434	1.480	2047.13	3029.62	0.643	1398.76	899.34
A_68_P28936499	chr13:34169593-34169637	NM_009450:263	Tubb2a	INSIDE	0.434	0.707	3359.06	2376.05	0.307	2486.24	763.25
A_68_P23547920	chr5:25035394-25035438	NR_027388:-419	1700096K18Rik	PROMOTER	0.433	0.574	3576.99	2052.69	0.249	2768.49	688.25
A_68_P27282447	chr10:79783116-79783160	NM_025521:155	2310011J03Rik	INSIDE	0.433	0.599	5286.50	3169.06	0.260	3798.53	986.03
A_68_P24052416	chr5:123271272-123271316	NM_001042491:54	Anapc5	INSIDE	0.433	0.665	1214.00	806.95	0.288	1049.39	302.30
A_68_P21423815	chr2:91490335-91490379	NM_146124:-3008	Arhgap1	PROMOTER	0.433	0.569	991.08	563.92	0.246	809.93	199.52
A_68_P31151212	chr17:34088387-34088432	NM_019420:24	B3galt4	INSIDE	0.433	0.350	2374.68	831.92	0.152	1767.64	268.00
A_68_P30684012	chr16:38089843-38089887	NR_033221:-518	BC031361	PROMOTER	0.433	0.387	1469.59	568.10	0.167	1398.26	234.14
A_68_P26467525	chr9:44225880-44225924	NM_201372:188	Ccdc84	INSIDE	0.433	0.632	3188.92	2014.72	0.274	2379.71	650.91
A_68_P24820862	chr6:125444303-125444347	NM_007657:449	Cd9	INSIDE	0.433	0.582	1893.00	1102.63	0.252	1613.75	407.23
A_68_P32143271	chr19:46402975-46403019	NM_133694:323	Fbxl15	INSIDE	0.433	0.654	1719.17	1123.56	0.283	1417.27	400.83
A_68_P23611439	chr5:37482314-37482358	NM_178394:40241	Jakmip1	INSIDE	0.433	0.619	2076.52	1285.31	0.268	1717.12	460.57
A_68_P25368688	chr7:107756761-107756805	NR_003559:-272	Mrpl48	PROMOTER	0.433	0.488	1437.47	702.13	0.212	1100.89	233.06
A_68_P20011680	chr1:6204723-6204767	NM_009826:2	Rb1cc1	INSIDE	0.433	0.385	1750.61	674.21	0.167	1388.61	231.75
A_68_P28328450	chr12:31596678-31596722	NM_013709:167	Sh3yl1	INSIDE	0.433	0.687	1307.89	898.56	0.297	1149.46	341.59
A_68_P22031742	chr3:30994277-30994321	NM_001039090:316	Skil	INSIDE	0.433	0.684	5333.16	3650.43	0.296	4142.42	1227.29
A_68_P28154494	chr11:115488974-115489018	NM_026071:457	Slc25a19	INSIDE	0.433	0.633	862.56	546.39	0.274	711.16	195.15
A_68_P23607365	chr5:36740222-36740266	NM_030889:544	Sorcs2	INSIDE	0.433	0.596	1044.48	622.61	0.258	879.21	227.18
A_68_P28054175	chr11:97914595-97914639	NM_146028:160	Stac2	INSIDE	0.433	0.528	3682.99	1946.43	0.229	2753.77	630.78
A_68_P24117827	chr5:136254305-136254349	NM_029659:-71	Styxl1	DIVERGENT_PROMOTER	0.433	0.535	1742.21	931.42	0.231	1395.04	322.94
A_68_P28871637	chr13:21292413-21292457	NM_009054:20607	Trim27	DOWNSTREAM	0.433	0.518	1248.32	647.22	0.225	964.05	216.53
A_68_P28155497	chr11:115676636-115676680	NM_029557:606	Tsen54	INSIDE	0.433	0.595	975.44	580.67	0.258	697.46	179.61
A_68_P31791610	chr18:67551054-67551098	NM_026473:692	Tubb6	INSIDE	0.433	0.494	1698.06	838.42	0.214	1422.44	304.23
A_68_P24385308	chr6:39822333-39822377			Unknown	0.433	0.450	1370.33	616.06	0.195	996.89	194.07
A_68_P31801898	chr18:69358247-69358291	AK080553:494		INSIDE	0.433	0.690	3138.24	2166.37	0.299	2347.69	702.46
A_68_P22947349	chr4:57794962-57795006	ENSMUST00000124581:-67		PROMOTER	0.433	0.629	2259.04	1420.75	0.272	2078.42	566.37
A_68_P28747155	chr12:113204858-113204902	NM_027360:308	2010107E04Rik	INSIDE	0.432	0.537	1594.75	856.04	0.232	1321.24	306.72
A_68_P29448496	chr14:21526704-21526748	NM_027996:-47	2310021P13Rik	PROMOTER	0.432	0.493	1547.75	762.95	0.213	1138.01	242.17
A_68_P28195050	chr12:3427455-3427499	NM_172421:593	Asxl2	INSIDE	0.432	0.652	2722.75	1775.44	0.282	1964.95	554.15
A_68_P24797813	chr6:120244449-120244493	NM_198884:107	B4galnt3	INSIDE	0.432	0.596	1611.33	960.49	0.258	1288.11	331.77
A_68_P21075526	chr2:25837853-25837902	NM_001115076:925	Camsap1	INSIDE	0.432	0.652	1123.64	733.04	0.282	904.28	254.82
A_68_P26971602	chr10:17443634-17443678	NM_010828:623	Cited2	INSIDE	0.432	0.712	3830.13	2727.47	0.307	2974.75	914.53
A_68_P30895371	chr16:78301854-78301898	NM_001025192:-59	Cxadr	PROMOTER	0.432	0.542	1773.20	961.47	0.234	1472.04	344.71
A_68_P28729569	chr12:109940441-109940485	NM_001171002:54	Degs2	INSIDE	0.432	0.678	1110.84	753.56	0.293	925.58	271.52
A_68_P23203729	chr4:109650347-109650391	NM_172296:-261	Dmrta2	PROMOTER	0.432	0.401	3107.48	1247.05	0.174	2233.97	387.65
A_68_P21909706	chr2:181022876-181022920	NM_198169:-227	Gmeb2	PROMOTER	0.432	0.624	1107.72	691.60	0.270	859.57	231.79
A_68_P26826863	chr9:110856302-110856347	NM_028838:2276	Lrrc2	INSIDE	0.432	0.537	1024.14	549.76	0.232	762.17	176.69
A_68_P24993428	chr7:20044025-20044069	NM_172279:-203	Mark4	PROMOTER	0.432	0.471	1471.90	693.97	0.204	1226.71	249.76
A_68_P23567792	chr5:29805215-29805259	NM_019944:-226	Mnx1	PROMOTER	0.432	0.649	2226.04	1445.38	0.281	1642.90	460.89
A_68_P30477985	chr15:98885628-98885672	NM_001163588:46	Prph	INSIDE	0.432	0.736	3231.96	2379.82	0.318	2337.44	743.16
A_68_P24045427	chr5:122043186-122043230	NM_009656:625	Aldh2	INSIDE	0.431	0.585	1349.74	789.32	0.252	1113.59	280.38
A_68_P27560709	chr11:4887252-4887296	NM_007454:367	Ap1b1	INSIDE	0.431	0.512	2650.54	1356.04	0.221	1850.24	408.37
A_68_P25954407	chr8:73363491-73363535	NM_027560:107	Arrdc2	INSIDE	0.431	0.629	4802.10	3020.09	0.271	3083.84	836.07
A_68_P25782090	chr8:36889097-36889141	NM_027998:495	Cldn23	INSIDE	0.431	0.540	1860.05	1004.54	0.233	1281.82	298.48
A_68_P31260713	chr17:57386929-57386973	NM_030084:114	Gpr108	INSIDE	0.431	0.560	1295.83	725.49	0.241	933.64	225.09
A_68_P28083441	chr11:102979217-102979261	NM_138753:1600	Hexim1	INSIDE	0.431	0.680	1269.78	863.31	0.293	1059.33	310.43
A_68_P22210773	chr3:67386862-67386906	NM_025813:195	Mfsd1	INSIDE	0.431	0.436	1431.44	623.47	0.188	1098.19	206.25
A_68_P22606647	chr3:144781543-144781587	NM_025714:1	Odf2l	INSIDE	0.431	0.515	2321.62	1194.95	0.222	1838.55	408.21

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31621135	chr18:36124744-36124788	NM_028707:278	Psd2	INSIDE	0.431	0.516	1453.25	750.11	0.222	1191.44	264.85
A_68_P27950225	chr11:79474212-79474256	NM_175543:69521	Rab11fip4	INSIDE	0.431	0.657	1815.22	1192.45	0.283	1417.94	401.57
A_68_P26567740	chr9:61761969-61762013	NM_018853:327	Rplp1	INSIDE	0.431	0.585	2880.40	1683.88	0.252	2159.08	544.13
A_68_P20250375	chr1:57026759-57026807	NM_139146:1396	Satb2	INSIDE	0.431	0.673	1459.32	981.68	0.290	1126.26	326.72
A_68_P23993055	chr5:113006360-113006404	NM_019982:-177	Sez6l	PROMOTER	0.431	0.471	1700.24	800.51	0.203	1326.27	268.88
A_68_P26996378	chr10:21714127-21714171	NM_011361:-323	Sgk1	PROMOTER	0.431	0.625	1978.07	1236.73	0.270	1444.33	389.40
A_68_P27277986	chr10:79100770-79100814	NM_001024539:-129	Shc2	PROMOTER	0.431	0.504	1121.40	564.70	0.217	942.73	204.84
A_68_P30405823	chr15:86045014-86045058	NM_145476:148	Tbc1d22a	INSIDE	0.431	1.568	5816.42	9120.58	0.677	3995.28	2702.95
A_68_P25948613	chr8:72426109-72426153	NM_032004:17	Tssk6	INSIDE	0.431	0.712	3179.15	2263.23	0.307	2270.51	697.43
A_68_P25670556	chr8:13785998-13786042	NM_025924:406	Upf3a	INSIDE	0.431	0.710	2540.02	1802.82	0.306	1946.37	595.74
A_68_P30489511	chr15:100909418-100909462	AK078004:-29		PROMOTER	0.431	0.598	1274.62	761.78	0.258	998.44	257.36
A_68_P20631365	chr1:135989841-135989885	AK155907:5872		DOWNSTREAM	0.431	0.431	2339.05	1008.26	0.186	1874.79	348.43
A_68_P22291856	chr3:84386605-84386649	NM_001081093:-79	Arfip1	PROMOTER	0.430	0.554	1121.05	621.23	0.238	1009.01	240.25
A_68_P26075475	chr8:96622393-96622437	NM_026116:297	Bbs2	INSIDE	0.430	0.383	1914.53	733.23	0.165	1329.59	219.11
A_68_P25093840	chr7:52825839-52825883	NM_009737:128	Bcat2	INSIDE	0.430	0.404	2126.05	858.33	0.174	1831.57	318.13
A_68_P30113000	chr15:31153773-31153829	NM_146057:-339	Dap	PROMOTER	0.430	0.513	1044.05	536.10	0.221	821.01	181.12
A_68_P24586430	chr6:81991869-81991913	NM_145570:269	Fam176a	INSIDE	0.430	0.583	1250.34	729.02	0.251	1000.94	251.16
A_68_P28084317	chr11:103128474-103128518	NM_016896:219	Map3k14	INSIDE	0.430	0.677	2901.94	1963.69	0.291	2093.48	609.49
A_68_P28084319	chr11:103128781-103128825	NM_016896:-87	Map3k14	PROMOTER	0.430	0.489	1810.48	884.93	0.210	1355.08	284.85
A_68_P31100481	chr17:25073380-25073424	NM_001163447:520	Mapk8ip3	INSIDE	0.430	0.494	1770.02	875.20	0.213	1269.58	270.08
A_68_P21151178	chr2:38780768-38780812	NM_010264:1191	Nr6a1	INSIDE	0.430	0.727	3471.77	2523.33	0.312	2582.24	806.87
A_68_P25368680	chr7:107755893-107755937	NM_001163663:-185	Rab6	PROMOTER	0.430	0.707	3728.15	2634.93	0.304	2431.82	739.73
A_68_P22450159	chr3:116297548-116297592	NM_028349:-355	Sass6	PROMOTER	0.430	0.525	1549.58	813.48	0.226	1281.98	289.46
A_68_P25016883	chr7:28140851-28140895	NM_138676:155	Shkbp1	INSIDE	0.430	0.495	3331.24	1648.27	0.213	2575.41	547.99
A_68_P20354817	chr1:75543227-75543271	NM_009208:408	Slc4a3	INSIDE	0.430	0.555	4935.41	2738.41	0.239	3596.93	858.77
A_68_P25007552	chr7:25740356-25740400			Unknown	0.430	0.573	4139.66	2372.16	0.246	2911.10	717.35
A_68_P20826030	chr1:173000636-173000680	ENSMUST00000164179:-5592		PROMOTER	0.430	0.494	5689.08	2813.03	0.213	4510.99	958.65
A_68_P27542784	chr10:128141723-128141767	NM_016756:363	Cdk2	INSIDE	0.429	0.608	1592.16	968.65	0.261	1257.00	327.89
A_68_P28778248	chr12:119437069-119437113	NM_010060:426	Dnahc11	INSIDE	0.429	0.600	1767.16	1059.95	0.257	1351.87	347.71
A_68_P23927139	chr5:100407949-100407993	NM_001077265:-13	Hnrnpd	PROMOTER	0.429	0.391	2458.35	960.66	0.168	1988.35	333.70
A_68_P32134218	chr19:44831888-44831933	NM_011037:27	Pax2	INSIDE	0.429	0.555	3005.41	1667.93	0.238	2302.50	547.97
A_68_P24829780	chr6:126889329-126889373	NM_009013:223	Rad51ap1	INSIDE	0.429	0.705	3601.47	2537.98	0.302	2733.45	825.52
A_68_P28036069	chr11:94871187-94871231	NM_146025:16	Samd14	INSIDE	0.429	0.511	1098.60	560.89	0.219	888.67	194.42
A_68_P30642392	chr16:30550884-30550928	NM_172614:-242	Tmem44	PROMOTER	0.429	0.604	2111.36	1275.91	0.259	1651.61	428.19
A_68_P22362402	chr3:98945208-98945252	NM_027462:218	Wars2	INSIDE	0.429	0.445	1547.83	688.13	0.191	1188.20	226.60
A_68_P24127316	chr5:138182800-138182844	NM_175521:-1596	6430598A04Rik	DIVERGENT_PROMOTER	0.428	0.443	1275.80	565.77	0.190	1132.49	214.71
A_68_P22451304	chr3:116510918-116510962	NM_001081326:144	Agl	INSIDE	0.428	0.535	1294.85	692.82	0.229	1035.02	236.91
A_68_P24039809	chr5:121063031-121063075	NM_028041:-86	Ddx54	DIVERGENT_PROMOTER	0.428	0.505	1103.35	556.80	0.216	981.25	212.11
A_68_P31065256	chr17:15512298-15512342	NM_007865:467	Dll1	INSIDE	0.428	1.381	2803.51	3870.71	0.591	2321.68	1371.13
A_68_P31610604	chr18:34166101-34166145	NM_013512:738	Epb4.1l4a	INSIDE	0.428	0.570	2976.61	1696.24	0.244	2147.76	523.49
A_68_P22369560	chr3:100293076-100293120	NM_001142952:17	Fam46c	INSIDE	0.428	0.481	4172.15	2006.74	0.206	3200.67	659.17
A_68_P22346159	chr3:95686322-95686366	NM_001033302:-193	Gm129	PROMOTER	0.428	0.460	1798.38	827.42	0.197	1429.60	281.50
A_68_P21054862	chr2:21289571-21289618	NM_001004761:401	Gpr158	INSIDE	0.428	0.553	984.62	544.69	0.237	837.31	198.19
A_68_P20442334	chr1:93310020-93310067	NM_019479:-244	Hes6	PROMOTER	0.428	0.626	971.17	607.78	0.268	735.86	196.96
A_68_P28066376	chr11:100006643-100006687	NM_008471:569	Krt19	INSIDE	0.428	0.638	1553.77	991.90	0.273	1163.22	317.88
A_68_P31220005	chr17:49071091-49071135	NM_027452:-794	Lrfn2	PROMOTER	0.428	0.459	1700.17	780.47	0.196	1290.14	253.30
A_68_P23278139	chr4:125773830-125773874	NM_001163266:-44	Lsm10	PROMOTER	0.428	0.502	1899.41	953.03	0.215	1425.24	306.22
A_68_P20293520	chr1:64664228-64664272	NM_025964:-508	Mettl21a	PROMOTER	0.428	0.546	1851.72	1011.72	0.234	1475.13	344.59
A_68_P27553117	chr11:3549252-3549296	NM_001159288:-222	Morc2a	DIVERGENT_PROMOTER	0.428	0.415	1488.45	617.90	0.178	1220.63	217.11
A_68_P20450137	chr1:94538493-94538537	NR_028108:11	Myeov2	INSIDE	0.428	0.339	3227.05	1092.73	0.145	2584.01	374.18
A_68_P31735610	chr18:57514422-57514466	NM_028447:58	Prrc1	INSIDE	0.428	0.533	3461.36	1846.17	0.228	2669.48	609.54

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26825596	chr9:110646504-110646548	NM_001083935:-336	Pth1r	PROMOTER	0.428	0.556	1547.35	860.35	0.238	1146.31	272.69
A_68_P31020008	chr17:5941641-5941685	NM_001113352:383	Synj2	INSIDE	0.428	0.643	1695.65	1090.26	0.275	1397.27	384.47
A_68_P23430517	chr4:153673893-153673937	NM_001112744:90	Arhgef16	INSIDE	0.427	0.712	1902.35	1355.25	0.304	1498.03	456.01
A_68_P21673355	chr2:138082825-138082869	NM_001025431:527	Btbd3	INSIDE	0.427	0.424	1382.18	586.22	0.181	991.91	179.61
A_68_P20351048	chr1:74931966-74932010	NM_153111:-6	Fev	PROMOTER	0.427	0.656	1876.17	1230.17	0.280	1690.43	473.23
A_68_P31759174	chr18:61852045-61852089	NM_019508:4478	Il17b	INSIDE	0.427	0.524	1291.49	676.38	0.224	892.38	199.63
A_68_P26531904	chr9:55394018-55394062	NM_027397:5085	Isl2	DOWNSTREAM	0.427	0.331	1731.85	572.49	0.141	1133.06	159.91
A_68_P29616405	chr14:55733423-55733480	NM_177049:2321	Jph4	INSIDE	0.427	7.920	2258.91	17890.37	3.382	1539.32	5205.58
A_68_P24129161	chr5:138612875-138612919	NR_029658:-5850	Mir106b	PROMOTER	0.427	0.734	4243.44	3116.55	0.314	2961.70	929.12
A_68_P25955964	chr8:73796836-73796880	NM_001142322:246	Myo9b	INSIDE	0.427	0.699	2481.41	1734.07	0.299	1887.62	563.56
A_68_P30778928	chr16:56029876-56029920	NM_001024622:-68	Pcnp	PROMOTER	0.427	0.540	1618.80	874.03	0.230	1205.16	277.78
A_68_P26469281	chr9:44542040-44542084	NM_153537:1215	Phldb1	INSIDE	0.427	0.714	4272.68	3050.03	0.305	3273.45	998.91
A_68_P28072822	chr11:101107992-101108036	NM_019444:367	Ramp2	INSIDE	0.427	0.617	1396.03	861.11	0.263	1052.20	276.94
A_68_P22312797	chr3:88058696-88058740	NM_021375:-112	Rhbg	PROMOTER	0.427	0.518	1100.66	569.84	0.221	865.57	191.15
A_68_P25834905	chr8:47296158-47296202	NM_007450:183	Slc25a4	INSIDE	0.427	0.363	3243.34	1176.72	0.155	2452.80	380.33
A_68_P31054933	chr17:13200672-13200716	NM_013671:-10	Sod2	PROMOTER	0.427	0.497	1484.39	737.22	0.212	1248.75	264.61
A_68_P26875193	chr9:119846837-119846881	NM_028735:135	Ttc21a	INSIDE	0.427	0.588	1305.35	767.49	0.251	976.75	245.21
A_68_P24066628	chr5:125870372-125870416	NM_019639:-7	Ubc	PROMOTER	0.427	0.549	1991.27	1093.22	0.234	1505.86	352.80
A_68_P28729766	chr12:109996154-109996198			Unknown	0.427	0.516	2795.74	1441.97	0.220	2269.90	499.67
A_68_P30367722	chr15:79489390-79489434	NM_029407:-26	4933432B09Rik	DIVERGENT_PROMOTER	0.426	0.502	1548.19	776.84	0.214	1181.94	252.65
A_68_P21110672	chr2:31543979-31544023	NM_001112703:-75	Abl1	PROMOTER	0.426	0.339	2003.50	680.11	0.144	1675.62	242.06
A_68_P26716243	chr9:90058080-90058124	NM_001003911:287	Adamts7	INSIDE	0.426	0.622	3260.24	2027.74	0.265	2504.27	662.96
A_68_P27279758	chr10:79389293-79389337	NM_007880:-502	Arid3a	PROMOTER	0.426	0.472	1199.10	565.47	0.201	934.58	187.72
A_68_P31095796	chr17:24306345-24306389	NR_037854:-26	Atp6v0c-ps2	PROMOTER	0.426	0.579	2335.57	1352.31	0.247	1816.59	447.87
A_68_P21425364	chr2:91761807-91761851	NM_007699:-517	Chrm4	PROMOTER	0.426	0.563	1003.42	564.90	0.240	792.85	190.09
A_68_P23202061	chr4:109349433-109349477	NM_007983:223	Faf1	INSIDE	0.426	0.363	1627.53	590.92	0.155	1325.49	204.86
A_68_P25528903	chr7:138686351-138686395	NM_008257:-104	Hmx3	PROMOTER	0.426	0.430	1802.03	775.35	0.183	1528.16	280.03
A_68_P23352779	chr4:139131562-139131606	NM_001205173:950	Iffo2	INSIDE	0.426	0.661	998.98	660.53	0.282	773.34	217.78
A_68_P31100079	chr17:25023157-25023201	NM_011956:117	Nubp2	INSIDE	0.426	0.469	5167.57	2423.85	0.200	3511.20	701.20
A_68_P26706481	chr9:87634446-87634490	NM_023814:-8373	Tbx18	PROMOTER	0.426	0.636	1528.24	972.50	0.271	1240.49	336.63
A_68_P25459062	chr7:125727948-125727992	NM_172476:230	Tmc7	INSIDE	0.426	0.646	1991.21	1286.03	0.275	1416.69	389.44
A_68_P24076587	chr5:127722499-127722543	NM_175432:325	Tmem132c	INSIDE	0.426	0.613	2255.62	1381.85	0.261	1684.29	439.13
A_68_P27563772	chr11:5421438-5421482	NM_013842:491	Xbp1	INSIDE	0.426	0.461	1736.71	800.62	0.196	1362.88	267.49
A_68_P21851439	chr2:169959243-169959287	NM_001033299:-2544	Zfp217	PROMOTER	0.426	0.618	1178.79	728.96	0.264	949.40	250.32
A_68_P27837321	chr11:59319755-59319799	NM_001130529:366	Zkscan17	INSIDE	0.426	0.460	1368.04	629.36	0.196	1124.79	220.27
A_68_P31465579	chr18:4922163-4922209	ENSMUST00000143254:463		INSIDE	0.426	0.612	1533.56	939.00	0.261	1233.66	322.04
A_68_P26584997	chr9:64808465-64808509	NM_001077631:-152	2010321M09Rik	DIVERGENT_PROMOTER	0.425	0.646	1408.86	910.69	0.275	1177.75	323.77
A_68_P29484385	chr14:27783967-27784011	NM_145221:-251	Appl1	PROMOTER	0.425	0.571	1575.58	900.31	0.243	1334.00	323.64
A_68_P31616437	chr18:35278200-35278244	NM_009818:-343	Ctnna1	PROMOTER	0.425	0.613	1314.59	806.16	0.261	1136.59	296.11
A_68_P30244835	chr15:57723554-57723598	NM_024207:397	Derl1	INSIDE	0.425	0.522	2550.26	1331.81	0.222	2025.95	449.64
A_68_P20366327	chr1:77511720-77511764	NM_007936:-79	Epha4	PROMOTER	0.425	0.615	5264.01	3234.77	0.261	3695.72	966.32
A_68_P24025033	chr5:118619514-118619558	NM_007545:-236	Hrk	PROMOTER	0.425	0.690	2723.58	1877.93	0.293	1906.88	558.84
A_68_P26445378	chr9:40608813-40608857	NM_031165:-521	Hspa8	PROMOTER	0.425	0.415	4533.39	1882.56	0.177	3146.44	555.59
A_68_P26644014	chr9:75289095-75289140	NM_001039522:-213	Leo1	PROMOTER	0.425	0.669	1036.55	693.78	0.284	843.34	239.68
A_68_P25905383	chr8:63111766-63111810	NM_027756:132	Mfap3l	INSIDE	0.425	0.452	2114.35	955.46	0.192	1973.04	379.33
A_68_P25585441	chr7:148067881-148067925	NM_001127351:-134	Sirt3	PROMOTER	0.425	0.664	2052.05	1362.14	0.282	1698.79	479.75
A_68_P25017007	chr7:28160302-28160347	NM_001199235:19201	Spnb4	INSIDE	0.425	0.702	1568.81	1101.78	0.298	1289.57	384.55
A_68_P26787851	chr9:103664317-103664362	NM_178638:-172	Tmem108	PROMOTER	0.425	0.641	1147.40	735.64	0.272	971.25	264.61
A_68_P32572889	chrX:100643328-100643372	NR_002844:16495	Tsix	INSIDE	0.425	3.366	7222.62	24314.54	1.431	2843.03	4068.66
A_68_P25500776	chr7:133630670-133630714	NM_001163713:-176	Tufm	PROMOTER	0.425	0.554	1769.13	980.78	0.236	1292.11	304.30
A_68_P30377738	chr15:81230455-81230499	NM_177310:-141	Xpnpep3	DIVERGENT_PROMOTER	0.425	0.585	3206.19	1874.83	0.248	2430.25	603.33

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P29750655	chr14:79700758-79700803	NM_025427:662	1190002H23Rik	INSIDE	0.424	0.631	2121.04	1338.95	0.267	1624.80	434.42
A_68_P26541144	chr9:57109788-57109832	NM_028820:596	1700017B05Rik	INSIDE	0.424	0.699	1446.44	1010.98	0.297	1101.96	326.77
A_68_P27945543	chr11:78640074-78640118	NM_001076681:0	1810012P15Rik	INSIDE	0.424	0.513	1366.42	701.09	0.218	1211.86	263.79
A_68_P28182352	chr11:119960513-119960557	NM_001110242:287	1810043H04Rik	INSIDE	0.424	0.680	1235.58	839.70	0.288	927.01	267.38
A_68_P26018414	chr8:86671587-86671631	NM_145970:44	Cc2d1a	INSIDE	0.424	0.656	1816.16	1190.95	0.278	1331.89	370.06
A_68_P24590977	chr6:82982750-82982794	NM_010070:693	Dok1	INSIDE	0.424	0.543	1563.64	848.90	0.230	1267.91	292.10
A_68_P26023052	chr8:87514587-87514631	NM_001167991:115	Hook2	INSIDE	0.424	0.642	1430.89	917.99	0.272	1070.13	290.93
A_68_P23253009	chr4:120419330-120419374	NM_001081142:429	Kcnq4	INSIDE	0.424	0.701	1634.38	1145.29	0.297	1213.62	360.38
A_68_P28748134	chr12:113382997-113383048	NM_001097621:-1396	Kif26a	PROMOTER	0.424	4.501	10309.02	46396.48	1.909	6069.03	11587.23
A_68_P24758095	chr6:113143886-113143930	NM_177763:1470	Lhfpl4	INSIDE	0.424	0.550	930.66	511.41	0.233	748.36	174.18
A_68_P27495998	chr10:119664180-119664224	NM_025431:87	Llph	INSIDE	0.424	0.414	1261.65	522.47	0.176	993.23	174.57
A_68_P25373934	chr7:108653145-108653191	NR_026574:53347	Pde2a	INSIDE	0.424	0.629	892.80	561.63	0.267	682.21	181.86
A_68_P24126055	chr5:137943429-137943477	NM_028753:205	Pop7	INSIDE	0.424	0.637	970.48	618.59	0.270	965.90	261.13
A_68_P21748795	chr2:152158169-152158213	NM_001083921:-29	Rbck1	PROMOTER	0.424	0.622	1354.24	841.74	0.264	1240.43	326.89
A_68_P23311883	chr4:131901216-131901260	NM_001197082:427	Rcc1	INSIDE	0.424	0.600	1049.23	629.95	0.255	818.84	208.65
A_68_P25605218	chr7:151361386-151361430	NM_001113373:-16	Shank2	PROMOTER	0.424	0.512	2129.65	1090.85	0.217	1528.90	332.09
A_68_P28096909	chr11:105451661-105451705	NM_181071:383	Tanc2	INSIDE	0.424	0.670	1636.27	1096.28	0.284	1449.26	411.89
A_68_P30510787	chr16:4558890-4558934	NM_031182:808	Tcfap4	INSIDE	0.424	0.614	7233.98	4440.62	0.260	4912.91	1279.00
A_68_P25947618	chr8:72178919-72178963	NM_001177527:486	Zfp964	INSIDE	0.424	0.654	853.37	558.16	0.277	599.49	166.07
A_68_P30337385	chr15:74317945-74317989			Unknown	0.424	0.401	1591.73	638.70	0.170	1276.67	217.40
A_68_P25827280	chr8:46020590-46020634	AK079043:-99		PROMOTER	0.424	0.592	933.24	552.39	0.251	682.70	171.43
A_68_P29699589	chr14:70552945-70552991	NM_146055:630	2610301G19Rik	INSIDE	0.423	5.739	4124.45	23669.03	2.427	2441.32	5924.78
A_68_P25962138	chr8:75094798-75094842	NM_172396:127	9130011J15Rik	INSIDE	0.423	0.533	1353.42	721.20	0.225	960.95	216.45
A_68_P24624508	chr6:88792125-88792169	NM_030251:-217	Abtb1	PROMOTER	0.423	3.214	16049.16	51578.49	1.361	9621.76	13091.91
A_68_P32030084	chr19:25580234-25580278	NM_015826:61	Dmrt1	INSIDE	0.423	0.495	2646.19	1309.16	0.210	2197.89	460.46
A_68_P23365986	chr4:141346174-141346218	NM_172338:363	Dnajc16	INSIDE	0.423	0.466	1787.12	833.14	0.197	1389.82	274.01
A_68_P28186834	chr11:120657869-120657913	NM_026824:-181	Dus1l	PROMOTER	0.423	0.567	2245.52	1272.24	0.240	1847.20	442.92
A_68_P24660676	chr6:95067884-95067930	NM_001008785:7	Kbtbd8	INSIDE	0.423	0.501	1384.91	693.50	0.212	1067.31	226.27
A_68_P25088287	chr7:51847145-51847189	NM_008422:911	Kcnc3	INSIDE	0.423	0.462	2111.75	976.07	0.195	1448.34	282.91
A_68_P23916638	chr5:98614079-98614123	NM_029947:4213	Prdm8	INSIDE	0.423	0.666	938.20	624.44	0.282	770.31	217.06
A_68_P26138376	chr8:108735052-108735096	NM_145404:121	Prmt7	INSIDE	0.423	0.530	1753.45	929.97	0.224	1499.64	336.49
A_68_P24061239	chr5:124875960-124876004	NM_001081203:-59	Sbno1	PROMOTER	0.423	0.464	2926.54	1357.27	0.196	2319.38	454.59
A_68_P20636517	chr1:136859020-136859067	NM_026024:-110	Ube2t	DIVERGENT_PROMOTER	0.423	0.447	1648.84	736.46	0.189	1452.07	274.19
A_68_P23584758	chr5:32913772-32913816	NM_001205132:251	Yes1	INSIDE	0.423	0.343	1952.00	669.02	0.145	1562.07	226.56
A_68_P24951777	chr7:5003100-5003144	NM_026900:-11	Zfp580	PROMOTER	0.423	0.626	1500.18	938.54	0.264	1245.68	329.43
A_68_P33008134	chr12:18521060-18521104	NM_001033157:-233	5730507C01Rik	PROMOTER	0.422	0.675	2966.19	2001.15	0.285	2172.47	618.07
A_68_P25958415	chr8:74225497-74225541	NM_028189:181	B3gnt3	INSIDE	0.422	0.737	2143.45	1580.77	0.311	1563.69	486.64
A_68_P31678448	chr18:46887631-46887675	NM_033037:344	Cdo1	INSIDE	0.422	0.460	2637.23	1212.62	0.194	1900.31	368.93
A_68_P24347497	chr6:33010009-33010053	NM_025336:122	Chchd3	INSIDE	0.422	0.536	1123.39	602.45	0.226	879.35	198.89
A_68_P20148457	chr1:36528751-36528795	NM_033570:331	Cnnm4	INSIDE	0.422	0.482	2547.50	1228.37	0.203	1966.77	399.81
A_68_P31100997	chr17:25150808-25150852	NM_020608:1345	Cramp1l	INSIDE	0.422	0.664	3615.04	2399.44	0.280	2718.26	761.40
A_68_P24467402	chr6:55067829-55067873	NM_009953:15116	Crhr2	INSIDE	0.422	0.608	2457.72	1493.45	0.257	2070.59	531.50
A_68_P26880506	chr9:120843223-120843267	NM_001165902:549	Ctnnb1	INSIDE	0.422	0.512	1548.12	792.34	0.216	1269.45	274.37
A_68_P21762927	chr2:154718076-154718120	NM_026030:544	Eif2s2	INSIDE	0.422	0.494	1295.85	640.47	0.209	1049.91	219.18
A_68_P25537048	chr7:140004752-140004796	NM_212473:105	Fam53b	INSIDE	0.422	0.395	1663.24	656.80	0.167	1453.98	242.25
A_68_P21477084	chr2:102290645-102290692	NM_010218:1281	Fjx1	INSIDE	0.422	0.535	1716.13	917.66	0.226	1340.04	302.63
A_68_P31614303	chr18:34879926-34879970	NM_010280:93	Gfra3	INSIDE	0.422	0.459	2095.67	961.61	0.193	1705.92	329.96
A_68_P31162040	chr17:36117126-36117170	NM_008136:249	Gnl1	INSIDE	0.422	0.509	1276.95	650.32	0.215	977.43	210.30
A_68_P30684006	chr16:38089070-38089114	NM_019827:6	Gsk3b	INSIDE	0.422	0.648	2453.27	1589.87	0.274	1758.48	480.99
A_68_P28043947	chr11:96205604-96205648	NM_010458:544	Hoxb3	INSIDE	0.422	0.531	2464.90	1309.04	0.224	1879.09	420.76
A_68_P23440918	chr4:155215643-155215688	NM_024263:1877	Mxra8	INSIDE	0.422	1.415	1342.30	1899.36	0.597	870.00	519.73

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P21853526	chr2:170337089-170337133	NM_001110152:381	Pfdn4	INSIDE	0.422	0.689	5002.07	3447.40	0.291	3516.04	1022.07
A_68_P30128575	chr15:34372745-34372789	NM_009083:214	Rpl30	INSIDE	0.422	0.412	1394.28	574.75	0.174	1238.70	215.54
A_68_P23240175	chr4:118081682-118081726	NM_198170:164	Szt2	INSIDE	0.422	0.619	2031.40	1257.39	0.261	1720.99	449.84
A_68_P27688949	chr11:32355960-32356004	NM_173784:611	Ubtd2	INSIDE	0.422	0.650	2519.59	1637.60	0.274	1965.94	539.05
A_68_P21780068	chr2:157767229-157767273	NM_198627:26862	Vstm2l	INSIDE	0.422	0.597	1879.46	1122.76	0.252	1501.75	379.02
A_68_P32300615	chrX:23270584-23270630	NM_175180:364	Wdr44	INSIDE	0.422	0.627	1040.85	652.64	0.264	459.39	121.46
A_68_P22864042	chr4:41678377-41678421	NM_001017362:-224	Arid3c	PROMOTER	0.421	1.491	3127.52	4663.60	0.627	2219.77	1392.00
A_68_P27445216	chr10:110182710-110182754	NM_178609:212	E2f7	INSIDE	0.421	0.462	1902.18	877.87	0.194	1517.45	294.85
A_68_P28101900	chr11:106349136-106349180	NM_023913:-48	Ern1	PROMOTER	0.421	0.508	2320.57	1179.85	0.214	1863.93	398.54
A_68_P28221291	chr12:8304878-8304922	NM_013527:3860	Gdf7	INSIDE	0.421	0.586	3303.52	1935.60	0.247	2268.27	559.55
A_68_P22767953	chr4:19968999-19969043	NM_010281:-178	Ggh	PROMOTER	0.421	0.429	1570.69	673.59	0.181	1388.11	250.57
A_68_P32152775	chr19:47993384-47993428	NM_001001738:383	Itprip	INSIDE	0.421	0.671	1366.53	916.97	0.282	1158.75	327.20
A_68_P23573586	chr5:30924517-30924565	NM_010608:33998	Kcnk3	INSIDE	0.421	0.568	1124.37	638.72	0.239	915.88	219.27
A_68_P33003688	chr1_random:342766-342810	NM_177389:125	Mia3	INSIDE	0.421	0.625	3157.26	1973.34	0.263	2445.27	642.87
A_68_P23985663	chr5:111847362-111847406	NM_001081235:199	Mn1	INSIDE	0.421	0.575	1005.17	578.01	0.242	781.17	189.07
A_68_P21731904	chr2:148557983-148558027	NM_019632:152	Napb	INSIDE	0.421	0.604	3761.23	2270.02	0.254	2478.43	630.22
A_68_P26640627	chr9:74710721-74710765	NM_008262:1015	Onecut1	INSIDE	0.421	0.493	2826.27	1394.05	0.208	2042.42	424.55
A_68_P27542730	chr10:128133098-128133142	NM_177411:204	Rab5b	INSIDE	0.421	0.635	1145.72	728.04	0.267	1055.13	282.18
A_68_P24755176	chr6:112646414-112646458	NM_001167730:228	Rad18	INSIDE	0.421	0.605	1133.64	685.89	0.255	962.43	245.03
A_68_P30393146	chr15:84022703-84022747	NM_178614:62	Samm50	INSIDE	0.421	0.447	1409.97	629.72	0.188	1155.30	217.45
A_68_P26506990	chr9:50816646-50816690	NM_178710:510	Sik2	INSIDE	0.421	0.666	1460.48	972.49	0.280	1189.96	333.71
A_68_P27181839	chr10:61158255-61158299	NM_027912:15	Tysnd1	INSIDE	0.421	0.715	1529.10	1092.85	0.301	1262.60	380.16
A_68_P26343012	chr9:20385783-20385830	NM_172919:35	Zfp846	INSIDE	0.421	0.679	981.98	666.79	0.286	714.64	204.52
A_68_P29478592	chr14:26426602-26426646	NM_183208:147954	Zmiz1	INSIDE	0.421	0.445	1472.58	655.05	0.187	1061.12	198.80
A_68_P31623418	chr18:36508869-36508913	NM_001081365:613	0610010O12Rik	INSIDE	0.420	0.560	1256.22	703.63	0.235	1148.09	270.04
A_68_P28182351	chr11:119960438-119960482	NM_001110242:213	1810043H04Rik	INSIDE	0.420	0.433	1670.26	723.07	0.182	1218.38	221.64
A_68_P31918872	chr19:3708434-3708478	NM_028077:124	1810055G02Rik	INSIDE	0.420	0.582	1229.51	715.50	0.245	1080.36	264.31
A_68_P20429507	chr1:91350965-91351009	NM_001037136:-399	Agap1	PROMOTER	0.420	0.601	947.41	568.97	0.252	814.03	205.32
A_68_P21073310	chr2:25463379-25463423	NM_001024616:566	B230208H17Rik	INSIDE	0.420	0.461	2280.92	1051.03	0.193	1867.74	361.13
A_68_P26168090	chr8:113917279-113917323	NM_178086:421	Fa2h	INSIDE	0.420	0.691	1285.10	888.34	0.290	1056.43	306.48
A_68_P24175497	chr5:148537110-148537154	NM_010228:432	Flt1	INSIDE	0.420	0.617	2038.47	1257.73	0.259	1729.64	447.73
A_68_P31347825	chr17:74059155-74059199	NM_027864:615	Galnt14	INSIDE	0.420	1.634	7514.33	12275.01	0.686	4948.64	3394.20
A_68_P21906911	chr2:180629180-180629224	NR_029538:458	Mir124a-3	DOWNSTREAM	0.420	0.570	2546.98	1450.56	0.239	2069.63	495.38
A_68_P24126542	chr5:138041887-138041931	NM_030037:360	Mospd3	INSIDE	0.420	0.710	3325.86	2360.03	0.298	2661.94	794.19
A_68_P21904887	chr2:180324446-180324490	NM_031373:357	Ogfr	INSIDE	0.420	0.370	1864.70	690.24	0.155	1417.92	220.43
A_68_P23527586	chr5:21243231-21243275	NM_028431:275	Pmpcb	INSIDE	0.420	0.735	5394.70	3965.09	0.308	3955.20	1219.56
A_68_P22315262	chr3:88520847-88520891	NM_001163310:93	Rit1	INSIDE	0.420	0.670	1279.17	857.61	0.281	1095.06	308.12
A_68_P31542490	chr18:21160400-21160444	NM_019706:581	Rnf138	INSIDE	0.420	0.671	2509.27	1684.57	0.282	2009.07	566.87
A_68_P29855886	chr14:102007246-102007295	NM_001081278:1138	Tbc1d4	INSIDE	0.420	0.592	1030.36	609.95	0.249	715.80	178.15
A_68_P26476239	chr9:45636484-45636528	NM_001081373:215	Cep164	INSIDE	0.419	0.600	4238.47	2542.52	0.251	2950.74	741.98
A_68_P31666413	chr18:44540296-44540340	NM_027490:165	Dcp2	INSIDE	0.419	0.438	2832.24	1241.26	0.184	2037.69	374.49
A_68_P24620356	chr6:88148509-88148553	NM_008090:-127	Gata2	PROMOTER	0.419	0.469	1442.64	676.95	0.197	1340.33	263.69
A_68_P27390319	chr10:99478265-99478309	NM_013598:-171	Kitl	PROMOTER	0.419	0.515	1992.06	1025.00	0.215	1728.00	372.28
A_68_P21309980	chr2:69424250-69424294	NM_001081088:-148	Lrp2	PROMOTER	0.419	0.613	2816.66	1727.82	0.257	2232.51	574.45
A_68_P30350168	chr15:76546311-76546355	NM_198119:6271	Lrrc24	INSIDE	0.419	0.423	1576.40	666.84	0.177	1146.32	203.17
A_68_P25210773	chr7:77502893-77502937	NM_009697:2565	Nr2f2	INSIDE	0.419	0.456	1637.13	746.81	0.191	1360.60	260.11
A_68_P24132961	chr5:139469670-139469719	NM_008808:1213	Pdgfa	INSIDE	0.419	0.450	1236.09	555.78	0.188	951.74	179.09
A_68_P28159660	chr11:116351347-116351391	NM_026364:292	Prpsap1	INSIDE	0.419	0.654	1739.53	1136.92	0.274	1497.75	409.90
A_68_P31154945	chr17:34769052-34769096	NM_030890:2444	Prrt1	INSIDE	0.419	0.664	859.65	571.17	0.279	659.58	183.75
A_68_P31065957	chr17:15635193-15635237	NM_011185:26	Psmb1	INSIDE	0.419	0.610	1107.75	675.79	0.255	837.69	213.89
A_68_P29619513	chr14:56340877-56340921	NM_019519:115	Rabggta	INSIDE	0.419	1.425	12228.98	17424.16	0.597	7695.71	4593.86

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31166377	chr17:37079998-37080042	NM_001099632:25	Rnf39	INSIDE	0.419	0.577	2136.79	1233.36	0.242	1870.24	452.19
A_68_P22347940	chr3:95976314-95976359	NM_153053:-136	Sf3b4	PROMOTER	0.419	0.579	1023.64	592.25	0.242	971.97	235.52
A_68_P26924749	chr10:8238335-8238379	NM_177387:267	Ust	INSIDE	0.419	0.480	2967.43	1423.15	0.201	2436.12	489.69
A_68_P25326410	chr7:99889553-99889597	NR_015510:395	4632427E13Rik	INSIDE	0.418	0.613	1591.85	975.17	0.256	1213.29	310.51
A_68_P28033281	chr11:94352708-94352752	NM_027984:8558	Epn3	INSIDE	0.418	0.713	1812.06	1292.17	0.298	1494.42	445.05
A_68_P25507025	chr7:134889380-134889424	NM_172748:-886	Fbxl19	PROMOTER	0.418	0.589	3043.86	1792.94	0.246	1889.60	465.46
A_68_P26897303	chr9:123761167-123761211	NM_001110253:-168	Fyco1	PROMOTER	0.418	0.378	2746.02	1037.60	0.158	2152.23	339.85
A_68_P30487410	chr15:100559585-100559629	NM_001161768:-8698	Galnt6	PROMOTER	0.418	0.526	1537.56	808.37	0.220	1232.61	271.10
A_68_P23416918	chr4:151534429-151534473	NM_008236:1475	Hes2	INSIDE	0.418	0.526	1120.01	589.36	0.220	990.52	218.07
A_68_P27050630	chr10:32610114-32610158	NM_001013411:-415	Nkain2	PROMOTER	0.418	0.558	3230.91	1803.75	0.233	2528.35	589.83
A_68_P32135820	chr19:45081022-45081066	NM_153796:-3	Peo1	DIVERGENT_PROMOTER	0.418	0.651	2097.28	1365.42	0.272	1519.11	413.74
A_68_P30452932	chr15:94373863-94373910	NM_172437:52	Pus7l	INSIDE	0.418	0.680	997.57	678.65	0.284	698.60	198.48
A_68_P26815242	chr9:108420124-108420168	NM_001114119:729	Qrich1	INSIDE	0.418	0.543	3343.99	1816.39	0.227	2647.85	600.78
A_68_P25617015	chr8:4275885-4275929	NM_011592:-1	Timm44	PROMOTER	0.418	0.466	1571.46	731.62	0.194	1206.45	234.55
A_68_P22722574	chr4:9787244-9787288	NM_013526:15748	Gdf6	INSIDE	0.417	0.641	1027.55	658.62	0.267	864.10	230.94
A_68_P24172322	chr5:148001001-148001045	NM_008178:751	Gsx1	INSIDE	0.417	0.428	1713.77	732.81	0.178	1429.29	255.11
A_68_P27234955	chr10:70811089-70811133	NM_027184:570	Ipmk	INSIDE	0.417	0.432	2655.26	1145.79	0.180	1984.07	356.94
A_68_P20832395	chr1:174256553-174256597	NM_008429:2820	Kcnj9	INSIDE	0.417	0.587	2183.54	1282.71	0.245	1782.70	436.35
A_68_P21902322	chr2:179959737-179959781	NM_001081171:806	Lama5	INSIDE	0.417	0.592	1520.26	899.44	0.246	1245.47	306.94
A_68_P29510443	chr14:32019604-32019648	NM_022656:386	Nisch	INSIDE	0.417	0.679	1573.09	1067.41	0.283	1272.08	360.07
A_68_P28946217	chr13:36061405-36061450	NM_029628:1653	Ppp1r3g	INSIDE	0.417	0.388	1422.88	552.68	0.162	1181.97	191.50
A_68_P21019039	chr2:13976814-13976858	NM_001012396:826	Ptpla	INSIDE	0.417	0.459	2459.88	1129.22	0.192	1945.14	372.64
A_68_P27926653	chr11:75345380-75345424	NM_001199283:-211	Slc43a2	PROMOTER	0.417	0.433	3188.26	1381.53	0.181	2533.47	457.61
A_68_P28712491	chr12:107248439-107248483	NM_001029843:-12	Vrk1	PROMOTER	0.417	0.553	1385.42	765.60	0.230	1094.21	251.90
A_68_P24816772	chr6:124696114-124696158	NM_007881:10369	Atn1	INSIDE	0.416	0.313	1682.71	526.81	0.130	1384.15	180.22
A_68_P31776699	chr18:64819875-64819919	NM_001001488:758	Atp8b1	INSIDE	0.416	0.645	1010.68	651.63	0.268	849.92	228.17
A_68_P31928284	chr19:5366667-5366713	NM_011793:-45	Banf1	DIVERGENT_PROMOTER	0.416	0.595	996.83	592.66	0.247	718.76	177.78
A_68_P20509929	chr1:108610390-108610434	NM_009741:455	Bcl2	INSIDE	0.416	0.638	1687.46	1076.52	0.265	1125.49	298.72
A_68_P21617362	chr2:127951410-127951454	NM_009754:-341	Bcl2l11	PROMOTER	0.416	0.608	2537.30	1542.87	0.253	1871.35	473.37
A_68_P21836878	chr2:167514004-167514048	NM_009883:-388	Cebpb	PROMOTER	0.416	0.532	1435.24	763.87	0.221	1226.46	271.50
A_68_P29249639	chr13:97908050-97908094	NM_177266:181	Gfm2	INSIDE	0.416	0.475	1662.26	789.34	0.197	1181.89	233.24
A_68_P21073109	chr2:25435334-25435378	NM_001005424:263	Gm996	INSIDE	0.416	0.678	2103.14	1425.89	0.282	1549.36	437.37
A_68_P25837684	chr8:47825681-47825725	NM_008391:604	Irf2	INSIDE	0.416	0.697	1597.32	1112.68	0.290	1181.44	342.31
A_68_P31929693	chr19:5610054-5610098	NR_037603:-369	Kat5	PROMOTER	0.416	0.475	1492.43	709.00	0.198	1082.98	214.21
A_68_P27922355	chr11:74584384-74584428	NM_026197:42	Mettl16	INSIDE	0.416	0.584	2413.79	1410.45	0.243	1906.66	463.72
A_68_P23585505	chr5:33128122-33128166	NM_177298:131	Pisd	INSIDE	0.416	0.458	1904.84	871.63	0.191	1459.14	278.02
A_68_P27568396	chr11:6315839-6315883	NM_008907:-12	Ppia	PROMOTER	0.416	0.551	1712.42	943.39	0.229	1413.81	323.65
A_68_P24043182	chr5:121654805-121654849	NM_011290:317	Rpl6	INSIDE	0.416	0.525	1530.53	802.85	0.218	1243.30	271.58
A_68_P29145778	chr13:74487536-74487580	NM_023281:130	Sdha	INSIDE	0.416	0.479	1256.33	601.51	0.199	969.17	193.08
A_68_P25827278	chr8:46020383-46020427	AK079043:109		INSIDE	0.416	0.517	1306.82	675.22	0.215	939.50	202.16
A_68_P29020720	chr13:48764426-48764470	NM_007526:6044	Barx1	DOWNSTREAM	0.415	0.533	3856.85	2055.47	0.221	2861.55	632.80
A_68_P27223320	chr10:68815779-68815823	NM_007659:-140	Cdk1	PROMOTER	0.415	0.495	1876.26	927.88	0.205	1570.55	321.96
A_68_P21421467	chr2:91077045-91077089	NM_028119:157	Ddb2	INSIDE	0.415	0.481	2729.92	1314.31	0.200	1977.93	395.17
A_68_P25151146	chr7:64764649-64764693	NM_176942:709	Gabra5	INSIDE	0.415	0.485	1209.79	586.31	0.201	1112.35	223.50
A_68_P22325407	chr3:90269682-90269726	NM_008727:84	Npr1	INSIDE	0.415	0.463	2335.39	1081.29	0.192	1864.58	358.54
A_68_P31161346	chr17:35998590-35998640	NM_134122:352	Nrm	INSIDE	0.415	1.623	3958.59	6423.63	0.673	2470.63	1663.50
A_68_P28055835	chr11:98210174-98210218	NM_144828:145	Ppp1r1b	INSIDE	0.415	0.626	3132.75	1960.48	0.260	2366.43	614.59
A_68_P28145824	chr11:113926254-113926298	NM_172800:989	Sdk2	INSIDE	0.415	0.423	2654.77	1123.94	0.176	1979.25	347.60
A_68_P23756359	chr5:65827367-65827411	NM_009466:-307	Ugdh	PROMOTER	0.415	0.455	1287.76	586.48	0.189	1071.15	202.44
A_68_P29433273	chr14:18005233-18005277			Unknown	0.415	0.554	1350.69	748.90	0.230	1047.01	241.07
A_68_P33012181	chr9_random:57403-57447	NR_027950:2732	4930526I15Rik	DOWNSTREAM	0.414	0.557	1497.55	834.42	0.231	1276.19	294.67

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25276880	chr7:89484688-89484732	NM_001190374:507	Adamtsl3	INSIDE	0.414	0.612	2844.93	1740.42	0.253	2171.37	549.74
A_68_P28430601	chr12:52695077-52695121	NM_001198835:771	Coch	INSIDE	0.414	0.570	1734.46	988.83	0.236	1303.88	307.67
A_68_P25952213	chr8:73017547-73017591	NM_018827:514	Crlf1	INSIDE	0.414	0.663	1178.42	780.87	0.274	916.86	251.36
A_68_P23574103	chr5:31013991-31014035	NM_023047:-255	Dpysl5	PROMOTER	0.414	0.710	1574.89	1118.13	0.294	1144.85	336.89
A_68_P22729550	chr4:11314133-11314177	NM_194055:-224	Esrp1	PROMOTER	0.414	0.637	3420.97	2180.31	0.264	2777.70	733.15
A_68_P24844081	chr6:129483283-129483327	NM_020590:95	Gabarapl1	INSIDE	0.414	0.481	1103.95	530.78	0.199	834.82	165.97
A_68_P21046072	chr2:19579131-19579175	NR_033642:372	Gm3230	INSIDE	0.414	0.580	1816.74	1053.00	0.240	1498.43	359.31
A_68_P28888885	chr13:24853671-24853715	NM_020567:114	Gmnn	INSIDE	0.414	0.546	1466.72	800.57	0.226	1159.39	261.93
A_68_P29223483	chr13:93125415-93125459	NM_010829:-478	Msh3	PROMOTER	0.414	0.660	1694.35	1118.52	0.273	1384.23	377.98
A_68_P22029225	chr3:30501383-30501427	NM_030557:396	Mynn	INSIDE	0.414	0.425	1483.23	631.03	0.176	1178.90	207.57
A_68_P23373719	chr4:142751586-142751630	NM_001081355:51004	Prdm2	INSIDE	0.414	0.600	2265.89	1359.50	0.248	1795.27	445.77
A_68_P26346146	chr9:21049162-21049206	NM_053190:3703	S1pr5	INSIDE	0.414	0.484	1981.32	959.66	0.200	1636.69	327.93
A_68_P31254157	chr17:56281353-56281397	NM_001130456:-1608	Sema6b	PROMOTER	0.414	0.648	3569.53	2312.29	0.268	2533.73	678.80
A_68_P32464768	chrX:71032322-71032366	NM_001166480:-22	Ssr4	DIVERGENT_PROMOTER	0.414	1.428	2322.49	3316.10	0.591	898.89	531.58
A_68_P23196100	chr4:108133295-108133339	NM_175472:1286	Zcchc11	INSIDE	0.414	0.646	1484.72	958.90	0.267	1125.04	300.94
A_68_P25027721	chr7:30303289-30303333	ENSMUST00000141713:-913		PROMOTER	0.414	0.420	1880.81	789.64	0.174	1529.55	265.75
A_68_P28463393	chr12:58677002-58677046	NM_001037743:11923	4921506M07Rik	INSIDE	0.413	0.680	1762.12	1197.90	0.281	1675.53	470.49
A_68_P22831249	chr4:34498566-34498610	NM_001007589:725	Akirin2	INSIDE	0.413	0.604	2742.82	1656.91	0.250	2173.52	542.87
A_68_P27539540	chr10:127534403-127534447	NM_054078:4586	Baz2a	INSIDE	0.413	0.431	2288.05	985.78	0.178	2055.08	365.44
A_68_P25565211	chr7:144506565-144506609	NM_001113414:-458	Ebf3	PROMOTER	0.413	0.566	1305.03	738.81	0.234	1040.78	243.47
A_68_P31157364	chr17:35202217-35202261	NR_001462:857	G6b	INSIDE	0.413	0.552	2616.09	1444.87	0.228	1893.95	432.00
A_68_P30925869	chr16:84835358-84835402	NM_008065:12	Gabpa	INSIDE	0.413	0.551	1057.97	583.26	0.228	789.20	179.70
A_68_P25715748	chr8:24367539-24367583	NM_001042484:-8	Golga7	PROMOTER	0.413	0.613	2389.75	1464.08	0.253	1668.08	421.69
A_68_P27767868	chr11:46250398-46250442	NM_001104530:-28	Med7	PROMOTER	0.413	0.663	990.79	656.77	0.274	789.79	216.19
A_68_P30232953	chr15:55388796-55388840	NM_026759:49	Mrpl13	INSIDE	0.413	0.473	2660.21	1257.09	0.195	2051.67	400.62
A_68_P29263987	chr13:100285787-100285831	NM_008634:749	Mtap1b	INSIDE	0.413	0.593	1126.62	667.52	0.245	890.06	217.62
A_68_P29055175	chr13:55566226-55566270	NM_001030296:621	Prr7	INSIDE	0.413	0.641	997.70	639.06	0.265	859.80	227.64
A_68_P25528063	chr7:138515003-138515047	NM_001039534:365	Pstk	INSIDE	0.413	0.557	1266.05	704.56	0.230	941.94	216.26
A_68_P30595257	chr16:21947236-21947280	NM_025693:367	Tmem41a	INSIDE	0.413	0.705	1335.69	942.24	0.291	1141.59	332.69
A_68_P27636579	chr11:21270946-21270990	NM_139297:-86	Ugp2	PROMOTER	0.413	0.627	3347.53	2100.29	0.259	2781.75	720.34
A_68_P29449769	chr14:21748618-21748662	NM_009502:-14	Vcl	PROMOTER	0.413	0.610	3674.94	2241.40	0.252	2828.59	712.86
A_68_P27992047	chr11:86806779-86806823	NM_001005341:464	Ypel2	INSIDE	0.413	0.672	4891.83	3288.84	0.278	3710.47	1030.84
A_68_P27111549	chr10:45206690-45206739	ENSMUST00000099849:-513		PROMOTER	0.413	0.474	1095.19	518.63	0.196	885.32	173.24
A_68_P23971472	chr5:108796224-108796268	ENSMUST00000100944:-2630		PROMOTER	0.413	0.564	1652.80	932.82	0.233	1237.91	288.34
A_68_P27970642	chr11:83116490-83116534	NM_001035854:314	Ap2b1	INSIDE	0.412	0.613	1542.09	945.94	0.253	1146.43	289.90
A_68_P25609691	chr7:152047946-152047990	NM_010202:678	Fgf4	INSIDE	0.412	0.492	1642.75	808.69	0.203	1186.41	240.81
A_68_P23018911	chr4:73659893-73659937	NM_172869:408	Frmd3	INSIDE	0.412	0.571	1375.71	786.02	0.235	1140.99	268.36
A_68_P32135887	chr19:45090142-45090186	NM_001130526:-2460	Lzts2	PROMOTER	0.412	0.691	1347.91	930.96	0.285	1100.25	313.42
A_68_P28192098	chr11:121563706-121563750	NM_144797:-12	Metrnl	PROMOTER	0.412	0.530	1369.10	725.65	0.218	1193.02	260.61
A_68_P25725384	chr8:26212812-26212856	NM_031257:-551	Plekha2	PROMOTER	0.412	0.703	3332.86	2343.63	0.290	2682.89	776.75
A_68_P31120663	chr17:28278567-28278611	NM_001004366:-882	Scube3	PROMOTER	0.412	0.452	1146.06	518.47	0.187	957.24	178.55
A_68_P30349611	chr15:76470372-76470416	NM_183091:-35	Tonsl	PROMOTER	0.412	1.668	9193.56	15333.36	0.687	5983.93	4113.26
A_68_P20636519	chr1:136859233-136859277	NM_026024:101	Ube2t	INSIDE	0.412	0.519	1782.14	924.96	0.214	1524.67	325.64
A_68_P20976549	chr2:5872087-5872131	NM_001081132:-406	Upf2	DIVERGENT_PROMOTER	0.412	0.537	2244.35	1204.12	0.221	1687.54	373.12
A_68_P22319094	chr3:89195751-89195795	NM_009565:1353	Zbtb7b	INSIDE	0.412	0.477	1482.92	707.26	0.196	1153.77	226.49
A_68_P30546660	chr16:11176366-11176410	NM_145931:98	Zc3h7a	INSIDE	0.412	0.489	1495.01	730.64	0.201	1359.83	273.69
A_68_P27846110	chr11:60836644-60836688	ENSMUST00000089184:601		INSIDE	0.412	0.609	938.36	571.87	0.251	789.61	198.33
A_68_P27255933	chr10:74780494-74780538	NM_009630:829	Adora2a	INSIDE	0.411	1.363	5453.48	7433.18	0.561	3819.41	2141.52
A_68_P26318243	chr9:14419424-14419468	NM_001081395:-2	Amotl1	PROMOTER	0.411	0.602	873.40	525.70	0.247	753.40	186.27
A_68_P21094157	chr2:28773265-28773309	NM_001164186:-1326	Barhl1	PROMOTER	0.411	0.696	2445.75	1702.23	0.286	1840.68	527.06
A_68_P25044994	chr7:35460266-35460310	NM_175140:137442	Chst8	INSIDE	0.411	0.599	1228.10	735.14	0.246	994.25	244.50

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P29506064	chr14:31293149-31293193	NM_133761:420	Dcp1a	INSIDE	0.411	0.548	1594.27	873.20	0.225	1172.68	263.71
A_68_P28069093	chr11:100480802-100480846	NM_019795:658	Dnajc7	INSIDE	0.411	0.700	1858.85	1301.35	0.288	1302.63	375.00
A_68_P21428049	chr2:92210891-92210935	NM_001166633:281	Gyltl1b	INSIDE	0.411	0.603	2316.06	1395.78	0.247	1656.29	409.93
A_68_P24942331	chr6:148779822-148779866	NM_001081113:145	Ipo8	INSIDE	0.411	0.555	1755.36	974.80	0.228	1369.02	312.29
A_68_P26585376	chr9:64868976-64869020	NM_021345:526	Ptplad1	INSIDE	0.411	0.593	1041.52	618.04	0.244	901.82	220.16
A_68_P25032745	chr7:31435198-31435242	NM_133693:27	Rbm42	INSIDE	0.411	0.643	1186.15	762.97	0.264	930.76	246.05
A_68_P26822087	chr9:110034313-110034357	NM_009211:-193	Smarcc1	PROMOTER	0.411	0.545	978.56	533.48	0.224	789.66	176.88
A_68_P30572948	chr16:17277681-17277725	NM_177473:1310	Tmem191c	INSIDE	0.411	0.419	1794.88	752.09	0.172	1424.21	245.03
A_68_P26596713	chr9:66891367-66891411	NM_001164252:290	Tpm1	INSIDE	0.411	0.633	1916.73	1214.25	0.260	1718.65	447.69
A_68_P24003597	chr5:114830959-114831004	NM_054093:366	Ube3b	INSIDE	0.411	0.529	4098.81	2167.91	0.218	3145.46	684.31
A_68_P31637164	chr18:39152519-39152563	NM_175164:-258	Arhgap26	PROMOTER	0.410	0.725	1703.48	1234.31	0.297	1219.68	361.91
A_68_P23201931	chr4:109330348-109330392	NM_007671:7607	Cdkn2c	DOWNSTREAM	0.410	0.428	2457.97	1053.23	0.176	2044.63	359.05
A_68_P26137946	chr8:108660718-108660762	NM_176838:134	Esrp2	INSIDE	0.410	0.672	6302.10	4233.59	0.275	4092.88	1126.41
A_68_P31099857	chr17:24987665-24987709	NM_001159626:75	Hagh	INSIDE	0.410	0.628	1229.78	771.74	0.257	1042.21	268.16
A_68_P27924564	chr11:74979683-74979728	NM_001098203:1949	Hic1	INSIDE	0.410	0.384	1585.65	608.64	0.157	1227.08	193.10
A_68_P29154205	chr13:76522219-76522263	NM_030174:-168	Mctp1	PROMOTER	0.410	0.580	1388.94	805.24	0.237	1088.20	258.36
A_68_P20221656	chr1:51535340-51535384	NM_028696:-119	Obfc2a	PROMOTER	0.410	0.578	4764.54	2752.21	0.237	3808.61	902.69
A_68_P25957670	chr8:74115606-74115650	NM_025396:-454	Pgls	PROMOTER	0.410	0.602	4980.29	3000.61	0.247	3676.46	907.74
A_68_P28071134	chr11:100820206-100820250	NM_008986:11703	Ptrf	INSIDE	0.410	0.593	2523.39	1495.35	0.243	1817.82	441.98
A_68_P20348987	chr1:74553038-74553082	NM_021383:427	Rqcd1	INSIDE	0.410	0.622	1929.98	1200.79	0.255	1468.88	374.64
A_68_P28168289	chr11:117830449-117830493	NM_007707:210	Socs3	INSIDE	0.410	0.498	1705.64	849.37	0.204	1381.55	281.93
A_68_P27682712	chr11:31269004-31269048	NM_011491:1035	Stc2	INSIDE	0.410	0.590	897.61	529.27	0.242	837.64	202.36
A_68_P21912033	chr2:181415118-181415162	NM_009326:126	Tcea2	INSIDE	0.410	0.504	1224.04	616.75	0.206	930.26	192.01
A_68_P25018704	chr7:28516297-28516346	NM_009560:-106	Zfp60	PROMOTER	0.410	0.489	1102.47	539.29	0.201	827.88	166.06
A_68_P21823447	chr2:165194226-165194272	NM_001005425:-6629	Zfp663	PROMOTER	0.410	0.586	1286.83	753.90	0.240	937.90	225.02
A_68_P24465594	chr6:54766604-54766648	NM_199143:-283	Znrf2	PROMOTER	0.410	0.537	1840.31	987.56	0.220	1516.27	333.72
A_68_P24430832	chr6:49024262-49024309	NM_029353:492	2410003K15Rik	INSIDE	0.409	0.678	1040.49	705.25	0.277	822.87	228.27
A_68_P22834883	chr4:35172926-35172970	NM_001081343:181	3110043O21Rik	INSIDE	0.409	0.669	955.75	639.50	0.274	791.03	216.49
A_68_P23442482	chr4:155484180-155484224	NM_145557:96	9430015G10Rik	INSIDE	0.409	0.431	1382.21	595.85	0.176	1104.16	194.66
A_68_P24046036	chr5:122161287-122161331	NM_009125:-309	Atxn2	PROMOTER	0.409	0.670	2342.01	1570.29	0.274	1840.76	505.08
A_68_P20849637	chr1:177622396-177622440	NM_021350:-3934	Chml	PROMOTER	0.409	0.736	3272.00	2406.68	0.301	2326.69	699.39
A_68_P28566344	chr12:79963184-79963228	NM_026114:148	Eif2s1	INSIDE	0.409	0.487	1532.72	745.90	0.199	1213.84	241.38
A_68_P31948452	chr19:10176316-10176360	NM_019699:-345	Fads2	PROMOTER	0.409	0.572	1284.29	734.28	0.234	1045.44	244.33
A_68_P20802626	chr1:168930754-168930798	NM_001160261:-771	Fam78b	DIVERGENT_PROMOTER	0.409	0.544	4120.83	2241.58	0.223	3702.58	824.57
A_68_P23226466	chr4:115563188-115563232	NM_001039124:6206	Kncn	DOWNSTREAM	0.409	0.556	1854.46	1030.70	0.227	1582.06	359.35
A_68_P31775847	chr18:64676070-64676114	NM_001142950:119	Nars	INSIDE	0.409	0.572	2345.12	1342.55	0.234	1852.25	434.23
A_68_P31626274	chr18:37107885-37107929	NM_007766:-4436	Pcdha4	PROMOTER	0.409	1.496	948.35	1419.04	0.612	808.66	495.14
A_68_P31921667	chr19:4192216-4192260	NM_031868:65	Ppp1ca	INSIDE	0.409	0.625	2319.46	1450.06	0.256	1886.44	482.61
A_68_P33012162	chr9_random:55248-55292	NM_011154:-238	Ppp2r3d	PROMOTER	0.409	0.688	1410.70	970.21	0.282	1027.25	289.29
A_68_P26609891	chr9:69138894-69138938	NM_013646:637308	Rora	INSIDE	0.409	0.527	2100.37	1107.77	0.215	1636.20	352.54
A_68_P25434394	chr7:121261406-121261450	NM_025846:-133	Rras2	PROMOTER	0.409	0.699	1787.85	1250.07	0.286	1426.98	408.44
A_68_P22917597	chr4:52452103-52452147	NM_008017:4	Smc2	INSIDE	0.409	0.450	1247.91	561.74	0.184	1050.69	193.22
A_68_P21070649	chr2:25080027-25080071	NM_146116:174	Tubb2c	INSIDE	0.409	0.478	1412.01	675.35	0.196	1110.29	217.23
A_68_P21070652	chr2:25080248-25080297	NM_146116:-50	Tubb2c	PROMOTER	0.409	0.423	1560.81	659.82	0.173	1088.84	188.17
A_68_P21070645	chr2:25079554-25079599	NM_146116:646	Tubb2c	INSIDE	0.409	0.491	1200.14	589.19	0.201	968.76	194.37
A_68_P28553596	chr12:77471058-77471102	NM_178744:-172	Zbtb1	DIVERGENT_PROMOTER	0.409	0.552	2284.85	1261.68	0.226	1750.16	395.07
A_68_P24973875	chr7:13551224-13551268	NM_178732:34	Zfp324	INSIDE	0.409	0.515	1331.45	685.54	0.210	1045.44	219.91
A_68_P31620880	chr18:36078887-36078931	AK021191:6123		DOWNSTREAM	0.409	0.618	2034.91	1258.42	0.253	1709.12	432.34
A_68_P21710705	chr2:144993065-144993109	ENSMUST00000110007:-403		PROMOTER	0.409	0.630	1657.26	1043.44	0.258	1328.30	342.45
A_68_P30560720	chr16:14159038-14159083	NM_001081154:307	4921513D23Rik	INSIDE	0.408	0.497	2073.99	1031.49	0.203	1636.44	332.16
A_68_P31953831	chr19:11023233-11023277	NM_023731:502	Ccdc86	INSIDE	0.408	0.643	889.16	571.31	0.262	716.46	187.98

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25501143	chr7:133709945-133709993	NM_146200:-88	Eif3c	PROMOTER	0.408	0.609	935.98	570.37	0.248	786.54	195.38
A_68_P25949228	chr8:72520400-72520444	NM_001113345:-144	Gatad2a	PROMOTER	0.408	0.489	2940.06	1438.94	0.200	2316.97	463.12
A_68_P22194396	chr3:63780003-63780047	NM_001033300:-40	Gmps	PROMOTER	0.408	0.683	1296.60	885.44	0.279	1021.69	284.75
A_68_P23541182	chr5:23857019-23857063	NM_013569:382	Kcnh2	INSIDE	0.408	0.563	1148.64	647.18	0.230	931.66	214.28
A_68_P24112795	chr5:135164074-135164118	NM_010717:364	Limk1	INSIDE	0.408	0.682	5503.00	3753.40	0.279	3918.82	1091.53
A_68_P22818617	chr4:32050724-32050768	NM_009316:-335	Map3k7	PROMOTER	0.408	0.377	1924.93	726.34	0.154	1466.92	225.63
A_68_P27293629	chr10:82226162-82226206	NM_010914:702	Nfyb	INSIDE	0.408	0.567	1982.74	1125.03	0.232	1672.39	387.54
A_68_P25373532	chr7:108599866-108599910	NR_026574:67	Pde2a	INSIDE	0.408	0.510	2866.26	1461.57	0.208	2125.20	441.78
A_68_P28107255	chr11:107331346-107331390	NM_145823:666	Pitpnc1	INSIDE	0.408	0.658	1864.59	1226.24	0.268	1561.88	419.27
A_68_P31940077	chr19:7557297-7557341	NM_053076:453	Rtn3	INSIDE	0.408	1.623	3523.70	5720.20	0.662	2531.91	1675.36
A_68_P21775423	chr2:156960457-156960501	NM_001139520:480	Samhd1	INSIDE	0.408	0.568	1117.04	634.74	0.232	1007.64	233.45
A_68_P24819294	chr6:125141350-125141400	NR_028517:-4925	Scarna10	PROMOTER	0.408	0.615	1712.69	1053.88	0.251	1327.18	332.98
A_68_P30580553	chr16:18581703-18581747	NM_011532:5338	Tbx1	DOWNSTREAM	0.408	0.656	1584.96	1040.01	0.267	1296.88	346.80
A_68_P22728296	chr4:11083878-11083922	NM_001199105:313	Trp53inp1	INSIDE	0.408	0.443	2227.67	986.41	0.181	1725.74	311.95
A_68_P21567191	chr2:118798466-118798510	AK184532:45580		INSIDE	0.408	0.507	2052.06	1040.89	0.207	1598.99	330.85
A_68_P23747544	chr5:64203539-64203583	NM_029554:-173	0610040J01Rik	PROMOTER	0.407	0.325	2198.01	714.47	0.132	1814.50	239.97
A_68_P26313777	chr9:13631232-13631276	NR_037622:243	Cep57	INSIDE	0.407	0.486	3391.82	1647.72	0.198	2734.82	540.70
A_68_P27284381	chr10:80085791-80085835	NM_001159591:-6588	Csnk1g2	PROMOTER	0.407	0.460	2111.74	970.58	0.187	1557.44	291.41
A_68_P24383688	chr6:39508034-39508079	NM_172477:-223	Dennd2a	PROMOTER	0.407	0.588	1614.11	949.25	0.239	1128.93	270.38
A_68_P26822030	chr9:110019511-110019555	NM_133347:-1446	Dhx30	PROMOTER	0.407	0.637	1377.60	877.71	0.260	1241.84	322.32
A_68_P27991096	chr11:86621298-86621342	NM_026191:-158	Dhx40	PROMOTER	0.407	0.538	1239.12	666.15	0.219	916.71	200.56
A_68_P27281569	chr10:79649352-79649396	NM_007909:7148	Efna2	INSIDE	0.407	1.541	1256.56	1936.53	0.627	969.03	607.79
A_68_P28924080	chr13:31718919-31718963	NM_010225:1256	Foxf2	INSIDE	0.407	0.689	3172.57	2185.00	0.281	2213.14	621.08
A_68_P31151371	chr17:34115239-34115283	NR_004446:476	H2-K2	INSIDE	0.407	0.456	1605.18	731.55	0.185	1385.24	256.72
A_68_P25098818	chr7:53652536-53652580	NM_001112739:692	Kcnc1	INSIDE	0.407	0.400	1311.52	524.24	0.163	975.14	158.73
A_68_P29110673	chr13:68720745-68720789	NM_172480:232	Mtrr	INSIDE	0.407	0.371	1931.95	716.22	0.151	1508.16	227.48
A_68_P24176700	chr5:148769468-148769512	NM_029920:595	Mtus2	INSIDE	0.407	0.526	1630.86	857.36	0.214	1291.13	276.17
A_68_P26610636	chr9:69245924-69245968	NM_145618:142	Narg2	INSIDE	0.407	0.384	5793.84	2227.06	0.156	4240.45	663.08
A_68_P29603748	chr14:52533567-52533611	NM_001145959:-425	Ndrg2	DIVERGENT_PROMOTER	0.407	0.480	1560.30	749.06	0.196	1153.20	225.46
A_68_P28614148	chr12:88443473-88443517	NM_022414:-5	Ngb	PROMOTER	0.407	0.415	1799.48	746.75	0.169	1681.23	284.09
A_68_P29701296	chr14:70843268-70843313	NM_025945:-12	Polr3d	DIVERGENT_PROMOTER	0.407	0.631	2190.63	1383.25	0.257	1603.41	411.96
A_68_P22889897	chr4:46663588-46663636	NM_198664:-541	Tbc1d2	PROMOTER	0.407	0.662	982.47	650.35	0.269	767.27	206.69
A_68_P29418923	chr14:14794239-14794283	NM_025435:-521	Thoc7	PROMOTER	0.407	0.537	1962.94	1053.66	0.218	1739.95	379.84
A_68_P27294064	chr10:82321765-82321809	NM_001042513:-164	Txnrd1	PROMOTER	0.407	0.407	1520.91	618.76	0.166	1187.54	196.62
A_68_P22704455	chr4:6118180-6118224	NM_026534:-49	Ubxn2b	PROMOTER	0.407	0.671	1912.76	1284.31	0.274	1666.37	455.81
A_68_P31175221	chr17:39982297-39982341	ENSMUST00000157647:-1752		PROMOTER	0.407	1.649	95563.17	157538.30	0.672	68246.85	45830.39
A_68_P28202484	chr12:4824078-4824122	NM_025323:-313	0610009D07Rik	PROMOTER	0.406	0.608	1944.10	1181.96	0.247	1603.98	395.49
A_68_P24167402	chr5:147042562-147042606	NM_153599:-666	Cdk8	DIVERGENT_PROMOTER	0.406	0.608	1352.14	821.47	0.246	1139.57	280.81
A_68_P21317592	chr2:70956339-70956383	NM_028593:250	Cybrd1	INSIDE	0.406	0.558	1737.90	970.02	0.226	1323.53	299.72
A_68_P28914787	chr13:30077407-30077451	NM_010093:504	E2f3	INSIDE	0.406	0.611	2612.84	1596.12	0.248	2058.37	509.93
A_68_P27897961	chr11:69734599-69734643	NM_001166596:-33	Eif5a	PROMOTER	0.406	0.463	1940.76	898.54	0.188	1546.60	290.79
A_68_P20826008	chr1:172995959-172996003	NM_010188:-6446	Fcgr3	PROMOTER	0.406	0.350	18198.05	6361.85	0.142	15322.08	2176.74
A_68_P29053524	chr13:55254501-55254545	NM_008011:344	Fgfr4	INSIDE	0.406	1.439	1816.38	2614.22	0.584	1466.89	857.10
A_68_P31347822	chr17:74058856-74058900	NM_027864:913	Galnt14	INSIDE	0.406	0.542	1480.35	802.89	0.220	1057.71	232.90
A_68_P27812596	chr11:54716387-54716431	NM_008161:-19	Gpx3	PROMOTER	0.406	0.537	985.97	529.92	0.218	768.72	167.64
A_68_P26134295	chr8:108042675-108042719	NM_008289:51	Hsd11b2	INSIDE	0.406	0.730	2677.10	1954.81	0.296	1979.05	586.14
A_68_P25780634	chr8:36651604-36651648	NM_001081279:775	Mfhas1	INSIDE	0.406	0.482	1783.48	859.18	0.196	1341.49	262.70
A_68_P31201772	chr17:45692808-45692853	NM_008690:166	Nfkbie	INSIDE	0.406	0.497	1713.85	852.26	0.202	1237.60	249.77
A_68_P20231215	chr1:53354231-53354281	NM_145517:318	Ormdl1	INSIDE	0.406	0.534	1129.37	603.42	0.217	980.16	212.39
A_68_P26546675	chr9:58094820-58094867	NM_008884:2750	Pml	INSIDE	0.406	0.442	1835.96	811.92	0.180	1371.08	246.26
A_68_P21103105	chr2:30272089-30272133	NM_138748:541	Ppp2r4	INSIDE	0.406	0.636	3968.58	2525.95	0.258	2830.49	731.40

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P30970947	chr16:92697153-92697197	NM_001111023:399	Runx1	INSIDE	0.406	0.515	2685.30	1382.40	0.209	2016.68	421.81
A_68_P30393147	chr15:84022777-84022821	NM_178614:136	Samm50	INSIDE	0.406	0.691	3994.97	2761.52	0.280	3060.42	858.38
A_68_P21597425	chr2:124435761-124435806	NM_172537:-248	Sema6d	PROMOTER	0.406	0.615	871.15	535.88	0.249	650.35	162.24
A_68_P27673282	chr11:29072968-29073015	NM_134034:85	Smek2	INSIDE	0.406	0.639	949.47	606.88	0.260	796.75	206.96
A_68_P27798797	chr11:52174094-52174138	NM_011694:-500	Vdac1	PROMOTER	0.406	0.650	1764.27	1146.33	0.264	1315.69	346.88
A_68_P25352337	chr7:104937215-104937259	ENSMUST00000172423:186		INSIDE	0.406	0.665	1482.59	985.69	0.270	1357.36	366.22
A_68_P25712955	chr8:23915948-23915992	NM_001122820:156	Ap3m2	INSIDE	0.405	0.626	938.42	587.32	0.253	785.72	199.13
A_68_P26132522	chr8:107778665-107778709	NM_178879:365	B3gnt9-ps	INSIDE	0.405	0.596	1716.07	1023.62	0.242	1234.29	298.28
A_68_P26349632	chr9:21741348-21741392	NM_144935:-1347	BC018242	PROMOTER	0.405	0.437	1486.50	649.65	0.177	1174.97	207.88
A_68_P26445764	chr9:40684336-40684380	NM_178245:2149	Bsx	INSIDE	0.405	0.423	1901.12	803.37	0.171	1525.03	260.78
A_68_P23271159	chr4:124613810-124613854	NM_026560:329	Cdca8	INSIDE	0.405	0.625	2290.39	1431.64	0.253	1723.95	436.25
A_68_P27173114	chr10:59681401-59681445	NM_016803:586	Chst3	INSIDE	0.405	0.480	1633.42	783.31	0.194	1275.03	247.62
A_68_P26248660	chr8:127472125-127472169	NM_053207:1008	Egln1	INSIDE	0.405	0.419	1430.66	598.91	0.170	1160.96	197.05
A_68_P23590781	chr5:34064587-34064631	NM_001163216:-346	Fgfr3	PROMOTER	0.405	0.530	3266.43	1729.91	0.215	2438.35	523.55
A_68_P22522346	chr3:129533887-129533931	NM_026578:406	Gar1	INSIDE	0.405	0.598	2284.02	1365.84	0.242	1847.04	446.89
A_68_P23404324	chr4:149475624-149475668	NM_177366:14035	Gpr157	INSIDE	0.405	1.773	2904.68	5150.79	0.719	2051.82	1474.86
A_68_P29010701	chr13:47026038-47026093	NM_010617:-978	Kif13a	PROMOTER	0.405	0.484	1767.47	854.99	0.196	1333.63	261.42
A_68_P28206071	chr12:5382006-5382050	NM_001164493:460	Klhl29	INSIDE	0.405	0.524	3088.99	1617.12	0.212	2432.86	515.70
A_68_P25279963	chr7:90017868-90017912	NM_175366:2048	Mex3b	INSIDE	0.405	0.636	1415.44	900.30	0.258	1133.24	291.99
A_68_P25953855	chr8:73284899-73284943	NM_183170:-100	Mpv17l2	PROMOTER	0.405	0.408	2453.08	1000.94	0.165	1787.56	295.51
A_68_P22705747	chr4:6380739-6380783	NM_010945:658	Nsmaf	INSIDE	0.405	0.415	1617.03	671.38	0.168	1348.70	226.72
A_68_P23308592	chr4:131393872-131393916	NM_001083119:299	Ptpru	INSIDE	0.405	1.432	2326.39	3331.75	0.580	1769.52	1025.80
A_68_P22129913	chr3:51288449-51288493	NM_016858:583	Rab33b	INSIDE	0.405	0.485	1658.46	804.34	0.196	1337.61	262.75
A_68_P23330841	chr4:135411994-135412038	NM_001080387:10	Srsf10	INSIDE	0.405	0.543	2145.64	1166.05	0.220	1597.74	351.61
A_68_P28037462	chr11:95085010-95085054	ENSMUST00000150818:1914		INSIDE	0.405	0.545	1408.10	767.79	0.221	1060.48	234.02
A_68_P28448910	chr12:55757351-55757395	NM_134054:187	1110002B05Rik	INSIDE	0.404	0.509	1885.11	959.65	0.206	1424.62	293.29
A_68_P29750659	chr14:79701095-79701139	NM_025427:326	1190002H23Rik	INSIDE	0.404	0.574	1404.21	805.56	0.232	1064.58	246.87
A_68_P26240062	chr8:126001616-126001660	NM_054070:-123	Afg3l1	PROMOTER	0.404	0.494	2109.64	1041.20	0.199	1607.97	320.67
A_68_P26236517	chr8:125394810-125394862	NM_007662:22563	Cdh15	DOWNSTREAM	0.404	1.403	1945.50	2728.65	0.566	1315.85	745.01
A_68_P30822062	chr16:64851258-64851302	NM_178647:-630	Cggbp1	PROMOTER	0.404	0.519	3183.58	1650.75	0.210	2462.97	516.24
A_68_P27284377	chr10:80085062-80085106	NM_134002:-440	Csnk1g2	PROMOTER	0.404	0.629	1419.87	892.51	0.254	1060.64	269.20
A_68_P24620360	chr6:88148968-88149012	NM_008090:333	Gata2	INSIDE	0.404	0.683	2322.07	1585.49	0.276	1713.63	472.62
A_68_P23318326	chr4:133140776-133140820	NM_133884:511	Gpn2	INSIDE	0.404	0.640	1169.25	748.32	0.259	985.30	254.87
A_68_P32090702	chr19:36629470-36629514	NM_001163471:364	Hectd2	INSIDE	0.404	0.272	2373.47	646.01	0.110	1953.97	214.88
A_68_P25616729	chr8:4238967-4239011	NM_001042557:249	Map2k7	INSIDE	0.404	0.580	2908.83	1687.64	0.234	2062.11	483.10
A_68_P29510753	chr14:32064135-32064185	NM_027949:244	Phf7	INSIDE	0.404	0.534	960.26	513.16	0.216	777.89	167.83
A_68_P31254158	chr17:56281426-56281470	NM_001130456:-1682	Sema6b	PROMOTER	0.404	0.581	2799.57	1627.69	0.235	2130.76	500.62
A_68_P27842505	chr11:60166539-60166583	NM_001039092:-153	Tom1l2	DIVERGENT_PROMOTER	0.404	0.361	1587.91	572.60	0.146	1187.68	172.87
A_68_P22869764	chr4:43071791-43071835	NM_001081413:-43	Unc13b	PROMOTER	0.404	0.501	1272.86	637.85	0.202	1133.30	229.43
A_68_P21622217	chr2:128769546-128769590	NM_020594:188	Zc3h8	INSIDE	0.404	0.554	1092.21	605.07	0.224	984.96	220.62
A_68_P22616117	chr3:146348087-146348133	ENSMUST00000147113:-2624		PROMOTER	0.404	1.480	1311.76	1941.95	0.598	1012.61	605.60
A_68_P28053985	chr11:97883420-97883464	NM_001159320:-3756	Cacnb1	PROMOTER	0.403	0.437	1225.57	535.50	0.176	1003.72	176.92
A_68_P26207422	chr8:120807660-120807704	NM_019707:28	Cdh13	INSIDE	0.403	0.463	1396.49	647.17	0.187	1115.55	208.39
A_68_P24799552	chr6:120615622-120615666	NM_001128151:-794	Cecr2	PROMOTER	0.403	0.603	3552.63	2143.25	0.243	2839.95	689.74
A_68_P31666414	chr18:44540418-44540462	NM_027490:287	Dcp2	INSIDE	0.403	0.471	1722.26	811.15	0.190	1330.43	252.26
A_68_P29702644	chr14:71041729-71041773	NM_008004:325	Fgf17	INSIDE	0.403	0.627	2188.74	1371.28	0.252	1859.32	469.04
A_68_P25361482	chr7:106530807-106530853	NM_201352:772	Gdpd5	INSIDE	0.403	1.577	1363.77	2150.15	0.636	979.45	622.45
A_68_P28744398	chr12:112723379-112723423	NM_001033248:634	Gm266	INSIDE	0.403	0.466	1750.51	815.19	0.188	1666.67	313.00
A_68_P24126241	chr5:137971926-137971970	NM_010312:2509	Gnb2	INSIDE	0.403	0.702	1875.13	1316.69	0.283	1528.56	432.65
A_68_P31940699	chr19:7686892-7686936	NM_025731:-144	Hrasls5	DIVERGENT_PROMOTER	0.403	0.677	2664.39	1803.92	0.273	1908.10	520.63
A_68_P31425157	chr17:88197480-88197524	NM_199251:-168	Kcnk12	PROMOTER	0.403	0.466	4375.97	2037.15	0.188	3471.60	651.98

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P29650241	chr14:62058563-62058607	NM_008466:200	Kpna3	INSIDE	0.403	0.405	1537.06	622.81	0.163	1438.25	235.02
A_68_P27890684	chr11:68505119-68505163	NM_175260:-276	Myh10	PROMOTER	0.403	0.664	1027.75	682.38	0.268	863.61	231.22
A_68_P26346140	chr9:21048545-21048589	NM_053190:4321	S1pr5	INSIDE	0.403	0.535	1135.96	608.15	0.216	1006.93	217.15
A_68_P22049514	chr3:34563117-34563161	NR_015580:103836	Sox2ot	INSIDE	0.403	0.484	2066.20	999.89	0.195	1574.89	307.29
A_68_P20353934	chr1:75419154-75419198	NM_001085370:36992	Speg	INSIDE	0.403	1.343	4896.31	6574.99	0.541	3345.01	1810.88
A_68_P30133048	chr15:35300905-35300956	NM_177151:-370	Vps13b	PROMOTER	0.403	0.492	1070.04	526.44	0.198	848.32	168.32
A_68_P24118436	chr5:136379600-136379644	NM_018871:30889	Ywhag	DOWNSTREAM	0.403	0.634	1135.29	719.87	0.256	915.76	234.26
A_68_P29604086	chr14:52604738-52604782	NM_001145921:253	Arhgef40	INSIDE	0.402	0.420	2403.91	1009.44	0.169	1831.28	309.16
A_68_P27129528	chr10:50312762-50312806	NM_001146089:310	Ascc3	INSIDE	0.402	0.639	3730.88	2382.81	0.257	3140.60	806.64
A_68_P20258660	chr1:58449893-58449937	NM_025824:-65	Bzw1	PROMOTER	0.402	0.379	2338.44	886.59	0.152	1931.23	294.39
A_68_P21425690	chr2:91804013-91804057	NM_138306:-314	Dgkz	PROMOTER	0.402	1.354	2042.05	2764.55	0.544	1585.34	862.03
A_68_P29257118	chr13:99124161-99124205	NM_008242:-17	Foxd1	PROMOTER	0.402	0.510	1490.33	760.15	0.205	1157.08	237.16
A_68_P24112565	chr5:134789851-134789895	NM_001080746:744	Gtf2i	INSIDE	0.402	0.714	2256.93	1612.52	0.287	1769.13	508.52
A_68_P23120716	chr4:94719068-94719112	NM_010591:-177	Jun	PROMOTER	0.402	0.423	1296.90	548.96	0.170	1043.85	177.68
A_68_P28961839	chr13:38726652-38726696	NM_139063:304	Muted	INSIDE	0.402	0.532	1082.81	575.86	0.214	844.67	180.51
A_68_P20039230	chr1:13116543-13116587	NM_001081209:680	Prdm14	INSIDE	0.402	0.572	3613.44	2067.32	0.230	2620.44	603.08
A_68_P31560663	chr18:24688162-24688206	NM_144861:521	Rprd1a	INSIDE	0.402	0.580	1300.04	753.96	0.233	1070.85	249.46
A_68_P28540843	chr12:75065592-75065636	NM_178392:98	Snapc1	INSIDE	0.402	0.389	1905.69	741.84	0.157	1618.55	253.52
A_68_P24880090	chr6:137684038-137684082	NM_011499:458	Strap	INSIDE	0.402	0.565	2008.73	1135.59	0.227	1503.42	341.29
A_68_P21818004	chr2:164287014-164287058	NM_025575:566	Sys1	INSIDE	0.402	0.517	1359.86	703.50	0.208	1188.15	247.05
A_68_P23223137	chr4:114730092-114730136	NM_011527:-2017	Tal1	PROMOTER	0.402	1.506	1521.71	2292.42	0.606	1280.29	776.17
A_68_P24452213	chr6:52663843-52663887	NM_025816:142	Tax1bp1	INSIDE	0.402	0.633	1114.69	706.07	0.255	971.26	247.36
A_68_P30344891	chr15:75741091-75741135	NM_178646:948	Tigd5	INSIDE	0.402	0.694	2910.45	2020.64	0.279	2088.38	583.52
A_68_P31951351	chr19:10630157-10630201	NM_026798:550	Tmem216	INSIDE	0.402	1.573	3244.90	5105.54	0.633	2382.85	1508.24
A_68_P28746254	chr12:113052004-113052048	NM_028875:26	Xrcc3	INSIDE	0.402	0.647	4008.98	2594.96	0.260	3067.97	797.87
A_68_P27541962	chr10:127984459-127984503	NM_134003:320	Zc3h10	INSIDE	0.402	0.565	1308.93	738.91	0.227	1006.35	228.22
A_68_P31166723	chr17:37139521-37139565	NR_033137:-1068	Zfp57	PROMOTER	0.402	0.568	1340.99	761.64	0.228	962.23	219.44
A_68_P20730836	chr1:156052430-156052474	NM_001204908:4136	Zfp648	INSIDE	0.402	0.615	1327.37	815.96	0.247	1041.18	257.49
A_68_P31063097	A_68_P31063097			Unknown	0.402	0.663	4637.87	3076.43	0.267	3485.76	929.33
A_68_P29848868	chr14:100685092-100685136	AK021307:-1508		PROMOTER	0.402	0.403	1857.91	748.70	0.162	1431.64	231.79
A_68_P27904030	chr11:70846911-70846955	NM_134022:187	6330403K07Rik	INSIDE	0.401	0.439	1364.46	599.38	0.176	1066.17	187.83
A_68_P31259844	chr17:57201624-57201668	NM_177638:-53	Crb3	DIVERGENT_PROMOTER	0.401	0.600	1139.58	684.20	0.241	965.34	232.70
A_68_P25588981	chr7:148648103-148648147	NM_001025103:1132	Efcab4a	INSIDE	0.401	0.489	1279.57	625.46	0.196	951.70	186.53
A_68_P28865541	chr13:20183122-20183166	NM_080288:769	Elmo1	INSIDE	0.401	0.362	2120.48	767.66	0.145	1712.97	248.82
A_68_P32219644	chr19:59541958-59542009	NM_010132:8804	Emx2	DOWNSTREAM	0.401	0.501	1502.12	752.11	0.201	1161.64	233.43
A_68_P31741004	chr18:58369796-58369845	NM_010181:-240	Fbn2	PROMOTER	0.401	0.672	1429.00	960.85	0.270	1189.50	320.74
A_68_P21137836	chr2:35960496-35960540	NM_001083126:-938	Lhx6	PROMOTER	0.401	1.336	8929.66	11925.85	0.536	6249.44	3346.87
A_68_P31601524	chr18:32323271-32323316	NM_011946:551	Map3k2	INSIDE	0.401	0.591	1415.59	837.13	0.237	1152.26	273.12
A_68_P27281301	chr10:79613466-79613510	NM_021565:2454	Midn	INSIDE	0.401	0.367	1465.23	537.97	0.147	1036.83	152.57
A_68_P30359767	chr15:78240574-78240618	NM_138670:3063	Mpst	INSIDE	0.401	0.682	1086.67	740.80	0.274	845.19	231.31
A_68_P26555228	chr9:59599330-59599374	NM_173018:372	Myo9a	INSIDE	0.401	0.623	1581.72	985.65	0.250	1278.00	319.75
A_68_P23328803	chr4:135050627-135050671	NM_028995:-229	Nipal3	DIVERGENT_PROMOTER	0.401	0.553	1557.06	861.22	0.222	1180.18	261.60
A_68_P28185376	chr11:120434174-120434218	NM_011032:54	P4hb	INSIDE	0.401	0.405	1978.78	800.88	0.162	1637.81	265.81
A_68_P27921382	chr11:74403457-74403501	NM_001015046:182	Rap1gap2	INSIDE	0.401	0.564	1202.64	678.74	0.227	932.96	211.38
A_68_P26874898	chr9:119803985-119804029	NM_026236:-6	Wdr48	PROMOTER	0.401	0.449	1258.18	565.02	0.180	961.70	173.28
A_68_P21394205	chr2:84554801-84554845	NM_144887:499	Zdhhc5	INSIDE	0.401	0.723	2712.89	1962.11	0.290	2037.85	590.93
A_68_P24465593	chr6:54766531-54766575	NM_199143:-357	Znrf2	PROMOTER	0.401	0.670	2222.15	1489.45	0.269	1707.36	459.35
A_68_P27852925	chr11:62062872-62062916	NM_007413:409	Adora2b	INSIDE	0.400	0.617	1152.32	711.48	0.247	829.07	204.77
A_68_P24050080	chr5:122842069-122842113	NM_019824:154	Arpc3	INSIDE	0.400	0.718	4394.64	3154.81	0.287	3316.23	952.58
A_68_P27826629	chr11:57458793-57458837	NM_134189:-129	Galnt10	PROMOTER	0.400	0.608	3664.79	2229.96	0.244	2544.15	619.66
A_68_P26445381	chr9:40609139-40609183	NM_031165:-195	Hspa8	PROMOTER	0.400	0.691	1034.99	714.85	0.276	879.47	242.73

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26258430	chr8:129118076-129118120	NM_001164598:-762	Irf2bp2	PROMOTER	0.400	0.721	1718.04	1238.29	0.289	1460.35	421.48
A_68_P30498330	chr15:102347068-102347112	NM_001163643:345	Map3k12	INSIDE	0.400	1.500	2499.08	3748.29	0.600	1607.42	964.83
A_68_P25009541	chr7:26082496-26082540	NM_008776:456	Pafah1b3	INSIDE	0.400	0.438	1706.65	746.98	0.175	1461.72	256.05
A_68_P25588866	chr7:148633186-148633239	NM_026020:-336	Rplp2	DIVERGENT_PROMOTER	0.400	0.587	1498.29	879.31	0.235	1091.39	255.97
A_68_P24591631	chr6:83086000-83086044	NM_009106:-1055	Rtkn	PROMOTER	0.400	0.655	1225.70	802.41	0.262	828.16	216.99
A_68_P31259829	chr17:57199355-57199400	NM_025877:-91	Slc25a23	DIVERGENT_PROMOTER	0.400	0.589	2001.97	1180.00	0.236	1472.23	347.15
A_68_P29218728	chr13:91601752-91601796	NM_024186:1073	Ssbp2	INSIDE	0.400	0.631	1627.78	1026.95	0.252	1284.93	323.86
A_68_P25184111	chr7:72838614-72838658	NM_026795:334	Tm2d3	INSIDE	0.400	0.349	1726.28	602.90	0.140	1348.93	188.30
A_68_P30660864	chr16:33966979-33967023	NM_009471:89	Umps	INSIDE	0.400	0.552	1618.29	893.67	0.221	1283.96	283.85
A_68_P24056367	chr5:124022745-124022789	NM_029929:258	Vps33a	INSIDE	0.400	0.514	1120.84	576.62	0.206	884.82	181.92
A_68_P25603239	chr7:151016135-151016179	NM_007856:7085	Dhcr7	INSIDE	0.399	0.597	1125.54	672.50	0.238	815.91	194.46
A_68_P23796637	chr5:73647888-73647932	NM_028194:-53	Fryl	PROMOTER	0.399	0.474	1998.35	946.81	0.189	1621.76	306.32
A_68_P26020978	chr8:87186231-87186275	NM_010499:499	Ier2	INSIDE	0.399	0.277	1961.30	542.96	0.110	1579.44	174.25
A_68_P24132967	chr5:139470355-139470399	NM_008808:531	Pdgfa	INSIDE	0.399	0.437	1789.36	781.96	0.174	1451.55	253.04
A_68_P23699207	chr5:53604122-53604166	NM_172710:547	Sel1l3	INSIDE	0.399	0.533	1774.42	945.20	0.212	1363.90	289.58
A_68_P21608668	chr2:126379204-126379249	NM_011978:467	Slc27a2	INSIDE	0.399	0.514	2438.81	1252.84	0.205	1823.73	373.99
A_68_P29455907	chr14:22808867-22808911	NM_145459:-65	Zfp503	PROMOTER	0.399	0.569	1604.07	911.92	0.227	1214.52	275.57
A_68_P31144955	chr17:32457753-32457797	NM_019774:324	Akap8	INSIDE	0.398	0.543	1365.85	741.62	0.216	1107.07	239.38
A_68_P30541084	chr16:10193396-10193440	NM_029253:420	Atf7ip2	INSIDE	0.398	0.608	995.72	605.68	0.242	813.64	197.17
A_68_P29480513	chr14:26747056-26747103	NM_025311:-343	D14Ertd449e	PROMOTER	0.398	0.358	1735.25	621.67	0.143	1456.35	207.60
A_68_P29651217	chr14:62268108-62268159	NR_028264:33077	Dleu2	INSIDE	0.398	0.543	1443.25	783.46	0.216	1158.50	250.08
A_68_P26957818	chr10:14264701-14264745	NM_001002268:120	Gpr126	INSIDE	0.398	0.467	1511.94	705.41	0.186	1275.00	236.56
A_68_P28833519	chr13:12742906-12742950	NR_003568:-266	Gpr137b-ps	PROMOTER	0.398	0.363	4391.82	1592.50	0.144	3385.93	488.41
A_68_P28157577	chr11:115999946-115999990	NM_024177:214	Mrpl38	INSIDE	0.398	0.493	3724.44	1836.53	0.196	2843.38	558.00
A_68_P21485378	chr2:103601161-103601205	NM_153126:225	Nat10	INSIDE	0.398	0.618	3637.53	2248.47	0.246	2544.68	625.73
A_68_P26349534	chr9:21722752-21722796	NM_031874:-209	Rab3d	PROMOTER	0.398	0.403	1561.47	629.94	0.160	1150.25	184.58
A_68_P28052672	chr11:97643844-97643889	NM_022891:-113	Rpl23	PROMOTER	0.398	0.606	1390.97	842.99	0.241	1054.91	254.30
A_68_P27891995	chr11:68714810-68714854	NM_009080:-235	Rpl26	PROMOTER	0.398	0.694	3449.52	2393.87	0.276	2457.62	679.51
A_68_P26316376	chr9:14081279-14081323	NM_030261:556	Sesn3	INSIDE	0.398	0.552	1345.98	743.47	0.220	1037.83	228.33
A_68_P29288689	chr13:104900121-104900165	NM_144838:273	Sgtb	INSIDE	0.398	0.583	3354.69	1956.35	0.232	2336.34	542.22
A_68_P20585378	chr1:127457195-127457239	NM_028787:-376	Slc35f5	PROMOTER	0.398	0.549	1232.48	677.04	0.218	1037.55	226.65
A_68_P26165834	chr8:113494088-113494132	NM_009179:50346	St3gal2	INSIDE	0.398	0.677	1222.12	827.61	0.269	901.87	242.81
A_68_P26644959	chr9:75458604-75458648	NM_016711:506	Tmod2	INSIDE	0.398	0.426	2977.71	1268.02	0.170	2449.97	415.69
A_68_P22323363	chr3:89884285-89884329	NM_022314:7691	Tpm3	INSIDE	0.398	0.365	1427.82	521.52	0.145	1038.00	150.77
A_68_P32700071	chrX:137134752-137134796	NM_001077364:287	Tsc22d3	INSIDE	0.398	3.957	5767.82	22822.44	1.575	2608.73	4107.70
A_68_P23862543	chr5:86601868-86601912	NM_172712:-122	Uba6	PROMOTER	0.398	0.692	2387.01	1652.51	0.275	1949.46	536.57
A_68_P29703308	chr14:71165727-71165771	NM_023045:687	Xpo7	INSIDE	0.398	0.702	1752.43	1229.46	0.279	1340.90	374.38
A_68_P33008825	chr4_random:109830-109874	NM_001033326:51	Dhrsx	INSIDE	0.397	0.470	1833.30	861.33	0.186	1457.07	271.74
A_68_P22318526	chr3:89120527-89120571	NM_010108:6253	Efna3	INSIDE	0.397	0.639	1485.97	948.79	0.254	1110.36	281.80
A_68_P26224353	chr8:123607977-123608021	NM_010426:-375	Foxf1a	PROMOTER	0.397	0.504	1890.38	952.54	0.200	1686.45	337.20
A_68_P21571367	chr2:119584322-119584366	NM_008523:-83	Ltk	PROMOTER	0.397	0.476	1630.05	775.10	0.189	1333.23	251.49
A_68_P26581610	chr9:64233768-64233812	NM_172522:358	Megf11	INSIDE	0.397	0.699	2374.21	1658.78	0.277	1758.64	487.33
A_68_P30232954	chr15:55388910-55388954	NM_001168250:-30	Mtbp	DIVERGENT_PROMOTER	0.397	0.432	3116.90	1347.01	0.172	2372.98	407.34
A_68_P29011114	chr13:47109579-47109623	NM_175340:619	Nhlrc1	INSIDE	0.397	0.517	1150.56	595.40	0.206	823.92	169.45
A_68_P24981712	chr7:17061914-17061958	NM_008718:193	Npas1	INSIDE	0.397	0.712	2890.67	2056.71	0.283	2241.41	633.52
A_68_P23820901	chr5:77739843-77739887	NM_153798:356	Polr2b	INSIDE	0.397	0.647	1612.02	1043.01	0.257	1284.16	330.01
A_68_P23301758	chr4:130219950-130220000	NM_001159603:701	Pum1	INSIDE	0.397	0.586	1032.44	605.24	0.232	893.17	207.63
A_68_P32741829	chrX:146893580-146893628	NM_001164683:89	Tmem29	INSIDE	0.397	0.687	1246.33	855.90	0.273	436.00	118.86
A_68_P22970878	chr4:63156551-63156595	NM_001008791:413	Whrn	INSIDE	0.397	0.613	3917.18	2399.98	0.243	2938.54	714.69
A_68_P24385306	chr6:39822132-39822176			Unknown	0.397	0.469	2589.32	1213.47	0.186	2062.60	383.60
A_68_P26640506	chr9:74696583-74696627	ENSMUST00000160842:-197		PROMOTER	0.397	0.658	970.12	638.12	0.261	740.58	193.51

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27835480	chr11:59021879-59021923	NM_024210:38	2310033P09Rik	INSIDE	0.396	0.576	2695.23	1552.55	0.228	1958.86	446.66
A_68_P24222134	chr6:7643189-7643233	NM_012055:-28	Asns	PROMOTER	0.396	0.542	2387.82	1293.90	0.215	2052.41	440.34
A_68_P24991257	chr7:19661336-19661380	NM_010058:-190	Dmwd	PROMOTER	0.396	0.616	1112.54	684.81	0.244	889.48	217.03
A_68_P29047193	chr13:54150633-54150677	NM_010076:373	Drd1a	INSIDE	0.396	0.545	2490.00	1356.97	0.216	1903.02	411.08
A_68_P31097235	chr17:24563756-24563800	NM_010023:151	Eci1	INSIDE	0.396	0.527	3129.78	1648.81	0.209	2436.59	508.04
A_68_P21202304	chr2:49307386-49307430	NM_172663:403	Epc2	INSIDE	0.396	0.453	2466.98	1117.64	0.179	1901.54	341.08
A_68_P26023481	chr8:87584180-87584224	NM_026791:185	Fbxw9	INSIDE	0.396	0.627	1561.81	978.68	0.248	1215.89	301.53
A_68_P22311356	chr3:87827542-87827586	NM_022031:3869	Hapln2	INSIDE	0.396	0.664	2761.76	1833.73	0.263	1981.97	520.78
A_68_P25196754	chr7:75097245-75097289	NM_010513:124	Igf1r	INSIDE	0.396	0.473	3320.88	1569.80	0.187	2477.45	464.14
A_68_P20833276	chr1:174412036-174412080	NM_001145800:-285	Igsf9	PROMOTER	0.396	0.574	1317.37	756.65	0.228	1156.57	263.21
A_68_P23399813	chr4:148681750-148681794	NM_207682:35	Kif1b	INSIDE	0.396	0.601	2997.35	1800.31	0.238	2346.60	557.57
A_68_P30482203	chr15:99603119-99603163	NM_028015:-194	Lass5	PROMOTER	0.396	0.596	2632.96	1568.15	0.236	2144.25	506.20
A_68_P27163119	chr10:57785941-57785985	NM_026148:-251	Lims1	PROMOTER	0.396	0.680	1897.17	1290.62	0.269	1413.46	380.81
A_68_P23839619	chr5:81758936-81758980	NM_198702:308341	Lphn3	INSIDE	0.396	1.822	2298.64	4187.16	0.722	1764.06	1273.14
A_68_P24792499	chr6:119280504-119280548	NM_001172207:-1304	Lrtm2	PROMOTER	0.396	0.523	1726.40	903.05	0.207	1158.45	239.74
A_68_P27940743	chr11:77796384-77796428	NM_174852:89	Phf12	INSIDE	0.396	0.423	4734.44	2004.16	0.168	3592.41	602.73
A_68_P20632578	chr1:136195654-136195698	NM_001144855:33829	Ppfia4	INSIDE	0.396	0.708	1305.46	924.84	0.281	1092.82	306.60
A_68_P21212092	chr2:51004822-51004866	NM_028810:-213	Rnd3	PROMOTER	0.396	0.586	1113.91	653.02	0.232	521.16	120.98
A_68_P22339768	chr3:94386146-94386190	NM_029721:456	Snx27	INSIDE	0.396	0.513	10731.28	5502.96	0.203	7576.74	1538.58
A_68_P23281702	chr4:126409701-126409745	NM_198960:3791	Tcfap2e	INSIDE	0.396	0.646	816.79	527.67	0.256	636.94	163.10
A_68_P23231032	chr4:116480068-116480112	NM_026654:74	Toe1	INSIDE	0.396	0.637	1622.39	1033.81	0.252	1277.20	322.39
A_68_P20293015	chr1:64579497-64579541	NM_001037726:141	Creb1	INSIDE	0.395	1.637	1498.43	2452.72	0.646	1044.74	674.70
A_68_P29571975	chr14:46276736-46276780	NM_001039106:1060	Ddhd1	INSIDE	0.395	0.513	2910.02	1493.49	0.203	2124.93	430.75
A_68_P23981089	chr5:111082753-111082797	NM_027156:305	Ddx51	INSIDE	0.395	1.415	2235.79	3162.99	0.559	1524.12	851.91
A_68_P23917030	chr5:98682994-98683038	NM_010203:-186	Fgf5	PROMOTER	0.395	0.553	1859.16	1027.23	0.218	1360.03	296.52
A_68_P29996526	chr15:7765753-7765797	NM_010275:4764	Gdnf	INSIDE	0.395	0.703	1521.03	1069.87	0.278	1204.55	334.90
A_68_P23571067	chr5:30482177-30482221	NM_145558:337	Hadhb	INSIDE	0.395	0.651	971.59	632.21	0.257	751.39	193.05
A_68_P27262211	chr10:75931408-75931452	NM_019434:-285	Mcm3ap	PROMOTER	0.395	0.628	2981.60	1872.43	0.248	2404.79	596.32
A_68_P30359739	chr15:78237110-78237154	NM_001162493:-9	Mpst	DIVERGENT_PROMOTER	0.395	0.517	1965.86	1015.55	0.204	1519.10	309.59
A_68_P22378553	chr3:101816844-101816888	NM_178777:2799	Nhlh2	INSIDE	0.395	0.497	2536.22	1261.46	0.197	2171.96	426.83
A_68_P28457454	chr12:57636900-57636944	NM_001146198:-829	Nkx2-1	PROMOTER	0.395	0.568	2415.54	1372.50	0.225	1730.29	388.75
A_68_P27283560	chr10:79958022-79958066	NM_139226:394	Onecut3	INSIDE	0.395	0.559	2970.49	1661.40	0.221	2195.37	484.90
A_68_P26823553	chr9:110310358-110310402	NM_001081043:334	Ptpn23	INSIDE	0.395	0.521	1283.21	669.17	0.206	1086.75	223.83
A_68_P27846981	chr11:60988586-60988630	NM_001004143:-47	Usp22	PROMOTER	0.395	0.591	3307.59	1953.18	0.233	2575.10	600.24
A_68_P28956456	chr13:37870834-37870878	ENSMUST00000122842:588		INSIDE	0.395	0.686	1883.01	1292.51	0.271	1291.09	350.38
A_68_P20262085	chr1:59176968-59177012	NM_001033449:-50	Als2cr4	PROMOTER	0.394	0.586	1764.61	1034.63	0.231	1379.76	318.35
A_68_P22407408	chr3:107399047-107399091	NM_007441:1120	Alx3	INSIDE	0.394	0.699	1352.07	945.75	0.276	993.19	273.74
A_68_P29020643	chr13:48755179-48755223	NM_007526:-3204	Barx1	PROMOTER	0.394	0.473	1255.55	593.95	0.186	993.02	185.15
A_68_P20616256	chr1:133424915-133424959	NM_175382:371	Fam72a	INSIDE	0.394	0.598	939.33	561.70	0.235	773.66	182.08
A_68_P24804136	chr6:121363612-121363660	NM_001033354:60060	Iqsec3	INSIDE	0.394	1.459	861.78	1257.28	0.575	728.64	419.21
A_68_P22934427	chr4:55544464-55544508	NM_010637:861	Klf4	INSIDE	0.394	0.566	1638.41	926.60	0.223	1245.95	277.60
A_68_P27351981	chr10:92624097-92624141	NR_035452:-1411	Mir1931	PROMOTER	0.394	0.461	1435.67	661.71	0.182	1234.00	224.27
A_68_P22029224	chr3:30501291-30501335	NM_030557:304	Mynn	INSIDE	0.394	0.491	1203.66	591.48	0.194	948.31	183.80
A_68_P22509733	chr3:127337069-127337113	NM_009718:1028	Neurog2	INSIDE	0.394	0.536	1400.00	750.34	0.211	1146.46	242.10
A_68_P29228004	chr13:93962351-93962395	NM_133905:-134	Papd4	PROMOTER	0.394	0.345	2639.04	910.03	0.136	2030.41	275.52
A_68_P27982131	chr11:85124251-85124295	NM_016910:-483	Ppm1d	PROMOTER	0.394	0.440	1279.88	563.48	0.173	1059.51	183.63
A_68_P31306706	chr17:66869156-66869200	NM_024448:-168	Rab12	PROMOTER	0.394	0.563	2387.55	1344.99	0.222	1888.64	419.35
A_68_P30425525	chr15:89329138-89329182	NM_021423:-1127	Shank3	PROMOTER	0.394	0.589	1347.03	794.03	0.232	1002.00	232.85
A_68_P24039146	chr5:120961225-120961269	NM_001177594:46	Slc24a6	INSIDE	0.394	0.528	3211.48	1697.21	0.208	2575.83	536.78
A_68_P31886106	chr18:84257584-84257628	NM_146090:57	Zadh2	INSIDE	0.394	0.377	3025.06	1141.33	0.149	2306.11	342.56
A_68_P25834611	chr8:47248829-47248873	NM_025747:-6059	4933411K20Rik	PROMOTER	0.393	0.377	1891.58	713.22	0.148	1452.97	215.28

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26397644	chr9:30729778-30729822	NM_001024139:237	Adamts15	INSIDE	0.393	0.551	1105.34	609.40	0.217	921.87	199.88
A_68_P27104595	chr10:43988364-43988408	NM_053069:223	Atg5	INSIDE	0.393	0.648	1331.05	862.37	0.255	1161.90	295.86
A_68_P27903680	chr11:70796542-70796586	NM_007573:-36	C1qbp	PROMOTER	0.393	0.533	1532.93	816.29	0.209	1280.18	267.89
A_68_P26527663	chr9:54613548-54613592	NM_013496:956	Crabp1	INSIDE	0.393	0.518	1434.66	742.44	0.203	1097.56	223.21
A_68_P32097101	chr19:37772874-37772918	NM_007811:599	Cyp26a1	INSIDE	0.393	0.426	1213.97	517.08	0.167	1052.81	176.09
A_68_P32030090	chr19:25580813-25580857	NM_015826:639	Dmrt1	INSIDE	0.393	0.736	4472.71	3292.67	0.289	3179.73	919.43
A_68_P24687559	chr6:99616974-99617018	NM_025829:-231	Eif4e3	PROMOTER	0.393	0.659	1635.27	1077.16	0.259	1160.44	300.29
A_68_P30261333	chr15:60656265-60656309	NM_001162926:349	Fam84b	INSIDE	0.393	0.655	1042.70	683.29	0.258	911.55	234.94
A_68_P28558324	chr12:78338946-78338990	NM_016893:-1039	Fut8	PROMOTER	0.393	0.501	2557.23	1281.73	0.197	2032.50	400.01
A_68_P27862299	chr11:63735880-63735924	NM_018805:-116	Hs3st3b1	PROMOTER	0.393	0.443	2224.84	984.97	0.174	1748.73	304.15
A_68_P28377243	chr12:40949898-40949942	NM_013562:-144	Ifrd1	PROMOTER	0.393	0.573	1938.73	1110.44	0.225	1465.35	330.17
A_68_P26345197	chr9:20842972-20843016	NR_035438:-6222	Mir1900	PROMOTER	0.393	0.633	1129.22	715.19	0.249	905.51	225.62
A_68_P29269917	chr13:101514369-101514413	NM_001190264:224	Mrps36	INSIDE	0.393	0.562	1483.16	833.55	0.221	1137.24	251.42
A_68_P25848475	chr8:49640835-49640879	NM_001145937:119188	Odz3	INSIDE	0.393	0.623	1717.71	1069.53	0.245	1357.53	332.13
A_68_P20412615	chr1:88425095-88425139	NM_008972:1806	Ptma	INSIDE	0.393	0.704	1399.14	985.11	0.277	1200.12	332.10
A_68_P23328512	chr4:134989887-134989933	NM_022980:-190	Rcan3	PROMOTER	0.393	0.620	1491.84	925.02	0.244	1175.09	286.59
A_68_P27911313	chr11:72224759-72224803	NM_177776:435	Smtnl2	INSIDE	0.393	0.562	1527.09	858.89	0.221	1231.22	271.86
A_68_P27792049	chr11:50872760-50872804	NM_009329:24	Zfp354a	INSIDE	0.393	0.466	1271.52	592.67	0.183	1116.60	204.33
A_68_P20258664	chr1:58450590-58450634	NM_025824:633	Bzw1	INSIDE	0.392	0.644	1254.18	807.72	0.252	1054.82	266.06
A_68_P25354352	chr7:105326428-105326472	NM_007602:253	Capn5	INSIDE	0.392	0.666	2220.45	1478.16	0.261	1546.65	403.21
A_68_P22523142	chr3:129672517-129672561	NM_025779:586	Ccdc109b	INSIDE	0.392	0.505	2604.71	1315.65	0.198	1951.55	386.76
A_68_P26085416	chr8:98331248-98331292	NM_001205226:92	Cnot1	INSIDE	0.392	0.403	2325.01	938.12	0.158	1832.93	289.72
A_68_P30648664	chr16:31663664-31663708	NM_007862:-438	Dlg1	PROMOTER	0.392	0.458	3597.39	1647.10	0.180	2613.64	469.67
A_68_P20317730	chr1:69154592-69154636	NM_010154:19	Erbb4	INSIDE	0.392	0.422	1426.54	601.74	0.165	1216.30	201.21
A_68_P23331511	chr4:135528428-135528472	NM_011942:59	Lypla2	INSIDE	0.392	0.473	1769.63	837.26	0.185	1552.06	287.58
A_68_P26884585	chr9:121550768-121550812	NM_026915:-106	Lyzl4	DIVERGENT_PROMOTER	0.392	0.586	1165.46	682.57	0.229	885.62	203.12
A_68_P22278905	chr3:82162143-82162187	NM_001081230:171	Mtap9	INSIDE	0.392	0.487	1290.87	628.19	0.191	1051.49	200.76
A_68_P26017700	chr8:86550149-86550193	NM_028877:4798	Palm3	INSIDE	0.392	1.362	4053.05	5519.11	0.533	2798.18	1491.77
A_68_P31207973	chr17:46766171-46766215	NM_175168:261	Ptk7	INSIDE	0.392	0.571	1376.75	786.16	0.224	1101.03	246.77
A_68_P24819295	chr6:125141439-125141483	NR_028517:-5011	Scarna10	PROMOTER	0.392	0.538	2141.51	1152.69	0.211	1553.71	328.17
A_68_P31260730	chr17:57388800-57388844	NM_134125:-51	Trip10	DIVERGENT_PROMOTER	0.392	0.608	3559.47	2163.18	0.238	2651.86	631.60
A_68_P31206982	chr17:46592667-46592712	NM_001162864:31935	Ttbk1	INSIDE	0.392	1.403	1399.62	1963.16	0.549	1059.83	582.08
A_68_P31206981	chr17:46592555-46592609	NM_001162864:32042	Ttbk1	INSIDE	0.392	1.717	3863.90	6635.69	0.673	2504.05	1685.58
A_68_P24974124	chr7:13594887-13594931	NM_001024699:241	Zbtb45	INSIDE	0.392	1.550	8940.84	13859.75	0.607	5657.47	3435.24
A_68_P20350710	chr1:74863740-74863784			Unknown	0.392	0.672	1297.47	872.32	0.264	974.28	257.03
A_68_P25890691	chr8:59819908-59819952	ENSMUST00000132988:9016		DOWNSTREAM	0.392	0.484	1350.03	653.38	0.189	1096.54	207.78
A_68_P29699594	chr14:70553626-70553670	NM_146055:-50	2610301G19Rik	PROMOTER	0.391	0.531	1427.31	757.25	0.207	1115.67	231.50
A_68_P21438173	chr2:93816579-93816623	NM_026944:34287	Alkbh3	DOWNSTREAM	0.391	0.698	1383.11	965.21	0.273	1073.71	293.35
A_68_P22503487	chr3:126300546-126300590	NM_001025438:678	Camk2d	INSIDE	0.391	0.431	2047.11	883.00	0.169	1532.12	258.42
A_68_P30026217	chr15:13103232-13103276	NM_007666:140	Cdh6	INSIDE	0.391	0.672	4209.50	2829.81	0.263	2762.48	726.88
A_68_P22550732	chr3:134875583-134875627	NM_173762:78	Cenpe	INSIDE	0.391	0.608	1219.19	740.70	0.237	914.46	216.97
A_68_P21132485	chr2:35111777-35111821	NM_001206367:-80	Gsn	PROMOTER	0.391	0.613	2026.14	1242.11	0.240	1463.14	350.71
A_68_P27497669	chr10:119912366-119912410	NM_010441:1603	Hmga2	INSIDE	0.391	0.640	1046.27	669.85	0.251	783.71	196.34
A_68_P25678163	chr8:15011860-15011904	NM_029116:858	Kbtbd11	INSIDE	0.391	0.478	1570.57	749.98	0.186	1240.73	231.39
A_68_P28089844	chr11:104092991-104093035	NM_001038609:263	Mapt	INSIDE	0.391	1.364	2693.55	3672.88	0.533	1860.12	991.85
A_68_P21817647	chr2:164229981-164230025	NM_013592:112	Matn4	INSIDE	0.391	0.476	1295.63	616.22	0.186	1035.52	192.49
A_68_P27184368	chr10:61595655-61595699	NM_009719:-161	Neurog3	PROMOTER	0.391	0.630	2160.43	1360.12	0.246	1755.04	431.48
A_68_P29075345	chr13:58907821-58907865	NM_008745:-114	Ntrk2	PROMOTER	0.391	0.692	1892.71	1310.54	0.271	1464.42	396.74
A_68_P30397294	chr15:84684736-84684780	NM_001081166:1801	Phf21b	INSIDE	0.391	0.463	1726.92	800.27	0.181	1439.78	261.16
A_68_P25435185	chr7:121419707-121419751	NM_011965:-98	Psma1	PROMOTER	0.391	0.724	2831.07	2050.70	0.283	2139.61	605.66
A_68_P28683722	chr12:101962780-101962824	NM_153587:436	Rps6ka5	INSIDE	0.391	0.589	1867.99	1100.53	0.230	1460.70	336.55

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26467387	chr9:44205049-44205093	NM_008063:-1188	Slc37a4	PROMOTER	0.391	0.721	1626.23	1172.93	0.282	1467.19	414.12
A_68_P20038594	chr1:12981919-12981963	NM_172841:-724	Slco5a1	PROMOTER	0.391	0.619	903.30	558.79	0.242	770.40	186.25
A_68_P22887519	chr4:46209270-46209318	NM_011728:-111	Xpa	PROMOTER	0.391	0.602	964.46	580.45	0.236	743.18	175.04
A_68_P26038366	chr8:90484574-90484618	NM_033327:-1102	Zfp423	PROMOTER	0.391	0.702	2889.02	2027.03	0.275	2132.18	585.63
A_68_P28577068	chr12:81793936-81793980	NM_001177503:371	3830431G21Rik	INSIDE	0.390	0.530	1326.37	703.50	0.207	1003.11	207.54
A_68_P30349161	chr15:76406872-76406916	NM_172960:106	Adck5	INSIDE	0.390	0.474	2356.78	1117.91	0.185	1905.00	352.18
A_68_P21151655	chr2:38863832-38863876	NM_028809:196	Arpc5l	INSIDE	0.390	0.589	4486.65	2640.44	0.230	3453.30	793.23
A_68_P24115147	chr5:135662582-135662626	NM_011714:-588	Baz1b	PROMOTER	0.390	0.583	2093.19	1220.19	0.227	1622.42	368.86
A_68_P25436575	chr7:121706623-121706670	NM_177382:-160	Cyp2r1	PROMOTER	0.390	0.629	1074.68	675.45	0.245	783.63	191.86
A_68_P21320095	chr2:71379350-71379394	NR_002854:-3424	Dlx1as	PROMOTER	0.390	0.546	2383.88	1302.44	0.213	1831.75	390.00
A_68_P25575621	chr7:146271919-146271963	NM_011993:41	Dpysl4	INSIDE	0.390	0.561	2409.39	1351.91	0.219	1732.06	378.82
A_68_P28158191	chr11:116099429-116099473	NM_025276:-45	Evpl	PROMOTER	0.390	0.689	1292.37	890.62	0.269	1148.19	308.81
A_68_P20339086	chr1:72872062-72872107	NM_008342:1008	Igfbp2	INSIDE	0.390	0.451	1799.04	811.95	0.176	1379.23	242.69
A_68_P21680286	chr2:139503286-139503330	NM_001126490:-605	Ism1	PROMOTER	0.390	0.557	2940.12	1637.95	0.217	2220.95	482.08
A_68_P32122223	chr19:42674559-42674603	NM_001164311:12716	Loxl4	INSIDE	0.390	1.433	1197.83	1716.78	0.559	945.09	528.24
A_68_P26319355	chr9:14588836-14588880	NM_018736:-292	Mre11a	DIVERGENT_PROMOTER	0.390	0.581	1999.35	1161.35	0.227	1453.26	329.26
A_68_P24643638	chr6:92133742-92133786	NM_025578:253	Mrps25	INSIDE	0.390	0.494	1982.78	978.66	0.192	1582.60	304.52
A_68_P25507198	chr7:134913587-134913631	NM_198424:280	Orai3	INSIDE	0.390	0.574	1146.27	658.43	0.224	942.27	210.99
A_68_P32240897	chrX:7499587-7499631	NM_013892:2661	Pcsk1n	INSIDE	0.390	1.478	1634.44	2416.47	0.577	700.79	404.31
A_68_P28107256	chr11:107331453-107331497	NM_145823:560	Pitpnc1	INSIDE	0.390	0.646	918.10	592.76	0.252	663.38	166.88
A_68_P20241613	chr1:55463553-55463597	NM_001114663:785	Plcl1	INSIDE	0.390	0.622	819.18	509.57	0.243	692.34	168.12
A_68_P27841333	chr11:59990255-59990299	NM_001037764:36693	Rai1	INSIDE	0.390	0.377	1620.98	611.52	0.147	1174.81	172.69
A_68_P21762361	chr2:154616920-154616964	NM_001139511:97	Raly	INSIDE	0.390	0.495	1287.23	637.07	0.193	1030.27	199.03
A_68_P27971294	chr11:83223607-83223651	NM_001013386:55	Rasl10b	INSIDE	0.390	0.597	1329.78	794.26	0.233	967.02	225.31
A_68_P22400156	chr3:105762584-105762628	NM_027432:191	Wdr77	INSIDE	0.390	0.258	3120.47	803.89	0.100	2417.29	242.77
A_68_P26065123	chr8:94880083-94880127	NR_033641:-85	4933436C20Rik	DIVERGENT_PROMOTER	0.389	1.413	1248.29	1763.93	0.550	857.60	471.77
A_68_P27958470	chr11:80965747-80965791	NM_007384:637	Accn1	INSIDE	0.389	0.643	2651.27	1705.25	0.250	2029.90	507.65
A_68_P23609440	chr5:37139337-37139381	NM_133724:560	Cno	INSIDE	0.389	0.426	1673.18	712.55	0.166	1430.27	236.80
A_68_P28143424	chr11:113544952-113544996	NM_138598:491	D11Wsu99e	INSIDE	0.389	0.525	2517.62	1321.72	0.204	2111.80	431.46
A_68_P30981933	chr16:94747960-94748013	NM_007834:250	Dscr3	INSIDE	0.389	0.617	1236.96	762.84	0.240	982.57	235.93
A_68_P22448211	chr3:115955166-115955210	NM_022427:1214	Gpr88	INSIDE	0.389	0.610	909.64	554.72	0.237	837.06	198.43
A_68_P27833729	chr11:58768398-58768446	NM_178218:236	Hist3h2a	INSIDE	0.389	0.527	1602.94	844.67	0.205	1168.73	239.53
A_68_P28290821	chr12:25335787-25335837	NM_178357:-423	Klf11	PROMOTER	0.389	0.533	1034.45	551.52	0.207	785.97	162.93
A_68_P27470613	chr10:115024518-115024562	NM_010195:296	Lgr5	INSIDE	0.389	0.548	1972.97	1081.22	0.213	1512.60	322.24
A_68_P23972003	chr5:108877737-108877781	NM_172883:152	Mfsd7a	INSIDE	0.389	1.422	4663.32	6629.61	0.553	3380.56	1869.85
A_68_P23985662	chr5:111847249-111847293	NM_001081235:85	Mn1	INSIDE	0.389	0.733	1915.89	1404.16	0.285	1480.94	422.52
A_68_P24009561	chr5:115886828-115886872	NM_008629:7157	Msi1	INSIDE	0.389	0.420	1710.15	717.48	0.163	1361.24	222.06
A_68_P27889080	chr11:68198460-68198504	NM_008744:1846	Ntn1	INSIDE	0.389	0.596	1947.38	1160.66	0.232	1552.36	359.66
A_68_P23308589	chr4:131393487-131393532	NM_001083119:684	Ptpru	INSIDE	0.389	1.782	9005.35	16046.43	0.693	5751.07	3988.01
A_68_P25617012	chr8:4275589-4275633	NM_011592:295	Timm44	INSIDE	0.389	0.352	1784.11	628.53	0.137	1462.47	200.17
A_68_P21765252	chr2:155208027-155208072	NM_178111:458	Trp53inp2	INSIDE	0.389	0.631	1550.89	978.36	0.246	1258.39	309.06
A_68_P24972904	chr7:13365807-13365851	NM_001017955:-4821	Zscan18	PROMOTER	0.389	0.658	2850.42	1874.64	0.256	2132.69	545.96
A_68_P27889191	chr11:68213826-68213870	ENSMUST00000108674:477		INSIDE	0.389	0.695	3044.74	2116.51	0.270	2024.29	547.54
A_68_P29940453	chr14:119105644-119105689	NM_001033336:-225	Abcc4	PROMOTER	0.388	0.553	937.89	518.53	0.215	799.90	171.59
A_68_P32094198	chr19:37248988-37249032	NM_198300:32773	Cpeb3	INSIDE	0.388	0.743	3061.68	2274.48	0.288	2444.14	704.83
A_68_P23270847	chr4:124559714-124559758	NM_177671:708	Epha10	INSIDE	0.388	0.609	2152.03	1311.03	0.237	1656.04	391.91
A_68_P23539568	chr5:23536418-23536462	NM_053090:61	Fam126a	INSIDE	0.388	0.364	2141.71	779.58	0.141	1832.65	259.00
A_68_P28079561	chr11:102299305-102299349	NM_199200:9651	Fam171a2	INSIDE	0.388	0.678	1299.25	880.31	0.263	929.75	244.30
A_68_P30501058	chr15:102797076-102797125	NM_010462:-126	Hoxc10	PROMOTER	0.388	0.430	1419.27	610.74	0.167	969.49	161.89
A_68_P29445595	chr14:21000753-21000797	NM_021542:230	Kcnk5	INSIDE	0.388	0.502	1115.45	560.30	0.195	1023.65	199.39
A_68_P26075859	chr8:96696623-96696667	NM_008630:127	Mt2	INSIDE	0.388	0.556	1281.29	712.61	0.216	1053.10	227.32

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31041951	chr17:11033242-11033286	NM_016694:15	Park2	INSIDE	0.388	0.416	1724.79	716.92	0.161	1429.97	230.49
A_68_P21818226	chr2:164323071-164323115	NM_133779:68	Pigt	INSIDE	0.388	0.636	1906.00	1212.07	0.247	1528.24	377.07
A_68_P21637464	chr2:131735522-131735570	NM_011170:-117	Prnp	PROMOTER	0.388	0.723	1662.95	1202.84	0.280	1338.97	375.41
A_68_P28107297	chr11:107340918-107340962	NM_025894:99	Psmd12	INSIDE	0.388	0.458	2343.59	1072.77	0.178	1712.82	304.09
A_68_P27943491	chr11:78279298-78279342	NM_026740:118	Slc46a1	INSIDE	0.388	0.632	956.21	604.78	0.245	777.95	190.79
A_68_P32136713	chr19:45218072-45218116	NM_021901:-7110	Tlx1	PROMOTER	0.388	0.621	874.63	543.49	0.241	668.88	161.26
A_68_P28614747	chr12:88540890-88540934	NM_001033475:267	Tmed8	INSIDE	0.388	0.434	1256.05	544.69	0.168	968.60	163.07
A_68_P26809359	chr9:107436884-107436928	NM_019704:631	Tmem115	INSIDE	0.388	0.468	1517.33	710.48	0.182	1120.49	203.73
A_68_P20937462	chr1:193150005-193150049	NM_025864:183	Tmem206	INSIDE	0.388	0.710	2924.08	2076.58	0.276	2035.80	561.01
A_68_P29117520	chr13:69878183-69878227	NM_001145162:571	Ube2ql1	INSIDE	0.388	0.642	1526.90	979.63	0.249	1303.06	324.09
A_68_P31092534	chr17:23729724-23729768	NM_011747:6708	Zfp13	INSIDE	0.388	0.519	1338.86	695.11	0.201	1137.36	229.06
A_68_P32007549	chr19:21727415-21727459	NM_025423:-155	1110059E24Rik	DIVERGENT_PROMOTER	0.387	0.465	1153.75	536.60	0.180	781.26	140.74
A_68_P28314428	chr12:29360059-29360103	NM_134052:9	Adi1	INSIDE	0.387	0.510	2484.60	1267.06	0.197	1921.23	379.24
A_68_P32795520	chrX:160347620-160347664	NM_026887:551	Ap1s2	INSIDE	0.387	1.410	2493.78	3516.61	0.546	1204.55	657.69
A_68_P21611139	chr2:126834542-126834586	NM_175550:118	Ap4e1	INSIDE	0.387	0.559	2168.56	1211.45	0.216	1837.20	397.00
A_68_P25587959	chr7:148480560-148480604	NM_007878:2678	Drd4	INSIDE	0.387	0.495	1097.57	543.76	0.192	917.90	175.85
A_68_P22702206	chr4:5571678-5571722	NM_173426:375	Fam110b	INSIDE	0.387	0.654	1996.63	1304.95	0.253	1615.37	408.64
A_68_P32386814	chrX:50622922-50622968	NM_001166365:38	Fam122b	INSIDE	0.387	3.956	2049.73	8109.44	1.532	750.92	1150.54
A_68_P25125435	chr7:59117580-59117624	NM_001115087:35	Fancf	INSIDE	0.387	0.389	1514.68	589.37	0.151	1241.29	186.88
A_68_P27897170	chr11:69615173-69615217	NM_010198:-67	Fgf11	PROMOTER	0.387	0.494	1422.97	703.22	0.191	1141.34	218.27
A_68_P22291215	chr3:84284164-84284208	NM_001205355:-773	Fhdc1	PROMOTER	0.387	0.475	3144.88	1494.82	0.184	2494.26	458.70
A_68_P21569058	chr2:119151824-119151868	NR_030683:87	Gm14207	INSIDE	0.387	0.398	1735.41	690.56	0.154	1256.20	193.45
A_68_P29613102	chr14:55196396-55196440	NM_010590:80	Jub	INSIDE	0.387	0.605	1082.21	654.80	0.234	895.45	209.49
A_68_P29696147	chr14:70008844-70008888	NM_033325:-416	Loxl2	PROMOTER	0.387	1.695	4811.56	8155.31	0.656	3027.77	1985.36
A_68_P26233415	chr8:124967303-124967347	NM_138656:-2	Mvd	PROMOTER	0.387	0.650	1192.88	775.28	0.251	953.11	239.48
A_68_P32147202	chr19:47090004-47090048	NM_001164363:-347	Nt5c2	PROMOTER	0.387	0.484	1367.29	661.09	0.187	1103.59	206.66
A_68_P31626368	chr18:37121882-37121926	NM_007767:-5505	Pcdha6	PROMOTER	0.387	1.503	820.70	1233.71	0.582	675.98	393.51
A_68_P23351038	chr4:138866454-138866498	NM_145384:139	Pqlc2	INSIDE	0.387	0.613	1241.01	761.20	0.237	955.93	226.87
A_68_P22346028	chr3:95659528-95659572	NM_027541:126	Prpf3	INSIDE	0.387	0.590	2572.21	1516.67	0.228	1976.81	451.55
A_68_P29502939	chr14:30781960-30782004	NM_019979:417	Selk	INSIDE	0.387	0.457	1368.15	625.57	0.177	965.93	170.93
A_68_P22200380	chr3:65331656-65331707	NM_178892:-687	Tiparp	PROMOTER	0.387	0.468	1309.30	612.30	0.181	1067.33	193.00
A_68_P30356632	chr15:77759535-77759579	NM_019913:-132	Txn2	PROMOTER	0.387	0.738	4818.93	3558.05	0.286	3258.39	931.89
A_68_P20827836	chr1:173341700-173341744	NM_009480:-89	Usf1	PROMOTER	0.387	0.638	846.99	540.07	0.247	766.48	189.14
A_68_P26721618	chr9:91273756-91273800	NM_009576:9969	Zic4	INSIDE	0.387	0.678	1231.49	835.37	0.263	838.63	220.15
A_68_P23283385	chr4:126738210-126738254	NM_026670:144	Zmym1	INSIDE	0.387	0.361	2545.42	917.71	0.139	2042.09	284.75
A_68_P28178207	chr11:119352476-119352520	NM_001164636:-162	A730011L01Rik	PROMOTER	0.386	0.699	1368.51	957.09	0.270	1069.81	288.84
A_68_P27508738	chr10:121886239-121886283	NM_016847:706	Avpr1a	INSIDE	0.386	0.565	1135.31	641.21	0.218	868.95	189.68
A_68_P23259659	chr4:122562951-122562995	NM_007598:152	Cap1	INSIDE	0.386	0.563	1933.48	1087.93	0.217	1356.49	294.41
A_68_P23196912	chr4:108293003-108293049	NM_177045:466	Cc2d1b	INSIDE	0.386	0.559	1352.55	755.60	0.215	918.88	197.95
A_68_P26790784	chr9:104164628-104164672	NM_001163026:610	Dnajc13	INSIDE	0.386	0.701	1651.99	1157.73	0.270	1188.76	321.22
A_68_P28155820	chr11:115719994-115720038	NM_145438:34645	Llgl2	DOWNSTREAM	0.386	0.695	1326.79	922.46	0.268	1040.21	279.24
A_68_P21122748	chr2:33495093-33495137	NM_010725:917	Lmx1b	INSIDE	0.386	0.530	1146.85	607.31	0.204	857.04	175.20
A_68_P22301529	chr3:86028379-86028423	NM_001077687:-211	Lrba	PROMOTER	0.386	0.501	2111.14	1058.28	0.193	1730.67	334.87
A_68_P29512324	chr14:32307722-32307766	NM_025907:419	Mettl6	INSIDE	0.386	0.405	1352.21	548.05	0.157	1069.13	167.34
A_68_P21350014	chr2:76244191-76244236	NM_145525:-381	Osbpl6	PROMOTER	0.386	0.500	1498.18	748.41	0.193	1241.20	239.14
A_68_P31066337	chr17:15701209-15701253	NM_144809:-943	Prdm9	PROMOTER	0.386	0.448	1781.88	799.01	0.173	1543.38	266.84
A_68_P31311919	chr17:67703480-67703524	NM_008984:297	Ptprm	INSIDE	0.386	0.444	1802.80	799.88	0.171	1378.61	235.92
A_68_P28291147	chr12:25393381-25393425	NM_009104:284	Rrm2	INSIDE	0.386	0.626	2599.15	1627.70	0.242	1944.45	469.87
A_68_P32116948	chr19:41817676-41817720	NM_015748:648	Slit1	INSIDE	0.386	0.671	4698.14	3152.91	0.259	3613.87	936.75
A_68_P20191545	chr1:43990635-43990679	NM_009418:-195	Tpp2	PROMOTER	0.386	0.587	1071.02	628.56	0.226	849.56	192.28
A_68_P21579903	chr2:121096750-121096794	NM_013735:350	Trp53bp1	INSIDE	0.386	1.499	10760.68	16131.09	0.578	7597.34	4390.72

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P22650340	chr3:152059616-152059660	NM_198416:-19	Zzz3	PROMOTER	0.386	0.628	997.79	626.69	0.242	807.48	195.68
A_68_P24973684	chr7:13513821-13513865	NM_029809:1078	2310014L17Rik	INSIDE	0.385	1.494	1749.65	2614.53	0.576	1454.10	837.63
A_68_P21072311	chr2:25316393-25316437	NM_153557:200	BC029214	INSIDE	0.385	0.633	2621.56	1659.14	0.244	1888.00	460.39
A_68_P23607907	chr5:36827498-36827542	NM_025725:284	Ccdc96	INSIDE	0.385	0.615	1350.55	830.38	0.236	1084.30	256.36
A_68_P27921507	chr11:74433104-74433148	NM_001013784:20	E130309D14Rik	INSIDE	0.385	0.588	2126.36	1249.32	0.226	1752.37	396.42
A_68_P21603035	chr2:125331152-125331196	NM_007993:1000	Fbn1	INSIDE	0.385	0.407	1662.11	676.94	0.157	1295.90	203.23
A_68_P21727937	chr2:147874425-147874470	NM_010446:-1742	Foxa2	PROMOTER	0.385	0.672	1303.99	875.82	0.258	1089.74	281.64
A_68_P30596435	chr16:22163008-22163052	NM_183029:342	Igf2bp2	INSIDE	0.385	0.488	2271.92	1109.15	0.188	1725.01	324.49
A_68_P26546364	chr9:58049788-58049832	NM_001161540:-204	Islr2	PROMOTER	0.385	1.676	3041.84	5098.28	0.646	2084.52	1346.23
A_68_P30483165	chr15:99803409-99803453	NM_001024526:220	Larp4	INSIDE	0.385	0.684	2794.77	1912.37	0.263	2103.85	553.97
A_68_P30513214	chr16:5013320-5013364	NM_133185:304	Rogdi	INSIDE	0.385	0.715	2269.83	1622.83	0.275	1581.98	435.04
A_68_P31841966	chr18:76400802-76400846	NM_010754:-754	Smad2	PROMOTER	0.385	0.482	2841.35	1370.16	0.186	2146.79	399.04
A_68_P30502555	chr15:102999581-102999625	NM_027885:-5887	Smug1	PROMOTER	0.385	0.569	3410.54	1941.02	0.219	2647.80	580.82
A_68_P25958201	chr8:74195222-74195266	NM_001029873:412	Unc13a	INSIDE	0.385	0.429	1736.62	744.39	0.165	1310.45	216.39
A_68_P26024223	chr8:87823249-87823293	NM_022997:126	Vps35	INSIDE	0.385	0.705	4010.05	2828.26	0.271	3021.53	820.03
A_68_P24648066	chr6:92893011-92893055	NR_015530:2457	9530026P05Rik	INSIDE	0.384	0.659	1940.02	1277.78	0.253	1367.67	346.12
A_68_P25354431	chr7:105343001-105343045	NM_001081167:4963	B3gnt6	INSIDE	0.384	0.645	1620.36	1045.61	0.248	1423.85	352.46
A_68_P25409556	chr7:116847071-116847115	NM_020616:-158	D930014E17Rik	PROMOTER	0.384	0.502	2548.77	1279.57	0.193	1928.95	371.99
A_68_P26157751	chr8:112089473-112089517	NM_178380:7	Dhx38	INSIDE	0.384	0.599	2610.74	1564.85	0.230	1737.08	399.73
A_68_P25637620	chr8:8661042-8661086	NM_010111:-291	Efnb2	PROMOTER	0.384	0.429	1357.65	581.82	0.165	1001.31	164.86
A_68_P28788493	chr13:3537834-3537878	NM_008112:536	Gdi2	INSIDE	0.384	0.541	1387.53	751.02	0.208	1088.91	226.22
A_68_P20451402	chr1:94728781-94728825	NM_016696:540	Gpc1	INSIDE	0.384	0.399	3973.72	1585.15	0.153	3108.58	475.88
A_68_P22565473	chr3:137528589-137528633	NM_016750:1048	H2afz	INSIDE	0.384	0.459	1411.87	647.69	0.176	1140.22	200.77
A_68_P28041913	chr11:95866656-95866701	NM_009951:580	Igf2bp1	INSIDE	0.384	0.502	1598.54	802.29	0.193	1273.94	245.79
A_68_P27927255	chr11:75444500-75444544	NM_008916:1	Inpp5k	INSIDE	0.384	0.649	799.68	519.12	0.249	623.68	155.52
A_68_P25727984	chr8:26707935-26707980	NM_173012:2	Letm2	INSIDE	0.384	0.742	5217.74	3873.84	0.285	3736.09	1064.50
A_68_P22180929	chr3:60807059-60807103	NM_008772:364	P2ry1	INSIDE	0.384	0.717	2585.02	1852.22	0.275	2083.51	573.97
A_68_P20184676	chr1:42754950-42754994	NM_008900:982	Pou3f3	INSIDE	0.384	0.530	1020.23	540.91	0.204	815.91	166.23
A_68_P31921665	chr19:4191850-4191903	NM_031868:-297	Ppp1ca	DIVERGENT_PROMOTER	0.384	0.618	906.79	560.73	0.238	670.71	159.33
A_68_P31925257	chr19:4811827-4811871	NM_019869:-214	Rbm14	PROMOTER	0.384	0.487	1962.26	954.80	0.187	1835.14	342.81
A_68_P32135692	chr19:45063608-45063652	NM_011976:-203	Sema4g	PROMOTER	0.384	0.700	3727.06	2609.07	0.269	2764.75	742.89
A_68_P28555630	chr12:77811318-77811362	NM_013675:194	Spnb1	INSIDE	0.384	0.669	1808.55	1209.90	0.257	1421.57	365.08
A_68_P26804665	chr9:106588204-106588248	NM_011573:-228	Tex264	PROMOTER	0.384	0.535	3120.21	1668.26	0.205	2397.02	492.12
A_68_P31140216	chr17:31649029-31649073	NM_021322:382	Wdr4	INSIDE	0.384	0.655	1367.68	895.97	0.252	1170.53	294.66
A_68_P28931387	chr13:32894954-32894998	NM_030215:1078	Wrnip1	INSIDE	0.384	0.617	1980.72	1221.55	0.237	1549.04	367.09
A_68_P21622286	chr2:128793161-128793205	NM_178404:45	Zc3h6	INSIDE	0.384	0.683	1457.58	995.55	0.262	1061.84	278.46
A_68_P26349728	chr9:21760084-21760135	NM_025870:-87	2310047B19Rik	PROMOTER	0.383	0.671	975.05	654.41	0.257	709.65	182.60
A_68_P22407409	chr3:107399162-107399206	NM_007441:1236	Alx3	INSIDE	0.383	0.530	2117.75	1122.27	0.203	1486.17	301.27
A_68_P32364050	chrX:45697107-45697151	NM_178782:2594	Bcorl1	INSIDE	0.383	9.469	12523.37	118577.60	3.626	5339.78	19361.94
A_68_P28959945	chr13:38437436-38437480	NM_007556:-126	Bmp6	PROMOTER	0.383	0.657	1024.36	673.30	0.252	703.83	177.12
A_68_P20456912	chr1:95582245-95582289	NM_016778:-4	Bok	PROMOTER	0.383	0.511	1064.21	543.39	0.196	812.05	158.91
A_68_P31001857	chr16:98143725-98143769	NM_174847:497	C2cd2	INSIDE	0.383	0.689	1211.64	834.54	0.264	935.34	246.86
A_68_P28331599	chr12:32184853-32184897	NM_134048:-469	Cbll1	PROMOTER	0.383	0.648	1114.88	722.24	0.248	898.13	223.06
A_68_P23271162	chr4:124614141-124614185	NM_026560:-1	Cdca8	DIVERGENT_PROMOTER	0.383	0.554	1874.20	1038.39	0.212	1341.22	284.79
A_68_P25957393	chr8:74067094-74067138	NM_028617:288	Fam125a	INSIDE	0.383	0.717	2146.50	1538.78	0.274	1662.90	456.22
A_68_P25307421	chr7:96553016-96553060	NM_008055:163	Fzd4	INSIDE	0.383	0.416	2360.05	981.14	0.159	1688.85	269.13
A_68_P28032111	chr11:94183206-94183250	NM_026313:-3	Luc7l3	DIVERGENT_PROMOTER	0.383	0.581	1257.23	730.56	0.223	890.55	198.18
A_68_P25756476	chr8:32278992-32279036	NM_026453:182	Mak16	INSIDE	0.383	0.614	1140.32	699.86	0.235	959.02	225.20
A_68_P29011119	chr13:47110041-47110085	NM_175340:157	Nhlrc1	INSIDE	0.383	0.608	5479.66	3332.96	0.233	4146.81	966.73
A_68_P29055509	chr13:55614601-55614645	NM_001114088:178	Pdlim7	INSIDE	0.383	0.398	3015.47	1199.10	0.152	2314.74	352.41
A_68_P27277400	chr10:78996361-78996405	NM_015817:150	Ppap2c	INSIDE	0.383	1.507	11061.78	16667.18	0.577	7272.18	4196.60

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P24447786	chr6:51962237-51962281	NM_018773:290	Skap2	INSIDE	0.383	0.510	1892.49	965.77	0.195	1579.61	308.51
A_68_P24974127	chr7:13595301-13595345	NM_001024699:-173	Zbtb45	PROMOTER	0.383	0.567	2246.83	1274.90	0.217	1400.51	304.31
A_68_P28712206	chr12:107201465-107201509	BC156654:163626		INSIDE	0.383	0.533	1030.53	549.68	0.204	761.18	155.41
A_68_P30421913	chr15:88721305-88721349	ENSMUST00000172019:63522		INSIDE	0.383	0.627	4361.14	2732.63	0.240	3076.36	738.59
A_68_P25668725	chr8:13494426-13494470	NM_019521:87	Gas6	INSIDE	0.382	0.445	3011.25	1340.42	0.170	2228.70	379.31
A_68_P28152427	chr11:115128177-115128221	NM_010350:359	Grin2c	INSIDE	0.382	0.620	2404.14	1491.55	0.237	1860.09	440.44
A_68_P29725078	chr14:75347229-75347273	NM_001033439:434	Lrch1	INSIDE	0.382	0.517	1295.66	669.60	0.198	1038.95	205.20
A_68_P20348983	chr1:74552547-74552591	NM_021383:-65	Rqcd1	PROMOTER	0.382	0.440	3658.22	1610.76	0.168	2627.28	441.91
A_68_P27280974	chr10:79564978-79565022	NM_183426:447	Sbno2	INSIDE	0.382	1.813	2958.89	5365.60	0.692	2160.66	1494.97
A_68_P32036092	chr19:26681843-26681887	NM_011416:2215	Smarca2	INSIDE	0.382	0.738	2246.36	1657.71	0.282	1648.69	464.78
A_68_P31909280	chr18:89063162-89063206	NM_018821:415	Socs6	INSIDE	0.382	0.706	2132.44	1504.63	0.269	1772.95	477.74
A_68_P25364623	chr7:107065859-107065903	NM_001164258:58153	Xrra1	INSIDE	0.382	0.552	1279.25	705.79	0.211	1061.22	223.43
A_68_P30369303	chr15:79763884-79763928	NM_144811:-830	Cbx7	PROMOTER	0.381	0.614	1036.84	637.03	0.234	902.92	211.45
A_68_P28396961	chr12:45311078-45311122	NM_013760:-45	Dnajb9	PROMOTER	0.381	0.457	2172.07	993.00	0.174	1688.94	294.02
A_68_P20825266	chr1:172837419-172837463	NM_001029984:5632	Fcrlb	INSIDE	0.381	1.347	2671.36	3598.72	0.514	2081.09	1068.86
A_68_P28083435	chr11:102978558-102978602	NM_138753:942	Hexim1	INSIDE	0.381	0.654	1619.45	1059.54	0.249	1327.14	331.08
A_68_P27534777	chr10:126676555-126676599	NM_001039000:23843	Kif5a	INSIDE	0.381	1.451	909.64	1320.23	0.554	735.03	406.86
A_68_P23391035	chr4:147242398-147242442	NM_001025365:408	Miip	INSIDE	0.381	0.537	1237.13	663.77	0.204	1010.63	206.44
A_68_P30359769	chr15:78240781-78240825	NM_138670:3269	Mpst	INSIDE	0.381	0.617	1060.37	654.13	0.235	771.69	181.47
A_68_P26268769	chr8:130881368-130881412	NM_008737:-1582	Nrp1	PROMOTER	0.381	0.592	1392.25	824.88	0.225	1178.98	265.85
A_68_P30961955	chr16:91271343-91271387	NM_016968:1351	Olig1	INSIDE	0.381	0.573	2374.04	1361.14	0.218	1834.52	400.26
A_68_P25370974	chr7:108160323-108160367	NM_008773:161	P2ry2	INSIDE	0.381	0.573	1520.90	870.99	0.218	1226.47	267.58
A_68_P31713373	chr18:53622483-53622527	NM_001033281:-1695	Prdm6	PROMOTER	0.381	0.623	1481.10	922.66	0.237	1180.35	279.88
A_68_P21762363	chr2:154617145-154617189	NM_001139511:321	Raly	INSIDE	0.381	0.604	2141.14	1293.22	0.230	1803.78	415.27
A_68_P30979319	chr16:94085864-94085908	NM_011377:382	Sim2	INSIDE	0.381	0.402	2426.59	975.03	0.153	1954.83	299.27
A_68_P28520026	chr12:71448401-71448445	NM_001110202:179	Trim9	INSIDE	0.381	0.608	867.71	527.28	0.232	729.99	169.06
A_68_P30592418	chr16:21423272-21423316	NM_001081366:104	Vps8	INSIDE	0.381	0.490	1413.78	693.21	0.187	1241.36	232.03
A_68_P22413520	chr3:108394071-108394115	NM_181400:-103	Wdr47	PROMOTER	0.381	0.485	1558.91	755.65	0.185	1300.47	240.11
A_68_P31926817	chr19:5088108-5088153	NM_026553:-407	Yif1a	DIVERGENT_PROMOTER	0.381	0.622	1033.89	643.35	0.237	751.85	178.03
A_68_P25827309	chr8:46024036-46024087	AK079043:-3548		PROMOTER	0.381	0.508	1156.37	586.87	0.193	855.25	165.37
A_68_P27809329	chr11:54117906-54117950	NM_001033597:223	Acsl6	INSIDE	0.380	0.691	3018.23	2086.45	0.262	2417.92	634.67
A_68_P25010985	chr7:26412400-26412444	NM_001036740:-220	B3gnt8	PROMOTER	0.380	1.663	4751.97	7900.87	0.632	3194.05	2020.21
A_68_P24158346	chr5:144578888-144578932	NM_013557:250	Eif2ak1	INSIDE	0.380	0.493	3030.88	1494.45	0.187	2286.94	428.01
A_68_P23404992	chr4:149611119-149611164	NM_023119:-164	Eno1	PROMOTER	0.380	0.563	1922.55	1081.72	0.214	1383.68	295.56
A_68_P32026412	chr19:24971921-24971965	NM_008022:3857	Foxd4	DOWNSTREAM	0.380	0.406	1833.59	744.71	0.154	1366.72	210.77
A_68_P27484948	chr10:117578776-117578823	NM_001162904:-43	Mdm1	PROMOTER	0.380	0.638	1123.74	716.89	0.242	880.61	213.36
A_68_P20551218	chr1:120218342-120218386	NM_026472:-55	Mki67ip	PROMOTER	0.380	0.521	1265.95	659.71	0.198	1035.88	204.88
A_68_P28039686	chr11:95446719-95446763	NM_033217:2272	Ngfr	INSIDE	0.380	0.690	1630.84	1125.96	0.262	1171.77	307.46
A_68_P22727582	chr4:10935187-10935231	NM_175175:-442	Plekhf2	PROMOTER	0.380	0.447	1915.38	856.58	0.170	1445.89	245.94
A_68_P25587156	chr7:148354570-148354614	NM_001172101:-7	Rnh1	PROMOTER	0.380	0.629	1970.53	1239.78	0.239	1596.49	381.57
A_68_P21328890	chr2:72819073-72819117	NM_001018042:-591	Sp3	PROMOTER	0.380	0.477	1207.64	576.04	0.181	1084.35	196.48
A_68_P28054167	chr11:97913713-97913757	NM_146028:1042	Stac2	INSIDE	0.380	0.687	2016.37	1385.58	0.261	1470.46	384.09
A_68_P24786878	chr6:118405236-118405280	NM_028335:266	Zfp248	INSIDE	0.380	0.605	1310.10	791.99	0.230	973.42	223.41
A_68_P32543330	chrX:93163948-93164001			Unknown	0.380	6.928	2107.39	14600.13	2.631	781.55	2056.51
A_68_P31215873	chr17:48232887-48232931	NM_026625:6327	1700067P10Rik	DOWNSTREAM	0.379	0.730	1820.06	1328.36	0.277	1416.41	391.83
A_68_P27187162	chr10:62114413-62114457	NM_053183:-488	Ddx50	PROMOTER	0.379	0.538	1677.62	902.00	0.204	1276.68	260.05
A_68_P29649840	chr14:61979049-61979093	NM_026598:212	Ebpl	INSIDE	0.379	0.627	961.94	602.95	0.238	806.22	191.53
A_68_P26761425	chr9:98855848-98855892	NR_003248:-141	Foxl2os	DIVERGENT_PROMOTER	0.379	0.439	1241.13	544.51	0.166	1052.26	175.12
A_68_P25025742	chr7:29956544-29956588	NM_182696:1158	Ggn	INSIDE	0.379	0.497	1466.17	729.41	0.189	1024.49	193.18
A_68_P21338737	chr2:74517808-74517856	NM_008273:-2617	Hoxd11	PROMOTER	0.379	0.653	1564.43	1021.20	0.247	1084.94	268.44
A_68_P25954140	chr8:73321012-73321061	NM_199308:-4704	Mast3	PROMOTER	0.379	3.708	4916.78	18230.35	1.407	3289.09	4627.57

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31400335	chr17:84105596-84105640	NM_001171053:116	Mta3	INSIDE	0.379	0.340	1941.82	660.09	0.129	1577.14	203.21
A_68_P30344755	chr15:75724584-75724628	NM_172607:305	Naprt1	INSIDE	0.379	0.701	5491.86	3848.68	0.265	3965.40	1052.51
A_68_P20354543	chr1:75501853-75501897	NM_178884:1153	Obsl1	INSIDE	0.379	0.484	1584.19	766.92	0.183	1259.54	231.06
A_68_P32141864	chr19:46131303-46131347	NM_001081214:296	Pprc1	INSIDE	0.379	0.651	3419.68	2226.53	0.247	2531.00	624.54
A_68_P25377920	chr7:109399308-109399352	NM_019566:-698	Rhog	PROMOTER	0.379	0.677	2603.19	1762.26	0.256	1904.52	488.06
A_68_P25585273	chr7:148043403-148043447	NM_053194:129	Ric8	INSIDE	0.379	0.593	1126.28	667.47	0.224	898.41	201.57
A_68_P31154751	chr17:34741404-34741448	NM_019403:-920	Rnf5	DIVERGENT_PROMOTER	0.379	0.539	1148.62	619.50	0.204	897.67	183.55
A_68_P23251106	chr4:120078426-120078470	NM_001159630:563	Scmh1	INSIDE	0.379	0.600	1674.00	1004.47	0.227	1603.57	364.74
A_68_P27844938	chr11:60624796-60624840	NM_009171:-51	Shmt1	PROMOTER	0.379	0.654	3482.45	2278.99	0.248	2969.94	736.22
A_68_P30464705	chr15:96471903-96471947	NM_134086:469	Slc38a1	INSIDE	0.379	0.501	1147.95	575.10	0.190	897.07	170.44
A_68_P21745018	chr2:151457749-151457793	NM_198214:499	Snph	INSIDE	0.379	0.513	1905.37	977.81	0.195	1525.99	296.87
A_68_P28909015	chr13:29050121-29050165	NM_009238:-4591	Sox4	PROMOTER	0.379	0.568	1790.08	1017.56	0.216	1321.89	285.13
A_68_P23382179	chr4:144836289-144836333	NM_011610:463	Tnfrsf1b	INSIDE	0.379	0.710	2172.27	1541.23	0.269	1510.46	406.10
A_68_P29260160	chr13:99660969-99661013	NM_001048267:7	Tnpo1	INSIDE	0.379	0.400	1452.88	581.14	0.152	1244.49	188.74
A_68_P26528457	chr9:54765090-54765134	NM_177351:16	Agphd1	INSIDE	0.378	0.546	1391.53	759.53	0.206	1175.08	242.26
A_68_P23332636	chr4:135762606-135762650	NM_001008232:349	Asap3	INSIDE	0.378	0.542	1377.48	746.30	0.205	1042.38	213.43
A_68_P27643056	chr11:22759939-22759983	NM_016888:-225	B3gnt2	PROMOTER	0.378	0.447	1284.53	574.01	0.169	1059.94	178.86
A_68_P28047198	chr11:96723388-96723432	NM_019877:12221	Copz2	DOWNSTREAM	0.378	0.520	2137.91	1110.95	0.196	1668.77	327.66
A_68_P30478214	chr15:98926989-98927033	NM_176835:-2904	Dnajc22	DIVERGENT_PROMOTER	0.378	0.414	1883.76	778.97	0.156	1542.55	241.04
A_68_P32140185	chr19:45811804-45811848	NM_001166361:5548	Fgf8	INSIDE	0.378	0.518	1130.07	584.84	0.196	886.64	173.41
A_68_P26467268	chr9:44187370-44187414	NM_021395:-180	Hyou1	PROMOTER	0.378	0.624	891.20	555.89	0.236	721.21	170.23
A_68_P25096453	chr7:53289096-53289140	NM_153057:53	Nomo1	INSIDE	0.378	0.555	1276.68	708.95	0.210	1041.00	218.28
A_68_P32107650	chr19:40346140-40346184	NM_016861:-56	Pdlim1	PROMOTER	0.378	0.425	1347.60	572.21	0.161	1066.57	171.25
A_68_P31254139	chr17:56278984-56279028	NM_013662:-5731	Sema6b	PROMOTER	0.378	0.495	2403.85	1190.58	0.187	1795.25	336.05
A_68_P21266387	chr2:61643809-61643853	NM_009322:1321	Tbr1	INSIDE	0.378	0.411	3510.27	1442.32	0.155	2675.82	415.74
A_68_P26817223	chr9:108838835-108838879	NM_025407:196	Uqcrc1	INSIDE	0.378	0.569	3102.80	1764.39	0.215	2284.53	491.08
A_68_P25087020	chr7:51615740-51615784	NM_027049:14638	1700008O03Rik	INSIDE	0.377	0.531	1102.21	585.73	0.200	868.73	174.08
A_68_P24104854	chr5:133019778-133019822	NM_177047:-1587	Auts2	PROMOTER	0.377	0.685	3249.49	2225.28	0.258	2618.90	676.35
A_68_P23069990	chr4:84322037-84322088	NM_172870:-1072	Bnc2	PROMOTER	0.377	0.582	919.68	535.21	0.219	725.51	159.22
A_68_P27987613	chr11:86014523-86014567	NM_178309:151	Brip1	INSIDE	0.377	0.519	1442.15	748.02	0.195	1105.35	215.97
A_68_P21875386	chr2:174264415-174264459	NM_022325:57	Ctsz	INSIDE	0.377	0.679	6326.25	4298.29	0.256	4237.74	1085.97
A_68_P32030091	chr19:25580881-25580925	NM_015826:707	Dmrt1	INSIDE	0.377	0.693	3461.68	2397.73	0.261	2630.53	687.09
A_68_P24994095	chr7:20158628-20158672	NM_027189:42	Gemin7	INSIDE	0.377	0.684	3085.38	2111.39	0.258	2288.35	590.73
A_68_P23190566	chr4:107108029-107108073	NM_147221:727	Glis1	INSIDE	0.377	1.478	4788.96	7077.76	0.556	3651.27	2031.75
A_68_P21073106	chr2:25434968-25435012	NM_001005424:629	Gm996	INSIDE	0.377	0.563	1539.04	865.75	0.212	1109.75	235.27
A_68_P23339949	chr4:137024813-137024857	NM_008305:117	Hspg2	INSIDE	0.377	0.550	1992.29	1095.14	0.207	1580.28	327.18
A_68_P24443347	chr6:51220315-51220359	NR_029719:-427	Mir148a	PROMOTER	0.377	0.701	1229.88	862.39	0.264	928.52	245.22
A_68_P23985674	chr5:111848466-111848510	NM_001081235:1303	Mn1	INSIDE	0.377	0.643	1622.85	1042.79	0.242	1169.35	283.36
A_68_P25111235	chr7:56502306-56502350	NM_175272:770	Nav2	INSIDE	0.377	0.475	2103.45	998.59	0.179	1602.07	287.07
A_68_P28224331	chr12:8779590-8779634	NM_011519:1411	Sdc1	INSIDE	0.377	0.650	3084.75	2005.47	0.245	2341.09	573.27
A_68_P25021279	chr7:29123215-29123259	NM_013676:502	Supt5h	INSIDE	0.377	0.553	3336.64	1843.66	0.208	2427.40	505.73
A_68_P30782603	chr16:56717699-56717743	NM_019678:-253	Tfg	PROMOTER	0.377	0.639	1044.09	666.87	0.241	911.00	219.11
A_68_P28074035	chr11:101327600-101327644	NM_012037:-109	Vat1	DIVERGENT_PROMOTER	0.377	0.555	2583.48	1432.77	0.209	1999.11	417.91
A_68_P28087340	chr11:103672887-103672931	NM_009521:37420	Wnt3	INSIDE	0.377	1.537	5118.67	7865.00	0.580	3885.97	2253.23
A_68_P21864322	chr2:172265854-172265898	NM_025542:-201	2410001C21Rik	PROMOTER	0.376	0.593	1408.80	834.79	0.223	1038.56	231.34
A_68_P22383903	chr3:102824344-102824388	NM_001161854:-102	Csde1	PROMOTER	0.376	0.647	808.74	523.50	0.243	705.15	171.62
A_68_P24008924	chr5:115750457-115750502	NM_019682:520	Dynll1	INSIDE	0.376	0.625	2770.59	1732.93	0.235	2047.53	481.21
A_68_P23570722	chr5:30431999-30432043	NM_001167879:285	Fam59b	INSIDE	0.376	0.492	1931.89	950.09	0.185	1357.36	250.70
A_68_P24620314	chr6:88143770-88143814	NM_008090:-4865	Gata2	PROMOTER	0.376	0.539	2269.98	1224.54	0.203	1815.15	368.02
A_68_P28071797	chr11:100941221-100941265	NM_010475:1518	Hsd17b1	INSIDE	0.376	0.473	1995.61	943.59	0.178	1426.12	253.51
A_68_P20778374	chr1:164478713-164478757	NM_144877:-258	Mettl13	PROMOTER	0.376	0.698	1673.31	1168.63	0.263	1374.55	360.91

						Sham group			TiO$_2$-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P21614449	chr2:127413281-127413325	NM_029963:141	Mrps5	INSIDE	0.376	0.672	1546.53	1039.02	0.253	1288.59	325.64
A_68_P30381132	chr15:81877600-81877644	NM_011482:406	Nhp2l1	INSIDE	0.376	0.482	2791.11	1346.58	0.181	2334.99	423.32
A_68_P27638910	chr11:21901664-21901708	NM_011023:-32	Otx1	PROMOTER	0.376	0.456	1923.97	876.51	0.171	1427.76	244.86
A_68_P22518747	chr3:128917569-128917613	NM_001042502:736	Pitx2	INSIDE	0.376	0.418	1871.32	782.01	0.157	1453.58	228.38
A_68_P26714904	chr9:89805072-89805116	NM_001039655:482	Rasgrf1	INSIDE	0.376	0.641	1055.56	676.09	0.241	881.96	212.28
A_68_P32365931	chrX:46048088-46048132	NM_173376:-70	Rbmx2	PROMOTER	0.376	0.657	1113.81	731.76	0.247	507.14	125.23
A_68_P26170969	chr8:114457634-114457678	NM_001033321:35	Tmem231	INSIDE	0.376	0.613	1831.69	1122.60	0.230	1433.18	330.11
A_68_P25598461	chr7:150254989-150255033	NM_001115085:-262	Tssc4	PROMOTER	0.376	0.561	1030.85	577.91	0.211	694.88	146.50
A_68_P27234634	chr10:70747646-70747690	NM_145420:342	Ube2d1	INSIDE	0.376	0.444	1934.49	859.07	0.167	1590.62	265.77
A_68_P26479797	chr9:46251878-46251922			Unknown	0.376	0.686	1076.23	738.81	0.258	831.21	214.40
A_68_P23319375	chr4:133312530-133312574	NM_001080819:-3026	Arid1a	PROMOTER	0.375	0.432	1290.39	557.28	0.162	1118.56	181.29
A_68_P23245373	chr4:119087968-119088012	NM_029286:136	Ccdc30	INSIDE	0.375	0.511	2076.30	1061.75	0.192	1777.26	340.50
A_68_P25948536	chr8:72413250-72413294	NM_026818:-1981	Cilp2	PROMOTER	0.375	0.550	2940.27	1616.09	0.206	2203.60	454.36
A_68_P21769581	chr2:155937720-155937764	NM_170588:-41	Cpne1	PROMOTER	0.375	0.652	1093.47	713.36	0.245	871.72	213.46
A_68_P29699000	chr14:70475029-70475073	NM_018781:-2201	Egr3	PROMOTER	0.375	0.542	1194.60	647.38	0.203	954.61	193.80
A_68_P22888257	chr4:46356845-46356889	NM_183298:-199	Foxe1	PROMOTER	0.375	0.620	1158.31	717.90	0.232	1056.51	245.61
A_68_P31484557	chr18:9214262-9214306	NM_008058:1431	Fzd8	INSIDE	0.375	0.660	1436.17	947.72	0.248	1152.02	285.42
A_68_P23627555	chr5:40036051-40036095	NM_010474:-202	Hs3st1	PROMOTER	0.375	0.628	1564.74	982.98	0.236	1171.99	276.35
A_68_P28079666	chr11:102317339-102317383	NM_010575:13837	Itga2b	INSIDE	0.375	0.568	2920.77	1658.07	0.213	2054.87	437.17
A_68_P26204800	chr8:120326079-120326123	NM_026758:-271	Mphosph6	PROMOTER	0.375	0.560	1128.23	632.06	0.210	997.82	209.56
A_68_P31205113	chr17:46247925-46247969	NM_026768:-6	Mrps18a	PROMOTER	0.375	0.423	1745.63	739.22	0.159	1403.26	222.69
A_68_P29554793	chr14:40285528-40285572	NM_001190187:826	Nrg3	INSIDE	0.375	0.638	1011.76	645.17	0.239	788.74	188.77
A_68_P20616242	chr1:133423393-133423437	NM_001081011:524	Srgap2	INSIDE	0.375	0.521	2544.03	1324.36	0.195	2056.63	401.09
A_68_P21729941	chr2:148220875-148220919	NM_009219:-216	Sstr4	PROMOTER	0.375	0.598	880.40	526.78	0.224	729.88	163.82
A_68_P22869602	chr4:43044144-43044188	NM_023231:90	Stoml2	INSIDE	0.375	0.633	1196.06	757.30	0.237	941.35	223.35
A_68_P22905511	chr4:49534082-49534127	NM_145547:16	Zfp189	INSIDE	0.375	0.545	1540.35	838.91	0.204	1299.90	265.54
A_68_P24385316	chr6:39823068-39823112			Unknown	0.375	0.399	1490.16	594.85	0.150	1111.59	166.61
A_68_P23437421	chr4:154624224-154624268	NM_001190445:172	2610002J02Rik	INSIDE	0.374	0.492	3337.24	1641.54	0.184	2477.98	456.36
A_68_P26023138	chr8:87531521-87531565	NM_001130193:6688	Best2	INSIDE	0.374	1.463	1331.75	1947.71	0.547	987.58	540.10
A_68_P29513184	chr14:32454218-32454262	NM_025295:-2	Btd	DIVERGENT_PROMOTER	0.374	0.584	1018.95	595.25	0.219	797.44	174.38
A_68_P28047526	chr11:96777751-96777795	NM_030248:23	Cdk5rap3	INSIDE	0.374	0.596	1501.27	895.07	0.223	1151.62	256.54
A_68_P29506063	chr14:31292967-31293011	NM_133761:238	Dcp1a	INSIDE	0.374	0.704	1577.12	1110.64	0.264	1229.62	324.21
A_68_P24607722	chr6:85978843-85978887	NM_012013:11680	Figla	DOWNSTREAM	0.374	0.504	1389.48	699.90	0.188	1073.81	202.30
A_68_P25656212	chr8:11555954-11555998	NM_011919:-89	Ing1	DIVERGENT_PROMOTER	0.374	0.539	1788.90	964.77	0.202	1283.50	259.05
A_68_P31425158	chr17:88197562-88197606	NM_199251:-250	Kcnk12	PROMOTER	0.374	0.571	1224.58	699.32	0.214	882.97	188.56
A_68_P32276229	chrX:16195746-16195790	NM_173740:-1055	Maoa	PROMOTER	0.374	0.575	1194.71	687.20	0.215	536.94	115.36
A_68_P27924663	chr11:74992086-74992130	NM_027136:202	Ovca2	INSIDE	0.374	0.551	1536.71	847.08	0.206	1192.92	246.00
A_68_P20740064	chr1:157659559-157659603	NM_001024945:449	Qsox1	INSIDE	0.374	0.659	3760.37	2479.17	0.246	2848.85	701.65
A_68_P29073052	chr13:58502691-58502735	NR_031761:-896	Rmi1	DIVERGENT_PROMOTER	0.374	0.699	1409.37	984.66	0.261	1116.26	291.50
A_68_P26609890	chr9:69138794-69138840	NM_013646:637208	Rora	INSIDE	0.374	0.598	1305.17	780.20	0.223	1018.95	227.73
A_68_P26084863	chr8:98240210-98240254	NM_001035123:420	Setd6	INSIDE	0.374	0.665	1819.01	1209.95	0.249	1391.57	346.00
A_68_P27630977	chr11:20232784-20232830	NM_018861:-90	Slc1a4	PROMOTER	0.374	0.620	1423.10	882.05	0.232	999.64	231.85
A_68_P25661254	chr8:12396094-12396138	NM_009233:598	Sox1	INSIDE	0.374	0.523	1735.04	908.20	0.196	1348.89	263.86
A_68_P27290695	chr10:81050342-81050386	NM_019725:12088	Tle2	INSIDE	0.374	1.682	2059.96	3464.99	0.629	1360.62	856.45
A_68_P23367600	chr4:141640361-141640405	NM_145402:-163	Tmem51	PROMOTER	0.374	0.680	2337.67	1589.41	0.254	1770.14	449.70
A_68_P25542187	chr7:140900886-140900932	NM_009479:70	Uros	INSIDE	0.374	0.654	1344.15	878.77	0.244	1112.54	271.69
A_68_P28611533	chr12:88019760-88019804	NM_177354:133	Vash1	INSIDE	0.374	0.304	2327.26	706.63	0.114	2022.48	229.66
A_68_P21538596	chr2:114027103-114027147	NM_175466:44	Zfp770	INSIDE	0.374	0.555	1476.51	818.98	0.207	1188.32	246.40
A_68_P25376020	chr7:109054295-109054339	NM_025605:-34	2400001E08Rik	PROMOTER	0.373	0.598	1246.58	744.90	0.223	882.36	196.69
A_68_P24219278	chr6:6906039-6906086	NM_001077713:45	Acn9	INSIDE	0.373	0.491	1636.84	803.46	0.183	1192.51	218.16
A_68_P24787432	chr6:118512444-118512488	NM_001081112:-192	Ankrd26	PROMOTER	0.373	1.366	2015.02	2752.25	0.509	1533.02	780.91

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27333413	chr10:89335981-89336025	NM_001128086:-251	Anks1b	PROMOTER	0.373	0.631	849.39	535.69	0.235	736.94	173.20
A_68_P25522113	chr7:137663240-137663284	NM_013799:-209	Ate1	PROMOTER	0.373	0.399	1322.65	527.16	0.149	1146.31	170.55
A_68_P25522115	chr7:137663415-137663459	NM_013799:-383	Ate1	PROMOTER	0.373	0.500	2341.57	1170.99	0.186	1742.52	324.88
A_68_P23585887	chr5:33206388-33206432	NM_177786:41	Depdc5	INSIDE	0.373	0.579	1412.99	817.53	0.216	1269.23	273.76
A_68_P25015867	chr7:27951865-27951909	NM_053208:-65	Egln2	PROMOTER	0.373	0.528	1116.01	589.21	0.197	856.52	168.89
A_68_P22367900	chr3:99966673-99966717	NM_010269:254	Gdap2	INSIDE	0.373	0.604	1259.37	760.79	0.225	960.25	216.33
A_68_P26810381	chr9:107578748-107578792	NM_008140:3153	Gnat1	INSIDE	0.373	0.650	3492.37	2268.41	0.242	2393.76	580.43
A_68_P20832289	chr1:174242640-174242684	NM_080419:125	Igsf8	INSIDE	0.373	0.710	3360.31	2386.34	0.265	2568.71	680.25
A_68_P30473040	chr15:97923295-97923339	NM_001163488:297	Pfkm	INSIDE	0.373	0.398	1591.36	632.58	0.148	1158.36	171.82
A_68_P21221438	chr2:52601606-52601650	NM_019667:-445	Stam2	PROMOTER	0.373	0.581	1188.08	689.77	0.217	877.37	190.01
A_68_P26696144	chr9:85736977-85737021	NM_001164792:540	Tpbg	INSIDE	0.373	0.555	3333.29	1850.00	0.207	2445.55	505.91
A_68_P26814408	chr9:108250538-108250582	NM_011678:399	Usp4	INSIDE	0.373	0.377	1442.99	543.97	0.141	1142.13	160.51
A_68_P26246901	chr8:127187263-127187307	NM_175149:-15	2310022B05Rik	PROMOTER	0.372	0.509	2820.86	1436.60	0.190	2109.31	399.83
A_68_P31201455	chr17:45643843-45643887	NM_198608:75	Aars2	INSIDE	0.372	0.561	1362.30	763.95	0.209	1028.70	214.79
A_68_P27448190	chr10:110735869-110735913	NM_027914:156	Bbs10	INSIDE	0.372	0.497	1259.28	626.04	0.185	941.39	173.95
A_68_P28449508	chr12:55963342-55963389	NM_007688:499	Cfl2	INSIDE	0.372	0.613	932.54	572.01	0.228	691.92	157.95
A_68_P27988567	chr11:86170969-86171013	NM_001080931:37	Med13	INSIDE	0.372	0.633	2475.01	1567.00	0.236	1888.51	445.29
A_68_P30365774	chr15:79158797-79158841	NM_001199023:-17	Pla2g6	PROMOTER	0.372	0.609	1039.23	633.31	0.227	829.12	187.89
A_68_P26585377	chr9:64869052-64869096	NM_021345:450	Ptplad1	INSIDE	0.372	0.622	923.15	574.18	0.231	836.12	193.53
A_68_P26936200	chr10:10277608-10277652	NM_026405:375	Rab32	INSIDE	0.372	0.664	4550.56	3021.23	0.247	3475.21	859.00
A_68_P29604814	chr14:52738859-52738903	NM_001168515:8303	Rpgrip1	INSIDE	0.372	0.434	1490.82	647.28	0.162	1149.00	185.61
A_68_P26237918	chr8:125626137-125626182	NM_016738:-90	Rpl13	PROMOTER	0.372	0.569	1555.77	885.91	0.212	1140.64	241.46
A_68_P20370954	chr1:78307126-78307170	NM_001004173:228	Sgpp2	INSIDE	0.372	0.570	1032.22	588.69	0.212	541.15	114.83
A_68_P28781844	chr12:120081565-120081609	NM_177082:-3215	Sp8	PROMOTER	0.372	0.462	2662.37	1228.89	0.172	2012.03	345.67
A_68_P25102503	chr7:54263926-54263970	NM_175318:-164	Spty2d1	PROMOTER	0.372	0.709	1940.59	1375.01	0.264	1561.52	412.11
A_68_P28071037	chr11:100800754-100800798	NM_011486:49	Stat3	INSIDE	0.372	0.701	1543.79	1082.81	0.261	1181.06	307.97
A_68_P22733170	chr4:12015068-12015112	NM_177861:14	Tmem67	INSIDE	0.372	0.333	1848.60	616.16	0.124	1452.29	180.16
A_68_P22982500	chr4:65266278-65266324	NM_001161782:281	Trim32	INSIDE	0.372	4.813	8083.80	38907.65	1.792	5043.12	9035.68
A_68_P27184874	chr10:61693685-61693729	NM_197996:260	Tspan15	INSIDE	0.372	0.456	2279.58	1039.91	0.170	1826.28	310.29
A_68_P29624841	chr14:57429933-57429977	NM_144842:599	Zmym5	INSIDE	0.372	0.460	1489.81	685.86	0.171	1148.41	196.90
A_68_P31402644	chr17:84496087-84496131	AK043195:-103		PROMOTER	0.372	0.554	2356.40	1306.16	0.206	1735.23	357.53
A_68_P26521201	chr9:53344702-53344746	NM_007499:52	Atm	INSIDE	0.371	0.563	1806.66	1017.29	0.209	1388.30	289.78
A_68_P24009173	chr5:115798570-115798614	NM_007748:372	Cox6a1	INSIDE	0.371	0.616	2290.27	1410.48	0.228	1743.29	397.93
A_68_P20457521	chr1:95698612-95698656	NM_001105667:-123	Dtymk	DIVERGENT_PROMOTER	0.371	0.592	1041.93	616.49	0.220	836.20	183.79
A_68_P29672520	chr14:65881704-65881748	NM_021458:-426	Fzd3	DIVERGENT_PROMOTER	0.371	0.390	1823.79	710.57	0.145	1432.21	207.20
A_68_P22310076	chr3:87600886-87600930	NM_011832:36	Insrr	INSIDE	0.371	0.623	1828.87	1138.98	0.231	1451.56	335.52
A_68_P22303234	chr3:86350689-86350733	NM_011839:1495	Mab21l2	INSIDE	0.371	0.692	3024.69	2091.84	0.257	2148.70	552.00
A_68_P20600071	chr1:130256165-130256209	NM_008567:47	Mcm6	INSIDE	0.371	0.330	1786.80	589.58	0.122	1566.63	191.87
A_68_P27555607	chr11:3996584-3996628	NM_026443:-1172	Mtfp1	PROMOTER	0.371	0.540	1683.71	909.01	0.200	1243.79	248.91
A_68_P26803472	chr9:106355981-106356025	NM_021567:-185	Pcbp4	PROMOTER	0.371	0.633	3803.95	2409.24	0.235	2799.94	658.50
A_68_P23542950	chr5:24104639-24104683	NM_025891:3160	Smarcd3	INSIDE	0.371	0.697	3373.47	2352.53	0.259	2692.22	697.16
A_68_P28744145	chr12:112683846-112683890	NM_009396:2997	Tnfaip2	INSIDE	0.371	0.520	2026.59	1053.27	0.193	1632.63	314.96
A_68_P25500777	chr7:133630795-133630839	NM_001163713:-52	Tufm	PROMOTER	0.371	0.604	2306.18	1393.18	0.224	1675.38	375.58
A_68_P29081868	chr13:59923934-59923978	NM_153538:552	Zcchc6	INSIDE	0.371	0.380	2426.51	922.15	0.141	2050.26	289.17
A_68_P27104120	chr10:43868558-43868602			Unknown	0.371	0.649	1984.04	1288.29	0.241	1465.56	353.43
A_68_P26812297	chr9:107888019-107888063	NM_026597:207	6230427J02Rik	INSIDE	0.370	0.566	1015.81	574.57	0.209	795.95	166.55
A_68_P21421624	chr2:91105178-91105222	NM_001166024:-71	Arfgap2	PROMOTER	0.370	0.643	1051.41	676.43	0.238	865.43	206.21
A_68_P24056050	chr5:123958945-123958990	NM_198611:-1501	B3gnt4	PROMOTER	0.370	0.545	1243.02	677.99	0.202	988.45	199.35
A_68_P28033137	chr11:94334569-94334613	NM_001112813:922	Cacna1g	INSIDE	0.370	0.334	2173.74	726.93	0.124	1681.55	207.80
A_68_P21976418	chr3:19594468-19594512	NM_205769:906	Crh	INSIDE	0.370	0.350	1613.65	564.62	0.130	1344.50	174.16
A_68_P30476581	chr15:98635925-98635969	NM_001013741:2410	Ddn	INSIDE	0.370	0.477	1136.62	541.64	0.176	853.54	150.62

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26810382	chr9:107578840-107578884	NM_008140:3061	Gnat1	INSIDE	0.370	0.562	2572.85	1446.90	0.208	1862.26	387.15
A_68_P24318697	chr6:28085365-28085421	NM_008174:-1023	Grm8	PROMOTER	0.370	0.524	1001.98	525.21	0.194	878.10	170.48
A_68_P26220486	chr8:123012400-123012445	NM_198671:-343	Gse1	PROMOTER	0.370	0.631	1511.00	953.06	0.233	993.55	231.90
A_68_P21906900	chr2:180627890-180627934	NR_029538:-832	Mir124a-3	PROMOTER	0.370	0.452	2903.67	1311.40	0.167	2160.01	361.10
A_68_P27924624	chr11:74986764-74986808	NR_029794:-103	Mir212	DIVERGENT_PROMOTER	0.370	0.589	886.91	522.01	0.218	675.07	146.83
A_68_P22129911	chr3:51288253-51288297	NM_016858:387	Rab33b	INSIDE	0.370	0.582	1602.37	932.44	0.215	1357.65	291.97
A_68_P20022049	chr1:9289822-9289866	NM_027671:-33	Sntg1	PROMOTER	0.370	0.527	1337.96	704.86	0.195	1107.80	216.19
A_68_P28909029	chr13:29051502-29051546	NM_009238:-5973	Sox4	PROMOTER	0.370	0.592	1691.19	1001.67	0.219	1214.69	266.31
A_68_P25576304	chr7:146373808-146373852	NM_021302:563	Stk32c	INSIDE	0.370	0.526	1714.22	901.08	0.195	1413.47	274.93
A_68_P20638619	chr1:137210199-137210243	NM_011590:94	Timm17a	INSIDE	0.370	0.694	1718.46	1192.95	0.257	1320.26	339.28
A_68_P23012911	chr4:71860767-71860811	NM_011599:1165	Tle1	INSIDE	0.370	0.453	1503.64	681.47	0.167	1141.27	191.14
A_68_P29428735	chr14:17198392-17198436	NM_009409:695	Top2b	INSIDE	0.370	0.674	1504.02	1014.20	0.249	1100.21	274.36
A_68_P22584284	chr3:141128445-141128489	NM_009472:-61	Unc5c	PROMOTER	0.370	0.575	2698.73	1551.80	0.213	2117.13	450.32
A_68_P26478900	chr9:46081259-46081303	NM_011752:134	Zfp259	INSIDE	0.370	0.476	1359.42	646.66	0.176	1243.16	218.91
A_68_P25063515	chr7:38556810-38556854	NM_172385:-2061	Zfp536	PROMOTER	0.370	0.645	1075.96	693.54	0.239	811.94	193.89
A_68_P27942257	chr11:78075584-78075628	NM_001002004:351	2610507B11Rik	INSIDE	0.369	0.544	2133.03	1160.71	0.201	1619.30	325.27
A_68_P27938080	chr11:77329296-77329340	NM_026185:700	Abhd15	INSIDE	0.369	0.522	1318.57	687.90	0.193	1028.42	198.06
A_68_P25050069	chr7:36371356-36371409	NM_178263:117	Ankrd27	INSIDE	0.369	0.612	860.19	526.55	0.226	672.05	151.87
A_68_P26356121	chr9:23026902-23026947	NM_028472:-595	Bmper	PROMOTER	0.369	1.643	1952.36	3208.29	0.606	1498.57	907.76
A_68_P31145617	chr17:32589667-32589711	NM_177307:21	Cyp4f39	INSIDE	0.369	1.547	1792.63	2772.84	0.571	1301.42	743.55
A_68_P22649279	chr3:151873278-151873322	NM_027287:-37	Dnajb4	DIVERGENT_PROMOTER	0.369	0.480	1350.69	648.44	0.177	1091.22	193.15
A_68_P24817442	chr6:124813681-124813725	NM_013533:233	Gpr162	INSIDE	0.369	0.432	2790.75	1206.46	0.159	2126.92	339.15
A_68_P30962573	chr16:91372961-91373005	NM_001110498:-45	Ifnar2	PROMOTER	0.369	1.806	1740.37	3143.44	0.667	1253.02	835.76
A_68_P31733116	chr18:57085552-57085596	NM_177115:-372	Marchf3	PROMOTER	0.369	0.549	1476.92	810.67	0.203	1171.17	237.29
A_68_P26134879	chr8:108137855-108137899	NR_035492:-1489	Mir1966	PROMOTER	0.369	0.547	1646.97	901.33	0.202	1453.38	293.57
A_68_P29448048	chr14:21460427-21460474	NM_021508:15312	Myoz1	DOWNSTREAM	0.369	0.591	1254.51	740.98	0.218	1043.25	227.15
A_68_P20010810	chr1:5906552-5906596	NM_010342:905	Npbwr1	INSIDE	0.369	1.711	2495.38	4269.75	0.631	1896.36	1195.84
A_68_P23354456	chr4:139384273-139384317	NM_011039:4589	Pax7	INSIDE	0.369	0.593	1252.20	742.35	0.219	1007.13	220.38
A_68_P23399007	chr4:148540337-148540381	NM_001081274:458	Pgd	INSIDE	0.369	0.494	3376.20	1667.68	0.182	2673.45	487.18
A_68_P26464018	chr9:43611946-43611990	NM_021424:59310	Pvrl1	INSIDE	0.369	1.592	2626.63	4180.82	0.588	2022.89	1189.23
A_68_P27943493	chr11:78279470-78279514	NM_026740:290	Slc46a1	INSIDE	0.369	0.544	1583.58	861.37	0.201	1242.60	249.24
A_68_P21836562	chr2:167456829-167456873	NM_023230:655	Ube2v1	INSIDE	0.369	0.640	7254.47	4646.42	0.236	5275.91	1247.68
A_68_P22039930	chr3:32716759-32716803	NM_001013024:233	Usp13	INSIDE	0.369	0.588	1373.60	807.09	0.217	1076.73	233.35
A_68_P24097670	chr5:131783250-131783294	NM_145218:120	Wbscr17	INSIDE	0.369	0.747	4369.97	3265.77	0.275	3230.56	889.72
A_68_P24686641	chr6:99471046-99471094	ENSMUST00000155466:145721		INSIDE	0.369	0.579	1235.84	715.32	0.213	1041.31	222.27
A_68_P25541690	chr7:140829066-140829110	NM_178115:-269	2700050L05Rik	PROMOTER	0.368	0.463	1801.90	834.44	0.170	1636.13	278.48
A_68_P27932871	chr11:76384753-76384797	NM_198895:102	Abr	INSIDE	0.368	0.676	4400.34	2973.23	0.248	3399.93	844.40
A_68_P21840065	chr2:168031845-168031889	NM_009628:696	Adnp	INSIDE	0.368	1.759	6730.07	11837.36	0.647	4875.54	3155.13
A_68_P30588537	chr16:20621774-20621818	NM_028420:-445	Camk2n2	DIVERGENT_PROMOTER	0.368	0.486	2447.06	1190.31	0.179	1934.82	346.13
A_68_P31921845	chr19:4215539-4215583	NM_019952:1169	Clcf1	INSIDE	0.368	0.459	4158.15	1906.85	0.169	3338.13	563.15
A_68_P29699020	chr14:70477756-70477800	NM_018781:527	Egr3	INSIDE	0.368	0.632	2005.00	1266.39	0.232	1471.41	341.64
A_68_P23968409	chr5:108150354-108150398	NM_010278:2987	Gfi1	INSIDE	0.368	0.440	2694.53	1186.86	0.162	2359.37	381.96
A_68_P25736704	chr8:28232129-28232173	NM_054044:35838	Gpr124	INSIDE	0.368	1.449	1249.75	1810.38	0.533	1079.04	575.38
A_68_P28089845	chr11:104093103-104093147	NM_001038609:375	Mapt	INSIDE	0.368	0.451	1322.61	596.24	0.166	913.25	151.68
A_68_P25578898	chr7:146768350-146768394	NR_027857:324	Nkx6-2	INSIDE	0.368	0.584	1587.11	927.23	0.215	1164.07	250.52
A_68_P24990654	chr7:19548318-19548362	NM_001029877:37104	Nova2	INSIDE	0.368	0.671	2332.29	1564.36	0.247	1919.15	473.29
A_68_P26567741	chr9:61762053-61762098	NM_018853:242	Rplp1	INSIDE	0.368	0.673	2655.14	1786.03	0.247	2042.06	505.38
A_68_P27924902	chr11:75027241-75027285	NM_177708:19768	Rtn4rl1	INSIDE	0.368	0.546	1933.57	1055.77	0.201	1441.23	289.59
A_68_P22169677	chr3:58496154-58496198	NM_009174:134	Siah2	INSIDE	0.368	0.501	1256.52	629.58	0.184	1022.76	188.36
A_68_P30544461	chr16:10785857-10785901	NM_009896:-249	Socs1	PROMOTER	0.368	0.595	1490.91	887.75	0.219	1122.29	245.84
A_68_P31752537	chr18:60784125-60784169	NM_177340:-187	Synpo	PROMOTER	0.368	0.713	2813.16	2005.75	0.262	2269.24	595.25

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P29855890	chr14:102007762-102007806	NM_001081278:624	Tbc1d4	INSIDE	0.368	0.515	2418.56	1245.80	0.190	1945.13	368.82
A_68_P25510961	chr7:135605591-135605635	NM_009383:-585	Tial1	PROMOTER	0.368	0.536	1014.76	543.51	0.197	867.11	170.87
A_68_P32144293	chr19:46574614-46574658	NM_053100:-1501	Trim8	PROMOTER	0.368	0.699	2968.85	2076.71	0.257	2146.07	552.02
A_68_P22552063	chr3:135102173-135102217	NM_025356:472	Ube2d3	INSIDE	0.368	0.625	1947.42	1216.38	0.230	1437.53	330.82
A_68_P32217702	chr19:59246036-59246083	NM_009501:-1540	Vax1	PROMOTER	0.368	1.763	2005.02	3535.34	0.650	1394.70	906.05
A_68_P23296404	chr4:129055173-129055217	NM_028603:78	Zbtb8a	INSIDE	0.368	0.554	1797.67	995.39	0.204	1518.39	309.05
A_68_P24958145	chr7:7074049-7074093	NM_172738:117	Zfp954	INSIDE	0.368	0.624	1752.32	1094.30	0.230	1266.05	290.61
A_68_P25470558	chr7:127974492-127974536			Unknown	0.368	0.698	1763.01	1231.02	0.257	1335.15	343.40
A_68_P28787949	chr13:3359101-3359145			Unknown	0.368	0.608	2079.16	1263.88	0.224	1629.70	364.41
A_68_P20774313	chr1:163806678-163806722	NM_172645:92	AI848100	INSIDE	0.367	0.580	4191.61	2429.48	0.213	2962.20	630.90
A_68_P20770398	chr1:163101115-163101159	NM_028664:28294	Ankrd45	DOWNSTREAM	0.367	0.706	2741.32	1934.83	0.259	2206.06	571.18
A_68_P25588372	chr7:148547330-148547384	NR_033532:3653	B230206H07Rik	INSIDE	0.367	4.016	965.36	3877.05	1.473	734.15	1081.55
A_68_P27854481	chr11:62352177-62352221	NM_028448:565	Cenpv	INSIDE	0.367	0.675	1792.10	1209.72	0.248	1317.70	326.44
A_68_P23155325	chr4:101169532-101169576	NM_198412:302	Dnajc6	INSIDE	0.367	0.589	1393.48	820.60	0.216	994.58	214.77
A_68_P22149459	chr3:54539268-54539312	NM_001163570:-4	Exosc8	DIVERGENT_PROMOTER	0.367	0.619	1633.62	1012.02	0.227	1454.55	330.87
A_68_P24784005	chr6:117866930-117866974	NM_001166427:-359	Hnrnpf	PROMOTER	0.367	0.586	1905.99	1117.24	0.215	1450.07	312.04
A_68_P31381041	chr17:80460590-80460634	NM_144802:1062	Hnrpll	INSIDE	0.367	0.428	2048.07	876.46	0.157	1597.30	250.70
A_68_P24171751	chr5:147888207-147888251	NM_080795:-80	Lnx2	DIVERGENT_PROMOTER	0.367	0.432	1415.22	610.72	0.159	1052.78	166.95
A_68_P29044037	chr13:53557736-53557785	NM_013601:10389	Msx2	DOWNSTREAM	0.367	0.659	1970.32	1299.01	0.242	1359.38	328.66
A_68_P25949908	chr8:72636524-72636568	NM_007789:8197	Ncan	INSIDE	0.367	0.582	1171.23	681.59	0.213	918.64	195.95
A_68_P27901894	chr11:70467828-70467872	NM_011072:302	Pfn1	INSIDE	0.367	0.660	1700.64	1122.36	0.242	1120.07	271.19
A_68_P28151618	chr11:115015440-115015484	NM_021411:-29	Rab37	PROMOTER	0.367	13.375	4190.60	56049.64	4.911	3112.74	15287.51
A_68_P20250386	chr1:57027876-57027920	NM_139146:280	Satb2	INSIDE	0.367	0.721	4515.25	3255.16	0.264	2873.17	759.41
A_68_P30546003	chr16:11066050-11066094	NM_009223:-318	Snn	PROMOTER	0.367	0.487	2775.35	1351.27	0.179	2112.81	377.92
A_68_P32957267	chr17:8477533-8477577	NM_018819:877	Brp44l	INSIDE	0.366	0.430	2294.45	985.74	0.157	1874.90	295.18
A_68_P26543685	chr9:57613651-57613695	NM_007713:-5	Clk3	PROMOTER	0.366	0.424	2415.65	1025.21	0.155	1907.78	296.45
A_68_P29611635	chr14:54873344-54873388	NM_001113358:238	Dad1	INSIDE	0.366	0.544	2468.07	1343.80	0.199	1980.63	394.71
A_68_P26468507	chr9:44412404-44412448	NM_001110826:-548	Ddx6	PROMOTER	0.366	0.641	1400.24	897.94	0.235	1104.97	259.50
A_68_P25082496	chr7:50720344-50720388	NM_026695:20854	Etfb	DOWNSTREAM	0.366	0.528	3554.86	1878.03	0.193	2621.67	506.75
A_68_P26593512	chr9:66359862-66359906	NM_175206:2516	Fbxl22	INSIDE	0.366	0.675	991.70	669.31	0.247	868.51	214.47
A_68_P23968432	chr5:108153037-108153081	NM_010278:305	Gfi1	INSIDE	0.366	0.652	2715.19	1770.48	0.239	2039.13	486.52
A_68_P25580591	chr7:147020155-147020199	NM_177469:104	Gpr123	INSIDE	0.366	0.556	951.68	528.86	0.204	821.51	167.20
A_68_P26526551	chr9:54434255-54434299	NM_029573:-41	Idh3a	PROMOTER	0.366	0.643	3186.60	2048.03	0.235	2635.93	620.29
A_68_P30350212	chr15:76553038-76553082	NM_198119:-457	Lrrc24	PROMOTER	0.366	0.490	1781.72	873.53	0.180	1217.47	218.75
A_68_P30939710	chr16:87432281-87432325	NM_001081068:549	Ltn1	INSIDE	0.366	0.682	1974.27	1347.44	0.250	1663.64	415.75
A_68_P31117836	chr17:27822046-27822090	NM_178365:-130	Pacsin1	PROMOTER	0.366	0.466	1736.60	809.51	0.171	1241.91	212.04
A_68_P21913217	chr2:181598855-181598899	NM_025901:-188	Polr3k	PROMOTER	0.366	0.499	1025.36	511.73	0.183	723.84	132.32
A_68_P31302583	chr17:66121848-66121892	NM_133685:222	Rab31	INSIDE	0.366	0.430	1523.83	655.05	0.157	1090.70	171.37
A_68_P24052512	chr5:123300221-123300265	NM_030564:46	Rnf34	INSIDE	0.366	0.692	1037.33	717.42	0.253	891.48	225.95
A_68_P22199716	chr3:65196136-65196183	NM_026155:316	Ssr3	INSIDE	0.366	1.567	1433.03	2244.91	0.573	1122.68	643.02
A_68_P27392328	chr10:99950341-99950385	NM_001110013:-381	Tmtc3	DIVERGENT_PROMOTER	0.366	0.500	3863.71	1931.11	0.183	2898.74	530.85
A_68_P27780095	chr11:48630257-48630301	NM_145377:615	Trim41	INSIDE	0.366	0.693	3398.98	2354.41	0.253	2424.95	614.69
A_68_P24950639	chr7:4764364-4764408	NM_133777:-444	Ube2s	PROMOTER	0.366	1.628	13007.66	21180.35	0.597	8763.23	5227.49
A_68_P26749716	chr9:96789602-96789646	NM_153420:217	Acpl2	INSIDE	0.365	0.604	8480.39	5122.60	0.220	5920.23	1304.23
A_68_P28450015	chr12:56085848-56085892	NM_013815:1453	Baz1a	INSIDE	0.365	0.680	2723.92	1851.08	0.248	2147.50	532.50
A_68_P26055734	chr8:93431736-93431780	NM_177224:79025	Chd9	INSIDE	0.365	0.516	1586.60	818.66	0.188	1265.60	238.22
A_68_P21818155	chr2:164312484-164312528	NM_001048229:-1104	Dbndd2	PROMOTER	0.365	0.680	1143.31	777.68	0.249	900.59	223.81
A_68_P31890268	chr18:84889452-84889496	NM_173770:-159	Fam69c	PROMOTER	0.365	0.519	1894.09	983.56	0.190	1558.48	295.66
A_68_P20351044	chr1:74931604-74931648	NM_153111:356	Fev	INSIDE	0.365	0.652	3328.55	2168.66	0.238	2335.52	555.21
A_68_P28924098	chr13:31721161-31721205	NM_010225:3498	Foxf2	INSIDE	0.365	0.641	1875.27	1201.92	0.234	1376.93	321.71
A_68_P24810880	chr6:122824802-122824859	NM_026267:256	Necap1	INSIDE	0.365	0.520	1498.27	778.43	0.190	1145.87	217.19

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26076074	chr8:96738369-96738413	NM_172410:-110	Nup93	PROMOTER	0.365	0.640	1151.63	737.03	0.234	880.41	205.75
A_68_P31929450	chr19:5560018-5560062	NM_019935:535	Ovol1	INSIDE	0.365	0.507	2049.44	1040.05	0.185	1613.64	299.18
A_68_P25373531	chr7:108599782-108599826	NR_026574:-17	Pde2a	PROMOTER	0.365	0.492	4645.45	2283.91	0.179	3315.28	594.43
A_68_P23228359	chr4:115894431-115894475	NM_181585:-66	Pik3r3	PROMOTER	0.365	0.529	1566.05	829.17	0.193	1213.12	234.41
A_68_P21115151	chr2:32251028-32251072	NM_133783:-359	Ptges2	DIVERGENT_PROMOTER	0.365	0.588	1314.57	772.59	0.214	1013.72	217.17
A_68_P32806533	chrX:162917564-162917608	NM_019773:213	Rab9	INSIDE	0.365	1.482	2254.55	3340.86	0.541	975.33	527.39
A_68_P21824257	chr2:165329532-165329576	NM_130451:77	Slc2a10	INSIDE	0.365	0.542	1306.20	707.64	0.198	1231.11	243.71
A_68_P30939796	chr16:87455183-87455227	NM_024258:-25	Usp16	PROMOTER	0.365	0.514	1171.02	601.72	0.188	1168.48	219.09
A_68_P28872662	chr13:21494612-21494656	NM_001145778:-10	Zkscan3	PROMOTER	0.365	0.728	2642.27	1922.65	0.266	2039.20	541.83
A_68_P32141578	chr19:46073169-46073219	NM_198296:-216	9130011E15Rik	DIVERGENT_PROMOTER	0.364	0.540	1105.89	596.97	0.197	794.71	156.33
A_68_P20632244	chr1:136131312-136131356	NM_001008533:670	Adora1	INSIDE	0.364	0.529	1761.63	931.49	0.193	1462.88	281.90
A_68_P20147467	chr1:36364433-36364477	NM_001172205:-123	Arid5a	PROMOTER	0.364	0.592	997.95	590.96	0.215	902.68	194.44
A_68_P25610231	chr7:152128709-152128753	NM_007631:-2900	Ccnd1	PROMOTER	0.364	0.447	1161.38	519.42	0.163	858.28	139.89
A_68_P31485624	chr18:9449444-9449488	NM_026484:682	Ccny	INSIDE	0.364	0.626	1079.22	675.59	0.228	843.35	192.32
A_68_P25587939	chr7:148477922-148477966	NM_007878:40	Drd4	INSIDE	0.364	0.465	1820.17	847.17	0.169	1494.82	252.94
A_68_P26954163	chr10:13686795-13686839	NM_010437:632	Hivep2	INSIDE	0.364	0.539	1026.28	553.65	0.197	946.65	186.06
A_68_P21233127	chr2:55289729-55289773	NM_008426:184	Kcnj3	INSIDE	0.364	0.622	1796.23	1116.79	0.226	1390.13	314.43
A_68_P20042289	chr1:13650498-13650542	NM_145381:70	Lactb2	INSIDE	0.364	0.613	1278.27	783.69	0.223	1015.13	226.65
A_68_P24994037	chr7:20147028-20147077	NM_199149:695	Lrrc68	INSIDE	0.364	0.492	1095.27	538.91	0.179	832.16	149.23
A_68_P23894277	chr5:92864276-92864320	NM_183392:-73	Nup54	PROMOTER	0.364	0.633	1620.81	1026.47	0.231	1304.06	301.01
A_68_P27311093	chr10:85379465-85379509	NM_181650:204	Prdm4	INSIDE	0.364	0.420	1790.11	751.12	0.153	1539.97	235.30
A_68_P22411529	chr3:108060296-108060340	NM_011967:475	Psma5	INSIDE	0.364	0.576	1211.32	697.48	0.210	1021.59	214.14
A_68_P20557415	chr1:121401606-121401656	NM_022327:-271	Ralb	PROMOTER	0.364	0.498	1170.49	582.38	0.181	884.83	160.09
A_68_P26588678	chr9:65477711-65477764	NM_028030:-651	Rbpms2	PROMOTER	0.364	0.429	1876.50	804.27	0.156	1567.11	244.47
A_68_P23328509	chr4:134989508-134989552	NM_022980:190	Rcan3	INSIDE	0.364	0.663	1405.51	931.59	0.241	1138.84	275.03
A_68_P26717018	chr9:90165190-90165234	NM_194334:395	Tbc1d2b	INSIDE	0.364	0.392	1692.75	663.34	0.143	1481.25	211.49
A_68_P21069043	chr2:24817956-24818000	NM_026044:37	Wdr85	INSIDE	0.364	0.709	2243.20	1589.40	0.258	1843.84	475.47
A_68_P25042342	chr7:34918494-34918538	NM_207212:-229	Wtip	PROMOTER	0.364	0.525	2836.45	1489.36	0.191	2244.05	429.00
A_68_P31469352	chr18:5591749-5591796	NM_011546:-116	Zeb1	PROMOTER	0.364	0.627	1055.27	661.74	0.228	870.77	198.86
A_68_P23590567	chr5:34035431-34035475	AK172441:89934		INSIDE	0.364	0.688	1155.60	795.45	0.250	972.46	243.58
A_68_P24617829	chr6:87682986-87683030	NM_001159697:2146	Ccdc48	INSIDE	0.363	0.632	1753.37	1108.15	0.229	1543.22	354.13
A_68_P20551457	chr1:120286262-120286306	NM_001081276:650	Clasp1	INSIDE	0.363	0.575	2595.78	1492.91	0.209	2048.58	427.43
A_68_P28610002	chr12:87763647-87763691	NM_011934:1075	Esrrb	INSIDE	0.363	0.588	2445.88	1437.16	0.213	1696.19	362.02
A_68_P28157765	chr11:116029229-116029273	NM_172571:242	Fbf1	INSIDE	0.363	0.488	2357.68	1150.60	0.177	1831.93	324.14
A_68_P28158431	chr11:116142573-116142617	NM_010254:342	Galr2	INSIDE	0.363	0.476	1565.55	745.74	0.173	1209.65	208.96
A_68_P27315611	chr10:86167975-86168019	NM_011631:193	Hsp90b1	INSIDE	0.363	0.537	1931.18	1037.46	0.195	1607.35	313.11
A_68_P30676660	chr16:36694130-36694174	NM_134109:29	Ildr1	INSIDE	0.363	0.478	1591.35	760.33	0.173	1257.76	217.96
A_68_P25952871	chr8:73119135-73119179	NM_023627:777	Isyna1	INSIDE	0.363	1.400	1995.11	2794.07	0.509	1512.14	769.49
A_68_P29668832	chr14:65271520-65271564	NM_001081177:175	Kif13b	INSIDE	0.363	0.514	2830.97	1454.50	0.186	2398.24	447.04
A_68_P28048328	chr11:96902741-96902785	NM_027026:-79	Lrrc46	DIVERGENT_PROMOTER	0.363	0.485	1848.56	896.38	0.176	1751.10	308.14
A_68_P29646483	chr14:61403303-61403351	NM_027436:-76	Mipep	PROMOTER	0.363	0.587	1104.41	648.00	0.213	803.94	171.19
A_68_P29773644	chr14:84845775-84845819	NM_001013753:2427	Pcdh17	INSIDE	0.363	0.422	2016.17	850.23	0.153	1558.98	238.72
A_68_P29482952	chr14:27488079-27488123	NM_178668:1232	Pde12	INSIDE	0.363	0.480	1875.53	900.54	0.174	1450.80	252.82
A_68_P28057823	chr11:98544328-98544372	NM_009439:483	Psmd3	INSIDE	0.363	0.643	1843.14	1185.27	0.233	1357.88	316.61
A_68_P26605678	chr9:68502422-68502466	NM_013646:836	Rora	INSIDE	0.363	0.530	2074.71	1099.56	0.193	1711.75	329.55
A_68_P28963699	chr13:39052582-39052626	NM_001170430:-198	Slc35b3	PROMOTER	0.363	0.673	1247.85	839.95	0.244	981.07	239.84
A_68_P25581334	chr7:147129626-147129670	NM_009482:-106	Utf1	PROMOTER	0.363	0.470	3752.43	1762.33	0.170	2832.98	482.46
A_68_P25063501	chr7:38555245-38555289	NM_172385:-495	Zfp536	PROMOTER	0.363	0.675	1965.18	1325.54	0.245	1624.38	397.88
A_68_P21810970	chr2:163029056-163029100	ENSMUST00000128999:-1210		PROMOTER	0.363	0.618	5459.74	3376.28	0.224	4376.05	981.33
A_68_P25594227	chr7:149558369-149558413	NM_177265:-226	6330512M04Rik	PROMOTER	0.362	1.697	3354.54	5691.01	0.614	2329.28	1430.01
A_68_P24455804	chr6:53237462-53237506	NR_015553:196	9430076C15Rik	INSIDE	0.362	0.441	1507.71	665.62	0.160	1198.21	191.54

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P23456811	chr5:5664103-5664147	NM_172447:108	A330021E22Rik	INSIDE	0.362	0.682	1203.11	820.16	0.247	905.36	223.21
A_68_P20596873	chr1:129670505-129670549	NM_028399:-214	Ccnt2	PROMOTER	0.362	0.696	1897.84	1321.27	0.252	1332.43	335.56
A_68_P30109623	chr15:30576998-30577042	NM_008729:474673	Ctnnd2	INSIDE	0.362	0.407	1353.05	550.99	0.148	980.81	144.78
A_68_P32328376	chrX:35918353-35918397	NM_001110142:10999	Cul4b	INSIDE	0.362	4.458	5368.72	23933.97	1.613	2521.92	4067.59
A_68_P25477510	chr7:129276573-129276617	NM_021608:40	Dctn5	INSIDE	0.362	0.494	1506.41	744.10	0.179	1229.40	219.58
A_68_P23803966	chr5:74931407-74931451	NM_001159573:-78	Fip1l1	DIVERGENT_PROMOTER	0.362	0.678	2028.43	1376.00	0.245	1754.68	430.30
A_68_P26244129	chr8:126756057-126756101	NM_139272:785	Galnt2	INSIDE	0.362	0.568	2036.88	1156.20	0.205	1543.13	317.06
A_68_P24449404	chr6:52196424-52196469	NM_010450:-680	Hoxa11	PROMOTER	0.362	0.568	1406.16	799.17	0.206	962.44	197.83
A_68_P23270091	chr4:124428867-124428911	NM_008385:9767	Inpp5b	INSIDE	0.362	0.653	4855.24	3170.40	0.236	3669.14	867.58
A_68_P27143272	chr10:53349951-53349995	NM_027830:273	Mcm9	INSIDE	0.362	1.819	5783.79	10523.23	0.659	3906.06	2574.75
A_68_P31753488	chr18:60934010-60934054	NM_020600:-217	Rps14	PROMOTER	0.362	0.383	1605.60	615.28	0.139	1190.38	165.27
A_68_P31142312	chr17:31992898-31992942	NM_010831:-183	Sik1	PROMOTER	0.362	0.545	1357.06	739.91	0.197	1298.38	256.01
A_68_P28535628	chr12:74213900-74213944	NM_011382:310	Six4	INSIDE	0.362	0.564	2662.05	1501.38	0.204	2072.53	422.87
A_68_P27480106	chr10:116661162-116661206	NM_026570:379	Yeats4	INSIDE	0.362	0.398	1735.68	690.14	0.144	1541.08	221.81
A_68_P30382915	chr15:82176602-82176646	NM_026914:149	1500032L24Rik	INSIDE	0.361	0.585	1133.20	662.59	0.211	926.82	195.82
A_68_P26584998	chr9:64808639-64808683	NM_175153:-83	2010321M09Rik	PROMOTER	0.361	0.740	2850.46	2110.58	0.268	2164.57	579.04
A_68_P32100295	chr19:38298465-38298509	NM_001081075:136	5730455O13Rik	INSIDE	0.361	0.520	1351.82	702.50	0.187	1104.35	206.90
A_68_P21782540	chr2:158187149-158187193	NR_015463:75	9430008C03Rik	INSIDE	0.361	0.611	1703.82	1041.43	0.221	1310.07	289.15
A_68_P30668268	chr16:35154633-35154677	NM_001012765:-1067	Adcy5	PROMOTER	0.361	0.385	3579.63	1378.53	0.139	2871.51	399.14
A_68_P24766252	chr6:114593333-114593377	NM_028835:212	Atg7	INSIDE	0.361	0.552	1095.39	605.07	0.200	843.59	168.36
A_68_P28680556	chr12:101437490-101437534	NM_009790:-238	Calm1	PROMOTER	0.361	0.354	2330.47	824.17	0.128	1909.05	243.64
A_68_P22752470	chr4:15872272-15872316	NM_026172:360	Decr1	INSIDE	0.361	0.715	5079.40	3632.75	0.258	4058.78	1046.83
A_68_P32030716	chr19:25684536-25684580	NM_177360:-468	Dmrt3	PROMOTER	0.361	0.667	1409.09	939.16	0.241	1098.30	264.44
A_68_P21439331	chr2:93998296-93998341	NM_019657:-252	Hsd17b12	PROMOTER	0.361	0.543	1429.19	775.83	0.196	1119.20	219.20
A_68_P22324048	chr3:90035364-90035413	NM_206924:-130	Jtb	PROMOTER	0.361	0.661	985.75	651.65	0.239	748.87	178.96
A_68_P24182265	chr5:149740293-149740337	NM_153572:-91	Katnal1	PROMOTER	0.361	0.641	1163.83	745.85	0.231	980.94	226.82
A_68_P20353555	chr1:75366170-75366222	NR_037976:5394	LOC100503248	INSIDE	0.361	1.945	2112.18	4107.44	0.702	1463.37	1026.86
A_68_P21309978	chr2:69424022-69424066	NM_001081088:80	Lrp2	INSIDE	0.361	0.507	1148.82	582.30	0.183	912.84	166.90
A_68_P21579978	chr2:121114942-121114992	NM_032393:-371	Mtap1a	PROMOTER	0.361	0.485	1371.23	664.89	0.175	1114.24	195.15
A_68_P30650229	chr16:31948693-31948737	NM_026554:83	Ncbp2	INSIDE	0.361	0.627	861.15	539.74	0.226	686.61	155.30
A_68_P27930798	chr11:76057462-76057506	NM_183263:247	Rnmtl1	INSIDE	0.361	0.646	1022.85	660.68	0.233	792.69	184.63
A_68_P30653349	chr16:32609415-32609459	NM_011638:455	Tfrc	INSIDE	0.361	0.620	1844.75	1144.05	0.224	1438.90	321.89
A_68_P31675646	chr18:46371668-46371712	NM_178872:571	Trim36	INSIDE	0.361	0.384	2178.47	836.93	0.139	1795.39	248.86
A_68_P28729765	chr12:109996083-109996127			Unknown	0.361	0.619	2317.95	1434.58	0.223	1833.24	409.44
A_68_P25007501	chr7:25733865-25733909			Unknown	0.361	0.616	1386.20	854.13	0.222	1143.68	254.25
A_68_P25415072	chr7:117911998-117912042	NM_009667:-4097	Ampd3	PROMOTER	0.360	0.535	1828.63	977.71	0.193	1638.59	315.51
A_68_P30499085	chr15:102501421-102501465	NM_026468:36	Atp5g2	INSIDE	0.360	0.503	1158.87	583.29	0.181	975.92	176.77
A_68_P28184671	chr11:120319473-120319517	NM_152807:52	Ccdc137	INSIDE	0.360	0.574	2047.05	1174.06	0.206	1632.56	336.62
A_68_P22882387	chr4:45355569-45355613	NM_153167:618	Dcaf10	INSIDE	0.360	0.511	1542.50	788.61	0.184	1163.88	214.04
A_68_P24213705	chr6:5955978-5956022	NM_001191023:280362	Dync1i1	INSIDE	0.360	0.613	1716.96	1051.72	0.220	1371.21	302.34
A_68_P26612672	chr9:69607372-69607416	NM_022378:1353	Foxb1	INSIDE	0.360	0.654	1741.68	1139.07	0.236	1300.54	306.29
A_68_P28080440	chr11:102467429-102467473	NM_020510:1706	Fzd2	INSIDE	0.360	0.368	2575.05	946.93	0.132	1850.97	244.83
A_68_P23592735	chr5:34511958-34512002	NM_146159:93	Haus3	INSIDE	0.360	0.510	2132.18	1087.18	0.184	1650.10	303.13
A_68_P28279803	chr12:21292038-21292083	NM_008403:38	Itgb1bp1	INSIDE	0.360	0.582	1324.20	770.93	0.210	996.58	208.90
A_68_P28513154	chr12:70269870-70269914	NM_001081406:92	Lrr1	INSIDE	0.360	0.440	1601.40	703.86	0.158	1276.28	202.13
A_68_P31827988	chr18:73975355-73975399	NM_145494:-330	Me2	PROMOTER	0.360	0.639	2932.55	1873.53	0.230	2291.93	527.23
A_68_P20849640	chr1:177622720-177622764	NM_010098:-21	Opn3	DIVERGENT_PROMOTER	0.360	0.638	877.37	559.53	0.230	784.04	180.03
A_68_P25366411	chr7:107376423-107376469	NM_027629:330	Pgm2l1	INSIDE	0.360	0.548	1061.66	581.90	0.197	888.06	175.38
A_68_P20956473	chr1:196446359-196446403	NM_008882:358	Plxna2	INSIDE	0.360	0.514	1066.96	548.68	0.185	944.67	175.10
A_68_P24034079	chr5:120131042-120131086	NM_011535:10387	Tbx3	INSIDE	0.360	0.706	2245.57	1586.31	0.255	1559.85	397.14
A_68_P23991446	chr5:112755370-112755414	NM_018783:4	Tfip11	INSIDE	0.360	0.584	1880.97	1097.98	0.210	1351.56	284.16

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P20354345	chr1:75476353-75476397	NM_177056:268	Tmem198	INSIDE	0.360	0.629	2696.14	1696.53	0.227	1869.52	423.62
A_68_P22015879	chr3:28162505-28162549	NM_001163009:391	Tnik	INSIDE	0.360	0.558	1455.69	812.90	0.201	1111.03	223.27
A_68_P25956520	chr8:73891092-73891136	NM_025917:-1	Use1	PROMOTER	0.360	0.672	1224.42	823.05	0.242	876.07	212.00
A_68_P31952190	chr19:10763362-10763406	NM_181403:80	Vps37c	INSIDE	0.360	0.419	2333.19	977.40	0.151	1928.16	290.51
A_68_P26011369	chr8:85298048-85298092	NM_145600:-45	Zfp330	PROMOTER	0.360	0.351	1589.13	558.40	0.127	1315.68	166.53
A_68_P29258005	chr13:99274267-99274314	AK135687:84155		INSIDE	0.360	0.528	1368.52	723.07	0.190	1005.85	191.27
A_68_P24872790	chr6:136419536-136419580	AK139818:7006		DOWNSTREAM	0.360	0.576	3420.64	1969.12	0.207	2700.33	559.33
A_68_P28068584	chr11:100389186-100389230	NM_001199296:106	Acly	INSIDE	0.359	0.592	1045.30	618.30	0.212	773.14	164.29
A_68_P23237358	chr4:117599846-117599890	NM_009711:2500	Artn	INSIDE	0.359	0.564	1056.45	596.23	0.202	882.24	178.51
A_68_P31791364	chr18:67503647-67503691	NR_033214:89	B430212C06Rik	INSIDE	0.359	0.645	4521.54	2917.14	0.231	3609.29	834.84
A_68_P28302020	chr12:27154103-27154147	NM_020557:45	Cmpk2	INSIDE	0.359	0.521	1941.54	1011.62	0.187	1587.41	297.21
A_68_P27297057	chr10:82823167-82823211	NM_026579:223	D10Wsu102e	INSIDE	0.359	0.481	2993.75	1439.96	0.172	2206.63	380.57
A_68_P23362370	chr4:140695629-140695673	NM_001025608:61	D4Ertd22e	INSIDE	0.359	0.621	2261.43	1403.38	0.223	1703.32	379.66
A_68_P21774638	chr2:156832712-156832756	NM_025853:77	Dsn1	INSIDE	0.359	0.581	1832.53	1065.41	0.209	1547.20	322.82
A_68_P28252857	chr12:14158564-14158621	NM_029007:252	Fam84a	INSIDE	0.359	0.700	1266.96	887.11	0.252	789.74	198.64
A_68_P26085828	chr8:98412281-98412325	NM_010325:-37	Got2	PROMOTER	0.359	0.707	2729.09	1929.90	0.254	2056.67	521.77
A_68_P21809532	chr2:162769099-162769143	NM_001081338:-80	L3mbtl1	PROMOTER	0.359	0.395	2115.44	834.65	0.142	1587.72	225.04
A_68_P29330805	chr13:112598506-112598550	NM_011945:663	Map3k1	INSIDE	0.359	0.432	2163.06	934.12	0.155	1715.14	265.84
A_68_P24258182	chr6:15671365-15671410	NM_175088:727	Mdfic	INSIDE	0.359	0.494	1383.43	683.28	0.177	1037.11	183.71
A_68_P28504593	chr12:68322368-68322415	NM_001193266:1145	Mdga2	INSIDE	0.359	1.495	2753.81	4116.16	0.536	1988.65	1066.51
A_68_P22314345	chr3:88340114-88340159	NM_001029890:3820	Mex3a	INSIDE	0.359	0.669	1173.92	785.40	0.240	815.67	195.79
A_68_P32118992	chr19:42165554-42165602	NM_145501:654	Pi4k2a	INSIDE	0.359	0.670	1833.56	1228.50	0.241	1273.81	306.48
A_68_P23062644	chr4:83131741-83131785	NM_133948:532	Psip1	INSIDE	0.359	0.513	1767.20	906.00	0.184	1327.78	244.70
A_68_P24777649	chr6:116623707-116623752	NM_178045:125	Rassf4	INSIDE	0.359	0.617	1306.76	805.96	0.221	923.35	204.47
A_68_P24089368	chr5:130007907-130007951	NM_172276:823	Sfswap	INSIDE	0.359	0.505	1512.54	763.12	0.181	1144.55	207.54
A_68_P25950471	chr8:72736718-72736765	NM_001007570:-561	Slc25a42	PROMOTER	0.359	0.590	1101.61	650.02	0.212	813.20	172.39
A_68_P22049393	chr3:34549575-34549619	NM_011443:670	Sox2	INSIDE	0.359	0.676	1895.61	1282.33	0.243	1431.82	348.20
A_68_P23991126	chr5:112706061-112706105	NM_009419:356	Tpst2	INSIDE	0.359	0.547	2099.86	1148.95	0.197	1642.33	322.96
A_68_P21311590	chr2:69735990-69736034	NM_001081548:710	Ubr3	INSIDE	0.359	1.511	6847.83	10349.14	0.543	5104.77	2769.63
A_68_P26238820	chr8:125778693-125778737	NM_020497:620	Zfp276	INSIDE	0.359	0.630	1063.44	669.45	0.226	921.19	207.92
A_68_P25505917	chr7:134656518-134656562	NR_024331:-157	1700008J07Rik	PROMOTER	0.358	0.593	1447.69	857.94	0.212	1201.80	254.90
A_68_P26749713	chr9:96789331-96789375	NM_153420:489	Acpl2	INSIDE	0.358	0.567	1211.53	687.33	0.203	931.50	189.06
A_68_P20149940	chr1:36766481-36766525	NM_146107:268	Actr1b	INSIDE	0.358	0.442	2835.28	1253.82	0.158	2026.68	321.20
A_68_P26055745	chr8:93433140-93433184	NM_177224:80429	Chd9	INSIDE	0.358	0.393	2705.33	1062.18	0.140	2181.41	306.28
A_68_P31286845	chr17:63230423-63230467	NM_010109:222	Efna5	INSIDE	0.358	0.701	2262.00	1584.83	0.251	1591.00	399.54
A_68_P25672217	chr8:14090101-14090145	NM_001034862:205	Erich1	INSIDE	0.358	0.615	2309.18	1420.87	0.220	1697.74	374.12
A_68_P26248321	chr8:127420511-127420555	NM_198103:1073	Exoc8	INSIDE	0.358	1.456	1115.06	1623.27	0.521	904.14	471.20
A_68_P31982708	chr19:16947889-16947933	NM_008023:410	Foxb2	INSIDE	0.358	0.689	1490.93	1026.98	0.247	1092.31	269.29
A_68_P31347823	chr17:74058995-74059039	NM_027864:775	Galnt14	INSIDE	0.358	0.577	2749.71	1586.43	0.207	2015.92	416.95
A_68_P23681255	chr5:50449451-50449501	NM_133911:759	Gpr125	INSIDE	0.358	0.666	1890.34	1259.88	0.238	1368.67	326.31
A_68_P24634427	chr6:90686065-90686109	NM_001134384:74031	Iqsec1	INSIDE	0.358	0.691	2105.16	1454.81	0.247	1692.06	418.36
A_68_P21233128	chr2:55289837-55289883	NM_008426:294	Kcnj3	INSIDE	0.358	0.376	1784.59	671.01	0.135	1342.96	180.69
A_68_P31074423	chr17:17761336-17761380	NM_172827:95	Lnpep	INSIDE	0.358	0.465	2106.22	978.49	0.166	1721.33	286.52
A_68_P23270752	chr4:124539019-124539063	NM_001007573:375	Maneal	INSIDE	0.358	0.505	1459.73	736.51	0.181	1129.54	203.96
A_68_P25023455	chr7:29551632-29551677	NM_010908:-111	Nfkbib	DIVERGENT_PROMOTER	0.358	0.514	1476.67	759.70	0.184	1146.83	211.30
A_68_P32319273	chrX:34138558-34138602	NM_016783:361	Pgrmc1	INSIDE	0.358	1.404	1678.06	2355.96	0.502	670.44	336.80
A_68_P27673275	chr11:29072187-29072231	NM_134034:-698	Smek2	PROMOTER	0.358	0.319	1615.34	515.58	0.114	1184.98	135.40
A_68_P21576016	chr2:120393619-120393664	NM_001177792:235	Snap23	INSIDE	0.358	0.463	1332.55	617.44	0.166	1159.23	192.38
A_68_P22871718	chr4:43455695-43455739	NM_011571:568	Tesk1	INSIDE	0.358	0.440	1213.47	533.81	0.157	959.00	150.94
A_68_P20076128	chr1:21069108-21069152	NM_133252:160	Tram2	INSIDE	0.358	0.673	900.90	606.18	0.241	699.67	168.66
A_68_P20046442	chr1:14497242-14497286			Unknown	0.358	0.709	1487.96	1054.72	0.253	1211.29	306.96

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P22900664	chr4:48553063-48553107	NM_028137:-286	5730528L13Rik	PROMOTER	0.357	0.645	1051.86	678.04	0.230	752.36	172.96
A_68_P25522114	chr7:137663333-137663377	NM_013799:-301	Ate1	PROMOTER	0.357	0.465	1593.89	741.10	0.166	1271.71	211.32
A_68_P28727506	chr12:109591095-109591139	NM_010010:18526	Cyp46a1	INSIDE	0.357	0.489	1756.76	859.13	0.175	1359.43	237.62
A_68_P30479790	chr15:99200609-99200653	NM_011711:267	Fmnl3	INSIDE	0.357	0.491	4277.39	2100.99	0.175	3175.08	557.23
A_68_P23607763	chr5:36807446-36807491	NM_024478:-365	Grpel1	PROMOTER	0.357	0.541	3092.77	1672.04	0.193	2365.57	457.16
A_68_P27315607	chr10:86167637-86167681	NM_011631:531	Hsp90b1	INSIDE	0.357	0.549	932.23	511.68	0.196	762.34	149.49
A_68_P30480286	chr15:99288275-99288319	NM_001001884:-117	Nckap5l	PROMOTER	0.357	0.659	2150.11	1417.18	0.235	1582.58	371.87
A_68_P21909038	chr2:180922669-180922713	NM_025598:643	Ppdpf	INSIDE	0.357	0.441	1594.20	703.42	0.158	1328.23	209.25
A_68_P21769937	chr2:156005990-156006034	NM_133242:-36	Rbm39	PROMOTER	0.357	0.439	1650.17	724.25	0.157	1330.90	208.68
A_68_P23234771	chr4:117169165-117169209	NM_025739:334	Rnf220	INSIDE	0.357	0.406	1995.83	810.02	0.145	1517.42	219.67
A_68_P26256736	chr8:128822425-128822469	NM_175434:-32	Slc35f3	PROMOTER	0.357	0.573	3684.64	2113.05	0.205	2919.91	597.22
A_68_P20799887	chr1:168309926-168309970	NM_030245:651	Tada1	INSIDE	0.357	0.628	1726.09	1083.70	0.224	1385.60	310.29
A_68_P21072876	chr2:25402210-25402254	NM_009422:182	Traf2	INSIDE	0.357	0.682	2963.88	2022.28	0.244	2354.67	574.25
A_68_P27929274	chr11:75779968-75780012			Unknown	0.357	0.735	2387.28	1754.62	0.262	1812.44	475.66
A_68_P31621018	chr18:36099359-36099403			Unknown	0.357	0.514	1567.26	805.09	0.183	1399.81	256.53
A_68_P30214228	chr15:51872101-51872145	NM_175503:470	Aard	INSIDE	0.356	0.516	1477.57	762.35	0.183	1221.35	224.04
A_68_P22058285	chr3:36374705-36374749	NM_009673:83	Anxa5	INSIDE	0.356	0.531	2081.16	1105.66	0.189	1468.31	277.93
A_68_P31102143	chr17:25321627-25321671	NM_183150:143	BC003965	INSIDE	0.356	0.693	1465.43	1015.66	0.247	1277.64	315.45
A_68_P30976751	chr16:93608089-93608133	NM_007620:29	Cbr1	INSIDE	0.356	0.552	1337.60	738.25	0.196	1234.39	242.53
A_68_P30511525	chr16:4679878-4679922	NM_030205:-180	Coro7	DIVERGENT_PROMOTER	0.356	0.547	1226.56	670.80	0.194	1036.47	201.52
A_68_P20149810	chr1:36748331-36748375	NM_009942:21	Cox5b	INSIDE	0.356	0.628	2340.02	1468.56	0.223	1593.40	356.01
A_68_P29659269	chr14:63741273-63741317	NM_007798:-7	Ctsb	PROMOTER	0.356	0.737	4175.57	3077.50	0.262	3408.61	893.77
A_68_P20578315	chr1:125942392-125942436	NM_199021:-278	Dpp10	PROMOTER	0.356	0.463	2751.40	1273.57	0.165	2109.16	347.79
A_68_P24921910	chr6:145197794-145197838	NM_021284:935	Kras	INSIDE	0.356	0.734	1962.50	1439.52	0.261	1309.32	341.84
A_68_P21794498	chr2:160193025-160193069	NM_010658:-245	Mafb	PROMOTER	0.356	0.738	4337.06	3202.29	0.263	3253.79	855.16
A_68_P25756477	chr8:32279067-32279111	NM_026453:108	Mak16	INSIDE	0.356	0.664	1383.78	919.33	0.237	1017.34	240.89
A_68_P27282971	chr10:79862699-79862743	NM_013595:-496	Mbd3	PROMOTER	0.356	0.579	916.64	530.98	0.206	663.01	136.66
A_68_P25423375	chr7:119369796-119369840	NM_001193305:469	Mical2	INSIDE	0.356	0.633	1366.45	865.08	0.225	1036.64	233.62
A_68_P30346980	chr15:76063274-76063318	NM_001163542:-1488	Plec	PROMOTER	0.356	0.316	3643.12	1151.50	0.112	2691.64	302.46
A_68_P23374046	chr4:142802052-142802101	NM_001081355:536	Prdm2	INSIDE	0.356	0.623	1062.06	661.45	0.222	812.48	180.01
A_68_P25030460	chr7:31017038-31017082	NM_025548:-12	Tbcb	DIVERGENT_PROMOTER	0.356	0.683	1744.35	1192.22	0.243	1387.00	337.08
A_68_P24127041	chr5:138125324-138125368	NM_178162:499	Agfg2	INSIDE	0.355	1.514	3297.19	4992.30	0.538	2537.47	1365.55
A_68_P30337616	chr15:74349537-74349581	NM_174991:2933	Bai1	INSIDE	0.355	0.591	1613.67	954.27	0.210	1301.66	273.33
A_68_P28072387	chr11:101035328-101035372	NM_007721:1407	Ccr10	INSIDE	0.355	0.389	2889.98	1123.43	0.138	2081.47	287.14
A_68_P25150558	chr7:64642169-64642213	NM_008074:51	Gabrg3	INSIDE	0.355	0.651	1083.07	704.54	0.231	988.34	228.09
A_68_P22788124	chr4:24825414-24825458	NM_026742:207	Ndufaf4	INSIDE	0.355	0.524	2453.41	1284.42	0.186	1765.45	328.39
A_68_P23198683	chr4:108673036-108673080	NM_146150:-351	Nrd1	PROMOTER	0.355	0.582	4518.05	2629.68	0.206	3154.75	650.95
A_68_P24479722	chr6:57642005-57642049	NM_025574:46	Pigy	INSIDE	0.355	0.466	1127.04	524.97	0.166	982.62	162.68
A_68_P25953979	chr8:73300434-73300478	NM_008841:155	Pik3r2	INSIDE	0.355	0.389	1578.56	614.04	0.138	1324.32	183.13
A_68_P26702535	chr9:86910781-86910825	NM_001037907:431	Ripply2	INSIDE	0.355	0.696	2712.26	1887.62	0.247	2398.42	591.77
A_68_P26766654	chr9:99775916-99775960	NM_011440:651	Sox14	INSIDE	0.355	0.531	1665.50	883.77	0.188	1293.35	243.31
A_68_P24993486	chr7:20055334-20055378	ENSMUST00000083454:-9072		PROMOTER	0.355	1.591	764.29	1215.86	0.564	667.29	376.32
A_68_P31465565	chr18:4920765-4920809	ENSMUST00000143254:-937		PROMOTER	0.355	0.446	2253.15	1003.98	0.158	1751.51	276.98
A_68_P24358388	chr6:34828039-34828083	NM_001135611:5	3110062M04Rik	INSIDE	0.354	0.388	2876.05	1117.23	0.138	2102.69	289.36
A_68_P22186536	chr3:62143169-62143213	NM_001081295:492	Arhgef26	INSIDE	0.354	0.261	2043.42	533.31	0.092	1705.32	157.56
A_68_P24050685	chr5:122952811-122952855	NM_009722:-598	Atp2a2	PROMOTER	0.354	0.571	2296.54	1311.45	0.202	1599.57	323.01
A_68_P25898923	chr8:61391591-61391635	NM_173411:1061	BC030500	INSIDE	0.354	0.612	1692.65	1035.71	0.217	1269.62	275.38
A_68_P29682515	chr14:67627653-67627697	NM_009761:40	Bnip3l	INSIDE	0.354	0.494	2395.59	1183.56	0.175	1697.55	297.00
A_68_P23590777	chr5:34064147-34064191	NM_001163215:-204	Fgfr3	PROMOTER	0.354	0.542	989.97	536.39	0.192	732.60	140.47
A_68_P25971956	chr8:77617525-77617569	NM_010442:30	Hmox1	INSIDE	0.354	0.623	977.54	608.67	0.220	790.71	174.17
A_68_P28043948	chr11:96205685-96205729	NM_010458:624	Hoxb3	INSIDE	0.354	0.495	1421.11	703.43	0.175	1108.68	194.20

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P20351506	chr1:74997489-74997533	NM_010544:715	Ihh	INSIDE	0.354	0.591	2779.98	1643.39	0.210	2146.31	449.65
A_68_P20285211	chr1:63160025-63160069	NM_001081436:795	Ino80d	INSIDE	0.354	0.658	1881.88	1237.76	0.233	1522.45	354.36
A_68_P31784506	chr18:66162058-66162102	NM_027400:209	Lman1	INSIDE	0.354	0.575	1069.30	614.96	0.204	917.62	186.92
A_68_P23192850	chr4:107475564-107475608	NM_001080926:723	Lrp8	INSIDE	0.354	0.541	1025.28	554.32	0.192	940.55	180.21
A_68_P26214833	chr8:122099237-122099281	NM_026648:124	Lrrc50	INSIDE	0.354	0.650	2180.92	1416.83	0.230	1885.31	433.04
A_68_P25537271	chr7:140044033-140044077	NM_028095:276	Mettl10	INSIDE	0.354	0.616	1386.53	854.61	0.218	1115.54	243.58
A_68_P27281287	chr10:79611758-79611802	NM_021565:746	Midn	INSIDE	0.354	0.514	2491.43	1281.64	0.182	1725.91	314.69
A_68_P24771973	chr6:115552217-115552261	NM_023290:283	Mkrn2	INSIDE	0.354	0.694	4289.30	2977.69	0.246	3154.72	776.37
A_68_P29446632	chr14:21212949-21212993	NM_025440:-193	Mrps16	PROMOTER	0.354	0.325	2585.87	839.18	0.115	2020.51	232.14
A_68_P29453025	chr14:22319120-22319164	NM_017479:136	Myst4	INSIDE	0.354	0.658	2124.63	1398.55	0.233	1702.60	396.53
A_68_P20559034	chr1:121734234-121734278	NM_019933:-608	Ptpn4	PROMOTER	0.354	0.690	1451.93	1001.36	0.244	1060.00	258.69
A_68_P31488616	chr18:10181915-10181959	NM_009071:-146	Rock1	PROMOTER	0.354	0.396	1867.11	738.84	0.140	1558.91	218.12
A_68_P24328152	chr6:29686394-29686438	NM_176996:920	Smo	INSIDE	0.354	0.516	2644.16	1363.26	0.182	1900.79	346.72
A_68_P23061865	chr4:82969752-82969796	NM_027238:319	Ttc39b	INSIDE	0.354	0.615	1060.46	651.68	0.217	895.67	194.79
A_68_P26041029	chr8:90977921-90977965			Unknown	0.354	0.646	1336.41	863.11	0.229	1041.25	238.25
A_68_P30483171	chr15:99804219-99804265	NR_028124:-524	2310068J16Rik	PROMOTER	0.353	0.557	1147.31	638.54	0.196	923.45	181.41
A_68_P31257262	chr17:56749026-56749070	NM_153152:146	2410015M20Rik	INSIDE	0.353	0.592	4505.74	2666.45	0.209	3180.53	664.58
A_68_P25954402	chr8:73362864-73362908	NM_027560:733	Arrdc2	INSIDE	0.353	0.510	1134.57	578.25	0.180	861.51	155.06
A_68_P24104846	chr5:133018497-133018541	NM_177047:-305	Auts2	PROMOTER	0.353	0.448	2293.45	1028.53	0.158	1553.00	245.62
A_68_P28175793	chr11:118951344-118951390	NM_007625:-3815	Cbx4	PROMOTER	0.353	1.551	4847.13	7516.25	0.547	3290.46	1798.99
A_68_P28752827	chr12:114066991-114067046	NM_028023:582	Cdca4	INSIDE	0.353	0.487	1401.24	682.63	0.172	1284.88	221.07
A_68_P21569219	chr2:119176997-119177041	NM_026929:41	Chac1	INSIDE	0.353	0.604	2071.02	1251.04	0.213	1652.42	352.12
A_68_P32145764	chr19:46837127-46837172	NM_001102471:1051	Cnnm2	INSIDE	0.353	0.643	939.54	603.88	0.227	684.27	155.44
A_68_P21818148	chr2:164311684-164311728	NM_026797:-248	Dbndd2	PROMOTER	0.353	0.450	1293.28	582.22	0.159	1044.82	166.10
A_68_P29702477	chr14:71018142-71018186	NM_013514:11797	Epb4.9	INSIDE	0.353	0.619	1580.18	978.14	0.219	1214.78	265.80
A_68_P23318324	chr4:133140609-133140653	NM_133884:343	Gpn2	INSIDE	0.353	0.556	1487.26	826.96	0.196	1219.44	239.12
A_68_P31400025	chr17:84030569-84030613	NM_153512:645	Kcng3	INSIDE	0.353	1.389	2456.92	3413.51	0.491	1758.85	863.10
A_68_P28292712	chr12:25659767-25659811	NM_001081378:-8	Kidins220	PROMOTER	0.353	0.596	1392.40	829.48	0.211	1030.84	217.06
A_68_P20806518	chr1:169618425-169618469	NM_033652:-1242	Lmx1a	PROMOTER	0.353	0.668	873.48	583.44	0.236	656.47	154.73
A_68_P27767867	chr11:46250322-46250367	NM_001104530:-104	Med7	PROMOTER	0.353	0.399	1342.28	535.92	0.141	1034.22	145.75
A_68_P21240006	chr2:56967343-56967388	NM_013613:84	Nr4a2	INSIDE	0.353	0.638	2028.46	1294.99	0.226	1598.35	360.64
A_68_P20826590	chr1:173126271-173126315	NM_025557:107	Pcp4l1	INSIDE	0.353	0.406	1496.51	607.24	0.143	1375.90	196.87
A_68_P31161701	chr17:36053710-36053754	NM_175934:-123	Ppp1r10	DIVERGENT_PROMOTER	0.353	0.690	1629.09	1124.65	0.244	1295.11	315.80
A_68_P27568682	chr11:6374896-6374940	NM_011221:1002	Purb	INSIDE	0.353	0.344	4121.48	1416.41	0.121	2880.64	349.66
A_68_P21986761	chr3:21975073-21975117	NM_030732:-479	Tbl1xr1	PROMOTER	0.353	0.519	2249.55	1167.90	0.183	1855.31	339.58
A_68_P21721821	chr2:146839369-146839413	NM_011917:595	Xrn2	INSIDE	0.353	0.440	1608.97	707.14	0.155	1283.99	199.43
A_68_P29478594	chr14:26426870-26426915	NM_183208:148222	Zmiz1	INSIDE	0.353	0.525	2428.51	1275.42	0.185	1639.02	303.99
A_68_P27498116	chr10:119990083-119990128			Unknown	0.353	0.617	866.96	534.53	0.217	633.36	137.70
A_68_P27223534	chr10:68861479-68861523	AK029407:-20		PROMOTER	0.353	0.642	1950.92	1253.00	0.227	1496.17	339.24
A_68_P28608855	chr12:87582934-87582978	NM_027405:129	1700020O03Rik	INSIDE	0.352	0.698	4032.55	2815.89	0.246	3252.59	799.85
A_68_P27851243	chr11:61743609-61743653	NM_019921:98	Akap10	INSIDE	0.352	0.516	2421.17	1248.76	0.182	1779.02	323.01
A_68_P30811313	chr16:62846874-62846918	NM_026577:-30	Arl13b	DIVERGENT_PROMOTER	0.352	0.563	1751.08	985.69	0.198	1531.81	303.94
A_68_P25354432	chr7:105343075-105343119	NM_001081167:4889	B3gnt6	INSIDE	0.352	0.593	1579.08	937.11	0.209	1334.57	278.92
A_68_P28688781	chr12:103213776-103213820	NM_016856:-385	Cpsf2	PROMOTER	0.352	0.697	2411.15	1679.69	0.245	1947.31	477.31
A_68_P28924020	chr13:31712001-31712045	NM_010225:-5662	Foxf2	PROMOTER	0.352	0.535	1077.89	576.66	0.188	951.86	179.28
A_68_P21052789	chr2:20890869-20890913	NR_033225:390	Gm13375	INSIDE	0.352	0.551	1205.68	664.22	0.194	1039.22	201.53
A_68_P27987929	chr11:86070620-86070664	NM_027421:428	Ints2	INSIDE	0.352	0.715	2228.60	1593.16	0.252	1750.76	440.53
A_68_P31150390	chr17:33896983-33897027	NM_008997:427	Rab11b	INSIDE	0.352	0.542	3620.11	1963.30	0.191	2748.19	524.49
A_68_P22312702	chr3:88045112-88045156	NM_021375:13472	Rhbg	DOWNSTREAM	0.352	0.647	817.10	528.52	0.228	713.72	162.42
A_68_P31560664	chr18:24688268-24688312	NM_144861:415	Rprd1a	INSIDE	0.352	0.523	1270.97	664.86	0.184	1047.90	192.85
A_68_P21078765	chr2:26300767-26300811	NM_153125:-52	Sec16a	PROMOTER	0.352	0.704	3435.76	2419.82	0.248	2631.82	652.80

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P29961839	chr14:122863102-122863146	NM_022987:1756	Zic5	INSIDE	0.352	0.604	916.24	552.97	0.212	774.75	164.57
A_68_P25940712	chr8:70586026-70586070	ENSMUST00000150169:137		INSIDE	0.352	0.610	1837.81	1120.58	0.215	1506.39	323.12
A_68_P29998440	chr15:8118886-8118930	NM_001162906:-197	2410089E03Rik	PROMOTER	0.351	0.576	1234.81	711.34	0.202	1166.72	235.67
A_68_P31111772	chr17:26813424-26813468	NM_025272:106	Atp6v0e	INSIDE	0.351	0.352	2011.81	708.90	0.124	1616.33	200.07
A_68_P24617811	chr6:87680675-87680719	NM_001159697:-166	Ccdc48	PROMOTER	0.351	0.727	4984.09	3625.21	0.256	3364.11	859.84
A_68_P24159039	chr5:144775595-144775639	NM_177682:106	Ccz1	INSIDE	0.351	0.622	2033.64	1265.35	0.219	1557.24	340.40
A_68_P26660362	chr9:78463468-78463512	NM_153098:138	Cd109	INSIDE	0.351	0.433	1680.35	727.12	0.152	1438.78	218.80
A_68_P31838825	chr18:75856820-75856864	NM_201354:508	Ctif	INSIDE	0.351	0.478	1876.78	897.37	0.168	1354.08	227.25
A_68_P28396959	chr12:45310845-45310889	NM_013760:189	Dnajb9	INSIDE	0.351	0.633	1982.31	1255.39	0.222	1490.06	331.30
A_68_P27612234	chr11:16652279-16652323	NM_007912:95	Egfr	INSIDE	0.351	0.580	936.29	543.40	0.204	700.44	142.85
A_68_P25416985	chr7:118225708-118225752	NM_001040131:814	Eif4g2	INSIDE	0.351	0.601	1018.69	611.78	0.211	908.92	191.53
A_68_P26761639	chr9:98886751-98886795	NM_001122851:-19	Faim	PROMOTER	0.351	0.484	3000.49	1451.66	0.170	2317.14	393.58
A_68_P23787826	chr5:72092511-72092555	NM_008069:1278	Gabrb1	INSIDE	0.351	0.641	1713.97	1097.91	0.225	1363.63	307.01
A_68_P29072860	chr13:58460543-58460587	NM_175214:-4341	Kif27	PROMOTER	0.351	0.430	4159.44	1787.57	0.151	3206.66	484.26
A_68_P22133744	chr3:51906476-51906520	NM_001004176:2430	Maml3	INSIDE	0.351	0.675	1006.00	679.14	0.237	777.73	184.13
A_68_P23188358	chr4:106739774-106739823	NM_025500:-327	Mrpl37	DIVERGENT_PROMOTER	0.351	0.625	3049.70	1907.51	0.219	2132.82	468.02
A_68_P21750258	chr2:152452780-152452824	NM_009047:59	Rem1	INSIDE	0.351	0.587	986.89	579.11	0.206	873.31	179.83
A_68_P28520022	chr12:71448035-71448079	NM_001110202:545	Trim9	INSIDE	0.351	0.558	2268.98	1265.65	0.196	1524.69	298.25
A_68_P31936615	chr19:6984479-6984523	NM_001166370:313	Trmt112	INSIDE	0.351	0.384	1480.45	568.66	0.135	1145.18	154.21
A_68_P20599496	chr1:130141494-130141539	NM_026390:759	Ubxn4	INSIDE	0.351	0.521	1427.11	743.99	0.183	1232.59	225.43
A_68_P24595030	chr6:83660707-83660751	NR_002873:198	Vax2os1	INSIDE	0.351	0.734	2299.57	1688.85	0.258	1778.87	458.13
A_68_P25504685	chr7:134377078-134377122	NM_146201:144	Zfp553	INSIDE	0.351	0.595	3038.36	1807.63	0.209	2190.21	457.91
A_68_P31809747	chr18:70631630-70631674	NM_172967:482	4930503L19Rik	INSIDE	0.350	0.589	1543.07	908.65	0.206	1154.66	237.68
A_68_P23542799	chr5:24082860-24082904	NM_001190443:403	Abcf2	INSIDE	0.350	0.633	2273.51	1438.78	0.221	1579.81	349.76
A_68_P28431152	chr12:52792067-52792111	NM_021710:136	Ap4s1	INSIDE	0.350	0.599	1966.91	1177.34	0.209	1515.36	317.08
A_68_P23332631	chr4:135762030-135762074	NM_001008232:-227	Asap3	PROMOTER	0.350	1.625	4946.21	8037.03	0.568	3366.45	1912.69
A_68_P25065442	chr7:38892952-38892996	NM_007633:-465	Ccne1	PROMOTER	0.350	0.497	4907.98	2437.19	0.174	3349.10	581.82
A_68_P22402364	chr3:106350168-106350212	NM_133869:489	Cept1	INSIDE	0.350	0.711	2349.11	1670.19	0.249	1749.54	435.91
A_68_P22318793	chr3:89154296-89154340	NM_029974:14843	Dcst1	INSIDE	0.350	0.467	1404.13	655.56	0.163	1222.06	199.72
A_68_P28103522	chr11:106650003-106650048	NM_007840:-217	Ddx5	DIVERGENT_PROMOTER	0.350	0.460	1898.40	874.02	0.161	1414.98	228.26
A_68_P26912795	chr10:5914411-5914463	NR_002891:-2938	Gm5512	PROMOTER	0.350	0.445	1369.32	609.20	0.156	961.81	149.71
A_68_P24053342	chr5:123439126-123439170	NM_001003953:-47	Kdm2b	PROMOTER	0.350	0.595	2810.70	1672.41	0.208	1999.93	416.43
A_68_P28049249	chr11:97049576-97049622	NM_008379:-392	Kpnb1	PROMOTER	0.350	0.517	3594.87	1860.24	0.181	2788.10	505.66
A_68_P28154418	chr11:115474202-115474246	NM_027162:-407	Mif4gd	PROMOTER	0.350	0.730	2201.37	1607.70	0.256	1623.92	415.03
A_68_P25111230	chr7:56501781-56501825	NM_175272:244	Nav2	INSIDE	0.350	0.442	2139.56	945.58	0.155	1491.83	231.03
A_68_P21018168	chr2:13714756-13714800	NM_145838:369	St8sia6	INSIDE	0.350	0.542	2894.52	1568.46	0.190	2206.39	418.34
A_68_P20352666	chr1:75207636-75207680	NM_011494:255	Stk16	INSIDE	0.350	0.663	1477.59	979.32	0.232	1157.58	268.18
A_68_P27383830	chr10:98378401-98378445	NM_026482:637	Atp2b1	INSIDE	0.349	0.489	1129.78	552.80	0.171	981.17	167.42
A_68_P24009177	chr5:115799028-115799072	NM_007748:-86	Cox6a1	PROMOTER	0.349	0.603	1919.81	1157.42	0.210	1453.08	305.38
A_68_P27865450	chr11:64250200-64250244	NR_028445:-46	F930015N05Rik	PROMOTER	0.349	0.551	1324.97	729.95	0.192	1103.99	212.10
A_68_P23317810	chr4:133035888-133035933	NM_175307:-137	Fam46b	PROMOTER	0.349	0.567	1302.78	738.54	0.198	1004.61	198.83
A_68_P32143272	chr19:46403086-46403130	NM_133694:435	Fbxl15	INSIDE	0.349	0.408	2457.72	1003.19	0.143	1919.29	273.60
A_68_P23404323	chr4:149475519-149475563	NM_177366:13929	Gpr157	INSIDE	0.349	1.558	2216.23	3452.56	0.543	1619.05	879.43
A_68_P28079750	chr11:102328735-102328779	NM_010575:2441	Itga2b	INSIDE	0.349	0.617	1324.91	817.38	0.215	995.03	214.03
A_68_P31863850	chr18:80559762-80559806	NM_001190373:1209	Kcng2	INSIDE	0.349	0.545	2077.46	1131.85	0.190	1568.32	297.86
A_68_P31936766	chr19:7008439-7008483	NM_008431:545	Kcnk4	INSIDE	0.349	0.559	2029.56	1134.32	0.195	1337.02	261.08
A_68_P26345199	chr9:20843307-20843352	NR_035438:-6557	Mir1900	PROMOTER	0.349	0.485	1410.84	684.42	0.169	1051.61	178.19
A_68_P31424458	chr17:88071727-88071771	NM_008628:-148	Msh2	PROMOTER	0.349	0.557	1109.81	618.20	0.194	936.25	181.98
A_68_P29962216	chr14:122933648-122933692	NM_144844:121	Pcca	INSIDE	0.349	0.590	1001.64	591.10	0.206	778.44	160.54
A_68_P25953920	chr8:73293490-73293534	NM_008841:7099	Pik3r2	INSIDE	0.349	0.679	1182.80	803.20	0.237	970.57	230.28
A_68_P27160897	chr10:57252403-57252448	NM_019760:-90	Serinc1	PROMOTER	0.349	0.466	1189.08	554.31	0.163	942.99	153.44

						Sham group			TiO$_2$-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P21478263	chr2:102499439-102499483	NM_001077514:621	Slc1a2	INSIDE	0.349	0.426	1244.38	530.24	0.149	1051.03	156.14
A_68_P29421302	chr14:15535329-15535377	NM_001033270:-186	Slc4a7	PROMOTER	0.349	0.445	1301.27	579.43	0.156	976.97	151.93
A_68_P20662734	chr1:141319149-141319193	NM_172643:211	Zbtb41	INSIDE	0.349	0.476	1372.99	652.86	0.166	1054.20	175.15
A_68_P31722245	chr18:55147700-55147744	NM_175751:2112	Zfp608	INSIDE	0.349	0.653	1413.12	922.57	0.228	1056.52	240.77
A_68_P28956447	chr13:37869883-37869931	ENSMUST00000122842:-362		PROMOTER	0.349	0.701	1554.95	1090.71	0.245	1060.64	260.00
A_68_P20914305	chr1:189432968-189433012	ENSMUST00000152927:-584		PROMOTER	0.349	0.609	991.74	604.21	0.212	800.97	170.14
A_68_P27212539	chr10:67011459-67011503	NM_001005419:223	Ado	INSIDE	0.348	0.474	1953.05	926.63	0.165	1854.02	305.70
A_68_P26595214	chr9:66643808-66643852	NM_177583:-600	Aph1b	PROMOTER	0.348	0.523	1276.14	666.86	0.182	948.74	172.32
A_68_P30365368	chr15:79091566-79091610	NM_177580:24351	Baiap2l2	INSIDE	0.348	0.686	2382.77	1635.65	0.239	2087.92	498.34
A_68_P27418182	chr10:105278621-105278665	NM_025602:108	Ccdc59	INSIDE	0.348	0.601	1307.64	785.41	0.209	1008.25	210.65
A_68_P23254629	chr4:120712162-120712206	NM_007741:14	Col9a2	INSIDE	0.348	0.656	1641.29	1076.36	0.228	1340.93	305.89
A_68_P23236051	chr4:117354667-117354711	NM_023178:142	Dmap1	INSIDE	0.348	0.512	2108.78	1079.77	0.178	1662.61	296.03
A_68_P31775663	chr18:64648900-64648944	NM_007998:-202	Fech	PROMOTER	0.348	0.574	2138.47	1228.40	0.200	1545.21	308.52
A_68_P23892220	chr5:92512615-92512659	NM_001080794:-53	G3bp2	PROMOTER	0.348	0.718	2229.52	1600.68	0.250	1610.20	402.39
A_68_P26345149	chr9:20836417-20836466	NM_008319:-40	Icam5	PROMOTER	0.348	0.531	1368.90	726.47	0.184	1163.21	214.58
A_68_P29233347	chr13:94944386-94944430	NM_172589:116658	Lhfpl2	INSIDE	0.348	0.730	2550.73	1860.93	0.254	1880.91	477.32
A_68_P24044318	chr5:121847841-121847885	NM_172722:-128	Naa25	PROMOTER	0.348	0.665	1669.70	1109.92	0.232	1353.75	313.59
A_68_P20140986	chr1:34906861-34906905	NM_145516:79	Plekhb2	INSIDE	0.348	0.565	3188.57	1800.24	0.196	2510.90	493.37
A_68_P26365988	chr9:25059616-25059661	NM_001205367:-401	Septin7	PROMOTER	0.348	0.689	1101.77	759.06	0.240	955.50	229.17
A_68_P25950463	chr8:72735887-72735931	NM_001007570:272	Slc25a42	INSIDE	0.348	0.612	1770.31	1082.71	0.213	1267.46	269.44
A_68_P26750480	chr9:96918879-96918923	NM_145134:-126	Spsb4	PROMOTER	0.348	0.445	1561.18	694.96	0.155	1344.12	208.26
A_68_P21587980	chr2:122590894-122590938	NM_001162503:-178	Sqrdl	PROMOTER	0.348	0.511	2170.79	1109.61	0.178	1708.45	303.97
A_68_P25158144	chr7:66483973-66484017	NM_173010:-125	Ube3a	PROMOTER	0.348	0.462	1876.60	866.42	0.161	1602.23	257.60
A_68_P26032506	chr8:89561850-89561894	ENSMUST00000085049:-9746		PROMOTER	0.348	0.594	1514.44	899.95	0.207	1154.36	238.56
A_68_P21812326	chr2:163244652-163244697	NM_025699:532	3230401D17Rik	INSIDE	0.347	0.550	1403.57	771.87	0.191	1069.58	204.11
A_68_P25286566	chr7:91235318-91235362	NM_030728:-325	9930013L23Rik	PROMOTER	0.347	0.623	1614.11	1006.39	0.216	1140.03	246.58
A_68_P24104848	chr5:133018792-133018836	NM_177047:-601	Auts2	PROMOTER	0.347	0.585	1578.68	923.29	0.203	1180.31	239.25
A_68_P24055190	chr5:123795453-123795497	NM_029850:1018	Bcl7a	INSIDE	0.347	0.730	2433.72	1775.81	0.253	1715.66	434.55
A_68_P21673353	chr2:138082625-138082669	NM_001025431:327	Btbd3	INSIDE	0.347	0.439	2287.72	1004.93	0.152	1958.63	298.59
A_68_P23410164	chr4:150482143-150482187	NM_001081557:753713	Camta1	INSIDE	0.347	0.648	3995.98	2590.53	0.225	2728.26	614.28
A_68_P22476389	chr3:121130415-121130465	NM_028044:982	Cnn3	INSIDE	0.347	0.478	2206.32	1053.53	0.166	1572.16	260.25
A_68_P30576344	chr16:17891528-17891572	NM_001109750:271	Dgcr2	INSIDE	0.347	0.526	2446.86	1286.03	0.182	1913.85	349.27
A_68_P21767850	chr2:155652193-155652237	NM_010579:447	Eif6	INSIDE	0.347	0.554	4497.99	2492.59	0.192	3414.99	656.39
A_68_P28072082	chr11:100981134-100981178	NM_026501:-18	Fam134c	PROMOTER	0.347	0.560	1409.76	789.69	0.194	1110.88	215.98
A_68_P31121749	chr17:28450313-28450357	NM_001163819:-140	Fance	PROMOTER	0.347	0.718	1420.58	1019.99	0.249	985.33	245.38
A_68_P32815027	chrX:164560836-164560880	NM_001033330:454307	Frmpd4	INSIDE	0.347	1.463	933.95	1366.66	0.508	557.14	283.14
A_68_P22522345	chr3:129533741-129533785	NM_026578:552	Gar1	INSIDE	0.347	0.613	2300.94	1410.15	0.212	1679.40	356.72
A_68_P31936768	chr19:7008741-7008785	NM_008431:243	Kcnk4	INSIDE	0.347	0.494	1948.28	962.37	0.172	1503.30	257.84
A_68_P30682961	chr16:37869139-37869183	NM_177093:675	Lrrc58	INSIDE	0.347	0.540	2018.30	1088.96	0.187	1581.02	295.65
A_68_P30498333	chr15:102347359-102347404	NM_001163643:54	Map3k12	INSIDE	0.347	0.557	1772.33	987.48	0.193	1335.19	258.25
A_68_P30499092	chr15:102502227-102502271	NR_030460:49	Mir688	INSIDE	0.347	0.636	921.97	586.04	0.220	662.62	145.96
A_68_P29615709	chr14:55633702-55633746	NM_026890:-566	Ngdn	PROMOTER	0.347	0.683	1576.78	1076.28	0.237	1163.61	275.85
A_68_P29428096	chr14:17075774-17075818	NM_021504:-6031	Ngly1	PROMOTER	0.347	0.351	1599.30	561.67	0.122	1270.14	154.81
A_68_P24152138	chr5:143005802-143005846	NM_019943:206	Papolb	INSIDE	0.347	1.795	1155.09	2073.25	0.622	916.43	569.98
A_68_P24591296	chr6:83028488-83028532	NM_197992:127	Pcgf1	INSIDE	0.347	0.334	2005.96	669.57	0.116	1555.03	180.15
A_68_P27901224	chr11:70353932-70353976	NM_008876:289	Pld2	INSIDE	0.347	0.608	2218.30	1348.45	0.211	1849.13	390.19
A_68_P21640034	chr2:132210975-132211019	NM_144944:187	Prokr2	INSIDE	0.347	0.605	1847.94	1118.73	0.210	1484.92	311.82
A_68_P23997297	chr5:113716248-113716292	NR_027934:-6649	Sgsm1	PROMOTER	0.347	0.691	2844.68	1966.65	0.240	2188.28	525.11
A_68_P30405820	chr15:86044641-86044685	NM_145476:-226	Tbc1d22a	PROMOTER	0.347	0.565	2300.99	1300.40	0.196	1734.31	339.90
A_68_P31620976	chr18:36093025-36093069			Unknown	0.347	0.557	5390.67	3000.63	0.193	4045.35	782.14
A_68_P25618381	chr8:4677445-4677489	ENSMUST00000058918:899		DOWNSTREAM	0.347	0.367	2027.50	744.77	0.127	1474.36	187.89

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P30711914	chr16:42875836-42875881	ENSMUST00000147181:-5		PROMOTER	0.347	0.456	1893.17	863.12	0.158	1430.09	226.24
A_68_P22862527	chr4:41454006-41454050	NM_028624:769	1110017D15Rik	INSIDE	0.346	0.574	1866.88	1070.67	0.199	1492.32	296.37
A_68_P25457394	chr7:125387430-125387474	NR_027879:32	4930583K01Rik	INSIDE	0.346	0.664	1675.75	1113.01	0.230	1298.59	298.55
A_68_P30380158	chr15:81702740-81702784	NM_080633:-130	Aco2	DIVERGENT_PROMOTER	0.346	0.562	1716.09	963.94	0.195	1293.49	251.63
A_68_P20837649	chr1:175297409-175297453	NM_053199:396	Cadm3	INSIDE	0.346	0.488	2611.70	1273.63	0.169	1819.80	306.71
A_68_P21601161	chr2:125073250-125073294	NM_023595:22	Dut	INSIDE	0.346	0.695	2144.94	1490.24	0.240	1617.56	388.64
A_68_P27289145	chr10:80826688-80826732	NM_028657:6396	F630110N24Rik	INSIDE	0.346	0.566	913.40	517.16	0.196	674.88	132.15
A_68_P31948451	chr19:10176193-10176237	NM_019699:-221	Fads2	PROMOTER	0.346	0.488	1341.38	654.93	0.169	1059.29	178.79
A_68_P23590168	chr5:33972239-33972283	NM_178390:24	Fam53a	INSIDE	0.346	0.261	2591.49	675.40	0.090	1961.12	176.96
A_68_P30347361	chr15:76124944-76124988	NM_001195537:103	Gm10345	INSIDE	0.346	0.670	2218.48	1486.76	0.232	1701.76	394.89
A_68_P31953771	chr19:11015569-11015613	NM_009962:3941	Gpr44	INSIDE	0.346	0.585	1188.64	695.44	0.203	938.38	190.04
A_68_P28033987	chr11:94490892-94490936	NM_133807:-223	Lrrc59	PROMOTER	0.346	0.467	1648.54	769.91	0.162	1465.96	236.99
A_68_P24994044	chr7:20147793-20147837	NM_199149:-67	Lrrc68	PROMOTER	0.346	0.375	1459.04	547.60	0.130	1273.98	165.40
A_68_P24362050	chr6:35489064-35489123	NM_008098:795	Mtpn	INSIDE	0.346	0.658	817.74	538.03	0.228	744.07	169.54
A_68_P29110674	chr13:68720849-68720893	NM_172480:128	Mtrr	INSIDE	0.346	0.543	6993.05	3796.75	0.188	5272.54	989.59
A_68_P29336879	chr13:113591191-113591235	NM_008903:82	Ppap2a	INSIDE	0.346	0.400	2048.00	818.63	0.138	1487.73	205.49
A_68_P31108134	chr17:26206603-26206648	NM_001162868:-503	Rab11fip3	PROMOTER	0.346	0.643	1198.34	770.82	0.223	907.53	202.24
A_68_P20269871	chr1:60624074-60624118	NM_001045513:-487	Raph1	PROMOTER	0.346	0.454	1323.52	601.18	0.157	1077.61	169.44
A_68_P30348858	chr15:76348557-76348601	NM_130893:3981	Scrt1	INSIDE	0.346	0.480	1591.67	763.81	0.166	1138.79	189.10
A_68_P30465070	chr15:96529072-96529122	NM_175121:1033	Slc38a2	INSIDE	0.346	0.434	1176.92	510.40	0.150	921.32	138.35
A_68_P28871638	chr13:21292545-21292595	NM_009054:20743	Trim27	DOWNSTREAM	0.346	0.415	1486.03	616.88	0.144	1132.32	162.54
A_68_P28160204	chr11:116442979-116443023	NM_173755:-239	Ube2o	PROMOTER	0.346	0.696	1128.49	785.63	0.241	927.90	223.53
A_68_P28730612	chr12:110132421-110132465	NM_177602:-39	Wdr25	DIVERGENT_PROMOTER	0.346	0.584	2508.95	1464.63	0.202	1879.81	379.22
A_68_P26891988	chr9:122812318-122812362	NM_001177505:14752	Zfp167	DOWNSTREAM	0.346	0.693	1775.77	1230.14	0.240	1231.48	295.22
A_68_P30501817	chr15:102890042-102890087	AK019974:-327		PROMOTER	0.346	0.576	963.56	555.05	0.199	698.64	139.06
A_68_P30557262	chr16:13437166-13437210	AK042946:-490		PROMOTER	0.346	0.563	1907.97	1074.44	0.195	1434.16	279.83
A_68_P23296887	chr4:129168766-129168810	NM_001085491:355	1700125D06Rik	INSIDE	0.345	0.541	2189.77	1184.01	0.187	1498.37	279.57
A_68_P22346556	chr3:95755077-95755121	NM_023210:21919	Anp32e	DOWNSTREAM	0.345	0.701	3316.82	2325.71	0.242	2505.96	606.98
A_68_P25616527	chr8:4206553-4206597	NM_207203:10738	BC068157	DOWNSTREAM	0.345	0.649	1674.15	1086.44	0.224	1142.10	256.05
A_68_P26600871	chr9:67607518-67607562	NM_001081314:297	C2cd4b	INSIDE	0.345	0.513	2348.85	1204.41	0.177	1940.66	343.40
A_68_P21477083	chr2:102290541-102290585	NM_010218:1387	Fjx1	INSIDE	0.345	0.690	1870.10	1290.36	0.238	1501.93	357.29
A_68_P24519505	chr6:66986497-66986541	NM_007836:883	Gadd45a	INSIDE	0.345	0.431	2343.74	1010.48	0.149	1850.66	274.91
A_68_P32048646	chr19:28752584-28752628	NM_175459:1961	Glis3	INSIDE	0.345	0.616	1558.16	960.44	0.212	1266.66	269.05
A_68_P22785948	chr4:24423938-24423984	NM_199467:352	Mms22l	INSIDE	0.345	0.554	922.74	511.39	0.191	630.84	120.57
A_68_P32142240	chr19:46211708-46211752	NM_008852:11085	Pitx3	INSIDE	0.345	0.537	1189.29	638.22	0.185	973.75	180.21
A_68_P27430005	chr10:107599244-107599288	NM_027892:-189	Ppp1r12a	PROMOTER	0.345	0.445	1358.46	604.42	0.153	1248.57	191.50
A_68_P29094234	chr13:63674256-63674300	NM_008957:-7450	Ptch1	PROMOTER	0.345	0.536	2331.34	1249.73	0.185	1792.86	331.49
A_68_P31682231	chr18:47526609-47526653	NM_018744:1892	Sema6a	INSIDE	0.345	0.668	2256.66	1506.77	0.230	1764.30	406.24
A_68_P22338873	chr3:94216925-94216977	NM_028307:-289	Tdrkh	PROMOTER	0.345	0.614	1227.17	753.72	0.212	819.41	173.68
A_68_P24162461	chr5:145528855-145528900	NM_001081362:-783	Trrap	DIVERGENT_PROMOTER	0.345	0.692	1276.24	883.62	0.239	930.82	222.09
A_68_P30125734	chr15:33617702-33617758	NM_001085421:-92	Tspyl5	PROMOTER	0.345	0.439	1748.06	767.52	0.151	1378.11	208.73
A_68_P29440562	chr14:19726350-19726394	NM_144839:-231	Ube2e2	PROMOTER	0.345	0.574	1097.38	629.74	0.198	820.14	162.60
A_68_P26467230	chr9:44169640-44169684	NM_027889:91	Vps11	INSIDE	0.345	0.616	3114.82	1920.10	0.213	2334.67	497.19
A_68_P30568843	chr16:16302936-16302980	NM_198246:-99	Yars2	PROMOTER	0.345	0.536	1519.30	813.81	0.185	1283.94	237.00
A_68_P31782009	chr18:65741080-65741124	NM_207255:1219	Zfp532	INSIDE	0.345	0.494	1236.74	611.02	0.170	956.13	162.83
A_68_P31491180	chr18:10707044-10707088	NM_134130:-372	Abhd3	PROMOTER	0.344	0.673	2149.10	1445.60	0.232	1657.30	383.91
A_68_P24469549	chr6:55401776-55401820	NM_001025372:-175	Adcyap1r1	PROMOTER	0.344	0.587	2809.37	1648.59	0.202	2108.33	425.67
A_68_P29486554	chr14:28149566-28149610	NM_027871:98364	Arhgef3	INSIDE	0.344	0.625	1140.57	712.63	0.215	936.30	201.24
A_68_P24059367	chr5:124566387-124566431	NM_144509:292	Arl6ip4	INSIDE	0.344	0.407	1975.84	804.76	0.140	1547.73	217.04
A_68_P24540589	chr6:72184688-72184732	NM_153778:861	Atoh8	INSIDE	0.344	0.409	3018.72	1233.51	0.140	2370.38	333.00
A_68_P31932217	chr19:6015773-6015817	NM_007600:-547	Capn1	PROMOTER	0.344	0.592	2441.53	1444.31	0.203	1880.58	382.65

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27563901	chr11:5442216-5442260	NM_134033:-18	Ccdc117	PROMOTER	0.344	0.718	1718.50	1233.47	0.247	1349.64	333.42
A_68_P28059228	chr11:98769471-98769515	NM_011799:28	Cdc6	INSIDE	0.344	1.407	1819.73	2560.78	0.484	1234.76	597.56
A_68_P31254442	chr17:56323432-56323476	NM_080837:-111	D17Wsu104e	PROMOTER	0.344	0.454	2548.60	1158.08	0.156	2023.79	315.92
A_68_P22998989	chr4:68615175-68615219	NM_019967:235	Dbc1	INSIDE	0.344	0.506	1069.98	541.88	0.174	790.43	137.54
A_68_P28914786	chr13:30077338-30077382	NM_010093:572	E2f3	INSIDE	0.344	0.459	3660.62	1681.12	0.158	2711.94	428.15
A_68_P29241614	chr13:96388371-96388415	NM_010169:-4	F2r	PROMOTER	0.344	0.540	2019.99	1091.38	0.186	1478.25	275.00
A_68_P24290978	chr6:22305712-22305756	NM_138587:347	Fam3c	INSIDE	0.344	0.380	2552.66	970.80	0.131	2087.58	273.19
A_68_P21339294	chr2:74585119-74585163	NM_010468:35091	Hoxd3	INSIDE	0.344	0.683	1523.36	1039.69	0.235	1194.89	280.82
A_68_P23193385	chr4:107552379-107552423	NM_010760:-17	Magoh	PROMOTER	0.344	0.587	1208.40	708.95	0.202	918.58	185.23
A_68_P21548581	chr2:115686326-115686370	NM_001159569:204009	Meis2	DOWNSTREAM	0.344	0.430	1557.31	669.02	0.148	1174.48	173.63
A_68_P28039696	chr11:95448025-95448069	NM_033217:966	Ngfr	INSIDE	0.344	0.554	1706.15	945.41	0.191	1239.07	236.27
A_68_P22350765	chr3:96512213-96512257	NM_001162925:249	Nudt17	INSIDE	0.344	0.488	1912.80	934.13	0.168	1486.44	249.62
A_68_P26463577	chr9:43553595-43553639	NM_021424:958	Pvrl1	INSIDE	0.344	0.566	943.26	534.19	0.195	727.92	141.86
A_68_P27704162	chr11:34934585-34934629	NM_011412:-351	Slit3	PROMOTER	0.344	0.467	1586.99	740.41	0.161	1269.13	203.90
A_68_P25425956	chr7:119822840-119822884	NM_001166584:29	Tead1	INSIDE	0.344	0.469	1119.16	524.58	0.161	856.78	138.13
A_68_P21736750	chr2:149656913-149656958	NM_001085521:417	Tmem90b	INSIDE	0.344	0.547	1978.60	1081.48	0.188	1688.29	317.19
A_68_P26447519	chr9:40964965-40965009	NM_176860:591	Ubash3b	INSIDE	0.344	0.430	1488.87	640.59	0.148	1269.45	188.16
A_68_P28881068	chr13:23461198-23461242	NM_001111107:-149	Zfp322a	PROMOTER	0.344	0.589	1652.29	972.74	0.202	1327.03	268.56
A_68_P25005239	chr7:25292778-25292822	NM_146183:695	Zfp428	INSIDE	0.344	0.540	2038.45	1099.97	0.185	1600.26	296.62
A_68_P26015764	chr8:86146384-86146428	AK160924:14211		INSIDE	0.344	0.699	2315.65	1618.31	0.240	1772.38	426.18
A_68_P21393923	chr2:84510529-84510573	NM_001033166:315	2700094K13Rik	INSIDE	0.343	0.538	1529.39	822.20	0.184	1088.64	200.69
A_68_P27255924	chr10:74779536-74779580	NM_009630:-129	Adora2a	PROMOTER	0.343	0.525	1504.76	790.52	0.180	1360.65	245.11
A_68_P25500900	chr7:133645875-133645919	NM_183020:920	Atxn2l	INSIDE	0.343	1.484	4817.28	7147.49	0.509	3484.37	1773.35
A_68_P32128433	chr19:43827788-43827832	NM_001113562:298	Cutc	INSIDE	0.343	0.633	2293.03	1451.94	0.217	1730.26	375.31
A_68_P24125310	chr5:137791448-137791492	NM_001159571:134	Ephb4	INSIDE	0.343	0.541	3935.14	2126.96	0.186	3267.51	606.59
A_68_P29644190	chr14:60997369-60997413	NM_001164705:268	Fam123a	INSIDE	0.343	0.602	1906.14	1146.59	0.206	1505.08	310.69
A_68_P30588159	chr16:20548466-20548510	NR_030670:141	Gm15760	INSIDE	0.343	0.695	1557.95	1083.45	0.238	1066.30	254.19
A_68_P28357924	chr12:37108183-37108227	NM_178629:99	Ispd	INSIDE	0.343	0.387	2597.33	1005.23	0.133	2013.78	267.18
A_68_P31156873	chr17:35118675-35118726	NM_001204274:-98	Lsm2	PROMOTER	0.343	0.633	1144.79	724.59	0.217	836.98	181.68
A_68_P26581615	chr9:64234276-64234320	NM_172522:866	Megf11	INSIDE	0.343	0.588	1478.56	868.87	0.202	1282.68	258.60
A_68_P25285353	chr7:91040923-91040967	NM_023403:435	Mesdc2	INSIDE	0.343	0.742	3615.43	2682.89	0.254	2438.90	620.28
A_68_P30559565	chr16:13903341-13903391	NM_001039533:-138	Pdxdc1	PROMOTER	0.343	0.446	1252.10	558.00	0.153	897.76	137.13
A_68_P23292761	chr4:128405549-128405608	NM_001195083:764	Phc2	INSIDE	0.343	0.648	904.44	586.46	0.222	564.26	125.50
A_68_P32322124	chrX:34731543-34731587	NM_153503:227	Rnf113a1	INSIDE	0.343	1.725	2033.00	3506.19	0.592	837.31	495.53
A_68_P30572152	chr16:17132713-17132758	NM_022324:-259	Sdf2l1	PROMOTER	0.343	0.652	972.55	634.34	0.223	716.56	160.11
A_68_P25265199	chr7:87331654-87331698	NM_013659:-50	Sema4b	PROMOTER	0.343	0.535	1137.27	608.78	0.184	971.67	178.54
A_68_P31351018	chr17:74737917-74737961	NM_001162870:-388	Spast	PROMOTER	0.343	0.531	1832.83	973.25	0.182	1583.59	288.44
A_68_P30251031	chr15:58765278-58765322	NM_175151:-15	Tatdn1	DIVERGENT_PROMOTER	0.343	0.550	962.61	529.46	0.189	846.52	159.61
A_68_P26564383	chr9:61220517-61220561	NM_001083927:366	Tle3	INSIDE	0.343	0.567	1269.16	720.00	0.195	923.94	179.79
A_68_P26815583	chr9:108480765-108480809	NM_031392:215	Wdr6	INSIDE	0.343	0.751	4941.07	3708.80	0.258	3387.87	873.24
A_68_P26228075	chr8:124175832-124175876	NM_080855:-21	Zcchc14	PROMOTER	0.343	0.463	2103.87	975.09	0.159	1537.21	244.55
A_68_P21749217	chr2:152239906-152239950	NM_175126:852	Zcchc3	INSIDE	0.343	0.609	1741.48	1060.96	0.209	1346.73	281.21
A_68_P27241481	chr10:72117558-72117607	NM_025635:-60	Zwint	PROMOTER	0.343	0.635	823.34	522.85	0.218	684.27	149.03
A_68_P28708612	chr12:106575527-106575571	ENSMUST00000138649:346		INSIDE	0.343	0.679	1199.68	814.38	0.233	942.32	219.70
A_68_P23281853	chr4:126430986-126431030	NM_133886:-5	AU040320	PROMOTER	0.342	0.470	1829.05	859.01	0.161	1333.78	214.08
A_68_P24218863	chr6:6829517-6829561	NM_010056:2530	Dlx5	INSIDE	0.342	0.489	2406.66	1176.53	0.167	1698.33	284.26
A_68_P26527191	chr9:54546796-54546840	NM_021422:-547	Dnaja4	PROMOTER	0.342	1.445	3453.02	4990.09	0.494	2623.13	1294.83
A_68_P25470622	chr7:127986473-127986517	NM_007908:98	Eef2k	INSIDE	0.342	0.620	2300.15	1425.40	0.212	1815.39	385.30
A_68_P25637619	chr8:8660957-8661001	NM_010111:-205	Efnb2	PROMOTER	0.342	0.556	1755.35	976.85	0.190	1389.17	264.38
A_68_P25609683	chr7:152047109-152047153	NM_010202:-160	Fgf4	PROMOTER	0.342	0.530	2799.23	1484.20	0.181	2301.08	416.77
A_68_P27561172	chr11:4963946-4963990	NM_001190406:1362	Gas2l1	INSIDE	0.342	1.478	1500.20	2217.22	0.505	1179.52	596.05

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P29703998	chr14:71290922-71290966	NM_008115:1008	Gfra2	INSIDE	0.342	0.467	2053.29	958.58	0.160	1567.16	250.28
A_68_P23927128	chr5:100406693-100406737	NM_001077265:1243	Hnrnpd	INSIDE	0.342	0.657	1887.39	1240.47	0.225	1455.95	326.96
A_68_P26222129	chr8:123260367-123260411	NM_008320:113	Irf8	INSIDE	0.342	0.452	1790.75	808.66	0.154	1437.85	222.07
A_68_P25587300	chr7:148380302-148380347	NM_153777:-717	Lrrc56	PROMOTER	0.342	0.583	3378.94	1968.59	0.199	2386.53	474.93
A_68_P28089843	chr11:104092753-104092797	NM_001038609:25	Mapt	INSIDE	0.342	0.509	1566.11	797.20	0.174	1253.98	218.61
A_68_P25370975	chr7:108160402-108160446	NM_008773:81	P2ry2	INSIDE	0.342	0.538	2527.30	1359.55	0.184	2030.92	373.19
A_68_P31632700	chr18:38371037-38371082	NM_029357:-1643	Pcdh1	PROMOTER	0.342	0.613	1613.63	988.37	0.209	1201.91	251.75
A_68_P23720369	chr5:58111053-58111097	NM_018764:1815	Pcdh7	INSIDE	0.342	0.626	2357.92	1475.45	0.214	1774.01	379.78
A_68_P25048763	chr7:36119695-36119739	NM_027897:461	Rhpn2	INSIDE	0.342	0.501	1703.30	852.57	0.171	1380.89	236.65
A_68_P20005837	chr1:4486985-4487029	NM_011441:-512	Sox17	PROMOTER	0.342	0.587	1511.13	887.02	0.201	1226.86	246.02
A_68_P26891990	chr9:122812568-122812612	NM_001177505:15002	Zfp167	DOWNSTREAM	0.342	0.659	1992.99	1312.63	0.226	1603.40	361.64
A_68_P23588919	chr5:33785607-33785651			Unknown	0.342	1.613	2761.60	4455.18	0.552	2013.65	1111.02
A_68_P31412804	chr17:86199724-86199768	AK142122:524		INSIDE	0.342	0.515	1096.31	564.62	0.176	957.34	168.75
A_68_P21503641	chr2:106814392-106814436	NM_173750:-3866	2700007P21Rik	PROMOTER	0.341	0.712	3658.98	2605.11	0.243	2707.00	657.80
A_68_P20443149	chr1:93437651-93437695	NM_023046:16	Asb1	INSIDE	0.341	0.604	982.35	593.63	0.206	826.95	170.48
A_68_P28181189	chr11:119803657-119803701	NM_001037754:-727	Baiap2	PROMOTER	0.341	0.550	2487.62	1367.46	0.187	1801.34	337.58
A_68_P23245376	chr4:119088209-119088253	NM_029286:-104	Ccdc30	PROMOTER	0.341	0.653	1052.61	687.63	0.223	849.73	189.12
A_68_P31125922	chr17:29231051-29231095	NM_007669:356	Cdkn1a	INSIDE	0.341	0.568	1745.25	992.08	0.194	1261.12	244.16
A_68_P30512427	chr16:4880947-4880994	NM_145359:-1119	Fam100a	DIVERGENT_PROMOTER	0.341	0.480	1328.98	638.19	0.164	886.08	144.97
A_68_P28669119	chr12:99497006-99497050	NM_008079:519	Galc	INSIDE	0.341	0.571	927.29	529.74	0.195	704.18	137.34
A_68_P28158436	chr11:116143049-116143093	NM_010254:818	Galr2	INSIDE	0.341	0.630	1348.14	848.69	0.215	926.83	199.12
A_68_P25089586	chr7:52095494-52095538	NM_010215:3859	Il4i1	INSIDE	0.341	0.638	2333.35	1487.96	0.218	1821.13	396.55
A_68_P21122681	chr2:33487222-33487266	NM_010725:8787	Lmx1b	INSIDE	0.341	0.593	1550.97	919.68	0.202	1177.14	238.06
A_68_P25279944	chr7:90015164-90015208	NM_175366:-656	Mex3b	PROMOTER	0.341	0.517	1609.49	832.10	0.176	1251.62	220.49
A_68_P27285693	chr10:80289215-80289268	NM_008753:-159	Oaz1	PROMOTER	0.341	0.565	1467.24	829.33	0.193	1028.09	198.41
A_68_P31757537	chr18:61559490-61559534	NM_133249:573	Ppargc1b	INSIDE	0.341	0.406	1984.91	805.32	0.138	1502.22	207.54
A_68_P27281038	chr10:79578186-79578230	NM_011492:-1072	Stk11	PROMOTER	0.341	0.659	910.75	600.38	0.225	707.91	159.15
A_68_P24671557	chr6:97129251-97129295	NM_001081111:-154	Tmf1	PROMOTER	0.341	0.658	1851.91	1218.68	0.224	1396.22	313.41
A_68_P24595035	chr6:83661384-83661428	NM_011912:149	Vax2	INSIDE	0.341	0.577	1338.25	772.15	0.197	927.73	182.45
A_68_P21394211	chr2:84555629-84555673	NM_144887:-329	Zdhhc5	PROMOTER	0.341	0.439	4734.44	2076.53	0.150	3532.02	528.54
A_68_P25264702	chr7:87226863-87226912	NM_175433:55774	Zfp710	INSIDE	0.341	1.610	1303.70	2098.42	0.549	951.92	522.55
A_68_P20046441	chr1:14497168-14497212			Unknown	0.341	0.529	1065.22	563.14	0.180	867.58	156.52
A_68_P22820135	chr4:32325268-32325312	ENSMUST00000108180:-488		PROMOTER	0.341	0.622	1872.87	1164.79	0.212	1430.32	303.75
A_68_P32260576	chrX:11705862-11705906	NM_001168321:31597	Bcor	INSIDE	0.340	1.523	1805.39	2748.90	0.517	603.83	312.24
A_68_P26815510	chr9:108472099-108472144	NM_026378:-101	Dalrd3	PROMOTER	0.340	0.353	2690.95	951.19	0.120	2178.95	261.88
A_68_P26878194	chr9:120402272-120402316	NM_026892:571	Eif1b	INSIDE	0.340	0.643	1232.01	792.49	0.219	908.79	198.62
A_68_P26132610	chr8:107792581-107792625	NM_015821:4055	Fbxl8	INSIDE	0.340	0.605	1463.87	886.37	0.206	1127.49	232.42
A_68_P27897164	chr11:69614462-69614506	NM_010198:643	Fgf11	INSIDE	0.340	0.317	2021.17	640.82	0.108	1463.23	157.89
A_68_P21221945	chr2:52717198-52717242	NM_172409:319	Fmnl2	INSIDE	0.340	0.583	2460.09	1434.58	0.198	1766.26	349.74
A_68_P20644037	chr1:138028308-138028352	NM_001039472:353	Kif21b	INSIDE	0.340	0.522	1919.86	1001.71	0.177	1596.07	282.84
A_68_P29110675	chr13:68720936-68720980	NM_172480:40	Mtrr	INSIDE	0.340	0.574	1799.72	1033.33	0.195	1338.83	261.01
A_68_P29773655	chr14:84847043-84847087	NM_001013753:3695	Pcdh17	INSIDE	0.340	0.515	1272.98	656.18	0.175	1056.78	185.20
A_68_P25030468	chr7:31017900-31017944	NM_027259:830	Polr2i	INSIDE	0.340	0.513	1782.34	914.06	0.174	1180.51	205.75
A_68_P25506340	chr7:134732564-134732608	NM_172281:375	Rnf40	INSIDE	0.340	1.706	2715.64	4631.89	0.579	1880.58	1089.29
A_68_P24007309	chr5:115462025-115462071	NM_029012:516	Sppl3	INSIDE	0.340	2.073	1933.68	4008.61	0.705	1553.83	1094.99
A_68_P30344892	chr15:75741160-75741204	NM_178646:1018	Tigd5	INSIDE	0.340	0.640	3566.60	2282.79	0.218	2745.60	597.69
A_68_P22856581	chr4:40216815-40216859	NM_134097:38	Topors	INSIDE	0.340	0.655	831.30	544.49	0.223	700.62	156.13
A_68_P31210125	chr17:47147460-47147504	NM_001177374:-1	Ubr2	PROMOTER	0.340	0.467	1693.61	790.74	0.159	1214.67	192.81
A_68_P24124995	chr5:137735672-137735716	NM_027356:-202	Ufsp1	PROMOTER	0.340	1.516	984.83	1492.78	0.515	738.67	380.39
A_68_P25581335	chr7:147129738-147129782	NM_009482:6	Utf1	INSIDE	0.340	0.504	2430.42	1224.45	0.171	1909.32	326.69
A_68_P24973141	chr7:13403835-13403879	NM_026046:353	Zfp329	INSIDE	0.340	0.530	1288.31	682.69	0.180	1080.60	194.90

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31256669	chr17:56651021-56651065	NM_011483:864	Znrf4	INSIDE	0.340	0.683	2859.56	1951.67	0.232	2164.65	503.03
A_68_P26892246	chr9:122859846-122859890	NM_025419:250	1110059G10Rik	INSIDE	0.339	0.569	2083.75	1185.89	0.193	1729.49	333.35
A_68_P28463397	chr12:58677434-58677478	NM_001037743:12355	4921506M07Rik	INSIDE	0.339	0.725	1649.62	1195.56	0.246	1211.69	298.10
A_68_P24122101	chr5:137043954-137043998	NM_009986:-675	Cux1	PROMOTER	0.339	0.571	1610.95	919.22	0.194	1380.86	267.45
A_68_P25952523	chr8:73063414-73063459	NM_007924:-137	Ell	PROMOTER	0.339	0.622	1705.78	1060.79	0.211	1280.19	269.65
A_68_P24859168	chr6:133985011-133985055	NM_007961:-692	Etv6	PROMOTER	0.339	0.684	2321.36	1588.07	0.232	1712.62	397.63
A_68_P24609727	chr6:86315530-86315574	NM_025591:-124	Fam136a	PROMOTER	0.339	0.705	6052.97	4269.05	0.239	4767.19	1140.80
A_68_P24992615	chr7:19895551-19895595	NM_008036:-178	Fosb	PROMOTER	0.339	0.558	1114.98	622.51	0.189	933.85	176.96
A_68_P22342884	chr3:95022045-95022089	NM_029885:-202	Gabpb2	PROMOTER	0.339	0.656	956.74	627.92	0.222	804.86	179.06
A_68_P29625860	chr14:57676319-57676363	NM_016975:442	Gja3	INSIDE	0.339	0.516	1227.11	632.98	0.175	1065.22	186.06
A_68_P25661487	chr8:12430676-12430720	NR_027975:44928	Gm5607	INSIDE	0.339	0.526	1959.63	1030.26	0.178	1552.09	276.81
A_68_P21283787	chr2:64861006-64861050	NM_016719:-205	Grb14	PROMOTER	0.339	0.576	1649.62	950.03	0.195	1437.21	280.90
A_68_P30880659	chr16:75766853-75766897	NM_030201:189	Hspa13	INSIDE	0.339	0.641	1975.32	1266.08	0.217	1430.94	311.12
A_68_P23277861	chr4:125724192-125724236	NM_025544:43	Mrps15	INSIDE	0.339	0.569	1751.68	996.75	0.193	1354.29	261.39
A_68_P30368846	chr15:79664558-79664602	NM_001013360:183	Npcd	INSIDE	0.339	0.432	1901.98	822.09	0.147	1392.49	204.25
A_68_P31731073	chr18:56722210-56722254	NM_001162989:10	Phax	INSIDE	0.339	0.611	1265.55	772.81	0.207	1014.37	209.81
A_68_P23610099	chr5:37261384-37261428	NM_172994:1598	Ppp2r2c	INSIDE	0.339	0.521	2486.87	1296.63	0.177	1877.70	331.55
A_68_P30577452	chr16:18089136-18089180	NM_011172:125	Prodh	INSIDE	0.339	0.406	1428.07	579.57	0.138	1030.07	141.71
A_68_P30348859	chr15:76348629-76348673	NM_130893:3909	Scrt1	INSIDE	0.339	0.476	1845.93	877.89	0.161	1351.96	218.04
A_68_P22683258	chr3:157694818-157694868	NM_001093753:-124	Srsf11	PROMOTER	0.339	0.643	1098.09	706.04	0.218	903.15	196.63
A_68_P31125470	chr17:29144780-29144824	NM_134115:80	Stk38	INSIDE	0.339	0.543	1290.56	700.74	0.184	959.77	176.47
A_68_P29730261	chr14:76244654-76244698	NM_009429:-386	Tpt1	PROMOTER	0.339	0.504	2082.32	1050.12	0.171	1574.00	269.35
A_68_P32700072	chrX:137134843-137134887	NM_001077364:197	Tsc22d3	INSIDE	0.339	7.001	3913.06	27395.46	2.371	1903.95	4514.37
A_68_P32134136	chr19:44821411-44821455			Unknown	0.339	0.671	2274.38	1526.71	0.228	1664.19	378.69
A_68_P20936907	chr1:193048234-193048279	ENSMUST00000169806:-94		PROMOTER	0.339	0.668	1059.66	707.40	0.226	850.47	192.23
A_68_P25093324	chr7:52722052-52722096	NM_007527:194	Bax	INSIDE	0.338	0.512	1886.42	965.17	0.173	1529.95	264.53
A_68_P24438772	chr6:50516320-50516364	NM_007808:131	Cycs	INSIDE	0.338	0.389	1792.99	697.19	0.131	1553.85	204.01
A_68_P24138252	chr5:140384071-140384115	NM_175522:196	Elfn1	INSIDE	0.338	0.583	1399.90	815.47	0.197	1168.09	230.30
A_68_P20317723	chr1:69154010-69154069	NM_010154:594	Erbb4	INSIDE	0.338	1.371	1345.01	1844.25	0.463	1261.90	584.09
A_68_P27267010	chr10:76721714-76721758	NR_026944:232	Gm10941	INSIDE	0.338	0.602	1017.53	612.92	0.204	810.65	165.13
A_68_P23819789	chr5:77524030-77524074	NM_001159900:240	Hopx	INSIDE	0.338	0.698	1624.76	1134.48	0.236	1430.51	337.68
A_68_P28043703	chr11:96176215-96176259	NR_029784:-2242	Mir10a	PROMOTER	0.338	0.480	1343.98	645.55	0.162	1215.40	197.05
A_68_P28055765	chr11:98199818-98199862	NM_010895:-8881	Neurod2	PROMOTER	0.338	0.529	1873.82	992.10	0.179	1372.85	245.61
A_68_P20418214	chr1:89406592-89406636	NM_019867:323	Ngef	INSIDE	0.338	0.484	3915.00	1895.24	0.164	3017.43	493.49
A_68_P22422580	chr3:109946888-109946938	NM_001163348:-522	Ntng1	PROMOTER	0.338	0.560	2088.91	1170.50	0.189	1590.07	301.02
A_68_P21913062	chr2:181572751-181572795	NM_153594:165	Pcmtd2	INSIDE	0.338	0.523	2130.87	1115.14	0.177	1539.97	272.28
A_68_P30652429	chr16:32431312-32431356	NM_001163160:19	Pcyt1a	INSIDE	0.338	0.624	1228.22	766.59	0.211	906.99	191.58
A_68_P26429011	chr9:36953245-36953299	NM_001029838:1579	Pknox2	INSIDE	0.338	0.468	1242.53	581.44	0.158	990.49	156.59
A_68_P23152967	chr4:100741468-100741512	NM_183024:-152	Raver2	PROMOTER	0.338	0.552	1400.97	773.23	0.187	1240.37	231.50
A_68_P28137844	chr11:112645388-112645432	NM_011448:1887	Sox9	INSIDE	0.338	0.507	1581.52	801.59	0.171	1241.06	212.67
A_68_P27006965	chr10:23869254-23869298	NM_016797:154	Stx7	INSIDE	0.338	0.311	1938.48	603.50	0.105	1686.79	177.73
A_68_P26564381	chr9:61220364-61220408	NM_001083927:214	Tle3	INSIDE	0.338	0.459	1810.81	831.47	0.155	1404.45	218.13
A_68_P28149096	chr11:114537102-114537146	NM_053273:343	Ttyh2	INSIDE	0.338	0.584	1186.00	692.48	0.197	917.64	181.19
A_68_P32321786	chrX:34650071-34650115	NM_026573:225	Upf3b	INSIDE	0.338	1.475	1569.57	2315.84	0.499	628.25	313.59
A_68_P30778633	chr16:55973743-55973787	NM_173026:-152	Zbtb11	PROMOTER	0.338	0.639	1822.62	1164.11	0.216	1614.97	348.49
A_68_P31918868	chr19:3708036-3708080	NM_028077:-274	1810055G02Rik	PROMOTER	0.337	0.436	1462.67	638.10	0.147	1340.36	196.90
A_68_P24430831	chr6:49024182-49024226	NM_029353:411	2410003K15Rik	INSIDE	0.337	0.620	1526.36	946.80	0.209	1324.44	277.11
A_68_P27285911	chr10:80318512-80318556	NM_175195:515	3110056O03Rik	INSIDE	0.337	0.551	1278.89	704.99	0.186	997.38	185.43
A_68_P28463396	chr12:58677361-58677405	NM_001037743:12281	4921506M07Rik	INSIDE	0.337	0.690	2575.94	1778.36	0.233	1996.79	464.33
A_68_P26132762	chr8:107813304-107813348	NM_001166394:102	4931428F04Rik	INSIDE	0.337	0.654	2913.44	1904.57	0.220	2154.06	474.43
A_68_P26505580	chr9:50583427-50583471	NM_133981:14	Alg9	INSIDE	0.337	0.698	2005.94	1400.85	0.235	1403.20	330.31

						Sham group			TiO$_2$-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31899554	chr18:86882710-86882754	NM_172633:293	Cbln2	INSIDE	0.337	0.554	1159.27	642.23	0.186	982.22	183.16
A_68_P22765609	chr4:19497322-19497369	NM_027769:-94	Cpne3	DIVERGENT_PROMOTER	0.337	0.512	3128.24	1601.48	0.173	2299.02	396.63
A_68_P31158507	chr17:35378777-35378821	NM_019693:108	Ddx39b	INSIDE	0.337	0.374	2398.36	896.01	0.126	1755.58	220.71
A_68_P30478222	chr15:98927785-98927829	NM_176835:-2108	Dnajc22	DIVERGENT_PROMOTER	0.337	0.662	1175.81	778.42	0.223	900.94	200.98
A_68_P30988904	chr16:95924063-95924107	NM_011809:71	Ets2	INSIDE	0.337	0.740	3358.88	2485.54	0.250	2387.72	596.09
A_68_P24620341	chr6:88146759-88146803	NM_008090:-1877	Gata2	PROMOTER	0.337	0.552	923.90	510.19	0.186	654.05	121.79
A_68_P26546339	chr9:58046840-58046884	NM_001161535:2660	Islr2	INSIDE	0.337	0.666	2409.98	1605.34	0.224	1693.87	379.84
A_68_P30477055	chr15:98701709-98701753	NM_001033276:-116	Mll2	PROMOTER	0.337	0.432	1460.87	630.65	0.146	1215.27	176.94
A_68_P30363155	chr15:78745009-78745053	NM_020271:682	Pdxp	INSIDE	0.337	0.682	2950.08	2011.01	0.229	1987.34	456.04
A_68_P22450818	chr3:116414578-116414622	NM_144902:598	Slc35a3	INSIDE	0.337	0.498	2384.90	1187.78	0.168	1934.40	324.78
A_68_P26363429	chr9:24578655-24578699	NM_194263:71	Tbx20	INSIDE	0.337	0.556	1024.81	569.50	0.187	912.00	170.62
A_68_P29733550	chr14:76815819-76815868	NM_207652:216	Tsc22d1	INSIDE	0.337	0.659	1206.39	794.62	0.222	889.10	197.56
A_68_P20858578	chr1:179187386-179187430	NM_011785:-8510	Akt3	PROMOTER	0.336	0.610	1755.05	1071.10	0.205	1321.79	271.31
A_68_P21007913	chr2:11700124-11700174	NM_177268:769	Ankrd16	INSIDE	0.336	0.538	1281.37	689.48	0.181	928.52	167.72
A_68_P23576171	chr5:31357229-31357273	NM_023525:67	Cad	INSIDE	0.336	0.693	1630.74	1130.54	0.233	1334.36	310.43
A_68_P26141981	chr8:109417694-109417738	NM_011574:177	Cirh1a	INSIDE	0.336	0.719	1877.59	1350.27	0.241	1458.53	352.21
A_68_P27800933	chr11:52578613-52578657	NM_177059:427	Fstl4	INSIDE	0.336	0.529	2350.07	1242.50	0.178	1799.39	319.63
A_68_P26886025	chr9:121766341-121766385	NM_001112668:287	Gm9790	INSIDE	0.336	0.568	3536.66	2007.95	0.191	2439.06	465.53
A_68_P21073102	chr2:25434469-25434514	NM_001005424:1128	Gm996	INSIDE	0.336	1.548	1725.74	2672.20	0.520	1236.81	642.79
A_68_P26875190	chr9:119846515-119846559	NM_028976:140	Gorasp1	INSIDE	0.336	0.582	3904.44	2271.27	0.196	2671.26	522.69
A_68_P24116811	chr5:136020789-136020833	NM_146001:182	Hip1	INSIDE	0.336	0.648	1656.74	1073.41	0.218	1180.12	256.84
A_68_P21902323	chr2:179959846-179959890	NM_001081171:696	Lama5	INSIDE	0.336	0.279	2052.96	573.01	0.094	1737.11	162.97
A_68_P27787817	chr11:50106087-50106131	NM_175334:-270	Maml1	PROMOTER	0.336	0.529	1025.84	543.18	0.178	817.07	145.50
A_68_P31161220	chr17:35978699-35978752	NM_001010833:283	Mdc1	INSIDE	0.336	0.678	1164.75	789.22	0.227	855.22	194.47
A_68_P29322931	chr13:111185370-111185414	NM_152804:141	Plk2	INSIDE	0.336	0.427	1874.97	800.72	0.143	1439.94	206.36
A_68_P21307667	chr2:69043827-69043871	NM_001199123:399	Spc25	INSIDE	0.336	0.484	1184.98	573.10	0.163	914.60	148.81
A_68_P21901050	chr2:179777293-179777337	NM_178750:127	Ss18l1	INSIDE	0.336	0.482	2057.89	992.10	0.162	1514.67	245.47
A_68_P22500445	chr3:125641287-125641331	NM_011674:160	Ugt8a	INSIDE	0.336	0.490	3569.56	1747.63	0.164	2752.41	452.21
A_68_P24541411	chr6:72330618-72330663	NM_001080742:-178	Vamp5	PROMOTER	0.336	0.706	1265.76	894.05	0.237	952.72	226.24
A_68_P20935796	chr1:192849520-192849564	NR_027298:313	A230020J21Rik	INSIDE	0.335	0.455	1278.55	582.32	0.153	988.28	150.85
A_68_P22055030	chr3:35653187-35653231	NM_029570:149	Atp11b	INSIDE	0.335	0.485	2517.63	1220.74	0.163	1939.55	315.50
A_68_P31936824	chr19:7016562-7016606	NM_007522:240	Bad	INSIDE	0.335	0.552	1852.09	1022.11	0.185	1346.95	248.86
A_68_P25313629	chr7:97592324-97592368	NM_145151:1056	Crebzf	INSIDE	0.335	0.576	3401.89	1959.86	0.193	2509.54	484.51
A_68_P25952440	chr8:73051499-73051543	NM_001111066:-121	Fkbp8	DIVERGENT_PROMOTER	0.335	0.630	1257.36	792.22	0.211	901.38	189.99
A_68_P23222364	chr4:114598169-114598213	NM_015758:428	Foxe3	INSIDE	0.335	0.481	2199.74	1058.09	0.161	1748.13	281.77
A_68_P24838573	chr6:128313280-128313324	NM_008021:291	Foxm1	INSIDE	0.335	0.536	2103.41	1127.86	0.179	1542.37	276.72
A_68_P31940698	chr19:7686824-7686868	NM_025731:-212	Hrasls5	DIVERGENT_PROMOTER	0.335	0.574	1405.93	806.98	0.192	1006.23	193.20
A_68_P20832488	chr1:174271323-174271367	NM_001039484:4	Kcnj10	INSIDE	0.335	0.681	2205.64	1501.20	0.228	1514.61	345.65
A_68_P23588231	chr5:33678100-33678145	NM_021500:-98	Maea	PROMOTER	0.335	0.614	2204.00	1352.69	0.206	1881.81	387.36
A_68_P24929768	chr6:146591129-146591173	NM_025315:50	Med21	INSIDE	0.335	0.478	1517.62	725.11	0.160	1248.74	199.94
A_68_P24008164	chr5:115608110-115608154	NM_175403:53	Mlec	INSIDE	0.335	0.375	1561.27	585.26	0.125	1484.05	186.17
A_68_P20088284	chr1:23390288-23390332	NM_001081079:-296	Ogfrl1	PROMOTER	0.335	0.497	1281.57	637.48	0.167	1031.91	171.96
A_68_P26980660	chr10:19077044-19077088	NM_053008:722	Olig3	INSIDE	0.335	0.729	7665.22	5584.24	0.244	5365.06	1310.44
A_68_P25184944	chr7:73007570-73007614	NM_011048:571	Pcsk6	INSIDE	0.335	0.459	2435.49	1117.45	0.154	1976.39	303.45
A_68_P20506801	chr1:108068058-108068102	NM_133821:-365	Phlpp1	PROMOTER	0.335	0.566	2301.60	1302.82	0.190	1736.91	329.71
A_68_P27509905	chr10:122115624-122115668	NM_176919:-171	Ppm1h	PROMOTER	0.335	0.507	1496.26	758.69	0.170	1244.74	211.29
A_68_P20083594	chr1:22540800-22540844	NM_001012623:271741	Rims1	INSIDE	0.335	0.662	1033.37	683.92	0.222	850.72	188.60
A_68_P24693485	chr6:100620652-100620698	NM_181590:477	Shq1	INSIDE	0.335	0.657	899.49	590.54	0.220	840.75	185.09
A_68_P25033088	chr7:31514777-31514828	NM_027215:-249	Tmem147	PROMOTER	0.335	0.447	1556.57	695.32	0.150	1142.35	171.09
A_68_P29493855	chr14:29319194-29319238	NM_009524:558	Wnt5a	INSIDE	0.335	0.439	1319.01	578.59	0.147	1027.20	150.84
A_68_P21747251	chr2:151855031-151855075			Unknown	0.335	0.666	1085.05	723.14	0.223	779.00	173.74

						Sham group			TiO$_2$-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28336337	chr12:33063533-33063581	NM_001162903:-97	2010109K11Rik	PROMOTER	0.334	1.633	1193.02	1947.75	0.545	864.99	471.39
A_68_P22987051	chr4:66064069-66064114	NM_019514:1426	Astn2	INSIDE	0.334	0.582	1421.91	827.13	0.194	1118.36	217.36
A_68_P21835087	chr2:167174410-167174454	NM_019835:246	B4galt5	INSIDE	0.334	0.599	1762.22	1055.89	0.200	1334.71	267.18
A_68_P22871974	chr4:43506583-43506627	NM_001037913:368	Ccdc107	INSIDE	0.334	0.565	1528.06	862.84	0.188	1207.56	227.47
A_68_P31376859	chr17:79754745-79754789	NM_026514:-335	Cdc42ep3	PROMOTER	0.334	0.667	1932.72	1289.86	0.223	1495.43	333.82
A_68_P30261335	chr15:60656490-60656535	NM_001162926:123	Fam84b	INSIDE	0.334	0.514	1333.29	684.70	0.171	964.41	165.17
A_68_P26085825	chr8:98411955-98411999	NM_010325:289	Got2	INSIDE	0.334	0.623	1481.30	923.05	0.208	1115.16	232.23
A_68_P25090530	chr7:52253328-52253372	NM_016849:321	Irf3	INSIDE	0.334	0.476	1097.47	522.34	0.159	967.49	153.74
A_68_P24055951	chr5:123939417-123939461	NM_001033461:105	Lrrc43	INSIDE	0.334	0.464	2379.21	1103.66	0.155	1826.63	283.02
A_68_P30547089	chr16:11254525-11254569	NR_035466:-8	Mir1945	PROMOTER	0.334	0.565	961.64	543.77	0.189	806.61	152.19
A_68_P22858433	chr4:40669503-40669547	NR_029594:-425	Mir207	PROMOTER	0.334	0.447	2107.54	941.45	0.149	1743.33	260.30
A_68_P28152870	chr11:115196117-115196161	NM_027132:91	Otop3	INSIDE	0.334	0.530	1083.19	574.39	0.177	850.05	150.77
A_68_P28940997	chr13:34966103-34966147	NM_013830:-1238	Prpf4b	PROMOTER	0.334	0.645	834.93	538.32	0.216	691.14	148.99
A_68_P25090924	chr7:52309475-52309519	NM_022999:7526	Prrg2	INSIDE	0.334	0.547	1987.85	1086.59	0.182	1528.63	278.69
A_68_P20240054	chr1:55084325-55084372	NM_031179:-26	Sf3b1	PROMOTER	0.334	0.467	1224.59	572.11	0.156	1049.46	163.67
A_68_P21319124	chr2:71205525-71205575	NM_172436:61	Slc25a12	INSIDE	0.334	0.604	1138.58	688.07	0.202	846.80	170.93
A_68_P29581356	chr14:47896866-47896910	NM_080843:71	Socs4	INSIDE	0.334	0.538	2225.72	1196.94	0.180	1783.39	320.60
A_68_P31383394	chr17:80879061-80879105	NM_009231:711	Sos1	INSIDE	0.334	0.444	2345.35	1041.49	0.149	1857.25	275.85
A_68_P21556051	chr2:116946577-116946621	NM_033524:-587	Spred1	PROMOTER	0.334	0.440	3528.51	1554.07	0.147	2790.48	410.47
A_68_P22894258	chr4:47365465-47365509	NM_009370:-690	Tgfbr1	PROMOTER	0.334	0.574	1331.23	764.62	0.192	892.00	171.18
A_68_P31004585	chr17:3327130-3327174	NM_001122998:580	Tiam2	INSIDE	0.334	0.526	1005.00	528.23	0.176	833.81	146.50
A_68_P24760052	chr6:113481369-113481416	NM_175101:240	Tmem111	INSIDE	0.334	0.605	898.06	543.45	0.202	731.96	147.75
A_68_P20151307	chr1:36996847-36996891	NM_018872:-496	Tmem131	PROMOTER	0.334	0.430	1668.97	718.43	0.144	1315.97	188.97
A_68_P32008155	chr19:21853166-21853210	NM_001033759:357	Tmem2	INSIDE	0.334	0.550	1254.36	689.67	0.184	1016.56	186.79
A_68_P26023333	chr8:87561242-87561290	NM_001122843:200	Tnpo2	INSIDE	0.334	5.335	1922.75	10257.39	1.781	1145.10	2039.63
A_68_P30250626	chr15:58704469-58704513	NM_026642:287	Trmt12	INSIDE	0.334	0.599	984.69	590.16	0.200	773.72	154.87
A_68_P29211814	chr13:90229104-90229154	NM_028012:85	Xrcc4	INSIDE	0.334	0.629	1117.32	703.03	0.210	843.60	177.21
A_68_P27896952	chr11:69579759-69579803	NM_029348:367	Zbtb4	INSIDE	0.334	0.685	1333.10	913.29	0.229	1059.80	242.41
A_68_P28050582	chr11:97301345-97301389	ENSMUST00000152933:3768		INSIDE	0.334	4.109	3066.02	12598.36	1.371	1895.49	2598.70
A_68_P29613712	chr14:55305381-55305425	NM_001085473:366	Acin1	INSIDE	0.333	0.693	1185.67	821.88	0.231	961.80	222.15
A_68_P21761657	chr2:154483014-154483064	NM_029362:277	Chmp4b	INSIDE	0.333	0.640	875.11	559.96	0.213	680.46	145.10
A_68_P28332514	chr12:32339519-32339563	NM_028002:151	Dus4l	INSIDE	0.333	0.443	1334.63	591.46	0.148	1132.44	167.14
A_68_P22318558	chr3:89124366-89124410	NM_010108:2413	Efna3	INSIDE	0.333	1.492	4248.51	6336.96	0.496	3141.81	1559.10
A_68_P25997733	chr8:82581462-82581506	NM_020259:423	Hhip	INSIDE	0.333	0.541	1886.99	1021.05	0.180	1655.06	298.20
A_68_P21339320	chr2:74588185-74588229	NM_010468:38157	Hoxd3	DOWNSTREAM	0.333	0.619	903.43	559.59	0.207	627.49	129.62
A_68_P26674977	chr9:81526156-81526200	NM_010482:-19	Htr1b	PROMOTER	0.333	0.609	1347.49	821.18	0.203	987.29	200.17
A_68_P30290896	chr15:66117380-66117424	NM_152923:384	Kcnq3	INSIDE	0.333	0.417	2616.11	1091.34	0.139	1995.45	277.20
A_68_P29694908	chr14:69809045-69809089	NM_010921:318	Nkx3-1	INSIDE	0.333	0.617	1285.66	793.18	0.206	1005.25	206.76
A_68_P23294683	chr4:128736055-128736099	NM_029219:562	Rnf19b	INSIDE	0.333	0.527	1567.38	825.96	0.176	1141.09	200.34
A_68_P30670710	chr16:35542481-35542525	NM_013661:1055	Sema5b	INSIDE	0.333	0.693	1104.16	765.26	0.231	916.15	211.69
A_68_P30979305	chr16:94083673-94083718	NM_011377:-1809	Sim2	PROMOTER	0.333	0.645	851.23	549.43	0.215	704.95	151.40
A_68_P28159866	chr11:116395212-116395256	NM_011451:-819	Sphk1	PROMOTER	0.333	0.717	1422.35	1020.19	0.239	1032.44	246.66
A_68_P23297755	chr4:129318416-129318460	NM_001199695:-129	Txlna	PROMOTER	0.333	0.698	1677.30	1170.21	0.232	1301.70	302.60
A_68_P23591876	chr5:34278835-34278879	NM_011914:51	Whsc2	INSIDE	0.333	0.638	1238.52	789.59	0.213	1098.24	233.43
A_68_P24973685	chr7:13513884-13513935	NM_029809:1145	2310014L17Rik	INSIDE	0.332	1.825	1243.46	2269.35	0.606	918.27	556.08
A_68_P23971890	chr5:108863226-108863271	NM_007507:149	Atp5k	INSIDE	0.332	1.509	3721.60	5614.14	0.501	2764.16	1385.19
A_68_P20561487	chr1:122239035-122239079	NM_207233:1898	C1ql2	INSIDE	0.332	0.481	1353.72	650.98	0.160	984.99	157.15
A_68_P21117007	chr2:32567836-32567880	NM_130860:446	Cdk9	INSIDE	0.332	0.453	2551.54	1156.85	0.151	1980.24	298.43
A_68_P22316449	chr3:88754686-88754730	NM_001164533:-504	Dap3	PROMOTER	0.332	0.575	2457.68	1412.69	0.191	2067.19	394.06
A_68_P29330069	chr13:112476100-112476144	NM_172593:-263	Mier3	PROMOTER	0.332	0.706	1932.94	1364.94	0.235	1389.53	326.18
A_68_P30424875	chr15:89209486-89209530	NM_001013022:177	Odf3b	INSIDE	0.332	0.576	1115.25	642.53	0.191	902.01	172.46

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P24117365	chr5:136165147-136165191	NM_008898:85	Por	INSIDE	0.332	0.379	3793.96	1439.74	0.126	2873.72	362.20
A_68_P20632576	chr1:136195378-136195427	NM_001144855:34103	Ppfia4	INSIDE	0.332	1.667	1077.95	1797.29	0.554	866.36	479.93
A_68_P21630920	chr2:130468079-130468124	NM_197945:438	Prosapip1	INSIDE	0.332	1.646	1718.94	2829.56	0.546	1116.46	609.97
A_68_P26997165	chr10:21879836-21879886	NM_009016:1446	Raet1a	INSIDE	0.332	0.691	1210.19	835.66	0.230	953.47	218.83
A_68_P25506338	chr7:134732367-134732411	NM_172281:177	Rnf40	INSIDE	0.332	0.539	3684.14	1985.86	0.179	2754.98	492.71
A_68_P27673287	chr11:29073384-29073428	NM_134034:500	Smek2	INSIDE	0.332	0.541	2795.39	1511.34	0.180	1975.10	354.87
A_68_P31123427	chr17:28758620-28758664	NM_016795:757	Srpk1	INSIDE	0.332	0.652	2257.58	1471.67	0.217	1739.13	376.59
A_68_P31952189	chr19:10763284-10763328	NM_181403:2	Vps37c	INSIDE	0.332	0.460	1485.26	682.69	0.153	1210.67	184.90
A_68_P30342959	chr15:75447008-75447052	NM_001044718:-84	Zfp41	PROMOTER	0.332	0.545	2116.98	1152.76	0.181	1691.87	305.67
A_68_P25029850	chr7:30875471-30875515	NM_152814:37	Zfp566	INSIDE	0.332	0.561	1419.16	795.82	0.186	1058.68	196.97
A_68_P24385317	chr6:39823195-39823239			Unknown	0.332	0.496	1570.25	779.16	0.165	1189.38	195.85
A_68_P28613111	chr12:88288337-88288381	NM_173735:66	2310044G17Rik	INSIDE	0.331	0.515	2181.83	1123.70	0.170	1614.00	274.96
A_68_P23562892	chr5:28791826-28791870	NR_015562:-1675	9530036O11Rik	PROMOTER	0.331	0.402	1583.43	637.04	0.133	1415.85	188.76
A_68_P26888668	chr9:122203107-122203151	NM_133979:364	Ano10	INSIDE	0.331	0.662	988.54	654.43	0.219	827.93	181.41
A_68_P29234322	chr13:95129157-95129201	NM_009680:264	Ap3b1	INSIDE	0.331	0.633	2204.00	1395.02	0.210	1681.11	352.45
A_68_P28331589	chr12:32183737-32183789	NM_134048:643	Cbll1	INSIDE	0.331	0.464	1148.20	533.15	0.154	969.88	149.27
A_68_P23979846	chr5:110877794-110877838	NM_001142642:-294	Fbrsl1	PROMOTER	0.331	0.624	3872.09	2414.63	0.206	2935.11	605.59
A_68_P32152397	chr19:47939957-47940001	NM_030051:-56	Gsto2	PROMOTER	0.331	0.475	1378.65	655.14	0.157	998.53	156.94
A_68_P22748787	chr4:15076098-15076142	NM_178617:158	Necab1	INSIDE	0.331	0.639	4194.84	2680.58	0.212	3139.91	664.84
A_68_P30655996	chr16:33056959-33057003	NM_021338:381	Rpl35a	INSIDE	0.331	0.584	1016.65	593.81	0.193	742.77	143.60
A_68_P24993674	chr7:20094360-20094415	NM_025960:310	Trappc6a	INSIDE	0.331	0.575	908.18	522.04	0.190	633.11	120.39
A_68_P32217657	chr19:59240762-59240806	NM_009501:3735	Vax1	INSIDE	0.331	0.488	1580.67	770.74	0.162	1310.75	211.81
A_68_P27086283	chr10:40603268-40603315	NM_031877:-48	Wasf1	DIVERGENT_PROMOTER	0.331	0.549	1332.25	731.06	0.182	1022.21	185.78
A_68_P31939560	chr19:7457601-7457645	NM_001033139:-106	AI846148	PROMOTER	0.330	0.526	1069.98	563.05	0.173	900.28	156.12
A_68_P27176098	chr10:60149935-60149979	NM_023370:9282	Cdh23	INSIDE	0.330	0.642	1312.10	842.19	0.212	1070.71	226.74
A_68_P28036768	chr11:94981457-94981501	NM_010055:48	Dlx3	INSIDE	0.330	0.663	6824.89	4524.71	0.219	4438.31	970.14
A_68_P20264182	chr1:59538765-59538809	NM_008057:-204	Fzd7	PROMOTER	0.330	0.652	1126.55	735.04	0.215	892.72	191.95
A_68_P21129649	chr2:34627324-34627368	NM_001163434:-263	Hspa5	PROMOTER	0.330	0.648	834.51	540.35	0.214	726.60	155.31
A_68_P20229133	chr1:52874369-52874413	NM_008384:142	Inpp1	INSIDE	0.330	0.522	1016.33	530.28	0.172	755.61	130.05
A_68_P29372955	chr13:120197789-120197833	NM_008710:8	Nnt	INSIDE	0.330	0.607	2162.56	1313.26	0.201	1778.37	356.82
A_68_P26079047	chr8:97219704-97219748	NM_026385:416	Pllp	INSIDE	0.330	0.562	2488.97	1399.13	0.186	1934.41	359.31
A_68_P31830207	chr18:74367434-74367478	NM_001164355:16	Ska1	INSIDE	0.330	0.675	1542.09	1040.85	0.223	1152.40	256.59
A_68_P29517799	chr14:33276809-33276853	NM_021712:1206	Slc18a3	INSIDE	0.330	0.644	1387.88	893.81	0.212	1161.94	246.74
A_68_P32239401	chrX:7215812-7215857	NM_009305:129	Syp	INSIDE	0.330	1.564	3404.39	5325.71	0.517	1357.55	701.23
A_68_P29189772	chr13:84361804-84361848	NM_175187:-74	Tmem161b	PROMOTER	0.330	0.647	2401.18	1552.43	0.213	1935.16	412.29
A_68_P29157708	chr13:77274951-77274995	NM_001081353:176	2210408I21Rik	INSIDE	0.329	0.475	1619.18	769.42	0.156	1366.62	213.73
A_68_P29480020	chr14:26662064-26662110	NM_013469:446	Anxa11	INSIDE	0.329	0.534	1751.87	934.91	0.176	1452.69	255.29
A_68_P21334162	chr2:73730864-73730908	NM_001025093:-201	Atf2	PROMOTER	0.329	0.595	1886.52	1122.96	0.196	1416.68	277.07
A_68_P24800932	chr6:120866913-120866957	NM_007544:-96	Bid	PROMOTER	0.329	0.520	1901.47	988.02	0.171	1443.08	246.66
A_68_P25594358	chr7:149573933-149573977	NM_009983:-179	Ctsd	PROMOTER	0.329	0.444	1208.99	536.50	0.146	972.25	141.86
A_68_P21601160	chr2:125073182-125073226	NM_023595:-46	Dut	PROMOTER	0.329	0.733	4470.05	3276.61	0.241	3542.84	855.05
A_68_P28158435	chr11:116142974-116143018	NM_010254:744	Galr2	INSIDE	0.329	0.538	3090.76	1662.50	0.177	2339.73	414.36
A_68_P28185092	chr11:120392138-120392182	NM_008101:120	Gcgr	INSIDE	0.329	0.476	2115.77	1007.90	0.157	1706.84	267.17
A_68_P24226572	chr6:8459387-8459431	NM_133236:-187	Glcci1	PROMOTER	0.329	0.407	1976.94	804.00	0.134	1662.49	222.59
A_68_P29569518	chr14:45840204-45840248	NM_027518:835	Gpr137c	INSIDE	0.329	0.680	1405.75	955.29	0.224	1019.18	227.96
A_68_P24589794	chr6:82723294-82723338	NM_013820:1132	Hk2	INSIDE	0.329	0.638	1871.92	1194.40	0.210	1528.37	321.29
A_68_P24449036	chr6:52153762-52153806	NM_010453:802	Hoxa5	INSIDE	0.329	0.520	1406.56	730.98	0.171	1068.76	182.49
A_68_P28104645	chr11:106861028-106861074	NM_010655:-211	Kpna2	PROMOTER	0.329	0.625	924.17	577.41	0.205	751.86	154.49
A_68_P31926078	chr19:4962474-4962518	NM_025553:191	Mrpl11	INSIDE	0.329	0.617	1433.26	883.99	0.203	1195.39	242.70
A_68_P27271611	chr10:77471981-77472025	NM_008826:539	Pfkl	INSIDE	0.329	0.529	1010.60	534.75	0.174	660.99	114.95
A_68_P27993894	chr11:87171685-87171729	NM_177167:790	Ppm1e	INSIDE	0.329	0.528	3696.59	1953.44	0.174	2917.15	507.29

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28074045	chr11:101329337-101329381	NM_009708:-293	Rnd2	DIVERGENT_PROMOTER	0.329	0.513	1295.32	664.66	0.169	1087.51	183.31
A_68_P27165500	chr10:58275328-58275372	NM_172788:-756	Sh3rf3	PROMOTER	0.329	0.424	1488.26	630.44	0.140	1073.55	149.81
A_68_P31929160	chr19:5510818-5510862	NM_001024560:-351	Snx32	PROMOTER	0.329	1.631	6529.73	10647.34	0.537	4546.26	2442.33
A_68_P23328077	chr4:134908288-134908332	NM_001130477:819	Srrm1	INSIDE	0.329	0.459	2385.61	1096.13	0.151	1846.87	279.42
A_68_P22411407	chr3:108029536-108029580	NM_008596:-41	Sypl2	PROMOTER	0.329	0.624	909.47	567.79	0.206	664.03	136.49
A_68_P27780098	chr11:48630599-48630643	NM_145377:273	Trim41	INSIDE	0.329	0.491	1747.72	857.96	0.161	1283.11	207.09
A_68_P23756354	chr5:65826840-65826884	NM_009466:219	Ugdh	INSIDE	0.329	0.477	1619.17	772.85	0.157	1266.07	199.08
A_68_P24135897	chr5:139960495-139960539	NM_001159908:-71	Zfand2a	PROMOTER	0.329	0.677	1149.23	777.68	0.223	972.75	216.67
A_68_P23417006	chr4:151552589-151552633	NM_001146057:-7632	Acot7	PROMOTER	0.328	0.435	1700.38	738.82	0.143	1283.70	183.01
A_68_P25352110	chr7:104886718-104886762	NM_175105:17	Aqp11	INSIDE	0.328	0.687	3990.52	2741.02	0.226	3126.19	705.20
A_68_P24735111	chr6:108610435-108610479	NM_011498:-166	Bhlhe40	PROMOTER	0.328	0.495	1175.97	581.53	0.162	957.28	155.05
A_68_P31764313	chr18:62708319-62708363	NM_134136:57	Fbxo38	INSIDE	0.328	0.651	1387.03	902.87	0.214	988.00	211.00
A_68_P21071306	chr2:25166855-25166901	NM_001177656:7805	Grin1	INSIDE	0.328	0.573	1554.63	890.80	0.188	1255.65	236.24
A_68_P23416912	chr4:151533736-151533780	NM_008236:783	Hes2	INSIDE	0.328	0.644	2289.50	1473.88	0.211	1490.45	314.73
A_68_P25092713	chr7:52625245-52625289	NM_011698:668	Lin7b	INSIDE	0.328	0.646	1494.01	964.68	0.212	1244.88	264.01
A_68_P28032108	chr11:94182771-94182815	NM_026313:433	Luc7l3	INSIDE	0.328	1.743	7729.97	13474.87	0.571	4792.05	2736.04
A_68_P30127810	chr15:34236528-34236572	NM_016762:115	Matn2	INSIDE	0.328	0.640	2207.22	1411.80	0.210	1655.60	346.92
A_68_P20156457	chr1:37947122-37947166	NM_026913:112	Mitd1	INSIDE	0.328	0.498	1063.49	529.09	0.163	719.51	117.41
A_68_P20185544	chr1:42908420-42908464	NM_023514:365	Mrps9	INSIDE	0.328	0.678	1127.31	763.76	0.222	885.66	196.52
A_68_P31934664	chr19:6428736-6428780	NM_001205234:10021	Nrxn2	INSIDE	0.328	0.603	1095.93	660.62	0.198	815.98	161.49
A_68_P21350016	chr2:76244453-76244497	NM_145525:-120	Osbpl6	PROMOTER	0.328	0.405	1936.43	783.94	0.133	1603.37	213.03
A_68_P31923508	chr19:4510485-4510529	NM_001162946:35	Pcx	INSIDE	0.328	0.570	1057.80	603.33	0.187	953.77	178.46
A_68_P30652430	chr16:32431382-32431427	NM_001163160:89	Pcyt1a	INSIDE	0.328	0.516	1340.09	691.10	0.169	1008.66	170.45
A_68_P24293210	chr6:22825825-22825869	NM_001081306:345	Ptprz1	INSIDE	0.328	0.540	1458.38	787.56	0.177	1115.51	197.31
A_68_P30575819	chr16:17807668-17807712	NM_153790:10316	Scarf2	INSIDE	0.328	0.515	3124.31	1609.55	0.169	2519.47	425.42
A_68_P27915802	chr11:73012820-73012864	NM_029031:-141	Shpk	DIVERGENT_PROMOTER	0.328	0.550	1385.83	762.72	0.180	1062.94	191.67
A_68_P23668849	chr5:48375003-48375047	NM_178804:631	Slit2	INSIDE	0.328	0.737	2370.43	1748.07	0.242	1695.31	409.93
A_68_P20625944	chr1:135060292-135060341			Unknown	0.328	0.625	1139.43	712.71	0.205	992.46	203.85
A_68_P21070791	chr2:25096537-25096581	NM_026415:-1141	2310002J15Rik	DIVERGENT_PROMOTER	0.327	0.621	1681.19	1044.39	0.203	1276.40	259.49
A_68_P24449864	chr6:52264164-52264215	NR_038163:637	5730457N03Rik	INSIDE	0.327	0.527	1015.98	535.84	0.173	706.77	122.05
A_68_P23364698	chr4:141102196-141102247	NR_030695:145	B330016D10Rik	INSIDE	0.327	0.686	1102.77	757.05	0.224	841.11	188.80
A_68_P27275483	chr10:78215546-78215590	NM_027630:244	Ccdc105	INSIDE	0.327	0.515	1222.98	630.21	0.168	988.39	166.34
A_68_P21715592	chr2:145760196-145760240	NM_025820:218	Crnkl1	INSIDE	0.327	0.435	1660.27	722.48	0.142	1238.30	176.21
A_68_P27288000	chr10:80652951-80652995	NM_007828:6310	Dapk3	INSIDE	0.327	1.782	1669.49	2975.08	0.583	1158.49	674.86
A_68_P21113205	chr2:31938737-31938781	NM_175511:467	Fam78a	INSIDE	0.327	0.594	2244.07	1333.68	0.194	1629.12	316.59
A_68_P31121750	chr17:28450482-28450526	NM_001163819:30	Fance	INSIDE	0.327	0.719	1777.05	1277.97	0.235	1349.73	317.35
A_68_P23917033	chr5:98683430-98683474	NM_010203:250	Fgf5	INSIDE	0.327	0.615	1605.45	987.03	0.201	1412.65	283.62
A_68_P23999715	chr5:114185534-114185578	NM_001010825:-234	Ficd	PROMOTER	0.327	0.464	2132.62	988.98	0.152	1495.81	226.98
A_68_P30925866	chr16:84835027-84835071	NM_008065:-320	Gabpa	PROMOTER	0.327	0.631	3756.39	2371.05	0.206	2791.11	575.64
A_68_P29660137	chr14:63870430-63870474	NM_008092:-6355	Gata4	PROMOTER	0.327	0.660	2536.61	1675.09	0.216	1862.65	402.08
A_68_P23576909	chr5:31481980-31482025	NM_027901:515	Gtf3c2	INSIDE	0.327	0.613	948.93	581.83	0.201	714.94	143.48
A_68_P30634660	chr16:29210031-29210075	NM_013751:272	Hrasls	INSIDE	0.327	2.119	4365.10	9249.79	0.692	3160.65	2188.69
A_68_P22311640	chr3:87886128-87886172	NM_001033484:178	Iqgap3	INSIDE	0.327	0.640	1080.27	691.66	0.209	843.99	176.78
A_68_P29508895	chr14:31764856-31764900	NM_011849:205	Nek4	INSIDE	0.327	0.545	1412.27	769.22	0.178	1179.76	209.82
A_68_P25948236	chr8:72356467-72356516	NM_001024954:-111	Pbx4	PROMOTER	0.327	0.419	1294.35	542.72	0.137	1029.47	141.14
A_68_P21580771	chr2:121240143-121240187	NM_007952:527	Pdia3	INSIDE	0.327	0.376	2675.08	1004.86	0.123	2061.48	253.29
A_68_P21706810	chr2:144194546-144194590	NM_001164813:-150	Pet117	PROMOTER	0.327	0.472	1145.94	541.12	0.155	963.15	148.85
A_68_P31108117	chr17:26204538-26204582	NM_001162868:1562	Rab11fip3	INSIDE	0.327	0.619	1921.83	1189.49	0.203	1359.32	275.42
A_68_P32203265	chr19:56896867-56896911	NM_001002238:-3810	Tdrd1	DIVERGENT_PROMOTER	0.327	0.652	2194.29	1431.00	0.214	1674.06	357.47
A_68_P26290457	chr9:8004110-8004154	NM_001171147:464	Yap1	INSIDE	0.327	0.634	3063.78	1942.36	0.207	2456.14	508.50
A_68_P20505868	chr1:107886770-107886814	NM_001122675:-190	Zcchc2	PROMOTER	0.327	0.533	1625.06	865.63	0.174	1208.30	210.16

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26568895	chr9:61969849-61969894	mmu-mir-5133:530		DOWNSTREAM	0.327	1.476	2048.18	3023.30	0.482	1436.89	692.68
A_68_P26888673	chr9:122203754-122203798	NM_133979:-284	Ano10	PROMOTER	0.326	1.412	6995.73	9875.00	0.460	4283.64	1970.44
A_68_P26797104	chr9:105297728-105297772	NM_001164828:-5367	Aste1	PROMOTER	0.326	0.267	2822.70	753.01	0.087	2039.80	177.66
A_68_P24800510	chr6:120786535-120786579	NM_153516:309	Bcl2l13	INSIDE	0.326	0.375	2013.72	755.91	0.122	1678.70	205.41
A_68_P27533698	chr10:126486217-126486263	NM_010009:939	Cyp27b1	INSIDE	0.326	0.365	1690.55	617.35	0.119	1110.02	132.01
A_68_P23222366	chr4:114598399-114598443	NM_015758:198	Foxe3	INSIDE	0.326	0.370	2556.91	946.80	0.121	2042.06	246.38
A_68_P26134292	chr8:108042458-108042502	NM_008289:-165	Hsd11b2	PROMOTER	0.326	0.425	1518.41	646.07	0.139	1128.21	156.61
A_68_P25965612	chr8:75877517-75877561	NM_010687:-1083	Large	PROMOTER	0.326	0.325	2752.12	893.29	0.106	1869.82	197.79
A_68_P25848476	chr8:49641034-49641078	NM_001145937:118988	Odz3	INSIDE	0.326	1.385	4524.73	6265.24	0.452	3103.08	1401.44
A_68_P25173477	chr7:70902398-70902442	NM_130880:312763	Otud7a	INSIDE	0.326	0.460	1275.32	586.99	0.150	1055.58	158.56
A_68_P22652203	chr3:152377356-152377400	NM_025662:315	Pigk	INSIDE	0.326	0.501	1096.58	549.24	0.163	905.32	147.86
A_68_P25589079	chr7:148660855-148660899	NM_025593:176	Polr2l	INSIDE	0.326	1.338	11219.53	15007.40	0.436	8052.58	3511.85
A_68_P21871015	chr2:173485606-173485650	NM_024436:283	Rab22a	INSIDE	0.326	0.522	1322.49	689.96	0.170	1079.65	183.49
A_68_P22449707	chr3:116211186-116211230	NM_025517:-115	Rtcd1	DIVERGENT_PROMOTER	0.326	0.545	1821.44	993.37	0.178	1535.89	273.01
A_68_P24325499	chr6:29222771-29222816	NM_023516:168	2310016C08Rik	INSIDE	0.325	0.492	1529.09	752.07	0.160	1159.55	185.56
A_68_P26397638	chr9:30729092-30729141	NM_001024139:921	Adamts15	INSIDE	0.325	0.630	1640.84	1034.07	0.205	1173.36	240.07
A_68_P27143033	chr10:53316773-53316825	NM_025541:32	Asf1a	INSIDE	0.325	0.576	1402.87	808.05	0.187	1079.97	202.03
A_68_P20936667	chr1:193007287-193007331	NM_007498:-96	Atf3	PROMOTER	0.325	0.558	3284.36	1832.38	0.182	2456.72	446.10
A_68_P25007802	chr7:25790777-25790821	NM_144921:116	Atp1a3	INSIDE	0.325	0.643	1282.34	824.20	0.209	1114.82	232.54
A_68_P20600402	chr1:130313507-130313551	NM_177445:465	Dars	INSIDE	0.325	0.686	1909.72	1310.50	0.223	1426.18	317.99
A_68_P21320135	chr2:71384020-71384064	NM_010054:769	Dlx2	INSIDE	0.325	0.585	2056.74	1203.82	0.190	1438.81	273.76
A_68_P26344425	chr9:20702979-20703023	NM_016876:34	Eif3g	INSIDE	0.325	0.497	2891.30	1437.01	0.162	2273.68	367.67
A_68_P21874766	chr2:174156274-174156318	NM_001077510:707	Gnas	INSIDE	0.325	0.643	1812.77	1166.24	0.209	1502.48	313.93
A_68_P21331225	chr2:73224765-73224809	NM_001190297:-331	Gpr155	PROMOTER	0.325	0.588	2712.39	1594.02	0.191	2026.63	386.67
A_68_P28614428	chr12:88487974-88488018	NM_010363:-671	Gstz1	PROMOTER	0.325	0.678	2336.86	1583.57	0.220	1908.15	420.14
A_68_P25502653	chr7:134005799-134005843	NM_172746:335	Hirip3	INSIDE	0.325	0.426	1549.80	659.52	0.138	1328.85	183.58
A_68_P26809753	chr9:107489861-107489907	NM_025903:-164	Ifrd2	PROMOTER	0.325	0.636	3494.17	2221.47	0.207	2465.15	509.70
A_68_P21147673	chr2:38210263-38210310	NM_010710:3459	Lhx2	INSIDE	0.325	0.537	2109.82	1133.30	0.174	1665.38	290.44
A_68_P22951805	chr4:58566279-58566323	NM_172989:-135	Lpar1	PROMOTER	0.325	0.581	1485.20	862.66	0.189	1231.58	232.16
A_68_P29348449	chr13:115608614-115608659	NM_001113374:192	Mocs2	INSIDE	0.325	0.651	973.07	633.63	0.211	793.11	167.72
A_68_P25578887	chr7:146767017-146767061	NR_027857:1658	Nkx6-2	INSIDE	0.325	0.674	1031.65	695.50	0.219	841.23	184.36
A_68_P21102303	chr2:30142233-30142277	NM_198304:302	Nup188	INSIDE	0.325	0.431	2753.10	1187.89	0.140	2026.23	284.10
A_68_P27840802	chr11:59919053-59919097	NM_009021:560	Rai1	INSIDE	0.325	0.609	4194.73	2555.13	0.198	3321.06	658.23
A_68_P22207866	chr3:66782104-66782148	NM_013665:3567	Shox2	INSIDE	0.325	0.738	3000.19	2215.07	0.240	2068.51	496.71
A_68_P30999921	chr16:97832578-97832622	NM_015775:202	Tmprss2	INSIDE	0.325	0.387	1770.06	685.77	0.126	1448.29	182.21
A_68_P23594730	chr5:34856051-34856097	NM_139064:554	Tnip2	INSIDE	0.325	1.737	1122.27	1949.46	0.565	867.02	490.08
A_68_P27780212	chr11:48650835-48650879	NM_053166:11217	Trim7	INSIDE	0.325	0.690	1523.39	1050.85	0.224	1105.36	247.47
A_68_P24287930	chr6:21801755-21801799	NM_173007:739	Tspan12	INSIDE	0.325	0.579	2836.66	1641.35	0.188	2156.87	406.19
A_68_P28332516	chr12:32339734-32339779	NM_001163126:23	Cog5	INSIDE	0.324	0.516	1819.70	938.79	0.167	1454.03	243.41
A_68_P28737540	chr12:111516152-111516199	NR_002866:103	Dio3os	INSIDE	0.324	0.378	1660.43	627.60	0.122	1385.18	169.57
A_68_P27928209	chr11:75609329-75609373	NM_007873:209	Doc2b	INSIDE	0.324	0.409	2502.99	1024.49	0.132	1958.78	259.37
A_68_P28863232	chr13:19711147-19711191	NM_134065:531	Epdr1	INSIDE	0.324	0.475	1194.76	568.01	0.154	934.33	143.87
A_68_P30089764	chr15:26824671-26824715	NM_176959:627	Fbxl7	INSIDE	0.324	0.629	2508.25	1578.89	0.204	1946.34	397.18
A_68_P23331228	chr4:135476820-135476864	NM_024243:202	Fuca1	INSIDE	0.324	0.616	1569.76	967.72	0.200	1295.05	258.75
A_68_P27826626	chr11:57458476-57458520	NM_134189:-445	Galnt10	PROMOTER	0.324	0.668	1176.19	786.21	0.217	976.16	211.69
A_68_P25952872	chr8:73119238-73119282	NM_023627:881	Isyna1	INSIDE	0.324	1.460	800.52	1168.77	0.473	778.01	367.89
A_68_P25954143	chr8:73321298-73321342	NM_199308:-4988	Mast3	PROMOTER	0.324	1.546	3449.19	5331.35	0.501	2349.00	1176.71
A_68_P21761151	chr2:154384393-154384437	NM_021546:175	Necab3	INSIDE	0.324	1.466	1381.50	2025.28	0.475	1131.57	537.67
A_68_P21820025	chr2:164659401-164659445	NM_001082974:-326	Neurl2	PROMOTER	0.324	0.551	2199.28	1212.46	0.178	1636.93	292.07
A_68_P26823555	chr9:110310525-110310569	NM_001081043:168	Ptpn23	INSIDE	0.324	0.428	1786.44	765.15	0.139	1351.38	187.53
A_68_P26628305	chr9:72379707-72379757	NM_001033536:-314	Rfx7	PROMOTER	0.324	0.657	823.83	540.96	0.213	566.59	120.64

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25408483	chr7:116662453-116662497	NM_011975:-234	Rpl27a	PROMOTER	0.324	0.709	2713.74	1924.57	0.230	1975.60	454.47
A_68_P27830409	chr11:58144073-58144117	NM_001161338:-125	Sh3bp5l	DIVERGENT_PROMOTER	0.324	0.681	1229.07	836.78	0.220	858.93	189.18
A_68_P28168283	chr11:117829826-117829870	NM_007707:832	Socs3	INSIDE	0.324	0.656	1019.69	668.44	0.212	822.72	174.58
A_68_P21749117	chr2:152222565-152222609	NM_011438:1196	Sox12	INSIDE	0.324	0.582	2264.60	1317.36	0.188	1759.69	331.63
A_68_P26504538	chr9:50412116-50412160	NM_013897:133	Timm8b	INSIDE	0.324	0.599	3069.78	1838.08	0.194	2210.71	428.87
A_68_P32742644	chrX:147091720-147091764	NM_001002272:237	Tro	INSIDE	0.324	1.623	1668.43	2707.75	0.526	803.83	423.10
A_68_P30084538	chr15:25914029-25914073	NM_144523:-70	Zfp622	PROMOTER	0.324	0.545	2913.87	1587.63	0.177	2220.02	392.50
A_68_P24397786	chr6:42300193-42300237	NM_011777:388	Zyx	INSIDE	0.324	0.509	3123.25	1591.09	0.165	2268.68	374.48
A_68_P24385307	chr6:39822258-39822302			Unknown	0.324	0.494	1253.82	618.76	0.160	1039.83	166.27
A_68_P30931901	chr16:85900910-85900966	NM_011782:432	Adamts5	INSIDE	0.323	0.482	1808.46	872.30	0.156	1374.78	214.52
A_68_P32202579	chr19:56797245-56797289	NM_007419:405	Adrb1	INSIDE	0.323	0.619	1423.99	880.90	0.200	1004.83	200.82
A_68_P23897552	chr5:93473776-93473820	NM_175270:250	Ankrd56	INSIDE	0.323	0.413	1290.56	532.86	0.133	1022.51	136.49
A_68_P23397203	chr4:148265241-148265285	NM_027195:86762	Casz1	INSIDE	0.323	0.745	3039.69	2264.27	0.241	2187.80	526.88
A_68_P24934669	chr6:147424894-147424938	NM_025911:524	Ccdc91	INSIDE	0.323	0.543	1210.07	657.52	0.175	1003.08	175.85
A_68_P30778453	chr16:55934660-55934704	NM_028815:279	Cep97	INSIDE	0.323	0.616	1514.17	932.49	0.199	1096.48	218.02
A_68_P21425776	chr2:91815643-91815687	NM_011957:48663	Creb3l1	DOWNSTREAM	0.323	0.554	1548.19	858.35	0.179	1192.03	213.29
A_68_P29446595	chr14:21207859-21207903	NM_134081:252	Dnajc9	INSIDE	0.323	0.410	2167.14	887.53	0.132	1525.68	201.53
A_68_P28865540	chr13:20183015-20183059	NM_080288:661	Elmo1	INSIDE	0.323	0.557	1580.09	880.66	0.180	1222.61	220.38
A_68_P26161392	chr8:112741955-112741999	NM_146215:117	Ftsjd1	INSIDE	0.323	0.714	3057.34	2182.95	0.231	2212.69	510.79
A_68_P25949229	chr8:72520506-72520550	NM_001113345:-250	Gatad2a	PROMOTER	0.323	0.338	3200.59	1082.52	0.109	2626.20	286.70
A_68_P23591967	chr5:34326256-34326300	NM_001033458:156	Gm1673	INSIDE	0.323	0.440	4056.81	1783.20	0.142	3021.30	429.15
A_68_P23134315	chr4:97438906-97438950	NM_001122953:-5388	Nfia	PROMOTER	0.323	0.625	892.54	557.84	0.202	796.05	160.61
A_68_P22558744	chr3:136333820-136333864	NM_008913:109	Ppp3ca	INSIDE	0.323	0.507	1318.47	668.10	0.164	975.43	159.85
A_68_P25091295	chr7:52384233-52384280	NM_009438:-151	Rpl13a	PROMOTER	0.323	0.453	1250.08	566.51	0.146	818.09	119.58
A_68_P26998899	chr10:22365156-22365200	NM_178934:362	Slc2a12	INSIDE	0.323	0.737	2954.87	2176.30	0.238	2393.14	568.74
A_68_P25576402	chr7:146399285-146399329	NM_001162540:-100	Stk32c	PROMOTER	0.323	0.472	2110.43	995.44	0.152	1549.76	236.26
A_68_P29243708	chr13:96731321-96731365	NM_029210:171190	Sv2c	INSIDE	0.323	0.541	1120.33	605.63	0.175	969.44	169.49
A_68_P32488666	chrX:78316434-78316478	NM_138751:474	Tmem47	INSIDE	0.323	1.684	2769.27	4664.43	0.545	987.39	537.79
A_68_P24629444	chr6:89594337-89594382	NM_001178058:378	Txnrd3	INSIDE	0.323	0.633	850.49	538.49	0.205	606.75	124.15
A_68_P24938726	chr6:148160773-148160817	NR_015615:-15	4732416N19Rik	PROMOTER	0.322	0.722	4696.46	3388.84	0.233	3349.09	778.85
A_68_P25471460	chr7:128126217-128126263	NM_028955:218	4933427G17Rik	INSIDE	0.322	0.594	1391.28	826.12	0.191	1011.77	193.60
A_68_P31145139	chr17:32487576-32487627	NM_017476:-79	Akap8l	PROMOTER	0.322	0.500	1310.92	655.00	0.161	954.49	153.79
A_68_P27912780	chr11:72503452-72503496	NM_009671:-29	Ankfy1	PROMOTER	0.322	1.388	2307.87	3202.55	0.447	1454.93	649.83
A_68_P25435069	chr7:121398243-121398287	NM_033370:-70	Copb1	PROMOTER	0.322	0.582	1570.16	913.29	0.187	1374.61	257.32
A_68_P32242173	chrX:7769712-7769759	NM_007898:903	Ebp	INSIDE	0.322	1.416	1649.64	2336.36	0.456	820.88	374.58
A_68_P20332287	chr1:71699659-71699703	NM_010233:65	Fn1	INSIDE	0.322	0.637	2362.01	1505.54	0.205	1784.10	366.11
A_68_P28703487	chr12:105711415-105711459	NM_010351:10	Gsc	INSIDE	0.322	0.584	988.58	576.92	0.188	823.69	154.66
A_68_P25957092	chr8:74012930-74012974	NM_032544:951	Gtpbp3	INSIDE	0.322	0.566	904.37	511.45	0.182	668.64	121.76
A_68_P27534887	chr10:126700073-126700117	NM_001039000:325	Kif5a	INSIDE	0.322	0.635	3511.08	2229.25	0.205	2525.28	516.91
A_68_P30350131	chr15:76541158-76541202	NM_145471:11	Lrrc14	INSIDE	0.322	0.642	2574.57	1652.84	0.207	1800.54	372.39
A_68_P31926004	chr19:4942668-4942712	NM_172835:402	Peli3	INSIDE	0.322	0.727	3180.37	2313.19	0.234	2465.11	577.80
A_68_P25308131	chr7:96665783-96665827	NM_029614:292	Prss23	INSIDE	0.322	0.621	1100.59	683.16	0.200	944.67	188.58
A_68_P30879835	chr16:75593202-75593246	NM_198302:89	Rbm11	INSIDE	0.322	0.573	1181.66	676.84	0.185	981.41	181.14
A_68_P28033654	chr11:94410127-94410174	NM_001013381:371	Rsad1	INSIDE	0.322	0.576	1069.18	615.52	0.186	777.58	144.35
A_68_P25504557	chr7:134351496-134351540	NM_144522:464	Tbc1d10b	INSIDE	0.322	0.584	1091.21	637.29	0.188	691.62	130.07
A_68_P23293635	chr4:128561085-128561129	NM_178110:-277	Trim62	PROMOTER	0.322	0.694	1071.89	743.45	0.224	794.08	177.50
A_68_P29005200	chr13:46059987-46060031	NM_009124:337	Atxn1	INSIDE	0.321	0.681	2019.49	1376.26	0.219	1592.59	348.06
A_68_P23094686	chr4:88922820-88922864	NM_001040654:5254	Cdkn2a	INSIDE	0.321	0.573	1402.32	803.61	0.184	1077.56	197.99
A_68_P31919590	chr19:3852379-3852423	NM_001025566:628	Chka	INSIDE	0.321	0.475	1951.50	927.80	0.152	1485.68	226.50
A_68_P25089991	chr7:52151549-52151593	NM_027376:122	Fuz	INSIDE	0.321	0.553	1968.66	1087.93	0.177	1562.48	277.33
A_68_P29338084	chr13:113784193-113784237	NM_001037914:139	Gm6320	INSIDE	0.321	0.575	1394.98	801.53	0.185	1268.59	234.19

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26546335	chr9:58046426-58046470	NM_001161535:3074	Islr2	INSIDE	0.321	0.410	1624.17	665.74	0.132	1391.94	183.04
A_68_P30964671	chr16:91730311-91730355	NM_001110276:717	Itsn1	INSIDE	0.321	0.667	3983.80	2655.88	0.214	2907.28	621.89
A_68_P23374709	chr4:142939818-142939864	NM_001162983:188	Lrrc38	INSIDE	0.321	0.588	916.58	538.54	0.188	728.77	137.35
A_68_P25279940	chr7:90014576-90014620	NM_175366:-1244	Mex3b	PROMOTER	0.321	0.602	1372.26	826.29	0.193	1055.62	203.99
A_68_P27567706	chr11:6191780-6191824	NM_010956:203	Ogdh	INSIDE	0.321	0.474	2299.39	1088.84	0.152	1778.73	270.62
A_68_P23720370	chr5:58111147-58111191	NM_018764:1909	Pcdh7	INSIDE	0.321	0.426	3975.06	1691.86	0.137	3268.28	446.41
A_68_P23593815	chr5:34679727-34679773	NM_011278:712	Rnf4	INSIDE	0.321	0.566	1040.25	588.55	0.181	829.14	150.44
A_68_P25091298	chr7:52384568-52384612	NM_009438:-485	Rpl13a	PROMOTER	0.321	0.469	1320.06	619.18	0.151	1028.48	154.80
A_68_P32036090	chr19:26681592-26681637	NM_011416:1965	Smarca2	INSIDE	0.321	1.760	1990.52	3503.15	0.564	1480.23	835.27
A_68_P25186101	chr7:73205809-73205860	NM_021336:613	Snrpa1	INSIDE	0.321	0.520	1014.95	527.50	0.167	724.25	120.79
A_68_P22339769	chr3:94386307-94386351	NM_029721:296	Snx27	INSIDE	0.321	0.349	4540.45	1585.08	0.112	3089.74	346.00
A_68_P20736172	chr1:157005611-157005658	NM_021433:-198	Stx6	PROMOTER	0.321	0.538	1076.13	578.77	0.173	864.75	149.38
A_68_P30574321	chr16:17530648-17530693	NM_026909:475	Thap7	INSIDE	0.321	0.704	1900.52	1338.88	0.226	1359.50	307.82
A_68_P31206979	chr17:46592282-46592326	NM_001162864:32320	Ttbk1	INSIDE	0.321	0.442	2903.34	1284.53	0.142	2013.32	286.35
A_68_P31131060	chr17:30141259-30141303	NM_148926:-751	Zfand3	PROMOTER	0.321	0.624	1409.90	879.83	0.200	1049.12	209.91
A_68_P31403204	chr17:84587274-84587318	NM_001001806:-9	Zfp36l2	PROMOTER	0.321	0.316	3508.71	1107.40	0.101	2651.07	268.22
A_68_P30261322	chr15:60654906-60654950	NR_030696:409	9930014A18Rik	INSIDE	0.320	1.433	1224.73	1755.61	0.458	1001.38	458.70
A_68_P21568396	chr2:119034800-119034844	NM_139139:-291	Dnajc17	PROMOTER	0.320	0.621	1302.31	808.98	0.199	1076.80	213.97
A_68_P23274592	chr4:125168108-125168152	NM_001081097:56	Grik3	INSIDE	0.320	0.504	1342.14	676.59	0.161	1178.43	190.25
A_68_P24982506	chr7:17200789-17200833	NM_172739:-468	Grlf1	PROMOTER	0.320	0.468	3258.55	1524.24	0.150	2453.71	366.86
A_68_P23352775	chr4:139130999-139131044	NM_001205173:387	Iffo2	INSIDE	0.320	0.390	1390.57	542.36	0.125	1300.49	162.46
A_68_P21842484	chr2:168426628-168426674	NM_001037178:505	Nfatc2	INSIDE	0.320	0.543	1560.13	847.85	0.174	1209.19	210.28
A_68_P22878698	chr4:44723640-44723686	NM_008782:-350	Pax5	PROMOTER	0.320	0.538	1095.77	589.27	0.172	901.83	155.05
A_68_P29753373	chr14:80173634-80173678	NM_001042726:-2537	Pcdh8	PROMOTER	0.320	0.556	1738.60	966.09	0.178	1417.39	252.02
A_68_P23232647	chr4:116806257-116806301	NM_013807:279	Plk3	INSIDE	0.320	0.519	1158.08	600.85	0.166	940.16	155.99
A_68_P27385035	chr10:98569435-98569486	NM_027740:-344	Poc1b	PROMOTER	0.320	0.651	1178.64	767.44	0.208	885.98	184.52
A_68_P26136633	chr8:108424693-108424737	NM_173432:341	Pskh1	INSIDE	0.320	0.553	2032.17	1122.90	0.177	1481.30	262.11
A_68_P28974206	chr13:40828928-40828972	NM_001122948:-3138	Tcfap2a	PROMOTER	0.320	0.595	1180.07	702.09	0.191	875.83	166.86
A_68_P22336416	chr3:93250348-93250392	NM_001163098:4119	Tchh	INSIDE	0.320	0.503	1545.93	777.32	0.161	1305.03	210.06
A_68_P21396040	chr2:84888732-84888776	NM_001081260:-1862	Tnks1bp1	PROMOTER	0.320	0.685	1542.69	1056.32	0.219	1141.47	250.15
A_68_P24950633	chr7:4763653-4763698	NM_133777:267	Ube2s	INSIDE	0.320	0.696	2552.57	1776.55	0.223	1803.54	401.60
A_68_P30084535	chr15:25913713-25913757	NM_144523:-386	Zfp622	PROMOTER	0.320	0.589	1339.31	788.35	0.188	1004.97	189.42
A_68_P31465567	chr18:4920993-4921047	ENSMUST00000143254:-703		PROMOTER	0.320	0.521	1024.66	534.01	0.167	865.10	144.32
A_68_P27765617	chr11:45869706-45869750	NM_009616:240	Adam19	INSIDE	0.319	0.584	2450.04	1431.58	0.186	1938.75	361.00
A_68_P32260348	chrX:11665608-11665652	NM_029510:-7951	Bcor	PROMOTER	0.319	0.565	1677.90	947.72	0.180	676.34	121.68
A_68_P23397714	chr4:148326567-148326611	NM_001159344:148088	Casz1	INSIDE	0.319	0.446	4925.34	2196.24	0.142	3600.04	511.90
A_68_P21325835	chr2:72314881-72314927	NM_025866:629	Cdca7	INSIDE	0.319	0.669	1191.25	796.55	0.214	945.63	201.98
A_68_P28143433	chr11:113546017-113546061	NM_177777:313	D11Wsu47e	INSIDE	0.319	0.698	1910.64	1333.85	0.222	1321.37	294.00
A_68_P29488027	chr14:28436033-28436077	NM_177814:427	Erc2	INSIDE	0.319	1.875	4506.26	8451.34	0.599	2846.84	1705.57
A_68_P32461568	chrX:70473551-70473595	NM_007978:-72	F8a	PROMOTER	0.319	1.492	1712.51	2555.71	0.476	617.47	293.75
A_68_P21784859	chr2:158593842-158593886	NM_027975:30	Fam83d	INSIDE	0.319	0.389	2629.73	1022.84	0.124	2015.92	250.46
A_68_P27561155	chr11:4962120-4962164	NM_001190406:3188	Gas2l1	INSIDE	0.319	0.639	1889.53	1208.16	0.204	1423.13	290.20
A_68_P24980081	chr7:16760697-16760741	NM_008627:-10	Meis3	PROMOTER	0.319	0.416	1308.51	543.77	0.133	1110.65	147.46
A_68_P25471699	chr7:128177893-128177937	NM_021554:-44	Mettl9	PROMOTER	0.319	0.628	917.67	575.84	0.200	724.47	145.05
A_68_P20224249	chr1:51972342-51972397	NM_001161817:449	Myo1b	INSIDE	0.319	0.593	953.15	565.63	0.189	766.66	145.17
A_68_P21199928	chr2:48804507-48804551	NR_033442:259	Orc4	INSIDE	0.319	0.641	1113.59	713.64	0.204	871.92	178.04
A_68_P24595788	chr6:83781684-83781728	NM_146169:29	Paip2b	INSIDE	0.319	0.442	1996.92	883.24	0.141	1585.98	223.94
A_68_P32089879	chr19:36483936-36483983	NM_029508:30403	Pcgf5	INSIDE	0.319	0.629	1456.26	915.91	0.201	1108.73	222.72
A_68_P30441118	chr15:92227846-92227890	NM_001164593:628	Pdzrn4	INSIDE	0.319	0.533	1499.69	799.03	0.170	1237.59	210.44
A_68_P31256335	chr17:56601867-56601911	NM_011218:14015	Ptprs	INSIDE	0.319	0.480	1171.26	561.67	0.153	790.94	121.16
A_68_P29430092	chr14:17408235-17408279	NM_011243:-532	Rarb	PROMOTER	0.319	0.438	2884.54	1262.51	0.140	2205.74	308.24

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P30575777	chr16:17802822-17802869	NM_153790:5471	Scarf2	INSIDE	0.319	0.660	996.82	658.39	0.211	732.58	154.45
A_68_P27131116	chr10:50614810-50614854	NM_011376:-624	Sim1	PROMOTER	0.319	0.516	2206.95	1138.45	0.164	1878.92	308.99
A_68_P24039147	chr5:120961336-120961380	NM_001177594:158	Slc24a6	INSIDE	0.319	0.473	1197.17	566.24	0.151	803.21	121.16
A_68_P27176491	chr10:60215496-60215540	NM_023596:12	Slc29a3	INSIDE	0.319	0.461	4027.72	1857.59	0.147	2857.79	420.10
A_68_P23322291	chr4:133899284-133899328	NM_001039677:322	Slc30a2	INSIDE	0.319	0.547	1470.19	804.25	0.174	1230.34	214.66
A_68_P31055162	chr17:13153233-13153278	NM_009338:336	Acat2	INSIDE	0.318	0.538	1930.12	1038.46	0.171	1383.85	236.51
A_68_P28109099	chr11:107655337-107655381	NM_019431:420	Cacng4	INSIDE	0.318	0.648	1051.32	681.39	0.206	825.45	170.02
A_68_P27533699	chr10:126486293-126486337	NM_010009:1013	Cyp27b1	INSIDE	0.318	0.531	2346.75	1245.55	0.169	1762.54	297.73
A_68_P22863377	chr4:41586983-41587027	NM_027147:331	Enho	INSIDE	0.318	0.518	2096.37	1085.56	0.165	1714.52	282.75
A_68_P32213509	chr19:58528941-58528985	NM_010279:-6	Gfra1	PROMOTER	0.318	0.585	1261.52	738.16	0.186	986.24	183.24
A_68_P26531906	chr9:55394278-55394322	NM_027397:5345	Isl2	DOWNSTREAM	0.318	0.540	1898.94	1024.76	0.172	1440.71	247.57
A_68_P31074431	chr17:17762209-17762253	NM_172827:-777	Lnpep	PROMOTER	0.318	0.525	2919.16	1531.48	0.167	2095.34	349.74
A_68_P22552361	chr3:135148732-135148776	NM_027288:180	Manba	INSIDE	0.318	0.553	1312.87	725.90	0.176	1150.75	202.41
A_68_P30345375	chr15:75828132-75828176	NM_177922:3956	Mapk15	INSIDE	0.318	0.516	1004.95	518.50	0.164	725.96	119.26
A_68_P28103512	chr11:106648993-106649037	NR_037224:-4941	Mir3064	PROMOTER	0.318	0.560	914.62	512.44	0.178	720.70	128.57
A_68_P30132611	chr15:35225684-35225737	NM_054049:-156	Osr2	PROMOTER	0.318	0.636	811.22	516.13	0.202	588.59	118.99
A_68_P27638907	chr11:21901433-21901477	NM_011023:200	Otx1	INSIDE	0.318	0.392	1595.62	626.26	0.125	1330.84	166.15
A_68_P31128228	chr17:29627044-29627088	NM_008842:-923	Pim1	PROMOTER	0.318	0.649	4174.97	2710.75	0.207	2967.55	613.15
A_68_P27430001	chr10:107598764-107598808	NM_027892:-669	Ppp1r12a	PROMOTER	0.318	0.448	3455.67	1549.30	0.143	2476.59	353.05
A_68_P31000873	chr16:97984845-97984902	NM_023663:489	Ripk4	INSIDE	0.318	0.584	961.88	561.91	0.186	623.95	115.79
A_68_P30655991	chr16:33056419-33056463	NM_001130485:-98	Rpl35a	DIVERGENT_PROMOTER	0.318	0.467	1287.12	601.27	0.149	957.31	142.25
A_68_P31257290	chr17:56753266-56753310	NM_018730:471	Rpl36	INSIDE	0.318	0.500	1535.88	768.11	0.159	1069.97	170.13
A_68_P25007067	chr7:25669258-25669302	NM_023133:-452	Rps19	PROMOTER	0.318	0.571	1920.01	1096.01	0.182	1364.94	247.75
A_68_P23271975	chr4:124744170-124744214	NM_175246:256	Snip1	INSIDE	0.318	0.459	1387.67	636.97	0.146	1112.09	162.20
A_68_P24838282	chr6:128250695-128250739	NM_001080979:115	Tead4	INSIDE	0.318	0.286	7210.52	2061.40	0.091	5771.82	524.63
A_68_P24981256	chr7:16985178-16985232	NM_198631:-1340	Zc3h4	PROMOTER	0.318	0.373	1449.53	540.10	0.118	1015.44	120.28
A_68_P30499541	chr15:102577044-102577088			Unknown	0.318	0.673	2925.98	1970.03	0.214	2076.54	444.32
A_68_P21761659	chr2:154483174-154483218	NM_029362:435	Chmp4b	INSIDE	0.317	0.423	1221.21	517.10	0.134	874.38	117.31
A_68_P24025032	chr5:118619420-118619464	NM_007545:-330	Hrk	PROMOTER	0.317	0.498	2773.27	1380.12	0.158	2013.37	317.57
A_68_P24025031	chr5:118619337-118619381	NM_007545:-414	Hrk	PROMOTER	0.317	0.580	2371.16	1376.46	0.184	1975.67	363.65
A_68_P25016220	chr7:28013751-28013795	NM_181593:-156	Itpkc	DIVERGENT_PROMOTER	0.317	0.561	2029.10	1138.64	0.178	1501.37	266.96
A_68_P21258085	chr2:60221190-60221234	NM_013825:76	Ly75	INSIDE	0.317	0.518	3628.14	1880.21	0.164	2695.63	442.78
A_68_P26075861	chr8:96696797-96696851	NM_008630:307	Mt2	INSIDE	0.317	0.474	1129.70	535.59	0.150	913.33	137.27
A_68_P32181719	chr19:53384898-53384942	NM_001008542:-75	Mxi1	PROMOTER	0.317	0.645	2113.80	1363.71	0.205	1652.54	338.46
A_68_P23592016	chr5:34338666-34338710	NM_001001985:56	Nat8l	INSIDE	0.317	0.731	2467.43	1804.16	0.232	2011.04	465.66
A_68_P31934468	chr19:6399999-6400043	NM_011242:-562	Rasgrp2	PROMOTER	0.317	0.548	4238.66	2323.82	0.174	3283.47	570.34
A_68_P25481826	chr7:130114107-130114151	NM_175023:51	Rbbp6	INSIDE	0.317	0.383	1654.05	634.13	0.121	1313.93	159.46
A_68_P26809957	chr9:107514932-107514976	NM_001042779:-3382	Sema3b	PROMOTER	0.317	0.678	2737.19	1855.43	0.215	2093.27	449.55
A_68_P21095246	chr2:28980261-28980312	NM_198033:-225	Setx	PROMOTER	0.317	0.507	1048.02	531.44	0.161	734.92	118.04
A_68_P27138497	chr10:52410862-52410906	NM_178675:578	Slc35f1	INSIDE	0.317	0.561	1223.00	686.52	0.178	1010.72	179.68
A_68_P24445012	chr6:51542432-51542476	NM_001127348:47933	Snx10	DOWNSTREAM	0.317	0.610	1280.18	781.43	0.193	957.39	185.08
A_68_P24521964	chr6:67485578-67485622	NM_020047:216	Tacstd2	INSIDE	0.317	0.706	1491.28	1053.38	0.224	1233.32	276.08
A_68_P27355935	chr10:93296839-93296883	NM_183199:2561	Usp44	INSIDE	0.317	0.467	2048.29	957.04	0.148	1560.01	231.12
A_68_P23164320	chr4:102786738-102786782	NM_146254:144	Wdr78	INSIDE	0.317	0.528	2194.19	1157.74	0.167	1559.94	260.85
A_68_P25600979	chr7:150631268-150631312			Unknown	0.317	0.360	1578.17	568.85	0.114	1241.19	141.74
A_68_P30402003	chr15:85476603-85476647	AK037366:-9471		PROMOTER	0.317	0.670	1375.33	921.96	0.213	1074.05	228.48
A_68_P24043270	chr5:121671022-121671067	ENSMUST00000119892:817		INSIDE	0.317	0.620	1458.64	904.56	0.196	1063.94	209.06
A_68_P28532685	chr12:73637141-73637185	NM_026327:-181	1810048J11Rik	PROMOTER	0.316	0.558	1404.89	784.23	0.176	1118.08	196.99
A_68_P20997485	chr2:9803030-9803074	NR_024257:180	4930412O13Rik	INSIDE	0.316	0.640	2306.32	1475.50	0.202	1708.55	345.24
A_68_P29480018	chr14:26661840-26661884	NM_013469:222	Anxa11	INSIDE	0.316	0.637	1341.51	853.91	0.201	1069.02	215.21
A_68_P29599143	chr14:51544686-51544730	NM_009687:85	Apex1	INSIDE	0.316	0.568	1054.30	599.15	0.180	808.85	145.22

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25429192	chr7:120352049-120352095	NM_007489:1094	Arntl	INSIDE	0.316	0.677	1310.12	886.85	0.214	1060.90	226.75
A_68_P23410311	chr4:150503055-150503099	NM_001081557:732801	Camta1	INSIDE	0.316	0.605	1254.59	758.51	0.191	959.68	183.07
A_68_P24084082	chr5:129107740-129107784	NM_175284:782	Fzd10	INSIDE	0.316	0.452	2566.07	1159.99	0.143	1964.88	281.06
A_68_P31876071	chr18:82575755-82575799	NM_008082:393	Galr1	INSIDE	0.316	0.578	2794.97	1614.79	0.182	2046.50	373.42
A_68_P25362934	chr7:106774303-106774347	NM_001195529:1289	Gm4980	INSIDE	0.316	0.565	1208.77	682.81	0.178	990.43	176.61
A_68_P28118144	chr11:109223851-109223895	NM_010303:-235	Gna13	PROMOTER	0.316	0.700	2039.32	1427.59	0.221	1392.58	307.64
A_68_P21114434	chr2:32143877-32143921	NM_001080968:126	Golga2	INSIDE	0.316	0.640	976.66	624.91	0.202	710.52	143.72
A_68_P27827763	chr11:57644849-57644893	NM_008213:779	Hand1	INSIDE	0.316	0.473	1204.13	569.65	0.150	795.06	118.89
A_68_P27185478	chr10:61802859-61802903	NM_001146100:289	Hk1	INSIDE	0.316	0.517	1844.88	953.18	0.163	1390.06	227.01
A_68_P21122772	chr2:33498002-33498046	NM_010725:-1993	Lmx1b	PROMOTER	0.316	0.547	2287.78	1251.52	0.173	1801.96	311.68
A_68_P31462759	chr18:4353279-4353323	NM_007746:-349	Map3k8	PROMOTER	0.316	0.508	2271.95	1155.14	0.161	1776.76	285.32
A_68_P23536404	chr5:22938833-22938877	NM_026984:-1392	Mll5	PROMOTER	0.316	1.442	6877.37	9913.78	0.456	4615.31	2104.90
A_68_P20023668	chr1:9690963-9691016	NM_008651:-699	Mybl1	PROMOTER	0.316	0.610	918.92	560.66	0.193	638.57	123.00
A_68_P28055689	chr11:98188746-98188790	NM_010895:2191	Neurod2	INSIDE	0.316	0.447	1637.45	732.22	0.141	1423.29	201.24
A_68_P20878432	chr1:182834386-182834430	NM_133705:4	Pycr2	INSIDE	0.316	0.464	1487.39	690.74	0.147	1191.12	174.93
A_68_P27209845	chr10:66560085-66560129	NM_001204915:-370	Reep3	PROMOTER	0.316	0.725	1973.20	1431.51	0.229	1480.80	338.96
A_68_P24604449	chr6:85282873-85282917	NM_178639:522	Sfxn5	INSIDE	0.316	0.519	1896.78	984.59	0.164	1488.04	243.94
A_68_P32182255	chr19:53465351-53465395	NM_172429:-309	Smndc1	PROMOTER	0.316	1.720	2194.67	3775.73	0.543	1466.27	796.49
A_68_P21106145	chr2:30808853-30808897	NM_133673:354	Tor1b	INSIDE	0.316	0.420	1700.27	714.36	0.133	1334.02	177.11
A_68_P30388853	chr15:83341230-83341274	NM_178869:85	Ttll1	INSIDE	0.316	0.708	2039.81	1444.84	0.224	1502.97	336.53
A_68_P27543029	chr10:128185074-128185118	NM_001170869:-481	Wibg	PROMOTER	0.316	0.494	1122.91	554.87	0.156	771.19	120.26
A_68_P25261707	chr7:86681146-86681190	ENSMUST00000141822:36166		DOWNSTREAM	0.316	0.710	2052.49	1457.51	0.225	1648.24	370.40
A_68_P24864301	chr6:134878457-134878501	NR_037955:-631	1190002F15Rik	PROMOTER	0.315	0.694	1887.29	1309.59	0.219	1288.40	281.77
A_68_P26217964	chr8:122637936-122637980	NM_001163762:-93	6430548M08Rik	PROMOTER	0.315	0.529	2610.81	1379.95	0.166	2055.91	341.82
A_68_P28574814	chr12:81360288-81360334	NM_134156:1048	Actn1	INSIDE	0.315	0.606	2559.63	1550.15	0.191	1984.65	378.58
A_68_P22864000	chr4:41672774-41672818	NM_001017362:5378	Arid3c	INSIDE	0.315	0.641	798.47	511.82	0.202	684.75	138.37
A_68_P23418117	chr4:151712690-151712736	NM_001081376:-47	Chd5	PROMOTER	0.315	0.338	2320.97	783.66	0.106	1837.66	195.40
A_68_P26665710	chr9:79567360-79567404	NM_007730:-897	Col12a1	PROMOTER	0.315	0.698	2718.00	1897.60	0.220	2040.62	448.42
A_68_P28924099	chr13:31721274-31721321	NM_010225:3613	Foxf2	INSIDE	0.315	0.404	1337.29	540.05	0.127	908.42	115.62
A_68_P27290416	chr10:81008062-81008106	NM_010301:-293	Gna11	PROMOTER	0.315	0.629	1392.76	876.66	0.199	1151.07	228.51
A_68_P22325243	chr3:90237709-90237753	NM_145540:-172	Ints3	PROMOTER	0.315	0.558	932.57	520.14	0.176	714.91	125.68
A_68_P28084316	chr11:103128366-103128410	NM_016896:327	Map3k14	INSIDE	0.315	0.533	2663.72	1420.95	0.168	1903.82	320.35
A_68_P25955963	chr8:73796755-73796799	NM_001142322:164	Myo9b	INSIDE	0.315	0.581	1757.69	1021.08	0.183	1279.05	233.95
A_68_P28077768	chr11:102007243-102007287	NM_178053:-415	Nags	PROMOTER	0.315	0.517	1829.39	945.43	0.163	1325.77	215.72
A_68_P30381130	chr15:81877398-81877442	NM_011482:608	Nhp2l1	INSIDE	0.315	0.708	1465.01	1036.69	0.223	1070.02	238.28
A_68_P31861995	chr18:80244514-80244558	NM_053117:903	Pard6g	INSIDE	0.315	0.662	1985.56	1314.53	0.208	1482.63	308.80
A_68_P22590679	chr3:142058808-142058852	NM_001190852:-170	Pdlim5	PROMOTER	0.315	0.562	1240.68	697.58	0.177	985.94	174.41
A_68_P26476668	chr9:45715123-45715167	NM_178709:-184	Rnf214	PROMOTER	0.315	0.693	1634.38	1132.30	0.219	1365.83	298.51
A_68_P29620552	chr14:56519022-56519066	NM_001082975:25	Sdr39u1	INSIDE	0.315	0.709	3748.22	2658.11	0.223	2769.29	618.42
A_68_P28778765	chr12:119540713-119540757	NM_001166385:-821	Sp4	PROMOTER	0.315	0.479	3913.42	1875.75	0.151	2958.73	446.12
A_68_P23819151	chr5:77403818-77403862	NM_025691:115	Srp72	INSIDE	0.315	0.455	1208.35	549.44	0.143	903.88	129.65
A_68_P27997502	chr11:87860747-87860791	NM_001078167:-404	Srsf1	PROMOTER	0.315	0.580	1194.48	693.03	0.183	953.83	174.32
A_68_P27269198	chr10:77068646-77068690	NM_019929:-310	Sumo3	PROMOTER	0.315	0.606	1287.95	780.64	0.191	1038.66	198.12
A_68_P28744144	chr12:112683687-112683731	NM_009396:2837	Tnfaip2	INSIDE	0.315	0.641	1159.38	742.68	0.202	841.52	169.59
A_68_P30207183	chr15:50721969-50722024	NM_032000:-409	Trps1	PROMOTER	0.315	0.446	1413.75	629.93	0.140	1070.76	150.24
A_68_P24954373	chr7:6124443-6124487	NM_001146024:350	Zfp444	INSIDE	0.315	1.391	1459.96	2030.37	0.438	1044.12	456.88
A_68_P28056476	chr11:98300031-98300075	NM_025559:250	1810046J19Rik	INSIDE	0.314	0.612	1741.14	1065.91	0.192	1258.27	241.81
A_68_P29654694	chr14:62911407-62911451	NM_173419:388	Dleu7	INSIDE	0.314	0.609	1151.47	700.81	0.191	1040.00	198.47
A_68_P28056287	chr11:98273671-98273715	NM_001003817:-105	Erbb2	PROMOTER	0.314	0.709	1513.44	1072.42	0.223	1206.13	268.51
A_68_P23973608	chr5:109123109-109123155	NM_001164259:-115	Fgfrl1	PROMOTER	0.314	0.691	5348.29	3695.93	0.217	4106.77	890.10
A_68_P31603480	chr18:32719536-32719580	NM_001048207:130	Gypc	INSIDE	0.314	0.565	2544.38	1437.98	0.178	2085.18	370.43

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25375733	chr7:108986683-108986727	NM_001122739:-366	Inppl1	PROMOTER	0.314	0.672	1783.11	1198.28	0.211	1355.05	285.97
A_68_P25574931	chr7:146132875-146132921	NM_028708:466	Jakmip3	INSIDE	0.314	0.348	1561.07	543.97	0.109	1085.34	118.67
A_68_P27836981	chr11:59263741-59263785	NM_001205068:216	Jmjd4	INSIDE	0.314	0.623	2470.69	1539.18	0.196	1856.16	362.91
A_68_P30366871	chr15:79335939-79335983	NM_008427:-289	Kcnj4	PROMOTER	0.314	0.643	1312.02	843.23	0.202	1044.58	210.62
A_68_P30347742	chr15:76181910-76181954	NM_001164607:209	Maf1	INSIDE	0.314	0.671	1461.02	980.13	0.211	1140.91	240.20
A_68_P26805732	chr9:106794296-106794340	NM_029103:-49	Manf	PROMOTER	0.314	0.556	969.69	538.82	0.174	714.03	124.51
A_68_P22317994	chr3:89031385-89031429	NR_030579:-286	Mir92b	DIVERGENT_PROMOTER	0.314	0.649	1222.94	793.11	0.204	839.30	170.98
A_68_P25953851	chr8:73284450-73284494	NM_183170:348	Mpv17l2	INSIDE	0.314	0.634	957.66	607.23	0.199	768.90	153.06
A_68_P23820898	chr5:77739527-77739571	NM_153798:40	Polr2b	INSIDE	0.314	0.429	1266.53	542.83	0.135	898.13	120.83
A_68_P21044982	chr2:19368271-19368321	NM_018809:1007	Ptf1a	INSIDE	0.314	0.649	1022.44	663.67	0.204	734.30	149.56
A_68_P20681326	chr1:145851560-145851609	NM_009061:-305	Rgs2	PROMOTER	0.314	0.576	1052.78	606.92	0.181	772.29	139.63
A_68_P29073051	chr13:58502488-58502536	NR_031761:-1096	Rmi1	DIVERGENT_PROMOTER	0.314	0.444	1268.57	563.20	0.139	1019.57	142.17
A_68_P20409777	chr1:87914871-87914915	NM_027029:-3624	Spata3	PROMOTER	0.314	0.683	2260.61	1543.56	0.215	1734.78	372.44
A_68_P24817040	chr6:124755640-124755684	NM_013539:-3296	Spsb2	PROMOTER	0.314	0.475	1229.87	584.16	0.149	957.83	142.90
A_68_P22338874	chr3:94217114-94217158	NM_028307:-103	Tdrkh	PROMOTER	0.314	0.599	1901.27	1139.41	0.188	1400.04	263.38
A_68_P23196088	chr4:108131810-108131854	NM_175472:-198	Zcchc11	PROMOTER	0.314	0.516	1517.11	783.36	0.162	1236.15	200.63
A_68_P32603683	chrX:109714707-109714751	NM_177747:594	Zfp711	INSIDE	0.314	1.682	1399.18	2352.86	0.527	652.40	343.98
A_68_P22283290	chr3:82932104-82932148	ENSMUST00000047876:1042		INSIDE	0.314	0.474	1142.87	541.57	0.149	816.45	121.55
A_68_P27835626	chr11:59041120-59041164	NM_001130408:522	Arf1	INSIDE	0.313	0.455	1172.79	533.81	0.143	912.01	130.09
A_68_P26035027	chr8:89996039-89996083	NM_019626:431	Cbln1	INSIDE	0.313	0.497	2682.57	1334.19	0.156	1960.44	305.02
A_68_P28175796	chr11:118951645-118951689	NM_007625:-4115	Cbx4	PROMOTER	0.313	0.570	1703.95	971.16	0.178	1352.97	241.16
A_68_P24432032	chr6:49269455-49269499	NM_175098:125	Ccdc126	INSIDE	0.313	0.599	1074.03	643.78	0.188	910.61	170.88
A_68_P28575796	chr12:81564448-81564492	NM_133798:389	Exd2	INSIDE	0.313	0.562	1070.64	601.76	0.176	932.09	164.02
A_68_P21569059	chr2:119151913-119151957	NR_030683:-1	Gm14207	PROMOTER	0.313	0.610	2568.77	1565.77	0.191	1984.18	378.63
A_68_P26346746	chr9:21172514-21172558	NM_001042708:90	Ilf3	INSIDE	0.313	0.616	1991.46	1226.19	0.193	1459.73	281.48
A_68_P24990788	chr7:19577261-19577305	NM_145579:689	Mypop	INSIDE	0.313	0.560	1902.02	1065.02	0.175	1477.16	258.81
A_68_P23362016	chr4:140633999-140634043	NM_025383:240	Necap2	INSIDE	0.313	0.457	1134.93	518.54	0.143	939.91	134.60
A_68_P24618280	chr6:87761089-87761133	NM_133717:-1362	Rab43	PROMOTER	0.313	0.552	1168.34	645.17	0.173	907.92	156.73
A_68_P31752099	chr18:60720832-60720876	NM_025776:415	Rbm22	INSIDE	0.313	0.499	1170.38	583.96	0.156	907.54	141.52
A_68_P21212090	chr2:51004592-51004636	NM_028810:17	Rnd3	INSIDE	0.313	0.287	2117.20	608.34	0.090	1693.31	152.40
A_68_P29448259	chr14:21493732-21493776	NM_001168273:212	Sec24c	INSIDE	0.313	0.592	2499.08	1480.28	0.186	1952.88	362.43
A_68_P21783956	chr2:158440051-158440100	NM_009508:3582	Slc32a1	INSIDE	0.313	0.568	940.57	534.46	0.178	693.97	123.49
A_68_P30398810	chr15:84962157-84962201	NM_080470:209	Smc1b	INSIDE	0.313	1.612	890.62	1435.72	0.504	837.68	422.05
A_68_P28137855	chr11:112646610-112646655	NM_011448:3109	Sox9	INSIDE	0.313	1.546	7635.10	11803.18	0.484	5030.24	2436.94
A_68_P24018832	chr5:117570657-117570701	NM_001199685:541	Taok3	INSIDE	0.313	1.384	2333.12	3228.26	0.433	1762.46	763.32
A_68_P27313251	chr10:85763083-85763128	NM_011595:-51	Timp3	PROMOTER	0.313	0.553	2251.16	1244.53	0.173	1867.17	322.71
A_68_P27892868	chr11:68884481-68884525	NM_025838:192	Tmem107	INSIDE	0.313	0.504	1047.51	528.00	0.158	754.41	119.00
A_68_P26958515	chr10:14425185-14425230	NM_025418:88	Vta1	INSIDE	0.313	0.701	1707.62	1197.33	0.220	1278.69	280.73
A_68_P29455869	chr14:22804369-22804413	NM_145459:4433	Zfp503	INSIDE	0.313	0.658	1731.42	1140.05	0.206	1176.21	242.46
A_68_P27678670	chr11:30168140-30168184	ENSMUST00000006629:7		INSIDE	0.313	0.535	3727.56	1993.03	0.167	2695.84	450.61
A_68_P22363031	chr3:99045299-99045347	ENSMUST00000151606:1019		INSIDE	0.313	0.523	1039.23	543.46	0.164	734.88	120.37
A_68_P30403121	chr15:85642175-85642219	NM_001164625:-69	2210021J22Rik	PROMOTER	0.312	0.575	3923.86	2255.17	0.179	2919.46	523.95
A_68_P24865610	chr6:135148284-135148328	NM_028982:302	8430419L09Rik	INSIDE	0.312	0.588	7845.62	4616.42	0.183	5418.44	993.91
A_68_P20632251	chr1:136132200-136132244	NM_001039510:-214	Adora1	PROMOTER	0.312	0.500	1936.92	968.66	0.156	1415.32	220.56
A_68_P31140915	chr17:31773909-31773953	NM_178224:146	Cbs	INSIDE	0.312	0.708	2004.67	1420.17	0.221	1690.64	373.21
A_68_P31919584	chr19:3851556-3851600	NM_001025566:-194	Chka	PROMOTER	0.312	0.613	1323.34	811.46	0.192	939.48	179.98
A_68_P23301437	chr4:129985225-129985269	NM_010174:-775	Fabp3	PROMOTER	0.312	0.537	3055.68	1641.66	0.168	2365.91	397.16
A_68_P32215807	chr19:58935699-58935743	NM_175199:-246	Hspa12a	PROMOTER	0.312	0.612	1871.08	1144.36	0.191	1301.11	248.26
A_68_P23094197	chr4:88783582-88783626	NM_024433:331	Mtap	INSIDE	0.312	0.678	1560.00	1057.61	0.212	1202.35	254.49
A_68_P29689075	chr14:68701929-68701973	NM_010910:10	Nefl	INSIDE	0.312	0.676	3074.89	2078.21	0.211	2344.48	495.11
A_68_P27567705	chr11:6191666-6191710	NM_010956:89	Ogdh	INSIDE	0.312	0.472	2945.64	1389.37	0.147	2126.37	313.31

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26381828	chr9:28211224-28211268	NM_177906:612393	Opcml	INSIDE	0.312	0.621	1967.48	1221.50	0.194	1602.77	310.66
A_68_P20350233	chr1:74795245-74795297	NM_153744:259	Prkag3	INSIDE	0.312	1.415	3788.79	5360.00	0.442	2741.39	1211.94
A_68_P21078762	chr2:26300450-26300494	NM_153125:264	Sec16a	INSIDE	0.312	0.477	1159.54	553.10	0.149	797.89	118.81
A_68_P28535335	chr12:74154555-74154606	NM_009189:-6881	Six1	PROMOTER	0.312	0.700	1656.51	1158.88	0.218	1212.57	264.27
A_68_P22031733	chr3:30992733-30992791	NM_001039090:-1220	Skil	PROMOTER	0.312	0.395	1342.75	530.78	0.123	1018.17	125.63
A_68_P29517796	chr14:33276471-33276515	NM_021712:1544	Slc18a3	INSIDE	0.312	0.704	4136.47	2914.05	0.220	2772.07	609.41
A_68_P31926382	chr19:5023935-5023979	NM_007854:-49	Slc29a2	PROMOTER	0.312	0.617	2154.83	1330.51	0.193	1509.83	290.69
A_68_P22825735	chr4:33296468-33296513	NM_177774:525	Srsf12	INSIDE	0.312	0.744	2829.04	2105.95	0.232	2326.52	540.72
A_68_P24134128	chr5:139676346-139676390	NM_024451:-255	Sun1	PROMOTER	0.312	0.728	2664.34	1940.32	0.227	1851.12	420.40
A_68_P31919105	chr19:3768272-3768316	NM_001167884:874	Suv420h1	INSIDE	0.312	0.488	1204.30	588.05	0.152	1004.06	153.05
A_68_P31213633	chr17:47825295-47825344	NM_001164729:16	Tomm6	INSIDE	0.312	0.539	1512.89	815.78	0.168	1072.92	180.78
A_68_P23269743	chr4:124370663-124370707	NM_026031:114	Utp11l	INSIDE	0.312	0.637	1271.91	810.07	0.198	1062.86	210.87
A_68_P31257263	chr17:56749175-56749221	NM_153152:-4	2410015M20Rik	DIVERGENT_PROMOTER	0.311	0.650	880.87	572.13	0.202	647.21	130.60
A_68_P25050066	chr7:36371059-36371104	NM_178263:-184	Ankrd27	DIVERGENT_PROMOTER	0.311	0.585	2004.59	1171.95	0.182	1608.09	292.19
A_68_P24992859	chr7:19945635-19945679	NM_145822:-824	Cd3eap	DIVERGENT_PROMOTER	0.311	0.402	3657.03	1470.39	0.125	2771.27	346.17
A_68_P26240285	chr8:126038733-126038778	NM_001170976:600	Dbndd1	INSIDE	0.311	0.647	2796.26	1808.64	0.201	2111.46	424.65
A_68_P23471509	chr5:9160963-9161011	NM_001110327:790	Dmtf1	INSIDE	0.311	0.645	1452.99	937.24	0.201	1079.13	216.46
A_68_P31258228	chr17:56904354-56904398	NM_144858:203	Dus3l	INSIDE	0.311	0.621	1871.83	1163.03	0.193	1359.56	262.92
A_68_P32242175	chrX:7769957-7770003	NM_007898:658	Ebp	INSIDE	0.311	0.625	1578.04	986.37	0.195	626.18	121.86
A_68_P22071595	chr3:38784639-38784683	NM_183221:-1201	Fat4	PROMOTER	0.311	0.651	2694.91	1753.61	0.202	1968.38	398.25
A_68_P28419966	chr12:50486205-50486249	NM_008241:2233	Foxg1	INSIDE	0.311	0.427	1752.30	747.96	0.133	1278.08	169.42
A_68_P20714215	chr1:153191431-153191475	NM_001039511:-175	Ivns1abp	PROMOTER	0.311	0.459	2192.95	1006.86	0.143	1657.53	236.40
A_68_P29668831	chr14:65271409-65271453	NM_001081177:63	Kif13b	INSIDE	0.311	0.676	1231.23	832.23	0.210	936.30	196.54
A_68_P29581489	chr14:47917977-47918021	NM_178684:10	Mapk1ip1l	INSIDE	0.311	0.520	1302.58	676.73	0.161	1067.60	172.28
A_68_P29589383	chr14:49284720-49284764	NM_144841:-2195	Otx2	DIVERGENT_PROMOTER	0.311	0.452	2371.68	1071.39	0.141	1728.89	243.22
A_68_P22031194	chr3:30894990-30895034	NM_008857:320	Prkci	INSIDE	0.311	0.483	2784.80	1344.04	0.150	2328.63	348.98
A_68_P20138944	chr1:34516811-34516856	NM_011206:243	Ptpn18	INSIDE	0.311	0.497	2255.29	1121.63	0.155	1747.96	270.79
A_68_P31306702	chr17:66868481-66868525	NM_024448:508	Rab12	INSIDE	0.311	0.641	2832.09	1816.20	0.199	2142.21	426.63
A_68_P28059598	chr11:98821127-98821171	NM_001176528:-636	Rara	PROMOTER	0.311	0.634	1923.06	1218.81	0.197	1477.29	291.35
A_68_P32289235	chrX:20194111-20194155	NM_001167775:-496	Rbm10	PROMOTER	0.311	1.498	1293.19	1937.09	0.466	657.26	305.99
A_68_P27807843	chr11:53841465-53841509	NM_019687:106	Slc22a4	INSIDE	0.311	0.656	1669.02	1095.08	0.204	1261.63	257.68
A_68_P23309110	chr4:131476820-131476864	NM_001201367:-843	Tmem200b	PROMOTER	0.311	0.637	1115.05	710.08	0.198	968.65	191.54
A_68_P32092598	chr19:36979096-36979151			Unknown	0.311	0.668	880.49	588.38	0.208	684.39	142.39
A_68_P24636065	chr6:90937787-90937831			Unknown	0.311	0.571	1217.42	694.78	0.178	949.28	168.57
A_68_P24043269	chr5:121670850-121670896	ENSMUST00000119892:645		INSIDE	0.311	0.642	1095.95	703.32	0.200	942.40	188.04
A_68_P23720350	chr5:58108862-58108920	NR_015588:268	4932441J04Rik	INSIDE	0.310	0.437	1280.56	560.18	0.136	858.56	116.48
A_68_P25435064	chr7:121397732-121397776	NM_033370:440	Copb1	INSIDE	0.310	0.674	942.61	635.01	0.209	784.38	164.07
A_68_P32031152	chr19:25747038-25747084	NM_145831:160	Dmrt2	INSIDE	0.310	0.686	1388.95	952.80	0.213	1035.27	220.16
A_68_P31130151	chr17:29979095-29979139	NM_001081160:45711	Mdga1	INSIDE	0.310	0.737	3923.97	2892.50	0.228	2840.85	649.04
A_68_P29330079	chr13:112477883-112477927	NM_172593:1519	Mier3	INSIDE	0.310	0.295	2250.96	664.54	0.092	1566.96	143.38
A_68_P31552999	chr18:23198421-23198469	NM_001161483:-1280	Nol4	PROMOTER	0.310	0.584	900.37	526.13	0.181	656.88	119.04
A_68_P31295073	chr17:64681710-64681754	NM_001025309:-509	Pja2	PROMOTER	0.310	0.447	1995.51	892.86	0.139	1482.72	205.45
A_68_P21110488	chr2:31509792-31509836	NM_001123362:14258	Prdm12	INSIDE	0.310	0.686	2682.89	1840.93	0.213	2519.68	535.54
A_68_P28137854	chr11:112646538-112646582	NM_011448:3037	Sox9	INSIDE	0.310	1.454	16942.70	24640.93	0.451	11286.38	5085.82
A_68_P23265704	chr4:123668100-123668144			Unknown	0.310	0.615	1201.34	739.05	0.191	965.10	184.15
A_68_P32050338	chr19:29038878-29038922	NM_198651:-256	4430402I18Rik	PROMOTER	0.309	0.540	1263.74	682.01	0.167	1227.41	204.57
A_68_P28078752	chr11:102158739-102158784	NM_001098836:-818	Atxn7l3	PROMOTER	0.309	0.699	1648.75	1152.08	0.216	1189.68	256.68
A_68_P25354426	chr7:105342464-105342508	NM_001081167:5499	B3gnt6	INSIDE	0.309	0.544	1800.99	980.45	0.168	1510.86	254.19
A_68_P23930021	chr5:100947315-100947359	NM_012001:9	Cops4	INSIDE	0.309	0.492	1167.19	573.85	0.152	881.98	133.94
A_68_P31458279	chr18:3383133-3383177	NM_029402:-68	Cul2	PROMOTER	0.309	0.489	1043.64	510.51	0.151	794.34	119.90
A_68_P28552887	chr12:77356011-77356057	NM_138745:-184	Mthfd1	DIVERGENT_PROMOTER	0.309	0.550	1015.45	558.66	0.170	708.43	120.50

						Sham group			TiO$_2$-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25098703	chr7:53632108-53632154	NM_010866:287	Myod1	INSIDE	0.309	0.465	1338.94	623.18	0.144	922.48	132.79
A_68_P26293544	chr9:8900444-8900488	NM_008829:634	Pgr	INSIDE	0.309	0.392	1565.31	613.31	0.121	1155.13	139.75
A_68_P26469278	chr9:44541688-44541732	NM_153537:1567	Phldb1	INSIDE	0.309	1.578	1314.26	2074.23	0.488	966.00	471.28
A_68_P23801769	chr5:74591333-74591377	NM_026878:4	Rasl11b	INSIDE	0.309	0.462	1675.56	773.71	0.143	1358.00	194.04
A_68_P32415814	chrX:58147306-58147350	NM_009237:-723	Sox3	PROMOTER	0.309	1.551	3090.46	4792.71	0.479	1344.24	644.52
A_68_P31106579	chr17:25969550-25969594	NM_019719:734	Stub1	INSIDE	0.309	0.732	2880.62	2110.02	0.227	2057.03	466.08
A_68_P24994888	chr7:20300800-20300844	NM_001109748:-44	Tomm40	PROMOTER	0.309	0.703	2686.35	1888.44	0.217	1825.38	396.24
A_68_P26132557	chr8:107783610-107783659	NM_001033161:4860	Tradd	INSIDE	0.309	0.384	1335.67	513.41	0.119	1041.01	123.64
A_68_P29102454	chr13:65343704-65343748			Unknown	0.309	1.347	2034.77	2740.19	0.416	1629.31	678.44
A_68_P28182349	chr11:119960272-119960316	NM_001110242:47	1810043H04Rik	INSIDE	0.308	0.394	1425.75	561.74	0.121	1015.23	123.11
A_68_P28755050	chr12:114394591-114394636	NM_134041:-18	4930427A07Rik	PROMOTER	0.308	0.424	2383.78	1010.51	0.131	1862.38	243.31
A_68_P22522754	chr3:129604639-129604686	NM_009811:320	Casp6	INSIDE	0.308	0.684	1224.78	837.20	0.210	872.90	183.60
A_68_P21821717	chr2:164938019-164938063	NM_174988:122197	Cdh22	INSIDE	0.308	0.461	1976.94	910.90	0.142	1492.14	211.67
A_68_P24141318	chr5:140895750-140895794	NM_133916:514	Eif3b	INSIDE	0.308	0.711	1372.71	975.79	0.219	1101.52	241.33
A_68_P28158771	chr11:116195721-116195765	NM_008240:926	Foxj1	INSIDE	0.308	0.423	1299.01	549.84	0.130	965.13	125.85
A_68_P31493068	chr18:11055096-11055140	NM_010258:2611	Gata6	INSIDE	0.308	0.658	1794.84	1180.78	0.203	1390.45	281.95
A_68_P28842019	chr13:15554706-15554754	NM_008130:-825	Gli3	PROMOTER	0.308	0.622	874.17	544.10	0.191	729.07	139.60
A_68_P30446028	chr15:93106155-93106199	NM_001033275:-661	Gxylt1	PROMOTER	0.308	0.455	1295.48	589.24	0.140	915.10	128.11
A_68_P25186204	chr7:73224455-73224499	NM_024439:-58	H47	PROMOTER	0.308	0.449	1540.45	691.17	0.138	1180.55	163.11
A_68_P20864304	chr1:180459747-180459791	NM_001161665:513	Kif26b	INSIDE	0.308	0.641	2569.97	1646.84	0.197	1831.57	361.10
A_68_P25187992	chr7:73532448-73532492	NM_146191:757	Lrrk1	INSIDE	0.308	0.500	1378.83	690.10	0.154	1171.14	180.40
A_68_P28184854	chr11:120345796-120345840	NM_027204:-164	Mrpl12	PROMOTER	0.308	0.415	1306.21	542.07	0.128	973.52	124.46
A_68_P32181743	chr19:53388066-53388111	NM_001008542:3093	Mxi1	INSIDE	0.308	0.429	1821.72	781.42	0.132	1669.23	220.66
A_68_P23185680	chr4:106323776-106323820	NM_001083887:125	Pars2	INSIDE	0.308	0.455	3076.60	1399.50	0.140	2264.92	317.68
A_68_P27551111	chr11:3188684-3188734	NM_019574:-1751	Patz1	PROMOTER	0.308	0.466	1570.97	731.51	0.143	1116.85	160.23
A_68_P24541329	chr6:72312280-72312324	NM_025607:73	Rnf181	INSIDE	0.308	0.662	938.17	621.52	0.204	767.13	156.66
A_68_P30382206	chr15:82054633-82054677	NM_028075:112	Tnfrsf13c	INSIDE	0.308	0.409	1535.29	628.63	0.126	1098.26	138.39
A_68_P26023338	chr8:87561856-87561900	NM_001122843:812	Tnpo2	INSIDE	0.308	0.563	1020.00	574.25	0.173	736.69	127.64
A_68_P24374361	chr6:37820805-37820849	NM_145076:16	Trim24	INSIDE	0.308	0.697	3366.12	2345.10	0.215	2760.08	592.80
A_68_P27589658	chr11:11016375-11016419	NM_177033:2378	Vwc2	INSIDE	0.308	0.325	1628.81	529.54	0.100	1221.17	122.11
A_68_P28813401	chr13:8870209-8870253	NM_172445:58	Wdr37	INSIDE	0.308	0.697	4478.10	3121.35	0.215	3238.33	695.05
A_68_P23429335	chr4:153515771-153515815	NM_021499:-688	Wdr8	DIVERGENT_PROMOTER	0.308	0.637	2009.41	1280.38	0.196	1424.96	279.41
A_68_P21143635	chr2:37558051-37558095	ENSMUST00000144206:597		INSIDE	0.308	1.781	4117.06	7332.92	0.548	2926.22	1604.18
A_68_P26870853	chr9:119066197-119066250	NM_146230:-12	Acaa1b	PROMOTER	0.307	0.623	1274.20	793.86	0.191	1075.27	205.65
A_68_P27560710	chr11:4887330-4887374	NM_007454:445	Ap1b1	INSIDE	0.307	0.582	2095.62	1219.07	0.178	1429.47	255.06
A_68_P25370485	chr7:108080406-108080454	NM_001081116:245	Arhgef17	INSIDE	0.307	0.324	1617.44	524.46	0.099	1238.33	123.19
A_68_P26544131	chr9:57684762-57684806	NM_019689:-2743	Arid3b	PROMOTER	0.307	0.536	1084.24	580.89	0.164	755.43	124.08
A_68_P31066946	chr17:15842783-15842827	NM_007690:874	Chd1	INSIDE	0.307	0.495	2613.42	1292.57	0.152	1867.71	283.26
A_68_P27990834	chr11:86571018-86571062	NM_001003908:-46	Cltc	PROMOTER	0.307	0.544	3606.28	1963.38	0.167	2688.21	449.14
A_68_P28266976	chr12:16818150-16818194	NM_033270:402	E2f6	INSIDE	0.307	0.572	2104.39	1204.19	0.176	1746.15	306.56
A_68_P29699029	chr14:70478786-70478830	NM_018781:1557	Egr3	INSIDE	0.307	0.538	1017.69	547.72	0.165	699.15	115.53
A_68_P30328924	chr15:73014625-73014669	NM_153178:731	Eif2c2	INSIDE	0.307	0.542	1536.65	832.16	0.166	1283.33	213.28
A_68_P25957752	chr8:74126620-74126664	NM_001166213:5098	Fam129c	INSIDE	0.307	0.565	1846.74	1043.92	0.174	1386.55	240.96
A_68_P25508346	chr7:135110839-135110887	NM_139149:-130	Fus	PROMOTER	0.307	0.360	1514.75	544.96	0.111	1206.26	133.34
A_68_P27543986	chr10:128371189-128371233	NM_008398:342	Itga7	INSIDE	0.307	0.442	2370.25	1048.13	0.136	1812.84	246.01
A_68_P31093374	chr17:23879287-23879335	NM_028416:3486	Kremen2	INSIDE	0.307	1.442	1137.02	1639.25	0.442	749.28	331.12
A_68_P31259252	chr17:57075335-57075382	NM_022328:-547	Mllt1	PROMOTER	0.307	0.600	906.69	544.44	0.184	647.94	119.41
A_68_P29448044	chr14:21459988-21460032	NM_021508:15752	Myoz1	DOWNSTREAM	0.307	0.627	2642.88	1657.82	0.193	2136.78	411.42
A_68_P31920554	chr19:4000379-4000423	NM_025529:-179	Nudt8	PROMOTER	0.307	0.519	1609.25	834.54	0.159	1305.69	207.58
A_68_P32099497	chr19:38171760-38171804	NM_181748:214	O3far1	INSIDE	0.307	0.500	1215.27	607.68	0.153	973.89	149.46
A_68_P22271765	chr3:80840549-80840593	NM_019971:233	Pdgfc	INSIDE	0.307	0.655	4758.85	3117.57	0.201	4044.76	812.21

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P32760541	chrX:152057603-152057648	NM_001093750:245	Ptchd1	INSIDE	0.307	1.655	2211.33	3659.14	0.508	896.80	455.50
A_68_P21085998	chr2:27532103-27532149	NM_011305:-594	Rxra	PROMOTER	0.307	0.619	1738.58	1075.62	0.190	1309.57	248.37
A_68_P23441761	chr4:155367293-155367337	NM_011341:292	Sdf4	INSIDE	0.307	0.477	1271.30	606.18	0.146	983.95	143.92
A_68_P25269485	chr7:88092809-88092853	NM_019951:-394	Sec11a	PROMOTER	0.307	0.634	826.34	523.49	0.194	636.34	123.60
A_68_P20149046	chr1:36613936-36613984	NM_001126047:1266	Sema4c	INSIDE	0.307	0.465	1165.59	542.06	0.143	881.56	125.81
A_68_P21101103	chr2:29918555-29918605	NM_001204875:-3413	Set	PROMOTER	0.307	0.409	1398.57	572.36	0.125	1078.77	135.35
A_68_P20870655	chr1:181447900-181447944	NM_027188:212	Smyd3	INSIDE	0.307	0.486	1813.14	881.71	0.149	1454.39	216.91
A_68_P27098028	chr10:42740979-42741023	NM_175407:153336	Sobp	INSIDE	0.307	0.630	2639.78	1664.18	0.194	2234.42	432.43
A_68_P24035159	chr5:120317204-120317248	NM_011537:32555	Tbx5	INSIDE	0.307	1.519	3033.48	4606.35	0.467	1973.23	920.98
A_68_P30255522	chr15:59481111-59481155	NM_144549:924	Trib1	INSIDE	0.307	0.739	3058.17	2261.46	0.227	2131.78	483.22
A_68_P27269296	chr10:77085151-77085195	NM_019803:107	Ube2g2	INSIDE	0.307	0.484	1202.52	581.61	0.149	974.75	144.97
A_68_P30084537	chr15:25913916-25913960	NM_144523:-182	Zfp622	PROMOTER	0.307	0.740	3944.02	2917.47	0.227	2881.16	654.34
A_68_P20530740	chr1:114313184-114313228			Unknown	0.307	0.555	1632.89	905.74	0.170	1256.17	213.62
A_68_P25827279	chr8:46020486-46020530	AK079043:5		INSIDE	0.307	0.687	1241.64	853.48	0.211	1006.72	212.50
A_68_P21108246	chr2:31170158-31170202	ENSMUST00000113532:246		INSIDE	0.307	0.715	3203.40	2289.58	0.220	2583.71	567.62
A_68_P29448465	chr14:21522444-21522488	NR_029446:-145	6230400D17Rik	PROMOTER	0.306	0.636	1615.46	1028.01	0.195	1214.50	236.56
A_68_P24383758	chr6:39523742-39523792	NM_178873:-108	Adck2	PROMOTER	0.306	0.501	1030.05	515.84	0.153	804.15	123.34
A_68_P22312956	chr3:88101171-88101215	NM_009836:136	Cct3	INSIDE	0.306	0.528	1948.15	1028.32	0.162	1464.90	236.89
A_68_P26336205	chr9:18096816-18096860	NM_025844:128	Chordc1	INSIDE	0.306	0.710	1483.02	1053.65	0.217	1106.17	240.51
A_68_P28143204	chr11:113511459-113511505	NM_013581:640	Cog1	INSIDE	0.306	0.631	855.45	539.61	0.193	733.34	141.68
A_68_P24008813	chr5:115729847-115729891	NM_026504:158	Coq5	INSIDE	0.306	0.650	876.70	569.85	0.199	685.97	136.62
A_68_P26665914	chr9:79607348-79607392	NM_009945:290	Cox7a2	INSIDE	0.306	0.600	2208.00	1325.14	0.183	1604.11	294.20
A_68_P20416436	chr1:89110508-89110552	NM_001039169:17	Eif4e2	INSIDE	0.306	0.609	1179.37	718.03	0.187	960.07	179.11
A_68_P30361561	chr15:78503090-78503140	NM_183141:45429	Elfn2	INSIDE	0.306	1.438	1384.09	1990.61	0.441	1048.42	461.94
A_68_P29448412	chr14:21515116-21515167	NM_028428:952	Fut11	INSIDE	0.306	0.604	948.23	572.44	0.185	646.75	119.45
A_68_P31123144	chr17:28712407-28712451	NM_026571:-235	Lhfpl5	PROMOTER	0.306	0.555	1443.17	800.38	0.170	1195.70	202.74
A_68_P21794488	chr2:160191953-160191997	NM_010658:827	Mafb	INSIDE	0.306	0.551	2432.00	1340.48	0.168	1838.20	309.53
A_68_P27287421	chr10:80568903-80568947	NM_023138:233	Map2k2	INSIDE	0.306	0.460	1148.19	528.02	0.141	830.12	116.64
A_68_P28103510	chr11:106648827-106648871	NR_037224:-4775	Mir3064	PROMOTER	0.306	0.692	3660.83	2533.29	0.211	2637.22	557.72
A_68_P31055439	chr17:13108867-13108911	NM_026310:69	Mrpl18	INSIDE	0.306	0.391	1728.34	675.39	0.119	1306.05	155.93
A_68_P24815139	chr6:124364839-124364883	NM_008995:225	Pex5	INSIDE	0.306	0.508	4295.46	2180.83	0.156	3282.57	510.53
A_68_P31655265	chr18:42554339-42554383	NM_138945:110	Pou4f3	INSIDE	0.306	0.476	4057.89	1932.58	0.146	2789.92	406.78
A_68_P21142186	chr2:37308087-37308131	NM_001033960:335	Rabgap1	INSIDE	0.306	0.685	1593.12	1091.59	0.209	1255.07	262.75
A_68_P20166592	chr1:39633542-39633586	NM_001033135:628	Rnf149	INSIDE	0.306	0.477	1657.94	791.46	0.146	1444.19	210.71
A_68_P27940386	chr11:77745058-77745102	NM_021286:636	Sez6	INSIDE	0.306	0.543	1094.97	595.09	0.166	867.73	144.19
A_68_P23767118	chr5:67698039-67698083	NM_178651:-135	Slc30a9	PROMOTER	0.306	0.696	2507.38	1744.43	0.213	1754.00	372.85
A_68_P28168277	chr11:117829266-117829310	NM_007707:1392	Socs3	INSIDE	0.306	0.439	1397.72	613.99	0.134	1080.52	145.26
A_68_P28750631	chr12:113749099-113749143	NM_178915:251	Tmem179	INSIDE	0.306	0.671	1006.20	675.06	0.205	723.82	148.36
A_68_P24459339	chr6:53768981-53769025	NM_025817:1817	Tril	INSIDE	0.306	0.465	1127.31	524.46	0.142	852.50	121.18
A_68_P22168174	chr3:58220683-58220727	NM_001081229:1094	Tsc22d2	INSIDE	0.306	0.620	1368.55	849.10	0.190	1397.48	265.58
A_68_P27513158	chr10:122634206-122634250	NM_027604:-249	Usp15	PROMOTER	0.306	0.705	4044.48	2850.09	0.216	3043.05	657.08
A_68_P25210203	chr7:77425760-77425806	AK148659:-1137		PROMOTER	0.306	0.698	1224.03	854.80	0.213	950.53	202.80
A_68_P23294134	chr4:128639387-128639431	NM_172875:253	Adc	INSIDE	0.305	0.550	936.37	514.76	0.168	720.57	120.90
A_68_P23882634	chr5:90794262-90794306	NM_030886:927	Ankrd17	INSIDE	0.305	0.569	5428.97	3088.89	0.173	3740.49	648.30
A_68_P26140015	chr8:109035666-109035710	NM_001037809:876	Cdh3	INSIDE	0.305	0.590	1353.51	798.17	0.180	1129.42	203.15
A_68_P21761660	chr2:154483260-154483304	NM_029362:521	Chmp4b	INSIDE	0.305	0.566	1615.67	914.49	0.173	1097.06	189.28
A_68_P31110712	chr17:26645159-26645203	NM_013642:237	Dusp1	INSIDE	0.305	0.685	1711.07	1171.73	0.209	1326.08	277.13
A_68_P20416756	chr1:89160739-89160787	NM_028889:-176	Efhd1	PROMOTER	0.305	0.479	1156.38	553.94	0.146	810.92	118.64
A_68_P23269774	chr4:124377782-124377826	NM_010213:-138	Fhl3	DIVERGENT_PROMOTER	0.305	0.537	3301.51	1771.42	0.163	2410.10	393.97
A_68_P24002949	chr5:114724178-114724222	NM_148935:-430	Foxn4	PROMOTER	0.305	0.583	2697.56	1572.79	0.178	1877.98	334.28
A_68_P22248622	chr3:75760179-75760223	NM_175193:553	Golim4	INSIDE	0.305	0.480	1318.91	632.79	0.146	1007.44	147.25

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P32399258	chrX:54306421-54306465	NM_028242:-304	Htatsf1	PROMOTER	0.305	1.509	1586.32	2393.78	0.460	638.68	293.87
A_68_P24591139	chr6:83004504-83004548	NM_019752:39	Htra2	INSIDE	0.305	0.427	1777.44	759.46	0.130	1307.76	170.57
A_68_P20391714	chr1:82287221-82287265	NM_010570:772	Irs1	INSIDE	0.305	0.492	1356.43	668.02	0.150	930.38	139.95
A_68_P32136346	chr19:45154510-45154554	NM_178929:3904	Kazald1	DOWNSTREAM	0.305	0.521	983.17	512.38	0.159	772.46	122.97
A_68_P25503740	chr7:134185787-134185831	NM_145588:126	Kif22	INSIDE	0.305	0.638	1173.06	748.72	0.195	861.63	167.91
A_68_P20864291	chr1:180458344-180458388	NM_001161665:-889	Kif26b	PROMOTER	0.305	0.559	3546.14	1982.41	0.171	2609.64	445.47
A_68_P24817385	chr6:124807053-124807099	NM_013534:629	Leprel2	INSIDE	0.305	0.543	992.44	539.18	0.165	751.11	124.31
A_68_P24563510	chr6:77193700-77193744	NM_028880:1012	Lrrtm1	INSIDE	0.305	0.625	2735.05	1709.24	0.191	2116.18	403.91
A_68_P25954146	chr8:73321652-73321696	NM_199308:-5342	Mast3	PROMOTER	0.305	0.487	1954.75	951.25	0.148	1418.66	210.64
A_68_P21099803	chr2:29701365-29701409	NR_029838:-139	Mir219-2	PROMOTER	0.305	0.588	2024.15	1190.18	0.179	1455.66	260.99
A_68_P32543772	chrX:93291348-93291392	NM_010833:-13	Msn	PROMOTER	0.305	2.325	4448.28	10340.82	0.709	1856.50	1315.46
A_68_P31112704	chr17:26975881-26975926	NM_008700:2607	Nkx2-5	INSIDE	0.305	0.598	3038.79	1816.48	0.182	2319.96	422.79
A_68_P29753340	chr14:80169561-80169605	NM_001042726:1537	Pcdh8	INSIDE	0.305	0.490	1698.45	832.13	0.149	1298.54	193.99
A_68_P25601371	chr7:150687585-150687629	NM_009434:823	Phlda2	INSIDE	0.305	0.640	2217.40	1418.70	0.195	1596.89	311.32
A_68_P29682921	chr14:67691110-67691154	NM_001205188:176	Ppp2r2a	INSIDE	0.305	0.434	5722.88	2483.43	0.132	4602.45	608.34
A_68_P22615129	chr3:146183762-146183806	NM_027371:603	Rpf1	INSIDE	0.305	0.649	994.91	646.00	0.198	927.29	183.38
A_68_P22388660	chr3:103718569-103718613	NM_172684:548	Rsbn1	INSIDE	0.305	0.619	849.22	525.31	0.189	611.07	115.40
A_68_P27286214	chr10:80363023-80363067	NM_013895:670	Timm13	INSIDE	0.305	0.591	2288.03	1351.38	0.180	1692.35	305.26
A_68_P28326655	chr12:31269403-31269447	NM_172049:117	Tmem18	INSIDE	0.305	0.464	1240.91	575.78	0.141	847.55	119.87
A_68_P32039604	chr19:27293281-27293330	NM_001161420:1796	Vldlr	INSIDE	0.305	0.474	1209.02	572.49	0.144	833.43	120.26
A_68_P26217896	chr8:122625507-122625560	NM_133967:-161	Zdhhc7	PROMOTER	0.305	0.442	1251.84	553.33	0.135	997.37	134.37
A_68_P23695857	chr5:53009885-53009931	ENSMUST00000064097:342		INSIDE	0.305	0.432	1681.15	726.32	0.132	1339.27	176.66
A_68_P31022091	chr17:6256702-6256746	ENSMUST00000121576:2822		DOWNSTREAM	0.305	0.404	2167.79	875.92	0.123	1904.63	234.91
A_68_P21707651	chr2:144353166-144353210	NM_172859:-54	6330439K17Rik	DIVERGENT_PROMOTER	0.304	0.336	2405.03	808.62	0.102	2017.05	206.21
A_68_P21061281	chr2:22923971-22924015	NM_001102437:-599	Acbd5	PROMOTER	0.304	0.505	1195.66	604.01	0.154	906.21	139.11
A_68_P32186059	chr19:54121110-54121154	NM_007417:1461	Adra2a	INSIDE	0.304	0.409	2147.85	877.83	0.124	1504.28	186.62
A_68_P25737281	chr8:28338526-28338570	NM_013462:1512	Adrb3	INSIDE	0.304	0.722	2240.17	1618.18	0.220	1672.88	367.55
A_68_P22408052	chr3:107498784-107498828	NM_145542:660	Ahcyl1	INSIDE	0.304	0.538	963.70	518.10	0.164	739.87	121.09
A_68_P21419446	chr2:90725823-90725867	NM_026161:-98	C1qtnf4	PROMOTER	0.304	0.498	1106.38	550.81	0.152	853.07	129.25
A_68_P21778673	chr2:157563323-157563367	NM_025680:208	Ctnnbl1	INSIDE	0.304	0.482	1643.11	792.00	0.147	1302.72	190.98
A_68_P24880220	chr6:137703212-137703256	NM_172733:137	Dera	INSIDE	0.304	0.674	1331.36	896.68	0.205	1083.34	222.02
A_68_P30600193	chr16:22857790-22857834	NM_001190804:-105	Dnajb11	DIVERGENT_PROMOTER	0.304	0.577	2072.81	1195.30	0.176	1427.93	250.66
A_68_P20457519	chr1:95698419-95698463	NM_001105667:71	Dtymk	INSIDE	0.304	0.502	1962.36	984.78	0.153	1438.06	219.73
A_68_P22010767	chr3:27270950-27270994	NM_177330:700	Ghsr	INSIDE	0.304	0.673	2032.00	1367.20	0.205	1465.99	299.92
A_68_P30547081	chr16:11253703-11253747	NM_001130008:694	Gspt1	INSIDE	0.304	0.491	2163.25	1062.04	0.149	1863.27	278.48
A_68_P31774691	chr18:64500742-64500786	NM_194268:747	Onecut2	INSIDE	0.304	0.612	2694.80	1648.87	0.186	1986.83	369.33
A_68_P28185658	chr11:120478932-120478976	NM_024229:250	Pcyt2	INSIDE	0.304	0.441	1269.98	560.42	0.134	936.43	125.46
A_68_P21888794	chr2:177877318-177877362	NM_028806:703	Phactr3	INSIDE	0.304	0.532	1007.53	536.11	0.162	746.47	120.70
A_68_P30447393	chr15:93350085-93350134	NM_001033217:76213	Prickle1	INSIDE	0.304	0.582	1032.40	600.49	0.177	940.59	166.16
A_68_P32225520	chr19:60543550-60543594	NM_201615:635	Prlhr	INSIDE	0.304	0.643	1273.50	819.03	0.196	1015.53	198.76
A_68_P23538312	chr5:23289160-23289204	NM_178403:297	Pus7	INSIDE	0.304	0.336	2362.92	793.83	0.102	1704.18	174.13
A_68_P21817911	chr2:164268487-164268531	NM_011521:180	Sdc4	INSIDE	0.304	0.522	1281.44	668.61	0.159	1064.40	169.09
A_68_P32185503	chr19:54020036-54020080	NM_019658:693	Shoc2	INSIDE	0.304	0.576	1786.87	1029.32	0.175	1393.04	243.57
A_68_P28186320	chr11:120574795-120574839	NM_016665:265	Stra13	INSIDE	0.304	0.653	1701.86	1111.63	0.199	1269.57	252.10
A_68_P28031414	chr11:94071733-94071777	NM_009427:-1013	Tob1	PROMOTER	0.304	0.584	957.13	559.06	0.178	830.53	147.57
A_68_P28788255	chr13:3477597-3477641	NR_015522:70	2810429I04Rik	INSIDE	0.303	0.585	2232.57	1306.06	0.177	1586.41	281.05
A_68_P21755509	chr2:153355180-153355224	NM_001134300:505	8430427H17Rik	INSIDE	0.303	0.536	4321.53	2314.36	0.162	3184.50	517.36
A_68_P21612948	chr2:127188974-127189018	NM_009633:-25	Adra2b	PROMOTER	0.303	0.563	1277.86	718.97	0.170	1108.29	188.80
A_68_P25089669	chr7:52105544-52105588	NM_026270:970	Akt1s1	INSIDE	0.303	0.509	1725.73	878.07	0.154	1072.00	165.37
A_68_P30421424	chr15:88650529-88650573	NM_029720:475	Creld2	INSIDE	0.303	0.531	1051.01	558.34	0.161	858.22	138.19
A_68_P31544272	chr18:21459015-21459059	NM_001033445:-396	Fam59a	PROMOTER	0.303	0.644	2589.20	1668.63	0.195	2037.40	398.16

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27800930	chr11:52578204-52578248	NM_177059:19	Fstl4	INSIDE	0.303	0.526	1767.90	929.20	0.159	1438.16	228.84
A_68_P28156837	chr11:115873664-115873708	NM_016905:347	Galk1	INSIDE	0.303	0.558	1834.42	1024.51	0.169	1392.43	235.32
A_68_P24864114	chr6:134847635-134847686	NM_001167697:-9783	Gpr19	PROMOTER	0.303	0.666	1646.81	1096.63	0.202	1249.68	252.28
A_68_P21319207	chr2:71227345-71227389	NM_026115:50	Hat1	INSIDE	0.303	0.421	1296.44	545.81	0.128	1004.31	128.31
A_68_P32123366	chr19:42854178-42854227	NM_019424:264	Hps1	INSIDE	0.303	0.504	1169.93	590.13	0.153	865.39	132.45
A_68_P31161217	chr17:35978332-35978376	NM_001010833:-88	Mdc1	DIVERGENT_PROMOTER	0.303	0.334	1856.65	620.90	0.101	1507.56	152.63
A_68_P21069127	chr2:24830756-24830800	NM_001031808:-160	Mrpl41	DIVERGENT_PROMOTER	0.303	0.401	1398.91	561.51	0.122	991.06	120.44
A_68_P23615663	chr5:38208346-38208390	NM_010835:7456	Msx1	DOWNSTREAM	0.303	1.765	3893.21	6873.03	0.535	2698.87	1444.12
A_68_P21821258	chr2:164860465-164860509	NM_144892:-207	Ncoa5	PROMOTER	0.303	0.546	1543.78	842.66	0.165	1208.50	199.80
A_68_P21350022	chr2:76245198-76245242	NM_145525:626	Osbpl6	INSIDE	0.303	0.669	3267.75	2185.75	0.202	2481.34	502.37
A_68_P32374343	chrX:48371227-48371271	NM_172413:-53	Rap2c	PROMOTER	0.303	5.261	4264.93	22436.89	1.595	2010.66	3206.85
A_68_P30670708	chr16:35542234-35542279	NM_013661:809	Sema5b	INSIDE	0.303	0.691	2015.11	1392.01	0.209	1485.20	310.35
A_68_P24604447	chr6:85282597-85282641	NM_178639:798	Sfxn5	INSIDE	0.303	0.371	2852.15	1057.76	0.112	2147.87	241.55
A_68_P20946924	chr1:194862258-194862302	NM_181546:-388	Syt14	PROMOTER	0.303	1.558	5136.92	8003.02	0.472	3535.96	1667.82
A_68_P30380081	chr15:81690360-81690404	NM_020507:-1626	Tob2	PROMOTER	0.303	0.448	1756.42	786.79	0.136	1382.89	187.56
A_68_P23865421	chr5:87233222-87233266	NM_177680:-270	Ythdc1	PROMOTER	0.303	0.584	2462.73	1439.18	0.177	1878.03	332.25
A_68_P27287622	chr10:80599571-80599615	NM_010731:577	Zbtb7a	INSIDE	0.303	0.454	1161.77	527.20	0.137	874.92	120.18
A_68_P29940450	chr14:119105251-119105295	NM_001033336:169	Abcc4	INSIDE	0.302	0.501	1987.26	995.31	0.151	1713.82	259.17
A_68_P26797759	chr9:105397652-105397696	NM_175025:-227	Atp2c1	PROMOTER	0.302	0.667	2789.01	1860.65	0.202	2145.78	432.40
A_68_P32050464	chr19:29064739-29064788	NM_025950:-220	Cdc37l1	PROMOTER	0.302	0.491	1312.98	644.98	0.148	1021.80	151.54
A_68_P20619646	chr1:134035792-134035836	NM_008795:448	Cdk18	INSIDE	0.302	0.491	1523.18	748.63	0.149	1239.82	184.16
A_68_P29659272	chr14:63741639-63741683	NM_007798:359	Ctsb	INSIDE	0.302	0.570	985.32	561.73	0.172	849.82	146.38
A_68_P26018981	chr8:86773349-86773396	NM_001007571:288	D8Ertd738e	INSIDE	0.302	0.479	1548.80	742.58	0.145	1177.15	170.63
A_68_P28914792	chr13:30078001-30078045	NM_010093:-90	E2f3	PROMOTER	0.302	0.519	1421.78	737.76	0.157	991.18	155.34
A_68_P31484555	chr18:9214035-9214079	NM_008058:1203	Fzd8	INSIDE	0.302	0.639	3884.69	2482.56	0.193	2795.20	539.70
A_68_P26458363	chr9:42705778-42705822	NM_175481:46654	Grik4	INSIDE	0.302	0.618	5699.87	3523.12	0.186	3862.16	719.99
A_68_P31159261	chr17:35606907-35606951	NM_010391:-105	H2-Q10	PROMOTER	0.302	0.564	1180.89	666.38	0.170	1060.75	180.49
A_68_P29071677	chr13:58230562-58230606	NM_029872:-667	Hnrnpa0	PROMOTER	0.302	0.622	3034.47	1887.17	0.188	2518.81	472.73
A_68_P23544150	chr5:24348013-24348057	NM_053075:145	Rheb	INSIDE	0.302	0.447	2693.22	1203.31	0.135	1930.51	260.66
A_68_P24057380	chr5:124199269-124199317	NM_001005525:129	Rsrc2	INSIDE	0.302	0.593	1203.73	713.96	0.179	876.61	156.88
A_68_P31412093	chr17:86084523-86084567	NM_011380:3050	Six2	INSIDE	0.302	0.590	1185.81	700.21	0.178	970.62	172.83
A_68_P32766763	chrX:153929218-153929262	NM_009214:738	Sms	INSIDE	0.302	1.425	1456.92	2076.00	0.431	606.78	261.41
A_68_P26882495	chr9:121186443-121186487	NM_177589:-174	Ulk4	PROMOTER	0.302	0.724	1738.14	1258.88	0.219	1360.39	297.54
A_68_P24817209	chr6:124779503-124779547	NM_013700:-59	Usp5	DIVERGENT_PROMOTER	0.302	0.503	1165.94	586.78	0.152	782.00	118.66
A_68_P23315907	chr4:132686541-132686585	NM_153423:15	Wasf2	INSIDE	0.302	0.494	1284.81	635.26	0.149	1019.39	152.15
A_68_P30673430	chr16:36041581-36041625	NM_027113:327	Wdr5b	INSIDE	0.302	0.628	1457.42	915.53	0.190	1119.50	212.43
A_68_P20352371	chr1:75165078-75165131	NM_001159905:-115	Zfand2b	PROMOTER	0.302	0.425	1698.12	721.94	0.128	1230.07	157.78
A_68_P24130230	chr5:138882841-138882885	NM_028130:159	Zfp157	INSIDE	0.302	0.705	1946.79	1372.41	0.213	1620.02	345.40
A_68_P25028819	chr7:30645245-30645299	NM_172740:275	Zfp420	INSIDE	0.302	0.593	957.43	567.41	0.179	679.63	121.45
A_68_P21568392	chr2:119034387-119034433	NM_001164827:-45	Zfyve19	PROMOTER	0.302	0.484	1173.15	567.34	0.146	828.70	121.06
A_68_P26200041	chr8:119502652-119502696	NM_027103:169	1700030J22Rik	INSIDE	0.301	0.583	1336.08	779.09	0.175	1050.21	184.17
A_68_P31619432	chr18:35813900-35813944	NM_027222:-4901	2010001M09Rik	PROMOTER	0.301	0.538	1419.87	764.60	0.162	1072.14	173.69
A_68_P20239573	chr1:54982711-54982755	NM_001081433:499	Ankrd44	INSIDE	0.301	0.566	2291.09	1296.37	0.170	1823.89	310.36
A_68_P21566797	chr2:118728139-118728183	NM_001045523:810	Bahd1	INSIDE	0.301	0.538	3665.07	1970.45	0.162	2797.55	451.99
A_68_P28356775	chr12:36883341-36883387	NM_025840:48	Bzw2	INSIDE	0.301	1.635	1872.76	3062.06	0.492	1394.80	686.87
A_68_P23467995	chr5:8422471-8422515	NM_001190717:224	Dbf4	INSIDE	0.301	0.385	1346.98	517.97	0.116	1040.47	120.50
A_68_P31166661	chr17:37125639-37125683	NM_001115075:789	H2-M5	INSIDE	0.301	0.729	2275.44	1658.37	0.220	1770.73	388.90
A_68_P26020977	chr8:87186135-87186179	NM_010499:595	Ier2	INSIDE	0.301	0.488	1879.99	917.11	0.147	1500.50	220.21
A_68_P26809754	chr9:107489944-107489988	NM_025903:-82	Ifrd2	PROMOTER	0.301	0.503	1227.58	618.03	0.152	1004.00	152.27
A_68_P27234954	chr10:70811019-70811063	NM_027184:500	Ipmk	INSIDE	0.301	0.628	4411.32	2769.91	0.189	3306.52	624.87
A_68_P29469008	chr14:24823022-24823066	NM_010610:383	Kcnma1	INSIDE	0.301	0.601	2823.74	1698.02	0.181	1847.96	333.96

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P30433465	chr15:90879520-90879574	NM_001109040:833	Kif21a	INSIDE	0.301	0.443	1163.02	514.88	0.133	904.58	120.45
A_68_P24517586	chr6:66485635-66485679	NM_019499:195	Mad2l1	INSIDE	0.301	0.648	1159.02	751.05	0.195	1025.09	199.61
A_68_P27284924	chr10:80164367-80164423	NM_172457:171	Mobkl2a	INSIDE	0.301	0.506	1100.89	556.99	0.153	794.12	121.12
A_68_P30018889	chr15:11834455-11834499	NM_001039181:953	Npr3	INSIDE	0.301	0.597	4118.83	2458.74	0.180	3024.13	543.61
A_68_P31258135	chr17:56890739-56890783	NM_008738:6193	Nrtn	INSIDE	0.301	1.430	1022.35	1462.25	0.430	808.62	347.81
A_68_P25507194	chr7:134913194-134913238	NM_198424:-112	Orai3	PROMOTER	0.301	0.468	1119.03	523.95	0.141	870.90	122.76
A_68_P25093637	chr7:52781402-52781446	NM_008654:214	Ppp1r15a	INSIDE	0.301	0.543	1675.58	909.14	0.163	1291.61	210.70
A_68_P23702720	chr5:54200876-54200920	NM_144517:33	Tbc1d19	INSIDE	0.301	0.709	1440.75	1020.80	0.213	1099.03	234.00
A_68_P27892869	chr11:68884583-68884627	NM_025838:294	Tmem107	INSIDE	0.301	0.451	1590.84	718.13	0.136	1179.13	160.48
A_68_P20076127	chr1:21068999-21069043	NM_133252:270	Tram2	INSIDE	0.301	0.699	3103.23	2169.79	0.210	2237.15	470.26
A_68_P31889607	chr18:84758993-84759052	NM_001033341:-126	Zfp407	PROMOTER	0.301	0.290	1917.24	556.95	0.087	1370.17	119.82
A_68_P27292200	chr10:81817022-81817066	DQ459435:45		INSIDE	0.301	0.538	1438.92	773.84	0.162	1087.39	175.96
A_68_P23349880	chr4:138686224-138686268	NR_033745:706	2310028O11Rik	INSIDE	0.300	0.640	828.17	529.84	0.192	621.75	119.45
A_68_P21441000	chr2:94246926-94246970	NR_027831:85	2810002D19Rik	INSIDE	0.300	0.402	1299.08	521.91	0.121	963.26	116.22
A_68_P29234321	chr13:95129057-95129101	NM_009680:164	Ap3b1	INSIDE	0.300	0.707	1455.47	1028.55	0.212	1162.74	246.57
A_68_P25657379	chr8:11758150-11758194	NM_001113518:-157	Arhgef7	PROMOTER	0.300	0.631	5001.76	3157.28	0.189	3997.93	757.01
A_68_P24004708	chr5:115021723-115021774	NM_001004180:3489	BC057022	INSIDE	0.300	0.522	1088.32	568.08	0.157	764.33	119.65
A_68_P21101914	chr2:30061663-30061707	NM_172404:-465	Ccbl1	PROMOTER	0.300	0.497	2037.06	1013.36	0.149	1516.18	226.33
A_68_P31252979	chr17:56098596-56098641	NM_028381:9	Ccdc94	INSIDE	0.300	0.628	842.30	529.27	0.189	638.62	120.51
A_68_P29098530	chr13:64471460-64471504	NM_009984:132	Ctsl	INSIDE	0.300	0.650	1179.67	766.37	0.195	936.16	182.74
A_68_P27180612	chr10:60915666-60915710	NM_010124:-271	Eif4ebp2	PROMOTER	0.300	2.127	3037.71	6460.83	0.637	2245.62	1431.38
A_68_P26761637	chr9:98886525-98886573	NM_001122851:-243	Faim	PROMOTER	0.300	0.342	1574.82	538.81	0.103	1150.49	118.07
A_68_P23320286	chr4:133523495-133523539	NM_016957:390	Hmgn2	INSIDE	0.300	0.453	3163.61	1431.56	0.136	2470.57	334.83
A_68_P29616408	chr14:55733743-55733787	NM_177049:2008	Jph4	INSIDE	0.300	0.666	2341.23	1558.41	0.200	1669.13	333.22
A_68_P28068130	chr11:100302472-100302516	NM_026561:-91	Nt5c3l	DIVERGENT_PROMOTER	0.300	0.677	1646.00	1113.66	0.203	1214.32	246.45
A_68_P30380501	chr15:81756859-81756907	NM_030229:-239	Polr3h	PROMOTER	0.300	0.498	1063.02	529.56	0.150	797.95	119.37
A_68_P21091470	chr2:28369078-28369122	NM_001145834:414	Ralgds	INSIDE	0.300	0.445	1702.64	757.67	0.133	1231.55	164.31
A_68_P22312700	chr3:88044849-88044893	NM_021375:13736	Rhbg	DOWNSTREAM	0.300	0.675	1054.10	712.01	0.203	878.09	177.91
A_68_P30013955	chr15:10966024-10966068	NM_178717:1677	Rxfp3	INSIDE	0.300	0.692	1201.59	831.41	0.208	816.46	169.56
A_68_P23441760	chr4:155367175-155367219	NM_011341:174	Sdf4	INSIDE	0.300	0.443	3597.37	1592.29	0.133	2849.65	378.39
A_68_P29337690	chr13:113717502-113717546	NM_028151:64	Skiv2l2	INSIDE	0.300	0.574	986.30	565.81	0.172	703.81	121.22
A_68_P31943156	chr19:8788183-8788228	NM_008577:182	Slc3a2	INSIDE	0.300	0.649	1373.09	891.78	0.195	937.37	182.55
A_68_P30600190	chr16:22857403-22857447	NM_001081368:218	Tbccd1	INSIDE	0.300	0.504	1833.25	923.31	0.151	1422.85	215.19
A_68_P27495880	chr10:119645922-119645966	NM_026617:63	Tmbim4	INSIDE	0.300	0.511	3248.99	1658.80	0.153	2547.88	389.68
A_68_P24304147	chr6:24906093-24906137	NM_177013:11	Tmem229a	INSIDE	0.300	0.461	2128.04	981.74	0.139	1780.30	246.61
A_68_P21768465	chr2:155755929-155755973	NM_018888:96	Uqcc	INSIDE	0.300	0.548	2307.00	1265.32	0.164	1686.87	277.31
A_68_P24156072	chr5:144090683-144090727	NM_028379:201	Zdhhc4	INSIDE	0.300	0.663	2941.05	1949.64	0.199	1987.61	394.70
A_68_P24951780	chr7:5003473-5003517	NM_026900:361	Zfp580	INSIDE	0.300	1.634	1369.84	2238.52	0.491	1043.17	511.69
A_68_P32133947	chr19:44792110-44792165			Unknown	0.300	2.020	1518.88	3068.14	0.605	1175.32	711.34
A_68_P28140562	chr11:113063090-113063135	NR_015556:40	2610035D17Rik	INSIDE	0.299	1.773	1746.44	3096.57	0.529	1170.83	619.76
A_68_P23545746	chr5:24606967-24607011	NR_027851:196	2900005J15Rik	INSIDE	0.299	0.607	2727.40	1655.22	0.181	2023.02	366.75
A_68_P27852924	chr11:62062701-62062745	NM_007413:237	Adora2b	INSIDE	0.299	0.603	1530.82	923.71	0.180	1165.56	210.17
A_68_P32183070	chr19:53603197-53603241	NM_001085390:-589	Dusp5	PROMOTER	0.299	0.465	1305.63	607.44	0.139	969.44	135.02
A_68_P23145544	chr4:99322690-99322737	NM_010425:-276	Foxd3	PROMOTER	0.299	0.633	841.55	532.51	0.189	638.07	120.81
A_68_P24078733	chr5:128112702-128112746	NM_177005:93	Glt1d1	INSIDE	0.299	0.428	1751.18	749.64	0.128	1530.19	195.95
A_68_P24111876	chr5:134660418-134660462	NM_053266:533	Gtf2ird2	INSIDE	0.299	0.639	1141.25	728.79	0.191	838.54	160.37
A_68_P21129656	chr2:34628056-34628100	NM_001163434:469	Hspa5	INSIDE	0.299	0.482	1166.19	562.07	0.144	957.86	138.21
A_68_P20409050	chr1:87791484-87791528	NM_022417:422	Itm2c	INSIDE	0.299	0.703	1596.53	1122.15	0.210	1179.45	247.88
A_68_P30325017	chr15:72376544-72376592	NM_001033876:141	Kcnk9	INSIDE	0.299	0.552	1254.57	692.97	0.165	989.60	163.53
A_68_P23990800	chr5:112657892-112657936	NR_003718:54	Miat	INSIDE	0.299	0.533	1405.27	749.37	0.160	1059.02	168.97
A_68_P22314346	chr3:88340207-88340251	NR_035434:76	Mir1905	INSIDE	0.299	0.671	973.25	653.32	0.201	734.20	147.55

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P30719817	chr16:44140456-44140500	NM_028108:557	Naa50	INSIDE	0.299	0.464	1161.17	538.28	0.139	895.49	124.12
A_68_P32116953	chr19:41818287-41818331	NM_015748:38	Slit1	INSIDE	0.299	1.381	5569.52	7689.30	0.412	4138.15	1705.80
A_68_P28615271	chr12:88641179-88641223	NM_011479:87980	Sptlc2	DOWNSTREAM	0.299	0.614	3622.78	2225.65	0.184	2774.53	509.31
A_68_P20616231	chr1:133422247-133422291	NM_001081011:1670	Srgap2	INSIDE	0.299	0.412	2073.72	854.41	0.123	1549.42	191.09
A_68_P24162465	chr5:145529208-145529252	NM_001081362:-430	Trrap	DIVERGENT_PROMOTER	0.299	0.611	1448.64	885.12	0.183	1176.65	214.85
A_68_P23872839	chr5:88993614-88993669	NM_023054:10134	Utp3	DOWNSTREAM	0.299	0.459	1123.80	515.85	0.137	847.87	116.46
A_68_P30588339	chr16:20591420-20591465	NM_182636:1788	Vwa5b2	INSIDE	0.299	0.507	1289.65	653.54	0.151	985.18	149.07
A_68_P26139675	chr8:108939273-108939317	NM_011764:56	Zfp90	INSIDE	0.299	0.494	1046.46	516.55	0.148	842.17	124.23
A_68_P29102450	chr13:65343136-65343180			Unknown	0.299	1.945	9762.87	18991.52	0.582	6538.54	3806.31
A_68_P26847337	chr9:114888048-114888092	CCDS52952.1:3755		DOWNSTREAM	0.299	0.443	1615.80	715.37	0.132	1356.59	179.48
A_68_P30003954	chr15:9000908-9000952	NM_001040395:-78	1110020G09Rik	PROMOTER	0.298	0.579	2192.77	1270.55	0.173	1518.52	262.25
A_68_P23547921	chr5:25035545-25035589	NR_027388:-269	1700096K18Rik	PROMOTER	0.298	0.568	3000.72	1704.54	0.169	2111.86	357.66
A_68_P20366321	chr1:77511149-77511206	NM_007936:486	Epha4	INSIDE	0.298	0.640	861.99	552.09	0.191	639.72	122.06
A_68_P22187976	chr3:62407890-62407934	NM_177346:1150	Gpr149	INSIDE	0.298	0.714	1701.46	1214.37	0.213	1269.21	269.94
A_68_P28067855	chr11:100259055-100259099	NM_010593:28	Jup	INSIDE	0.298	0.567	1550.90	879.40	0.169	1126.51	190.56
A_68_P26068286	chr8:95379269-95379313	NM_173014:42	Lpcat2	INSIDE	0.298	0.635	3188.41	2024.16	0.189	2268.79	429.12
A_68_P31127333	chr17:29463770-29463814	NM_023734:7966	Pi16	INSIDE	0.298	0.554	1109.54	614.43	0.165	771.49	127.28
A_68_P20956472	chr1:196446255-196446299	NM_008882:254	Plxna2	INSIDE	0.298	0.634	1595.91	1012.02	0.189	1163.51	219.86
A_68_P30481816	chr15:99532450-99532494	NM_031842:-245	Smarcd1	PROMOTER	0.298	0.641	1203.61	771.11	0.191	906.16	172.95
A_68_P23328078	chr4:134908468-134908512	NM_001130477:639	Srrm1	INSIDE	0.298	0.722	1561.86	1128.40	0.215	1225.60	263.61
A_68_P22570423	chr3:138406072-138406116	NM_019571:936	Tspan5	INSIDE	0.298	0.557	5007.03	2790.18	0.166	3779.51	627.44
A_68_P31256670	chr17:56651120-56651164	NM_011483:764	Znrf4	INSIDE	0.298	0.618	1002.25	619.27	0.184	778.98	143.56
A_68_P26199436	chr8:119387539-119387583			Unknown	0.298	0.553	1498.46	827.95	0.165	1152.91	189.92
A_68_P23611141	chr5:37420204-37420248	ENSMUST00000165557:12659		DOWNSTREAM	0.298	0.484	1064.67	514.90	0.144	836.75	120.56
A_68_P25010197	chr7:26180486-26180536	NR_015569:78	4732471J01Rik	INSIDE	0.297	0.409	1377.94	563.29	0.121	1038.30	126.07
A_68_P25509654	chr7:135381359-135381407	NM_177001:163	9130023H24Rik	INSIDE	0.297	0.455	3341.32	1521.88	0.135	2245.49	303.74
A_68_P21763873	chr2:154899789-154899833	NM_016661:423	Ahcy	INSIDE	0.297	0.646	938.05	605.85	0.192	870.33	166.71
A_68_P27981860	chr11:85048235-85048279	NM_025825:366	Appbp2	INSIDE	0.297	0.566	1614.72	914.38	0.168	1238.42	208.60
A_68_P31152216	chr17:34256835-34256882	NR_037970:-13	Brd2	PROMOTER	0.297	0.664	1305.39	866.95	0.197	878.61	173.17
A_68_P26811951	chr9:107838581-107838626	NM_145621:353	Camkv	INSIDE	0.297	0.469	1168.01	548.13	0.139	860.37	119.89
A_68_P31932216	chr19:6015590-6015634	NM_007600:-365	Capn1	PROMOTER	0.297	0.502	2108.34	1058.29	0.149	1674.37	249.26
A_68_P30431389	chr15:90510273-90510317	NM_025815:-475	Cpne8	PROMOTER	0.297	0.635	897.45	569.88	0.189	639.64	120.75
A_68_P26350219	chr9:21855638-21855682	NM_010487:807	Elavl3	INSIDE	0.297	0.704	4462.12	3140.26	0.209	3223.27	674.40
A_68_P20332283	chr1:71699233-71699279	NM_010233:489	Fn1	INSIDE	0.297	0.563	930.89	524.18	0.167	694.08	116.20
A_68_P24816733	chr6:124690988-124691032	NM_013535:87	Grcc10	INSIDE	0.297	0.555	943.86	524.02	0.165	731.22	120.76
A_68_P28066377	chr11:100006745-100006792	NM_008471:465	Krt19	INSIDE	0.297	0.402	1333.60	536.05	0.120	1037.15	124.01
A_68_P22082267	chr3:40754901-40754949	NM_001040399:372	Larp1b	INSIDE	0.297	0.561	1498.78	841.48	0.167	1141.79	190.57
A_68_P27996401	chr11:87630681-87630732	NM_080420:8910	Lpo	INSIDE	0.297	0.421	1352.36	569.03	0.125	910.85	113.94
A_68_P24563511	chr6:77193808-77193857	NM_028880:1122	Lrrtm1	INSIDE	0.297	0.467	1187.23	554.94	0.139	858.30	119.33
A_68_P26018712	chr8:86722479-86722523	NR_029740:-9916	Mir23a	PROMOTER	0.297	0.641	891.06	570.89	0.190	782.87	148.91
A_68_P29667754	chr14:65059716-65059760	NM_026322:15002	Msra	INSIDE	0.297	0.607	853.63	518.11	0.181	685.33	123.71
A_68_P23617866	chr5:38550212-38550259	NM_010942:471	Nsg1	INSIDE	0.297	0.618	826.48	510.65	0.183	640.65	117.53
A_68_P21096076	chr2:29107825-29107869	NM_133500:-4286	Ntng2	PROMOTER	0.297	0.598	1790.03	1071.17	0.178	1394.41	247.93
A_68_P23184552	chr4:106136609-106136653	NM_153565:300	Pcsk9	INSIDE	0.297	0.606	1091.54	661.02	0.180	828.68	148.97
A_68_P20832748	chr1:174307013-174307057	NM_026234:373	Pigm	INSIDE	0.297	0.667	1648.01	1099.60	0.198	1331.03	263.79
A_68_P25265835	chr7:87439504-87439548	NM_145150:176	Prc1	INSIDE	0.297	0.555	1443.64	800.97	0.165	1176.43	193.63
A_68_P27806201	chr11:53520531-53520577	NM_009012:267	Rad50	INSIDE	0.297	0.617	1174.44	724.17	0.183	1066.68	195.06
A_68_P30572549	chr16:17209535-17209579	NM_001033338:1329	Rimbp3	INSIDE	0.297	0.528	4076.18	2153.37	0.157	2939.18	460.39
A_68_P25090672	chr7:52271527-52271571	NM_001008422:71	Scaf1	INSIDE	0.297	0.495	1154.40	571.19	0.147	814.15	119.77
A_68_P31331157	chr17:71203092-71203136	NM_001164074:-242	Tgif1	PROMOTER	0.297	0.622	1196.16	744.42	0.185	981.70	181.46
A_68_P27804179	chr11:53138214-53138260	NM_026479:46	Zcchc10	INSIDE	0.297	0.393	1423.03	559.29	0.117	1016.64	118.57

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26342786	chr9:20326146-20326190	NM_001082485:-305	Zfp266	PROMOTER	0.297	0.434	5985.65	2600.73	0.129	4200.66	542.84
A_68_P21820483	chr2:164736035-164736086	NM_199027:1190	Zfp335	INSIDE	0.297	0.551	1094.05	603.28	0.164	734.59	120.43
A_68_P32133946	chr19:44791974-44792031			Unknown	0.297	1.535	635.12	975.02	0.456	484.85	221.10
A_68_P21516740	chr2:109533518-109533562	NM_001048142:-179	Bdnf	PROMOTER	0.296	0.561	933.08	523.23	0.166	766.95	127.48
A_68_P25094588	chr7:52960776-52960821	NM_016974:182	Dbp	INSIDE	0.296	0.354	1557.36	551.37	0.105	1140.67	119.71
A_68_P27171638	chr10:59414463-59414507	NM_029083:34	Ddit4	INSIDE	0.296	0.266	2024.13	537.73	0.079	1482.62	116.59
A_68_P29615094	chr14:55545462-55545506	NM_010112:141	Efs	INSIDE	0.296	0.619	1572.86	974.21	0.183	1139.18	208.54
A_68_P21727914	chr2:147871631-147871680	NM_010446:1050	Foxa2	INSIDE	0.296	0.644	871.17	561.09	0.191	628.51	119.74
A_68_P28989502	chr13:43398690-43398734	NM_001033399:829	Gfod1	INSIDE	0.296	0.541	2800.65	1514.17	0.160	1873.14	299.96
A_68_P22875166	chr4:44085073-44085117	NM_001190414:451	Gne	INSIDE	0.296	0.428	2122.03	909.19	0.127	1602.89	203.35
A_68_P21489523	chr2:104333403-104333447	NM_001145824:1222	Hipk3	INSIDE	0.296	0.446	1339.26	596.69	0.132	1022.60	134.85
A_68_P29484662	chr14:27852087-27852131	NM_134437:-78	Il17rd	PROMOTER	0.296	0.552	2127.06	1175.11	0.164	1552.07	254.16
A_68_P26884586	chr9:121550854-121550898	NM_026915:-192	Lyzl4	DIVERGENT_PROMOTER	0.296	0.488	2617.71	1278.25	0.145	1836.94	265.46
A_68_P28831282	chr13:12350227-12350271	NM_001081128:19	Mtr	INSIDE	0.296	0.473	2220.29	1050.04	0.140	1540.42	215.54
A_68_P23120296	chr4:94645934-94645983	NM_177239:-167	Mysm1	PROMOTER	0.296	0.501	1093.13	547.24	0.148	809.97	119.88
A_68_P25507195	chr7:134913265-134913309	NM_198424:-42	Orai3	PROMOTER	0.296	0.416	2043.31	849.01	0.123	1541.67	189.67
A_68_P31655275	chr18:42555427-42555471	NM_138945:1198	Pou4f3	INSIDE	0.296	0.603	906.72	546.45	0.179	676.84	120.93
A_68_P25048759	chr7:36119164-36119208	NM_027897:-69	Rhpn2	PROMOTER	0.296	0.480	1957.54	939.90	0.142	1650.02	234.47
A_68_P25475987	chr7:129008610-129008655	NM_011325:8	Scnn1b	INSIDE	0.296	0.444	2237.84	992.61	0.131	1674.89	219.88
A_68_P20353582	chr1:75371730-75371774	NM_007463:-119	Speg	DIVERGENT_PROMOTER	0.296	0.693	2142.52	1484.62	0.205	1623.95	333.44
A_68_P29647965	chr14:61656646-61656690	NM_001164155:156	Tnfrsf19	INSIDE	0.296	0.424	1805.28	765.52	0.125	1451.09	182.03
A_68_P32010024	chr19:22213827-22213871	NM_001035239:242	Trpm3	INSIDE	0.296	0.576	1073.25	617.71	0.170	900.06	153.11
A_68_P24974297	chr7:13623923-13623967	NM_001168469:-325	Ube2m	PROMOTER	0.296	0.616	967.88	596.50	0.182	764.16	139.33
A_68_P30385944	chr15:82817919-82817963	ENSMUST00000170562:4641		INSIDE	0.296	0.710	2401.77	1704.86	0.210	1866.07	392.23
A_68_P26822985	chr9:110207937-110207981	NM_001081381:263	2610002I17Rik	INSIDE	0.295	0.546	2450.33	1336.68	0.161	1753.18	282.25
A_68_P33012180	chr9_random:57290-57334	NR_027950:2620	4930526I15Rik	DOWNSTREAM	0.295	0.671	1868.30	1253.84	0.198	1395.16	276.24
A_68_P24007907	chr5:115569084-115569128	NM_007383:216	Acads	INSIDE	0.295	0.630	2283.44	1438.67	0.186	1678.89	311.69
A_68_P23294136	chr4:128639545-128639589	NM_172875:95	Adc	INSIDE	0.295	0.686	6057.50	4153.97	0.202	4127.09	835.52
A_68_P30113930	chr15:31296769-31296813	NM_001164441:724	Ankrd33b	INSIDE	0.295	0.568	2634.76	1497.79	0.168	2118.43	355.51
A_68_P32795517	chrX:160347213-160347257	NM_026887:143	Ap1s2	INSIDE	0.295	2.033	1837.35	3735.54	0.599	901.22	540.07
A_68_P21040966	chr2:18620478-18620522	NM_001001334:-148	BC061194	PROMOTER	0.295	0.461	1908.34	880.42	0.136	1521.56	207.18
A_68_P25944440	chr8:71258901-71258945	NM_172753:119	Csgalnact1	INSIDE	0.295	0.632	2416.83	1526.41	0.186	1907.58	355.01
A_68_P28914783	chr13:30077028-30077072	NM_010093:882	E2f3	INSIDE	0.295	0.653	1692.28	1105.35	0.193	1342.03	258.74
A_68_P26986431	chr10:20067872-20067916	NM_027930:270	Fam54a	INSIDE	0.295	0.482	1155.15	557.13	0.142	860.19	122.49
A_68_P27357056	chr10:93498664-93498716	NM_053072:-55	Fgd6	DIVERGENT_PROMOTER	0.295	0.553	975.06	538.97	0.163	744.85	121.32
A_68_P20294266	chr1:64784611-64784655	NM_001042659:-308	Fzd5	PROMOTER	0.295	0.531	1159.38	615.42	0.156	868.90	135.84
A_68_P24429122	chr6:48693166-48693210	NM_008376:4143	Gimap1	INSIDE	0.295	1.877	2991.48	5614.39	0.554	2024.80	1121.84
A_68_P28563524	chr12:79327386-79327430	NM_145965:-233	Gphn	PROMOTER	0.295	0.680	1080.98	735.04	0.201	887.89	178.22
A_68_P24129157	chr5:138612451-138612495	NR_029658:-5426	Mir106b	PROMOTER	0.295	0.501	2923.33	1464.32	0.148	2009.96	297.20
A_68_P23579047	chr5:31916324-31916368	NM_025796:23	Mrpl33	INSIDE	0.295	0.611	1447.93	884.64	0.180	1142.65	205.92
A_68_P31331867	chr17:71340037-71340081	NM_023402:-202	Myl12b	PROMOTER	0.295	0.729	5895.03	4299.37	0.215	4404.46	949.13
A_68_P23199842	chr4:108874395-108874439	NM_133885:461	Osbpl9	INSIDE	0.295	0.672	3598.78	2417.08	0.198	2579.37	511.68
A_68_P28940998	chr13:34966207-34966251	NM_013830:-1134	Prpf4b	PROMOTER	0.295	0.510	3080.41	1569.79	0.150	2126.73	319.29
A_68_P31256438	chr17:56615517-56615561	NM_011218:365	Ptprs	INSIDE	0.295	0.397	1320.98	524.04	0.117	1033.69	120.88
A_68_P30132017	chr15:35085586-35085630	NM_019635:-47	Stk3	PROMOTER	0.295	0.488	4603.04	2246.98	0.144	3782.78	544.91
A_68_P25701519	chr8:18950799-18950843	NM_001113350:153	Xkr5	INSIDE	0.295	0.550	1900.50	1045.48	0.162	1597.83	258.98
A_68_P21749218	chr2:152239987-152240031	NM_175126:772	Zcchc3	INSIDE	0.295	0.353	1958.83	690.72	0.104	1453.63	151.39
A_68_P25089142	chr7:52003877-52003921	NM_178734:89	Zfp473	INSIDE	0.295	0.530	1007.57	533.75	0.156	772.53	120.81
A_68_P21782538	chr2:158186969-158187016	NR_015463:253	9430008C03Rik	INSIDE	0.294	0.433	1475.14	638.46	0.127	1038.55	132.14
A_68_P23299521	chr4:129662643-129662687	NM_001199696:343	Bai2	INSIDE	0.294	0.677	1184.37	801.57	0.199	840.45	167.23
A_68_P27315615	chr10:86168388-86168432	NM_001003939:-145	BC030307	DIVERGENT_PROMOTER	0.294	0.445	1172.76	521.83	0.131	927.24	121.32

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26790789	chr9:104165231-104165275	NM_001163026:8	Dnajc13	INSIDE	0.294	0.439	2216.01	973.37	0.129	1782.78	230.03
A_68_P32315762	chrX:33428641-33428685	NM_001009947:-164	Dock11	PROMOTER	0.294	1.708	1636.37	2794.21	0.503	769.78	386.90
A_68_P23202063	chr4:109349653-109349697	NM_007983:443	Faf1	INSIDE	0.294	0.447	2022.94	904.09	0.131	1611.81	211.86
A_68_P24607724	chr6:85978997-85979041	NM_012013:11834	Figla	DOWNSTREAM	0.294	0.395	1372.49	541.51	0.116	1018.25	118.25
A_68_P29329254	chr13:112280052-112280096	NM_001122963:175	Gpbp1	INSIDE	0.294	1.470	5825.93	8562.02	0.432	3881.47	1675.84
A_68_P27924588	chr11:74982421-74982465	NM_001098203:-788	Hic1	PROMOTER	0.294	0.429	2116.45	908.35	0.126	1711.04	216.24
A_68_P26809702	chr9:107483108-107483152	NM_178020:-496	Hyal3	PROMOTER	0.294	0.647	961.49	622.42	0.190	705.09	134.26
A_68_P21569912	chr2:119303420-119303464	NM_026574:-77	Ino80	PROMOTER	0.294	0.436	3829.81	1671.27	0.128	2908.06	373.43
A_68_P27894946	chr11:69224331-69224375	NM_001017426:2825	Kdm6b	INSIDE	0.294	1.983	6938.02	13758.22	0.582	4494.01	2616.74
A_68_P31545963	chr18:21811255-21811299	NM_001081403:-407	Klhl14	PROMOTER	0.294	0.461	1899.45	876.38	0.136	1439.61	195.37
A_68_P30498285	chr15:102340830-102340876	NM_001163643:6583	Map3k12	INSIDE	0.294	0.625	860.46	537.87	0.183	666.50	122.30
A_68_P23985671	chr5:111848092-111848136	NM_001081235:929	Mn1	INSIDE	0.294	0.648	3672.91	2380.26	0.191	2489.23	474.22
A_68_P30346947	chr15:76059642-76059686	NM_201385:263	Plec	INSIDE	0.294	0.451	1296.40	584.06	0.132	922.68	122.12
A_68_P25093690	chr7:52793837-52793881	NM_148927:12159	Plekha4	INSIDE	0.294	0.540	1520.91	820.86	0.159	1147.84	182.08
A_68_P31918147	chr19:3575682-3575726	NM_001164159:45	Ppp6r3	INSIDE	0.294	0.652	4055.20	2645.44	0.192	2867.08	549.30
A_68_P21831536	chr2:166539405-166539449	NM_177782:-94	Prex1	PROMOTER	0.294	2.047	14771.77	30234.45	0.602	9815.80	5904.42
A_68_P24119440	chr5:136578358-136578403	NM_133914:18595	Rasa4	INSIDE	0.294	0.548	1458.41	798.68	0.161	1075.99	172.99
A_68_P28956734	chr13:37918572-37918616	NM_001177868:-186	Rreb1	PROMOTER	0.294	0.423	4304.25	1818.77	0.124	3030.87	376.08
A_68_P30463774	chr15:96291694-96291742	NM_028148:-444	Scaf11	PROMOTER	0.294	0.501	1219.43	610.39	0.147	812.36	119.44
A_68_P28535264	chr12:74146664-74146708	NM_009189:1013	Six1	INSIDE	0.294	0.589	1124.15	662.40	0.173	841.12	145.60
A_68_P27082611	chr10:39861509-39861553	NM_001114332:530	Slc16a10	INSIDE	0.294	0.612	888.49	543.96	0.180	686.30	123.72
A_68_P23542947	chr5:24104268-24104313	NM_025891:3530	Smarcd3	INSIDE	0.294	0.462	1776.32	820.22	0.136	1418.76	192.66
A_68_P21328878	chr2:72817077-72817121	NM_001098425:240	Sp3	INSIDE	0.294	0.405	3871.91	1567.02	0.119	2908.63	345.72
A_68_P29116720	chr13:69750085-69750129	NM_175283:235	Srd5a1	INSIDE	0.294	0.327	1824.07	596.40	0.096	1215.67	116.70
A_68_P32340127	chrX:39265129-39265173	NM_001033422:-72	Thoc2	PROMOTER	0.294	2.007	3746.06	7518.66	0.590	1500.11	884.89
A_68_P26465329	chr9:43851804-43851848	NM_009382:360	Thy1	INSIDE	0.294	0.683	1981.00	1352.86	0.201	1441.04	289.23
A_68_P32289749	chrX:20281744-20281788	NM_145628:732	Usp11	INSIDE	0.294	1.410	2905.22	4097.29	0.415	1322.34	549.07
A_68_P25505268	chr7:134488780-134488824	NM_146202:26	Zfp768	INSIDE	0.294	0.541	5020.78	2714.09	0.159	3484.95	553.49
A_68_P26710503	chr9:88418332-88418377	ENSMUST00000034997:-633		PROMOTER	0.294	0.533	1182.90	630.60	0.157	966.47	151.49
A_68_P24975023	chr7:13863906-13863950	NM_177312:142	6330408A02Rik	INSIDE	0.293	0.622	2851.13	1773.84	0.182	2030.50	369.65
A_68_P22765602	chr4:19496630-19496674	NM_027769:599	Cpne3	INSIDE	0.293	0.649	793.67	514.74	0.190	700.35	132.94
A_68_P26585431	chr9:64880028-64880087	NM_028906:-207	Dpp8	PROMOTER	0.293	0.440	1159.20	509.86	0.129	948.77	122.08
A_68_P21129653	chr2:34627681-34627725	NM_001163434:93	Hspa5	INSIDE	0.293	0.620	2180.82	1351.86	0.182	1776.45	322.79
A_68_P20453278	chr1:94998327-94998371	NM_001110315:94	Kif1a	INSIDE	0.293	0.550	2648.99	1458.18	0.161	1809.39	291.67
A_68_P31784508	chr18:66162318-66162362	NM_027400:-51	Lman1	PROMOTER	0.293	0.509	1077.33	548.48	0.149	878.66	130.92
A_68_P27535211	chr10:126748493-126748537	NM_001003913:328	Mars	INSIDE	0.293	0.523	4633.52	2422.92	0.153	3347.90	513.77
A_68_P29612399	chr14:55051483-55051527	NM_008608:1064	Mmp14	INSIDE	0.293	0.657	2064.39	1357.11	0.193	1585.31	305.40
A_68_P28831283	chr13:12350347-12350391	NM_001081128:-101	Mtr	PROMOTER	0.293	0.527	1009.78	532.47	0.155	763.32	117.96
A_68_P22310998	chr3:87774969-87775013	NM_016701:-24	Nes	PROMOTER	0.293	0.474	2870.67	1359.97	0.139	2059.17	285.72
A_68_P26021880	chr8:87308048-87308097	NM_001081981:-9804	Nfix	PROMOTER	0.293	0.697	1850.78	1289.55	0.204	1327.75	271.33
A_68_P28049717	chr11:97141114-97141159	NM_008942:754	Npepps	INSIDE	0.293	1.593	6250.36	9956.81	0.467	4024.92	1879.83
A_68_P22393105	chr3:104583807-104583851	NM_027982:-145	Ppm1j	DIVERGENT_PROMOTER	0.293	0.463	1284.55	594.17	0.135	951.62	128.90
A_68_P24834763	chr6:127718286-127718330	NM_201371:439	Prmt8	INSIDE	0.293	0.528	1007.47	531.79	0.155	788.32	122.03
A_68_P24170392	chr5:147657058-147657102	NM_026864:434	Rasl11a	INSIDE	0.293	0.666	1475.99	983.08	0.195	1211.41	236.39
A_68_P28172265	chr11:118430608-118430652	NM_001024931:340256	Rbfox3	INSIDE	0.293	0.490	1592.34	780.22	0.143	1158.14	166.16
A_68_P23893504	chr5:92738668-92738712	NM_172713:360	Sdad1	INSIDE	0.293	0.723	2304.22	1666.04	0.212	1683.50	357.23
A_68_P32036095	chr19:26682223-26682267	NM_011416:2595	Smarca2	INSIDE	0.293	0.657	1770.36	1162.95	0.192	1363.01	261.99
A_68_P22958421	chr4:59819390-59819434	NM_172468:891	Snx30	INSIDE	0.293	0.701	1625.10	1138.38	0.205	1357.73	278.35
A_68_P31104791	chr17:25707616-25707662	NM_011447:-7	Sox8	DIVERGENT_PROMOTER	0.293	0.529	1282.74	678.92	0.155	1010.72	156.57
A_68_P28070590	chr11:100721997-100722041	NM_001164062:221	Stat5a	INSIDE	0.293	0.592	1196.98	709.14	0.173	945.49	164.00
A_68_P25728415	chr8:26787130-26787174	NM_001081269:36397	Whsc1l1	INSIDE	0.293	1.637	516.31	845.41	0.479	525.16	251.72

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P29063254	chr13:56854688-56854732	AK131829:478		INSIDE	0.293	0.469	1402.36	658.19	0.137	1260.98	173.38
A_68_P27776267	chr11:47801865-47801909	ENSMUST00000128558:585		INSIDE	0.293	0.659	1202.52	792.78	0.193	943.05	182.10
A_68_P28743981	chr12:112661620-112661664	NM_028807:6002	1200009I06Rik	INSIDE	0.292	0.533	994.97	530.58	0.156	775.75	120.64
A_68_P26920089	chr10:7383225-7383269	NR_030698:78	A630066F11Rik	INSIDE	0.292	0.506	2660.02	1345.58	0.148	2036.56	300.51
A_68_P26397645	chr9:30729921-30729965	NM_001024139:95	Adamts15	INSIDE	0.292	0.587	2655.06	1559.55	0.172	1935.71	332.19
A_68_P25700847	chr8:18846041-18846085	NM_026792:-216	Agpat5	PROMOTER	0.292	0.411	1275.85	524.29	0.120	1017.50	121.91
A_68_P26913680	chr10:6079737-6079781	NM_031185:454	Akap12	INSIDE	0.292	0.593	2600.83	1542.13	0.173	2115.32	366.03
A_68_P23882635	chr5:90794338-90794382	NM_030886:851	Ankrd17	INSIDE	0.292	0.690	3054.67	2107.60	0.202	2236.75	451.10
A_68_P25429189	chr7:120351704-120351748	NM_007489:748	Arntl	INSIDE	0.292	0.529	1000.70	529.57	0.155	829.35	128.15
A_68_P25585263	chr7:148042305-148042349	NM_018742:-44	Bet1l	DIVERGENT_PROMOTER	0.292	0.591	2650.92	1565.37	0.172	2027.12	349.16
A_68_P28453879	chr12:56937597-56937641	NM_001037756:266	Brms1l	INSIDE	0.292	0.517	3907.17	2021.34	0.151	2900.31	438.81
A_68_P21221048	chr2:52531254-52531298	NM_001037099:825	Cacnb4	INSIDE	0.292	0.484	1120.73	542.76	0.141	907.44	128.19
A_68_P27479232	chr10:116500293-116500343	NM_007636:552	Cct2	INSIDE	0.292	0.702	1693.56	1188.50	0.205	1169.03	239.89
A_68_P32121691	chr19:42593347-42593391	NM_177464:74	D19Ertd386e	INSIDE	0.292	0.582	2611.01	1518.40	0.170	1878.54	318.97
A_68_P28737548	chr12:111517382-111517429	NM_172119:-34	Dio3	DIVERGENT_PROMOTER	0.292	0.621	840.39	522.19	0.182	664.86	120.84
A_68_P21585577	chr2:122124337-122124381	NM_025777:-277	Duoxa2	DIVERGENT_PROMOTER	0.292	0.597	901.23	537.78	0.174	691.95	120.45
A_68_P27554562	chr11:3795169-3795213	NM_173745:-52	Dusp18	DIVERGENT_PROMOTER	0.292	0.588	1725.53	1014.44	0.172	1300.49	223.61
A_68_P22369562	chr3:100293420-100293464	NM_001142952:-327	Fam46c	PROMOTER	0.292	0.710	1428.78	1014.97	0.207	1178.39	244.24
A_68_P23807224	chr5:75471627-75471671	NM_133256:23	Gsx2	INSIDE	0.292	0.511	2343.80	1198.27	0.149	1839.49	274.26
A_68_P26812406	chr9:107905251-107905295	NM_013785:294	Ip6k1	INSIDE	0.292	0.362	1542.06	558.32	0.106	1152.15	121.73
A_68_P24142813	chr5:141177968-141178012	NM_028833:342	Iqce	INSIDE	0.292	0.567	1355.69	769.13	0.166	1178.25	195.26
A_68_P27947413	chr11:78959127-78959171	NM_013571:708	Ksr1	INSIDE	0.292	0.652	3720.80	2427.69	0.190	2729.19	519.38
A_68_P23956961	chr5:106161428-106161472	NM_178701:31622	Lrrc8d	INSIDE	0.292	1.627	5444.91	8860.01	0.475	3636.37	1726.04
A_68_P21550149	chr2:115888052-115888096	NM_001159569:2283	Meis2	INSIDE	0.292	0.513	1690.71	867.77	0.150	1157.09	173.65
A_68_P23265180	chr4:123581921-123581965	NM_019660:-313	Mycbp	PROMOTER	0.292	0.604	2027.64	1224.95	0.177	1616.30	285.42
A_68_P21485380	chr2:103601403-103601448	NM_153126:-18	Nat10	PROMOTER	0.292	0.351	1473.67	517.41	0.102	1179.32	120.82
A_68_P26373646	chr9:26838450-26838494	NM_178113:713	Ncapd3	INSIDE	0.292	0.575	1380.17	793.06	0.168	1032.90	173.47
A_68_P32140280	chr19:45823401-45823445	NM_008723:631	Npm3	INSIDE	0.292	0.529	1686.66	892.00	0.154	1223.51	188.69
A_68_P29437679	chr14:19071747-19071791	NM_011584:-148	Nr1d2	PROMOTER	0.292	1.714	1886.57	3233.78	0.501	1321.71	662.59
A_68_P22422579	chr3:109946712-109946764	NM_001163348:-348	Ntng1	PROMOTER	0.292	0.564	929.84	524.30	0.164	728.06	119.75
A_68_P31062919	chr17:15098706-15098750	NM_024250:-491	Phf10	PROMOTER	0.292	1.357	6416.10	8704.67	0.397	4682.72	1856.94
A_68_P32141867	chr19:46131714-46131758	NM_001081214:708	Pprc1	INSIDE	0.292	0.549	3380.16	1854.29	0.160	2755.75	441.96
A_68_P31117588	chr17:27771794-27771838	NM_025963:371	Rps10	INSIDE	0.292	0.554	999.66	554.01	0.162	735.73	119.24
A_68_P32775570	chrX:156065828-156065872	NM_001135727:511	Sh3kbp1	INSIDE	0.292	1.517	2708.20	4109.38	0.443	1044.62	462.77
A_68_P25908463	chr8:63702506-63702553	NM_021506:-438	Sh3rf1	PROMOTER	0.292	0.459	1306.91	599.66	0.134	1163.87	156.17
A_68_P20005839	chr1:4487234-4487278	NM_011441:-762	Sox17	PROMOTER	0.292	0.467	1142.06	533.59	0.137	911.72	124.50
A_68_P25307027	chr7:96487209-96487253	NM_028343:67	Tmem135	INSIDE	0.292	0.414	3962.50	1640.35	0.121	3189.47	386.18
A_68_P22728289	chr4:11083171-11083217	NM_001199105:-393	Trp53inp1	PROMOTER	0.292	0.528	1082.70	572.05	0.155	783.13	121.02
A_68_P23185865	chr4:106351237-106351283	NM_001172073:31	Ttc4	INSIDE	0.292	0.596	911.39	542.97	0.174	694.48	121.01
A_68_P28694456	chr12:104187580-104187626	NM_001081017:534	Unc79	INSIDE	0.292	0.413	1388.25	573.76	0.121	1017.38	122.81
A_68_P26038378	chr8:90485888-90485932	NM_033327:-2416	Zfp423	PROMOTER	0.292	0.628	2432.62	1528.64	0.183	1809.04	331.51
A_68_P21579347	chr2:120996224-120996271	NM_178889:638	Zscan29	INSIDE	0.292	0.364	1531.16	556.88	0.106	1135.92	120.64
A_68_P31801899	chr18:69358377-69358422	AK080553:625		INSIDE	0.292	0.667	1113.72	742.71	0.195	949.58	184.96
A_68_P21109229	chr2:31315525-31315569	ENSMUST00000142448:13292		INSIDE	0.292	0.651	4225.22	2750.87	0.190	3018.17	574.58
A_68_P31833165	chr18:74938885-74938929	NM_177470:41	Acaa2	INSIDE	0.291	0.576	3477.89	2001.80	0.168	2416.86	404.97
A_68_P22858339	chr4:40650160-40650206	NM_025545:-233	Aptx	PROMOTER	0.291	0.556	3699.17	2057.41	0.162	2715.18	439.07
A_68_P21073893	chr2:25562488-25562532	NM_023326:112	Bmyc	INSIDE	0.291	0.518	2191.14	1134.96	0.151	1771.29	267.16
A_68_P30793143	chr16:58728472-58728525	NM_171826:342	Cldnd1	INSIDE	0.291	0.516	1065.71	549.69	0.150	790.94	118.52
A_68_P27998412	chr11:88007125-88007169	NM_001172099:24080	Cuedc1	INSIDE	0.291	1.632	1600.20	2611.79	0.474	1254.77	595.27
A_68_P26240284	chr8:126038626-126038670	NM_001170976:707	Dbndd1	INSIDE	0.291	0.626	2142.22	1340.42	0.182	1685.82	306.92
A_68_P28593179	chr12:84861421-84861470	NM_001165256:-5553	Dcaf4	PROMOTER	0.291	0.541	1017.28	550.51	0.157	825.27	129.77

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P30648665	chr16:31663764-31663808	NM_007862:-338	Dlg1	PROMOTER	0.291	0.436	1220.85	532.57	0.127	933.67	118.67
A_68_P28962021	chr13:38750788-38750832	NM_025380:87	Eef1e1	INSIDE	0.291	0.640	1197.51	766.37	0.186	937.50	174.80
A_68_P20091639	chr1:24106505-24106549	NM_026604:654	Fam135a	INSIDE	0.291	0.529	1272.08	672.54	0.154	1041.98	160.09
A_68_P32920574	chr13:50513406-50513450	NM_175401:183	Fbxw17	INSIDE	0.291	0.407	1725.21	703.01	0.119	1387.43	164.75
A_68_P24173495	chr5:148211661-148211705	NM_010229:383	Flt3	INSIDE	0.291	0.651	1303.31	848.05	0.189	1103.09	208.52
A_68_P25089992	chr7:52151653-52151697	NM_027376:226	Fuz	INSIDE	0.291	0.609	1832.41	1115.85	0.178	1331.80	236.40
A_68_P20264196	chr1:59540370-59540414	NM_008057:1402	Fzd7	INSIDE	0.291	0.647	4951.91	3202.58	0.188	3716.89	699.77
A_68_P28553835	chr12:77507209-77507257	NM_008301:1876	Hspa2	INSIDE	0.291	0.577	2070.19	1195.39	0.168	1492.84	250.92
A_68_P24334773	chr6:30907971-30908017	NM_001135093:996	Klf14	INSIDE	0.291	0.529	1220.51	645.44	0.154	916.79	140.84
A_68_P27535212	chr10:126748563-126748607	NM_001003913:258	Mars	INSIDE	0.291	0.641	1250.46	802.14	0.187	1011.00	188.76
A_68_P29701300	chr14:70843636-70843680	NR_029802:342	Mir320	DOWNSTREAM	0.291	0.415	1340.23	556.11	0.121	1026.45	123.74
A_68_P27838143	chr11:59475883-59475927	NM_012027:-92	Mprip	PROMOTER	0.291	0.608	848.32	515.51	0.177	678.35	119.82
A_68_P24161584	chr5:145307316-145307360	NM_016789:583	Nptx2	INSIDE	0.291	0.593	925.50	548.83	0.173	691.26	119.32
A_68_P22705746	chr4:6380618-6380662	NM_010945:778	Nsmaf	INSIDE	0.291	0.598	1501.04	897.31	0.174	1239.58	215.96
A_68_P21495957	chr2:105515455-105515507	NM_013627:-1121	Pax6	DIVERGENT_PROMOTER	0.291	0.604	1261.47	761.99	0.176	908.46	159.49
A_68_P28083253	chr11:102941713-102941757	NM_152813:21238	Plcd3	INSIDE	0.291	0.571	954.33	545.03	0.166	734.64	122.25
A_68_P28055837	chr11:98210403-98210447	NM_144828:373	Ppp1r1b	INSIDE	0.291	0.565	4091.51	2311.88	0.164	2917.39	479.12
A_68_P26809514	chr9:107456460-107456504	NM_019713:-504	Rassf1	PROMOTER	0.291	0.569	1935.92	1101.47	0.166	1313.80	217.82
A_68_P22286829	chr3:83568459-83568506	NM_009144:-1760	Sfrp2	PROMOTER	0.291	0.395	1409.56	556.86	0.115	1077.22	124.04
A_68_P28050118	chr11:97224447-97224491	NM_138657:604	Socs7	INSIDE	0.291	0.494	1273.59	629.35	0.144	1088.65	156.52
A_68_P31931515	chr19:5893867-5893911	NM_198634:219	Tigd3	INSIDE	0.291	0.584	1366.26	798.07	0.170	1106.96	187.96
A_68_P30374042	chr15:80542447-80542491	NM_144812:726	Tnrc6b	INSIDE	0.291	0.565	2485.99	1404.12	0.164	1757.12	288.84
A_68_P27564839	chr11:5662438-5662482	NM_001077661:-81	Urgcp	PROMOTER	0.291	0.643	1337.79	860.34	0.187	1214.75	227.24
A_68_P26805312	chr9:106725024-106725068	NM_001015507:740	Vprbp	INSIDE	0.291	0.639	1814.16	1159.24	0.186	1451.16	269.83
A_68_P31149742	chr17:33766187-33766231	NM_026712:172	Zfp414	INSIDE	0.291	0.445	6747.39	3002.33	0.129	5296.35	685.64
A_68_P26036154	chr8:90184192-90184236	NM_033327:299280	Zfp423	DOWNSTREAM	0.291	0.573	7295.16	4182.97	0.167	4961.94	828.90
A_68_P20936657	chr1:193006272-193006316	NM_007498:918	Atf3	INSIDE	0.290	0.486	1095.96	532.55	0.141	829.74	116.77
A_68_P24115149	chr5:135662813-135662862	NM_011714:-355	Baz1b	PROMOTER	0.290	0.480	1075.80	516.45	0.139	874.52	121.72
A_68_P24467398	chr6:55067497-55067541	NM_009953:15448	Crhr2	INSIDE	0.290	0.491	1247.82	612.33	0.142	865.93	123.04
A_68_P26248320	chr8:127420438-127420486	NM_198103:1143	Exoc8	INSIDE	0.290	1.552	928.99	1442.11	0.450	780.54	351.57
A_68_P25011168	chr7:26444266-26444310	NM_138586:117	Exosc5	INSIDE	0.290	0.569	3894.44	2214.29	0.165	2797.00	460.86
A_68_P30589004	chr16:20693747-20693792	NM_133778:-1360	Fam131a	PROMOTER	0.290	0.623	818.12	509.47	0.180	636.34	114.76
A_68_P30347858	chr15:76199296-76199340	NM_021555:-9	Fam203a	PROMOTER	0.290	0.590	980.36	578.65	0.171	721.73	123.65
A_68_P25035344	chr7:31935750-31935794	NM_027898:297	Gramd1a	INSIDE	0.290	0.720	2585.09	1861.85	0.209	1791.82	374.37
A_68_P32539365	chrX:91787127-91787171	NM_019791:265	Maged1	INSIDE	0.290	1.612	4543.27	7325.31	0.468	1646.10	770.57
A_68_P32696393	chrX:136405600-136405644	NM_001193309:571	Morc4	INSIDE	0.290	1.434	3195.96	4582.39	0.415	1254.52	520.76
A_68_P21138065	chr2:35991976-35992020	NM_026422:81	Mrrf	INSIDE	0.290	0.380	1379.22	524.74	0.110	1059.61	116.93
A_68_P20258949	chr1:58502448-58502495	NM_027351:-141	Ppil3	DIVERGENT_PROMOTER	0.290	0.508	1199.71	609.82	0.147	786.45	115.84
A_68_P29950631	chr14:120878349-120878398	NM_029519:691	Rap2a	INSIDE	0.290	0.569	1022.09	582.08	0.165	727.34	120.08
A_68_P28741734	chr12:112278458-112278502	NM_198023:472	Rcor1	INSIDE	0.290	0.583	1825.48	1065.11	0.169	1419.55	240.15
A_68_P26770648	chr9:100543417-100543473	NM_009282:-597	Stag1	PROMOTER	0.290	0.551	990.61	545.74	0.160	756.42	120.75
A_68_P31104079	chr17:25611509-25611553	NM_027951:2996	Tekt4	INSIDE	0.290	0.538	2290.27	1232.73	0.156	1651.83	258.06
A_68_P29619287	chr14:56300293-56300337	NM_145705:340	Tinf2	INSIDE	0.290	0.359	1619.23	581.11	0.104	1191.14	123.90
A_68_P24092036	chr5:130555652-130555696	NM_001130476:319	Tpst1	INSIDE	0.290	0.699	1632.32	1140.96	0.203	1334.75	270.58
A_68_P26228083	chr8:124177031-124177079	NM_080855:-1221	Zcchc14	PROMOTER	0.290	0.456	1346.16	613.25	0.132	940.16	124.30
A_68_P21101316	chr2:29949011-29949055	NM_001037762:123	Zdhhc12	INSIDE	0.290	0.613	1506.51	923.59	0.178	1068.77	190.18
A_68_P31620728	chr18:36049609-36049656			Unknown	0.290	0.600	983.92	590.81	0.174	694.27	120.75
A_68_P25653637	chr8:11187883-11187927	ENSMUST00000151014:150		INSIDE	0.290	0.475	1405.38	667.83	0.138	1005.54	138.45
A_68_P26973142	chr10:17742734-17742778	NM_028440:302	3110003A17Rik	INSIDE	0.289	0.605	3596.24	2174.83	0.175	2581.80	450.71
A_68_P29005206	chr13:46060896-46060940	NM_009124:-573	Atxn1	PROMOTER	0.289	0.533	1901.12	1013.24	0.154	1466.43	226.22
A_68_P25843138	chr8:48798881-48798925	NM_172407:383	Cdkn2aip	INSIDE	0.289	0.518	1190.71	616.78	0.150	980.32	146.98

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27183505	chr10:61441491-61441535	NM_007731:344	Col13a1	INSIDE	0.289	0.464	1189.96	552.60	0.134	898.88	120.49
A_68_P23361908	chr4:140616772-140616816	NM_001145958:-334	Crocc	PROMOTER	0.289	0.442	4975.18	2200.64	0.128	3735.03	476.92
A_68_P21134666	chr2:35477528-35477572	NM_001114124:50	Dab2ip	INSIDE	0.289	0.413	1276.03	527.55	0.119	1055.63	126.06
A_68_P21102299	chr2:30141747-30141791	NM_177648:106	Dolk	INSIDE	0.289	0.581	2654.39	1542.59	0.168	1932.29	324.04
A_68_P32219504	chr19:59526023-59526072	NR_002863:7078	Emx2os	INSIDE	0.289	0.588	883.92	519.35	0.170	746.75	126.83
A_68_P30364009	chr15:78873840-78873884	NM_015738:1548	Galr3	INSIDE	0.289	0.709	2482.84	1759.91	0.205	1813.34	372.01
A_68_P31469355	chr18:5592249-5592293	NR_033552:165	Gm10125	INSIDE	0.289	0.412	1288.43	530.38	0.119	982.72	116.95
A_68_P26546363	chr9:58049670-58049721	NM_001161540:-89	Islr2	PROMOTER	0.289	1.612	3806.23	6134.04	0.466	2481.86	1156.46
A_68_P28997683	chr13:44829152-44829196	NM_001205043:2535	Jarid2	INSIDE	0.289	0.517	2630.47	1360.22	0.150	1836.55	274.76
A_68_P25349935	chr7:104480504-104480548	NM_001039039:-306	Kctd21	DIVERGENT_PROMOTER	0.289	0.299	1729.33	516.53	0.086	1377.68	118.82
A_68_P21309972	chr2:69423381-69423427	NM_001081088:720	Lrp2	INSIDE	0.289	0.553	1038.24	574.28	0.160	761.29	121.55
A_68_P23260021	chr4:122638391-122638435	NM_029662:19	Mfsd2a	INSIDE	0.289	0.622	1411.09	877.56	0.180	1126.79	202.73
A_68_P23349653	chr4:138648926-138648970	NM_008675:-63	Nbl1	PROMOTER	0.289	0.597	1053.71	628.70	0.173	887.58	153.14
A_68_P26075123	chr8:96560510-96560557	NM_026623:406	Nudt21	INSIDE	0.289	0.604	1360.52	822.02	0.175	1087.56	189.83
A_68_P25957680	chr8:74116556-74116600	NM_025396:496	Pgls	INSIDE	0.289	0.479	1111.20	531.95	0.138	852.96	118.07
A_68_P21110347	chr2:31491119-31491163	NM_001123362:-4416	Prdm12	PROMOTER	0.289	0.605	2072.75	1254.06	0.175	1628.91	285.24
A_68_P27954278	chr11:80242652-80242696	NM_178616:558	Psmd11	INSIDE	0.289	0.570	2297.37	1309.55	0.165	1732.48	285.19
A_68_P26463575	chr9:43553383-43553427	NM_021424:746	Pvrl1	INSIDE	0.289	0.468	1102.54	516.48	0.136	899.37	121.89
A_68_P27896515	chr11:69495196-69495240	NM_030702:254	Senp3	INSIDE	0.289	0.519	2388.39	1238.44	0.150	1846.44	276.67
A_68_P31351306	chr17:74795028-74795072	NM_144798:79	Slc30a6	INSIDE	0.289	0.614	1014.56	622.62	0.177	846.16	150.14
A_68_P29341537	chr13:114407731-114407779	NM_130796:1018	Snx18	INSIDE	0.289	0.539	1023.50	551.54	0.156	768.99	119.62
A_68_P30380073	chr15:81689400-81689446	NM_020507:-666	Tob2	PROMOTER	0.289	0.544	1004.28	546.65	0.157	757.58	119.12
A_68_P22382654	chr3:102538511-102538562	NM_027533:-156	Tspan2	PROMOTER	0.289	0.588	1057.44	621.30	0.170	758.81	128.76
A_68_P23984910	chr5:111714358-111714402	NM_024477:405559	Ttc28	INSIDE	0.289	1.503	3161.06	4751.77	0.435	2197.69	954.94
A_68_P27796900	chr11:51813767-51813811	NM_009458:180	Ube2b	INSIDE	0.289	0.391	1321.77	517.13	0.113	1046.13	118.28
A_68_P20023918	chr1:9737605-9737655	NM_173443:833	Vcpip1	INSIDE	0.289	0.585	1069.26	625.55	0.169	683.09	115.38
A_68_P30246279	chr15:57972958-57973002	NM_029734:-10	Wdyhv1	DIVERGENT_PROMOTER	0.289	0.601	950.62	571.54	0.174	671.27	116.80
A_68_P30000714	chr15:8519221-8519268			Unknown	0.289	0.626	1571.37	983.84	0.181	1190.85	215.58
A_68_P31215882	chr17:48233958-48234004	NM_026625:7399	1700067P10Rik	DOWNSTREAM	0.288	0.584	897.20	524.07	0.168	720.02	121.27
A_68_P24127511	chr5:138220691-138220735	NM_027242:567	2010007H12Rik	INSIDE	0.288	0.582	1030.64	599.67	0.168	736.02	123.52
A_68_P31609279	chr18:33954809-33954858	NR_038151:288	2410004N09Rik	INSIDE	0.288	0.536	1097.38	588.01	0.154	778.08	120.08
A_68_P31119198	chr17:28046785-28046829	NM_181413:522	Anks1	INSIDE	0.288	0.366	1475.23	539.44	0.105	1139.79	119.99
A_68_P26569955	chr9:62189553-62189597	NM_009672:425	Anp32a	INSIDE	0.288	2.218	7454.98	16534.36	0.638	4783.60	3051.89
A_68_P27970640	chr11:83116209-83116256	NM_001035854:34	Ap2b1	INSIDE	0.288	0.506	1137.54	576.09	0.146	795.64	115.97
A_68_P21334163	chr2:73730945-73730989	NM_001025093:-281	Atf2	PROMOTER	0.288	0.498	1166.27	581.04	0.143	875.44	125.49
A_68_P26818136	chr9:108976442-108976486	NM_172774:174	Atrip	INSIDE	0.288	0.607	3567.99	2164.71	0.175	2549.16	444.92
A_68_P24942635	chr6:148844880-148844924	NM_181541:-254	Caprin2	PROMOTER	0.288	0.636	1656.30	1053.88	0.183	1278.52	233.94
A_68_P32130472	chr19:44181487-44181534	NM_001162410:457	Chuk	INSIDE	0.288	1.567	5209.02	8160.95	0.451	3712.27	1672.88
A_68_P26875482	chr9:119892235-119892279	NM_153287:1520	Csrnp1	INSIDE	0.288	0.343	3301.34	1132.11	0.099	2401.95	236.83
A_68_P32040826	chr19:27504142-27504186	NM_177474:146	D19Bwg1357e	INSIDE	0.288	0.614	4153.16	2551.77	0.177	3232.43	572.62
A_68_P20769690	chr1:162964920-162964964	NR_002840:-354	Gas5	DIVERGENT_PROMOTER	0.288	0.565	4380.48	2475.69	0.163	3082.19	500.88
A_68_P32119983	chr19:42330356-42330400	NM_027694:150	Golga7b	INSIDE	0.288	0.578	1822.77	1053.90	0.167	1356.45	226.09
A_68_P30021004	chr15:12251953-12252003	NM_025673:728	Golph3	INSIDE	0.288	0.608	1180.07	717.61	0.175	896.26	157.00
A_68_P26023020	chr8:87509915-87509959	NM_001167991:-4557	Hook2	DIVERGENT_PROMOTER	0.288	0.510	1072.57	546.88	0.147	953.13	140.17
A_68_P30966735	chr16:92059004-92059048	NM_080456:446	Mrps6	INSIDE	0.288	0.491	1978.11	971.22	0.141	1636.30	231.32
A_68_P29689305	chr14:68743026-68743070	NM_008691:13	Nefm	INSIDE	0.288	0.449	5041.87	2261.94	0.129	4106.09	529.88
A_68_P22872800	chr4:43644731-43644775	NM_173788:-54	Npr2	PROMOTER	0.288	1.511	5436.31	8213.47	0.435	3337.09	1451.11
A_68_P29094165	chr13:63665588-63665632	NM_008957:1218	Ptch1	INSIDE	0.288	0.668	891.25	595.20	0.193	622.39	119.82
A_68_P27568683	chr11:6374982-6375033	NM_011221:913	Purb	INSIDE	0.288	0.450	1239.90	558.31	0.130	910.10	117.95
A_68_P23576450	chr5:31396001-31396045	NM_011773:-122	Slc30a3	PROMOTER	0.288	1.336	4328.71	5783.69	0.384	2888.85	1109.73
A_68_P30570744	chr16:16870950-16870994	NM_011624:-11	Top3b	DIVERGENT_PROMOTER	0.288	0.325	1641.88	533.84	0.094	1394.13	130.41

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27565815	chr11:5856146-5856195	NM_019661:410	Ykt6	INSIDE	0.288	0.510	1006.23	512.70	0.147	829.23	121.49
A_68_P27855686	chr11:62603073-62603117	NM_138949:-175	Zfp286	PROMOTER	0.288	0.383	1745.56	669.02	0.110	1299.64	143.42
A_68_P25827306	chr8:46023782-46023826	AK079043:-3291		PROMOTER	0.288	1.370	3272.86	4484.89	0.394	2326.64	917.67
A_68_P22964961	chr4:62186403-62186447	NM_177607:22	4933430I17Rik	INSIDE	0.287	0.665	1107.30	735.94	0.191	996.80	190.04
A_68_P28191919	chr11:121534104-121534151	NM_178664:338	B3gntl1	INSIDE	0.287	0.630	876.92	552.82	0.181	659.65	119.51
A_68_P29856057	chr14:102039624-102039668	NM_001033132:42	Commd6	INSIDE	0.287	0.454	4775.14	2167.54	0.130	3500.99	456.54
A_68_P21320122	chr2:71382362-71382406	NM_010054:2427	Dlx2	INSIDE	0.287	0.503	1577.81	794.03	0.145	1323.44	191.28
A_68_P28158449	chr11:116144557-116144601	NM_010254:2326	Galr2	INSIDE	0.287	0.402	1510.04	606.34	0.115	1072.64	123.66
A_68_P23968443	chr5:108154493-108154537	NM_010278:-1151	Gfi1	PROMOTER	0.287	0.572	2172.92	1242.44	0.164	1848.78	303.22
A_68_P30641174	chr16:30309847-30309891	NM_008148:997	Gp5	INSIDE	0.287	0.678	1551.89	1052.21	0.194	1119.97	217.67
A_68_P30964672	chr16:91730394-91730438	NM_001110276:801	Itsn1	INSIDE	0.287	0.630	1288.50	812.30	0.181	1078.75	195.21
A_68_P30347741	chr15:76181792-76181836	NM_001164607:91	Maf1	INSIDE	0.287	1.738	3682.37	6398.89	0.498	2466.15	1228.36
A_68_P21722732	chr2:147010130-147010174	NR_030769:334	Nkx2-2as	INSIDE	0.287	0.629	1165.97	732.92	0.181	992.36	179.16
A_68_P20797862	chr1:167933482-167933526	NM_011137:-739	Pou2f1	PROMOTER	0.287	0.503	2291.28	1152.49	0.144	1791.86	258.47
A_68_P25574424	chr7:146038574-146038618	NM_026391:528	Ppp2r2d	INSIDE	0.287	0.623	1761.29	1097.13	0.179	1484.25	265.10
A_68_P22558749	chr3:136334580-136334624	NM_008913:869	Ppp3ca	INSIDE	0.287	0.530	2584.21	1369.02	0.152	2083.54	316.64
A_68_P24155046	chr5:143874559-143874603	NM_080561:119	Rnf216	INSIDE	0.287	0.548	1427.99	782.23	0.157	1146.26	180.05
A_68_P28035860	chr11:94840370-94840414	NM_009161:-2751	Sgca	PROMOTER	0.287	0.710	1261.96	896.40	0.204	952.35	194.21
A_68_P27899519	chr11:70034182-70034226	NM_172371:292	Slc16a13	INSIDE	0.287	0.677	2138.90	1448.28	0.194	1471.59	286.19
A_68_P29664621	chr14:64562219-64562263	NM_011446:-302	Sox7	PROMOTER	0.287	0.675	1774.40	1198.17	0.194	1488.83	288.88
A_68_P25507645	chr7:134985062-134985106	NM_009294:-237	Stx4a	PROMOTER	0.287	0.454	1433.00	651.08	0.130	1154.76	150.48
A_68_P31102174	chr17:25326044-25326091	NM_001197024:723	Unkl	INSIDE	0.287	2.199	2892.25	6361.48	0.630	1885.87	1188.62
A_68_P26814409	chr9:108250644-108250688	NM_011678:505	Usp4	INSIDE	0.287	0.698	3306.90	2307.48	0.200	2490.18	499.03
A_68_P26232278	chr8:124805221-124805265	NM_009569:-798	Zfpm1	PROMOTER	0.287	0.706	2890.92	2040.33	0.203	2183.91	442.96
A_68_P29102445	chr13:65342650-65342694			Unknown	0.287	1.640	2950.27	4839.63	0.471	2013.34	948.92
A_68_P30421541	chr15:88667971-88668015	ENSMUST00000083457:2263		DOWNSTREAM	0.287	0.499	3431.56	1713.57	0.143	2458.73	352.67
A_68_P27633580	chr11:20731422-20731466	NM_173752:-333	1110067D22Rik	PROMOTER	0.286	0.403	2112.75	851.46	0.115	1634.76	188.73
A_68_P24183686	chr5:149995738-149995782	NR_015478:-121	5730422E09Rik	DIVERGENT_PROMOTER	0.286	0.546	995.30	543.23	0.156	763.11	119.15
A_68_P24007906	chr5:115568969-115569013	NM_007383:332	Acads	INSIDE	0.286	1.430	1816.65	2597.95	0.409	1297.06	531.05
A_68_P32180647	chr19:53217337-53217384	NM_013758:-1126	Add3	PROMOTER	0.286	0.567	1104.47	626.67	0.162	889.75	144.36
A_68_P26199828	chr8:119467966-119468010	NM_177700:696	Atmin	INSIDE	0.286	0.586	1366.95	801.42	0.168	1053.01	176.42
A_68_P20878149	chr1:182781262-182781306	NM_145943:3	BC031781	INSIDE	0.286	0.625	917.25	573.30	0.179	688.08	123.08
A_68_P30940063	chr16:87495606-87495650	NM_009840:486	Cct8	INSIDE	0.286	0.625	3419.51	2137.75	0.179	2726.76	487.36
A_68_P24359958	chr6:35083871-35083915	NM_001164412:-155	Cnot4	PROMOTER	0.286	0.570	1444.44	823.65	0.163	1111.87	181.03
A_68_P28528482	chr12:72932824-72932868	NM_026102:782	Daam1	INSIDE	0.286	0.443	1250.67	554.25	0.127	919.50	116.72
A_68_P24449227	chr6:52175677-52175721	NM_010456:1671	Hoxa9	INSIDE	0.286	0.577	1083.34	625.13	0.165	906.20	149.66
A_68_P28553824	chr12:77505751-77505795	NM_008301:416	Hspa2	INSIDE	0.286	0.465	1427.90	663.73	0.133	1109.00	147.26
A_68_P24759769	chr6:113432843-113432887	NM_134159:11416	Il17rc	INSIDE	0.286	0.272	2040.65	555.79	0.078	1604.13	124.97
A_68_P21680283	chr2:139502974-139503018	NM_001126490:-917	Ism1	PROMOTER	0.286	0.499	2705.45	1349.99	0.142	2069.31	294.85
A_68_P23120703	chr4:94717558-94717602	NM_010591:1333	Jun	INSIDE	0.286	0.666	949.37	632.09	0.191	754.96	143.85
A_68_P30478813	chr15:99054103-99054147	NM_010601:-1282	Kcnh3	PROMOTER	0.286	0.493	1168.71	575.72	0.141	913.16	128.58
A_68_P31156874	chr17:35118802-35118846	NM_001204273:-250	Lsm2	PROMOTER	0.286	0.428	2081.23	890.56	0.122	1752.74	214.56
A_68_P23588230	chr5:33678025-33678069	NM_021500:-174	Maea	PROMOTER	0.286	0.374	1878.77	703.16	0.107	1386.19	148.30
A_68_P30575358	chr16:17722742-17722786	NM_001040683:259	Med15	INSIDE	0.286	0.453	1994.93	904.08	0.130	1685.87	218.73
A_68_P28177558	chr11:119251624-119251668	NR_035453:-139	Mir1932	PROMOTER	0.286	0.462	4271.84	1973.19	0.132	3223.29	425.76
A_68_P29701298	chr14:70843425-70843469	NR_029802:130	Mir320	DOWNSTREAM	0.286	0.682	3204.31	2185.44	0.195	2370.08	462.40
A_68_P29689083	chr14:68703035-68703085	NM_010910:1120	Nefl	INSIDE	0.286	0.585	1767.07	1033.39	0.167	1351.09	226.08
A_68_P29023783	chr13:49283461-49283505	NM_013610:567	Ninj1	INSIDE	0.286	0.600	926.87	555.99	0.171	682.64	116.94
A_68_P23271479	chr4:124664198-124664242	NM_138683:547	Rspo1	INSIDE	0.286	1.542	9361.65	14434.57	0.442	6803.05	3005.24
A_68_P28224313	chr12:8777876-8777920	NM_011519:-303	Sdc1	PROMOTER	0.286	0.478	1159.22	553.62	0.137	887.67	121.34
A_68_P23993052	chr5:113005975-113006019	NM_019982:209	Sez6l	INSIDE	0.286	0.594	2040.56	1211.37	0.170	1645.50	279.06

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28534662	chr12:74040869-74040913	NM_011384:-41	Six6	PROMOTER	0.286	0.575	2021.53	1162.50	0.164	1466.62	240.87
A_68_P27779980	chr11:48613984-48614028	NR_028563:-1528	Snord96a	PROMOTER	0.286	0.484	1131.53	548.14	0.139	850.77	118.00
A_68_P32136797	chr19:45228297-45228341	NM_021901:3114	Tlx1	INSIDE	0.286	0.574	1014.95	582.93	0.164	765.50	125.67
A_68_P27842502	chr11:60166254-60166298	NM_001039092:131	Tom1l2	INSIDE	0.286	0.524	2049.56	1073.20	0.150	1540.13	230.37
A_68_P21070648	chr2:25079927-25079971	NM_146116:274	Tubb2c	INSIDE	0.286	0.550	2642.39	1453.91	0.157	2034.13	319.71
A_68_P27992046	chr11:86806680-86806725	NM_001005341:562	Ypel2	INSIDE	0.286	0.717	2621.91	1881.13	0.205	2013.03	413.64
A_68_P21121777	chr2:33324228-33324287	NM_001025594:-205	Zbtb43	PROMOTER	0.286	0.607	860.01	521.62	0.174	684.62	118.83
A_68_P24114682	chr5:135565443-135565487			Unknown	0.286	0.542	1537.77	833.26	0.155	1383.43	214.26
A_68_P21904833	chr2:180317770-180317815	NM_028479:1784	1600027N09Rik	INSIDE	0.285	0.714	1518.90	1083.89	0.203	1141.79	231.82
A_68_P30380159	chr15:81702880-81702926	NM_080633:10	Aco2	INSIDE	0.285	0.550	1078.74	593.74	0.157	764.99	119.88
A_68_P32019520	chr19:23832652-23832703	NM_177034:-688	Apba1	PROMOTER	0.285	0.633	849.54	537.40	0.180	663.11	119.36
A_68_P24798779	chr6:120442774-120442818	NM_033567:1029	Cecr6	INSIDE	0.285	0.473	2029.78	960.77	0.135	1580.40	213.41
A_68_P23415476	chr4:151308731-151308775	NM_172704:924	Dnajc11	INSIDE	0.285	0.476	1138.93	542.64	0.136	972.31	132.01
A_68_P23270909	chr4:124571706-124571750	NM_177671:12700	Epha10	DOWNSTREAM	0.285	0.701	1547.42	1084.80	0.200	1080.50	215.98
A_68_P28158782	chr11:116197021-116197065	NM_008240:-374	Foxj1	PROMOTER	0.285	0.470	1201.62	564.88	0.134	868.88	116.34
A_68_P29484665	chr14:27852530-27852574	NM_134437:366	Il17rd	INSIDE	0.285	0.660	1194.43	787.81	0.188	981.10	184.21
A_68_P28832394	chr13:12553847-12553891	NM_001199043:137	Lgals8	INSIDE	0.285	0.707	1827.52	1291.24	0.201	1343.56	270.44
A_68_P26465868	chr9:43938018-43938064	NM_023061:-4700	Mcam	PROMOTER	0.285	0.654	1067.23	697.96	0.186	841.86	156.71
A_68_P30575357	chr16:17722612-17722656	NM_001040683:389	Med15	INSIDE	0.285	0.581	1108.52	643.61	0.165	918.66	151.83
A_68_P28010558	chr11:90110449-90110493	NM_026178:-319	Mmd	PROMOTER	0.285	0.653	1230.30	802.83	0.186	966.13	179.74
A_68_P31257925	chr17:56857454-56857498	NM_027244:292	Ndufa11	INSIDE	0.285	0.710	2636.33	1871.06	0.202	1931.98	390.66
A_68_P26400217	chr9:31194116-31194160	NM_172766:362	Nfrkb	INSIDE	0.285	0.582	1195.13	695.01	0.166	970.54	160.97
A_68_P21070361	chr2:25036829-25036873	NM_025980:573	Nrarp	INSIDE	0.285	0.691	2563.98	1771.64	0.197	1831.98	361.15
A_68_P23618580	chr5:38668967-38669011	NM_172709:346	Otop1	INSIDE	0.285	0.445	2069.17	921.27	0.127	1547.19	196.57
A_68_P20370400	chr1:78193226-78193270	NM_001159520:463	Pax3	INSIDE	0.285	0.398	2203.97	877.86	0.114	1787.04	203.17
A_68_P23438160	chr4:154735910-154735954	NM_008860:-432	Prkcz	PROMOTER	0.285	0.346	1560.54	540.03	0.099	1188.92	117.20
A_68_P32071917	chr19:32831118-32831162	NM_008960:-926	Pten	PROMOTER	0.285	0.460	1600.62	735.67	0.131	1213.86	159.15
A_68_P27541276	chr10:127848724-127848768	NM_001164237:75	Rnf41	INSIDE	0.285	0.346	1482.41	512.45	0.098	1202.87	118.41
A_68_P21567499	chr2:118860959-118861006	NM_173450:457	Rpusd2	INSIDE	0.285	0.431	1203.70	518.34	0.123	946.80	116.40
A_68_P28151695	chr11:115024532-115024576	NM_012030:-100	Slc9a3r1	PROMOTER	0.285	0.480	1527.52	733.96	0.137	1217.10	166.40
A_68_P28744656	chr12:112777247-112777291	NR_033168:-1888	Snora28	PROMOTER	0.285	0.489	1390.09	679.70	0.139	1202.16	167.57
A_68_P27569494	chr11:6526399-6526444	NM_001130457:-351	Tbrg4	PROMOTER	0.285	0.562	990.46	556.67	0.160	735.74	117.74
A_68_P22336429	chr3:93251869-93251913	NM_001163098:5639	Tchh	INSIDE	0.285	0.544	3864.49	2102.53	0.155	2807.29	435.78
A_68_P25042335	chr7:34917422-34917466	NM_207212:843	Wtip	INSIDE	0.285	0.712	3656.96	2605.57	0.203	2868.96	581.90
A_68_P20252951	chr1:57463816-57463860	NM_001037742:-320	1110034B05Rik	PROMOTER	0.284	0.480	1330.48	639.27	0.137	1073.59	146.60
A_68_P30092465	chr15:27396520-27396564	NM_020332:111	Ank	INSIDE	0.284	1.666	1809.05	3014.71	0.474	1329.51	630.30
A_68_P29047195	chr13:54150782-54150826	NM_010076:223	Drd1a	INSIDE	0.284	0.507	2712.96	1375.12	0.144	2034.05	293.08
A_68_P29150855	chr13:75845818-75845862	NM_138953:909	Ell2	INSIDE	0.284	0.551	3812.96	2100.90	0.157	2775.00	434.36
A_68_P26137945	chr8:108660566-108660610	NM_176838:286	Esrp2	INSIDE	0.284	0.703	2587.98	1818.11	0.200	1926.67	384.79
A_68_P24423931	chr6:47544220-47544264	NM_001146689:787	Ezh2	INSIDE	0.284	0.462	1665.91	770.07	0.131	1313.21	172.63
A_68_P20352246	chr1:75139198-75139242	NM_170755:-139	Fam134a	DIVERGENT_PROMOTER	0.284	0.487	2793.58	1360.33	0.138	2206.11	305.33
A_68_P29659636	chr14:63796998-63797042	NM_010191:-390	Fdft1	PROMOTER	0.284	0.459	1214.26	557.87	0.130	912.10	118.93
A_68_P31214659	chr17:48009732-48009776	NM_001110824:51827	Foxp4	INSIDE	0.284	1.607	1108.44	1780.99	0.456	915.59	417.32
A_68_P24519510	chr6:66987027-66987071	NM_007836:353	Gadd45a	INSIDE	0.284	0.657	4073.48	2676.09	0.187	3289.26	613.92
A_68_P21073093	chr2:25433409-25433453	NM_001005424:2189	Gm996	INSIDE	0.284	0.705	1422.20	1002.37	0.201	1083.70	217.30
A_68_P29936841	chr14:118536110-118536156	NM_021434:-216	Gpr180	DIVERGENT_PROMOTER	0.284	0.645	846.89	546.24	0.183	635.90	116.38
A_68_P26803573	chr9:106367885-106367929	NM_001159652:365	Gpr62	INSIDE	0.284	0.609	1636.61	996.12	0.173	1176.95	203.18
A_68_P28056595	chr11:98319477-98319521	NM_010346:11351	Grb7	DOWNSTREAM	0.284	0.545	2796.07	1523.32	0.155	2077.31	321.17
A_68_P31152954	chr17:34401924-34401968	NM_207105:1775	H2-Ab1	INSIDE	0.284	0.659	7394.39	4874.37	0.187	5405.93	1010.72
A_68_P28153966	chr11:115375918-115375967	NM_008258:-258	Hn1	PROMOTER	0.284	0.639	827.18	528.47	0.181	663.28	120.28
A_68_P31672396	chr18:45718914-45718958	NM_080465:-871	Kcnn2	PROMOTER	0.284	0.728	2275.19	1655.82	0.207	1551.17	320.94

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P24932467	chr6:147040098-147040142	NM_001081237:524	Klhdc5	INSIDE	0.284	0.423	1233.08	521.35	0.120	989.84	118.70
A_68_P31861993	chr18:80244305-80244349	NM_053117:693	Pard6g	INSIDE	0.284	0.562	1948.38	1094.44	0.160	1442.57	230.37
A_68_P23977768	chr5:110530421-110530465	NR_027665:865	Plcxd1	INSIDE	0.284	0.388	1783.69	692.33	0.110	1272.40	140.06
A_68_P24946434	chr7:3581622-3581669	NM_001159714:59	Prpf31	INSIDE	0.284	0.510	1092.30	557.24	0.145	808.75	117.27
A_68_P32758876	chrX:151651017-151651061	NM_009121:-86	Sat1	PROMOTER	0.284	1.456	2986.18	4346.66	0.413	1226.63	506.19
A_68_P29034451	chr13:51888679-51888723	NM_013660:313	Sema4d	INSIDE	0.284	0.409	1636.17	668.85	0.116	1261.66	146.71
A_68_P27632486	chr11:20531998-20532042	NM_001038625:41	Sertad2	INSIDE	0.284	0.465	1105.30	514.01	0.132	894.76	118.22
A_68_P28137827	chr11:112643586-112643636	NM_011448:87	Sox9	INSIDE	0.284	0.588	894.94	526.10	0.167	709.87	118.32
A_68_P25507650	chr7:134985680-134985724	NM_009294:381	Stx4a	INSIDE	0.284	0.495	1378.96	682.77	0.140	986.11	138.42
A_68_P26812057	chr9:107853467-107853511	NM_011634:195	Traip	INSIDE	0.284	0.576	971.65	559.31	0.163	761.10	124.36
A_68_P23200902	chr4:109079361-109079406	NM_153392:-321	Ttc39a	PROMOTER	0.284	0.620	851.96	528.47	0.176	666.06	117.44
A_68_P28751784	chr12:113917844-113917888	NM_001100460:816	Zbtb42	INSIDE	0.284	0.714	2093.79	1494.32	0.202	1495.49	302.64
A_68_P24973507	chr7:13483057-13483103	NM_001001447:-83	Zscan22	PROMOTER	0.284	0.539	1225.76	660.50	0.153	1031.70	157.85
A_68_P31494029	chr18:11239912-11239962			Unknown	0.284	0.583	1388.36	809.79	0.165	1143.48	189.14
A_68_P23074276	chr4:85160312-85160356	ENSMUST00000147066:104		INSIDE	0.284	0.554	1526.93	845.46	0.157	1213.88	191.03
A_68_P24329526	chr6:29935479-29935523	ENSMUST00000165864:147		INSIDE	0.284	0.737	3587.73	2644.21	0.210	3018.58	632.81
A_68_P30003953	chr15:9000818-9000866	NM_001040395:-166	1110020G09Rik	PROMOTER	0.283	0.592	1047.71	620.19	0.167	721.25	120.70
A_68_P22834880	chr4:35172594-35172638	NM_001081343:513	3110043O21Rik	INSIDE	0.283	0.592	889.38	526.11	0.167	743.22	124.48
A_68_P31152225	chr17:34257765-34257809	NR_037970:-941	Brd2	PROMOTER	0.283	0.657	5608.29	3685.58	0.186	3785.75	703.50
A_68_P22340676	chr3:94590702-94590746	NM_001037711:-287	Cgn	PROMOTER	0.283	0.421	1390.08	584.89	0.119	1001.79	119.45
A_68_P31937160	chr19:7062391-7062440	NM_020566:4347	Dnajc4	INSIDE	0.283	0.419	1358.98	569.90	0.119	987.10	117.28
A_68_P26132768	chr8:107814026-107814070	NM_177788:5950	Exoc3l	INSIDE	0.283	0.585	3362.80	1968.90	0.166	2244.27	371.46
A_68_P30261327	chr15:60655565-60655617	NM_001162926:1045	Fam84b	INSIDE	0.283	0.608	919.35	558.71	0.172	699.74	120.36
A_68_P20351018	chr1:74928813-74928857	NM_153111:3148	Fev	INSIDE	0.283	0.642	3070.75	1970.84	0.181	2408.62	436.84
A_68_P29531949	chr14:35632705-35632749	NM_008166:-595	Grid1	PROMOTER	0.283	0.450	1149.77	517.11	0.127	930.75	118.36
A_68_P28152305	chr11:115111838-115111882	NM_010350:16697	Grin2c	INSIDE	0.283	0.446	2260.91	1009.37	0.126	1592.06	201.15
A_68_P24804130	chr6:121363049-121363093	NM_001033354:60626	Iqsec3	INSIDE	0.283	0.662	1510.78	1000.13	0.187	1176.93	220.64
A_68_P24816264	chr6:124612578-124612622	NM_145130:-521	Lpcat3	PROMOTER	0.283	0.591	1112.55	657.42	0.167	968.93	162.25
A_68_P23905257	chr5:96639210-96639261	NM_001039084:102	Mrpl1	INSIDE	0.283	0.603	1236.33	745.79	0.171	1003.15	171.15
A_68_P22339052	chr3:94247698-94247742	NM_030116:463	Mrpl9	INSIDE	0.283	0.443	1707.10	755.57	0.125	1209.25	151.40
A_68_P22509724	chr3:127336069-127336113	NM_009718:28	Neurog2	INSIDE	0.283	0.382	1512.09	576.95	0.108	1244.62	134.27
A_68_P25171969	chr7:70590173-70590217	NM_130880:537	Otud7a	INSIDE	0.283	0.433	1666.98	721.11	0.123	1482.49	181.72
A_68_P20506802	chr1:108068165-108068215	NM_133821:-255	Phlpp1	PROMOTER	0.283	0.571	3301.60	1885.10	0.162	2325.73	376.11
A_68_P30520835	chr16:6349110-6349154	NM_021477:464247	Rbfox1	INSIDE	0.283	0.648	1817.20	1176.68	0.183	1424.51	260.77
A_68_P31560661	chr18:24687904-24687948	NM_144861:779	Rprd1a	INSIDE	0.283	0.622	1662.70	1033.75	0.176	1292.73	227.47
A_68_P31682227	chr18:47526193-47526237	NM_018744:2308	Sema6a	INSIDE	0.283	0.385	1381.04	532.08	0.109	1066.25	116.36
A_68_P31834370	chr18:75160579-75160623	NR_028552:-121	Snord58b	PROMOTER	0.283	0.716	2081.82	1491.03	0.203	1612.49	326.96
A_68_P28307239	chr12:28024428-28024472	NM_009234:3133	Sox11	INSIDE	0.283	0.476	3106.48	1479.64	0.135	2467.91	332.14
A_68_P30377735	chr15:81230102-81230146	NM_133726:0	St13	INSIDE	0.283	0.741	7066.61	5237.90	0.210	4964.21	1042.96
A_68_P30423272	chr15:88953588-88953632	NM_001163319:-30	Tubgcp6	PROMOTER	0.283	1.407	1974.38	2777.34	0.398	1327.48	528.47
A_68_P28567993	chr12:80273243-80273287	NM_016800:181	Vti1b	INSIDE	0.283	0.629	1090.67	686.21	0.178	868.86	154.77
A_68_P21492627	chr2:104967572-104967616	NM_144783:909	Wt1	INSIDE	0.283	0.572	1330.60	761.18	0.162	1090.85	176.72
A_68_P27287609	chr10:80598116-80598160	NM_010731:-877	Zbtb7a	PROMOTER	0.283	0.701	1844.23	1292.99	0.198	1148.37	227.51
A_68_P30498878	chr15:102455997-102456041	NM_146065:-166	Atf7	PROMOTER	0.282	0.534	1176.12	627.93	0.151	1056.04	159.25
A_68_P24921625	chr6:145159463-145159508	NM_177222:5	Casc1	INSIDE	0.282	0.611	1361.87	831.85	0.172	1001.41	172.43
A_68_P25086654	chr7:51559898-51559942	NM_009131:2409	Clec11a	INSIDE	0.282	0.664	848.05	563.18	0.187	640.56	119.90
A_68_P31126792	chr17:29375212-29375256	NM_153166:-499	Cpne5	PROMOTER	0.282	0.570	3122.91	1781.38	0.161	2326.13	373.64
A_68_P30106579	chr15:30102117-30102161	NM_008729:-209	Ctnnd2	PROMOTER	0.282	0.616	1878.08	1157.70	0.174	1487.11	258.73
A_68_P24449834	chr6:52260814-52260866	NM_007966:-2651	Evx1	PROMOTER	0.282	0.540	1031.45	557.14	0.153	762.12	116.28
A_68_P29543502	chr14:37948492-37948546	NM_078478:-10	Ghitm	PROMOTER	0.282	0.619	908.79	562.64	0.175	668.07	116.73
A_68_P21565608	chr2:118528286-118528330	NM_001081971:1391	Gm1337	INSIDE	0.282	0.716	1588.94	1138.16	0.202	1307.35	264.36

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P29619000	chr14:56254517-56254561	NM_024267:-23	Ipo4	PROMOTER	0.282	0.292	2453.01	716.88	0.083	1878.48	155.04
A_68_P22843571	chr4:36897285-36897329	NM_001165999:1471	Lingo2	INSIDE	0.282	0.649	1776.84	1152.69	0.183	1408.41	258.00
A_68_P27533640	chr10:126478229-126478273	NM_001205036:200	LOC100504608	INSIDE	0.282	0.361	2077.96	751.15	0.102	1620.47	165.27
A_68_P30340467	chr15:74786292-74786336	NM_001164040:779	Ly6e	INSIDE	0.282	0.517	1075.37	555.47	0.146	812.49	118.44
A_68_P31829416	chr18:74225103-74225147	NM_172632:-521	Mapk4	PROMOTER	0.282	0.460	1360.36	626.05	0.130	1238.03	160.75
A_68_P28461539	chr12:58331901-58331948	NM_001164370:513	Mipol1	INSIDE	0.282	0.490	1182.98	579.77	0.138	918.97	126.93
A_68_P27903939	chr11:70833307-70833351	NM_025993:216	Mis12	INSIDE	0.282	0.431	1217.58	524.45	0.121	981.65	119.22
A_68_P22129478	chr3:51212746-51212790	NM_025523:109	Ndufc1	INSIDE	0.282	0.487	2313.80	1126.57	0.137	1725.09	237.16
A_68_P21070362	chr2:25036916-25036960	NM_025980:661	Nrarp	INSIDE	0.282	0.637	3173.71	2022.47	0.180	2317.54	416.33
A_68_P30650143	chr16:31933937-31933981	NM_172822:22	Pigz	INSIDE	0.282	0.517	1181.84	610.58	0.146	846.76	123.55
A_68_P30513992	chr16:5132390-5132436	NM_008909:162	Ppl	INSIDE	0.282	0.468	1156.38	540.83	0.132	902.55	119.09
A_68_P31928437	chr19:5388969-5389013	NM_016882:-287	Sart1	PROMOTER	0.282	0.529	1120.54	592.66	0.149	886.23	131.98
A_68_P27915807	chr11:73013310-73013355	NM_029031:349	Shpk	INSIDE	0.282	0.649	903.19	586.29	0.183	628.50	114.93
A_68_P31412155	chr17:86092046-86092090	NM_011380:-4474	Six2	PROMOTER	0.282	0.451	1703.10	768.03	0.127	1391.83	176.85
A_68_P28187724	chr11:120812178-120812222	NM_001038653:1820	Slc16a3	INSIDE	0.282	0.610	2676.51	1632.44	0.172	1910.64	329.15
A_68_P20788009	chr1:166179184-166179228	NM_054087:21	Slc19a2	INSIDE	0.282	0.531	3660.11	1942.01	0.150	2936.10	439.37
A_68_P31151612	chr17:34168426-34168470	NM_001077709:187	Slc39a7	INSIDE	0.282	0.441	1242.25	547.48	0.124	937.67	116.51
A_68_P27162286	chr10:57514696-57514740	NM_020561:369	Smpdl3a	INSIDE	0.282	0.475	1179.15	559.67	0.134	929.07	124.20
A_68_P31123424	chr17:28758327-28758378	NM_016795:1047	Srpk1	INSIDE	0.282	0.529	1613.63	853.61	0.149	1237.90	184.37
A_68_P27941695	chr11:77979180-77979227	NM_009423:-151	Traf4	PROMOTER	0.282	0.538	1100.62	591.94	0.152	926.94	140.73
A_68_P24777346	chr6:116578724-116578768	NM_026057:249	Zfp422	INSIDE	0.282	0.553	3244.64	1793.90	0.156	2317.78	361.06
A_68_P24605099	chr6:85401740-85401787	NR_028081:201	1700040I03Rik	INSIDE	0.281	0.630	892.75	562.20	0.177	656.57	116.23
A_68_P21864323	chr2:172265966-172266010	NM_025542:-89	2410001C21Rik	PROMOTER	0.281	0.572	1502.08	859.66	0.161	1181.28	190.27
A_68_P30931898	chr16:85900536-85900586	NM_011782:810	Adamts5	INSIDE	0.281	0.421	1248.03	525.97	0.118	984.46	116.54
A_68_P28959953	chr13:38438458-38438503	NM_007556:896	Bmp6	INSIDE	0.281	0.617	2412.64	1488.63	0.173	1731.52	299.91
A_68_P23296726	chr4:129139208-129139252	NM_133889:308	Bsdc1	INSIDE	0.281	0.461	1182.13	545.33	0.130	890.14	115.58
A_68_P23818502	chr5:77286666-77286710	NM_001163793:17065	C530008M17Rik	INSIDE	0.281	1.592	1314.50	2092.35	0.447	973.85	434.84
A_68_P30836893	chr16:67620755-67620799	NM_001145977:377	Cadm2	INSIDE	0.281	0.666	1005.38	669.65	0.187	645.82	120.96
A_68_P23898891	chr5:93696983-93697027	NM_007635:406	Ccng2	INSIDE	0.281	0.502	1240.12	622.20	0.141	890.36	125.31
A_68_P30431388	chr15:90510200-90510246	NM_025815:-403	Cpne8	PROMOTER	0.281	0.443	1325.88	587.98	0.124	1014.18	126.26
A_68_P28036957	chr11:95006662-95006706	NM_007867:431	Dlx4	INSIDE	0.281	0.651	2321.49	1510.92	0.183	1744.75	318.99
A_68_P22392957	chr3:104561384-104561428	NM_183224:19059	Fam19a3	DOWNSTREAM	0.281	0.477	1131.90	540.11	0.134	907.71	121.49
A_68_P24084083	chr5:129107881-129107932	NM_175284:926	Fzd10	INSIDE	0.281	0.500	1019.37	509.94	0.141	844.22	118.86
A_68_P29338085	chr13:113784265-113784309	NM_001037914:211	Gm6320	INSIDE	0.281	0.575	1191.92	685.22	0.161	977.43	157.79
A_68_P28150124	chr11:114712661-114712705	NM_001110337:-163	Gprc5c	PROMOTER	0.281	0.342	1622.76	555.06	0.096	1266.11	121.86
A_68_P23600193	chr5:35732106-35732150	NM_010445:363	Hmx1	INSIDE	0.281	0.444	3075.14	1366.56	0.125	2298.91	286.79
A_68_P28153290	chr11:115265346-115265390	NM_026729:289	Ict1	INSIDE	0.281	0.584	2127.27	1242.61	0.164	1491.93	245.07
A_68_P27353694	chr10:92916374-92916418	NM_008517:256	Lta4h	INSIDE	0.281	0.461	1176.69	542.62	0.130	913.09	118.37
A_68_P30423406	chr15:88971030-88971074	NM_013871:81	Mapk12	INSIDE	0.281	0.716	2592.92	1857.68	0.201	1804.08	363.14
A_68_P29613303	chr14:55236595-55236639	NR_030457:-994	Mir686	PROMOTER	0.281	0.556	1034.77	575.14	0.156	921.06	143.94
A_68_P23188355	chr4:106739488-106739543	NM_025500:-44	Mrpl37	DIVERGENT_PROMOTER	0.281	0.506	1134.27	573.53	0.142	858.86	121.88
A_68_P30126794	chr15:34012255-34012299	NM_026002:-197	Mtdh	PROMOTER	0.281	0.703	2580.46	1815.24	0.197	1925.28	380.12
A_68_P25115904	chr7:57230774-57230819	NM_001037906:77	Nell1	INSIDE	0.281	1.345	2100.10	2825.20	0.378	1473.11	556.36
A_68_P21079208	chr2:26358390-26358438	NM_008714:928	Notch1	INSIDE	0.281	0.633	1567.20	991.68	0.178	1075.31	191.03
A_68_P31626861	chr18:37249454-37249501	NM_001003671:-312	Pcdhac1	PROMOTER	0.281	0.621	990.47	615.09	0.175	820.09	143.12
A_68_P27970618	chr11:83112471-83112515	NM_134025:-13	Pex12	DIVERGENT_PROMOTER	0.281	0.631	2669.29	1685.21	0.177	1858.05	329.27
A_68_P27796196	chr11:51671860-51671916	NM_199299:-905	Phf15	PROMOTER	0.281	0.635	916.81	581.81	0.179	685.66	122.42
A_68_P29480407	chr14:26722558-26722602	NM_207229:-201	Plac9	PROMOTER	0.281	0.690	7465.52	5150.73	0.194	6608.79	1282.54
A_68_P28083254	chr11:102941888-102941932	NM_152813:21062	Plcd3	INSIDE	0.281	0.719	1777.53	1277.53	0.202	1219.75	246.12
A_68_P22411526	chr3:108059982-108060035	NM_011967:165	Psma5	INSIDE	0.281	0.631	1111.74	702.05	0.177	808.70	143.42
A_68_P22399296	chr3:105603567-105603617	NM_145541:662	Rap1a	INSIDE	0.281	0.550	973.04	534.79	0.154	755.33	116.69

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P29578867	chr14:47501948-47501992	NM_001037221:-669	Samd4	PROMOTER	0.281	0.414	1606.07	665.62	0.117	1240.06	144.55
A_68_P28164067	chr11:117127295-117127344	NM_001113487:-240	Septin9	PROMOTER	0.281	0.545	1091.92	594.59	0.153	785.44	120.04
A_68_P28164072	chr11:117127975-117128019	NM_001113487:437	Septin9	INSIDE	0.281	0.414	1960.82	810.94	0.116	1462.50	170.22
A_68_P32427552	chrX:61530169-61530213	NM_178740:-19	Slitrk4	PROMOTER	0.281	1.914	10588.74	20265.47	0.537	4113.15	2209.98
A_68_P28058193	chr11:98603344-98603393	NM_178060:182	Thra	INSIDE	0.281	0.339	1682.81	571.28	0.095	1271.26	121.06
A_68_P30478054	chr15:98904927-98904971	NM_001162506:-455	Troap	PROMOTER	0.281	0.675	1353.53	913.56	0.189	969.68	183.59
A_68_P27056226	chr10:34017317-34017361	NM_030203:112	Tspyl4	INSIDE	0.281	0.464	1299.68	602.88	0.130	1003.98	130.86
A_68_P32975183	chr9:108393525-108393569	NM_027804:540	Usp19	INSIDE	0.281	0.533	1036.90	552.26	0.149	786.82	117.61
A_68_P31147012	chr17:32925128-32925172	NM_172458:82	Zfp871	INSIDE	0.281	0.683	1074.16	733.40	0.192	783.56	150.47
A_68_P28680480	chr12:101425351-101425395	ENSMUST00000146364:-805		PROMOTER	0.281	0.547	1067.99	584.66	0.154	783.96	120.42
A_68_P23349886	chr4:138686821-138686865	NR_033745:110	2310028O11Rik	INSIDE	0.280	0.548	2023.91	1109.13	0.153	1605.35	246.22
A_68_P20347693	chr1:74331033-74331077	NM_001190444:258	Aamp	INSIDE	0.280	0.431	1648.02	710.43	0.121	1313.97	158.37
A_68_P32143651	chr19:46469679-46469723	NM_016860:525	Actr1a	INSIDE	0.280	0.608	1106.56	672.40	0.170	919.00	156.10
A_68_P21754296	chr2:153171121-153171165	NM_001039939:-732	Asxl1	PROMOTER	0.280	0.543	1780.67	966.24	0.152	1397.73	212.40
A_68_P22803192	chr4:28742495-28742539	NM_001122889:2222	Epha7	INSIDE	0.280	0.395	2846.75	1124.65	0.110	2230.06	246.37
A_68_P27845566	chr11:60745169-60745219	NR_027800:175	Gm16516	INSIDE	0.280	0.512	1039.71	532.39	0.144	807.31	115.86
A_68_P24156213	chr5:144125893-144125937	NM_133355:328	Grid2ip	INSIDE	0.280	0.387	1715.24	664.49	0.108	1251.75	135.75
A_68_P26936713	chr10:10408926-10408970	NM_001114333:393181	Grm1	INSIDE	0.280	0.386	1984.50	765.94	0.108	1707.58	184.84
A_68_P30547086	chr16:11254244-11254288	NM_001130008:152	Gspt1	INSIDE	0.280	0.440	2981.65	1312.19	0.123	2199.17	271.37
A_68_P28547080	chr12:76277679-76277723	NM_172805:619	Kcnh5	INSIDE	0.280	0.403	1318.92	531.28	0.113	1070.99	120.62
A_68_P23955794	chr5:105948943-105948987	NM_133897:475	Lrrc8c	INSIDE	0.280	0.579	1273.90	737.70	0.162	967.85	156.87
A_68_P30365874	chr15:79178468-79178512	NM_010755:383	Maff	INSIDE	0.280	1.627	4199.84	6834.63	0.455	2838.74	1291.98
A_68_P27281289	chr10:79611936-79611980	NM_021565:924	Midn	INSIDE	0.280	0.643	839.66	539.96	0.180	664.72	119.56
A_68_P29675623	chr14:66424674-66424718	NM_023209:-51	Pbk	PROMOTER	0.280	0.597	1015.90	606.75	0.167	859.53	143.56
A_68_P31252242	chr17:55851800-55851847	NM_028370:103	Pot1b	INSIDE	0.280	0.616	2320.37	1429.39	0.173	1799.85	310.91
A_68_P28119824	chr11:109512145-109512189	NM_021880:-96	Prkar1a	PROMOTER	0.280	0.460	1170.83	538.40	0.129	901.30	116.04
A_68_P27098034	chr10:42741868-42741912	NM_175407:152446	Sobp	INSIDE	0.280	0.645	1619.54	1043.79	0.181	1356.07	244.96
A_68_P27255276	chr10:74674681-74674725	NM_153406:-115	Specc1l	PROMOTER	0.280	0.566	2185.57	1237.33	0.158	1688.67	267.56
A_68_P23590348	chr5:34001258-34001302	NM_001040435:485	Tacc3	INSIDE	0.280	0.502	1566.40	786.82	0.141	1212.27	170.46
A_68_P24946431	chr7:3581260-3581308	NM_023524:202	Tfpt	INSIDE	0.280	0.468	1175.23	549.55	0.131	910.45	119.17
A_68_P30653345	chr16:32608966-32609010	NM_011638:7	Tfrc	INSIDE	0.280	0.544	1547.28	841.30	0.152	1262.45	192.09
A_68_P28975560	chr13:41111770-41111814	NM_025387:174	Tmem14c	INSIDE	0.280	0.644	1020.72	657.77	0.181	830.66	150.02
A_68_P23621601	chr5:38952237-38952281	NM_011715:576	Wdr1	INSIDE	0.280	0.536	1344.69	721.07	0.150	1059.34	159.06
A_68_P31925602	chr19:4878554-4878607	NM_001168516:-87	Zdhhc24	DIVERGENT_PROMOTER	0.280	0.366	1495.19	546.60	0.102	1195.49	122.29
A_68_P31002111	chr16:98183558-98183609	NM_001081684:203	Zfp295	INSIDE	0.280	0.548	1006.51	551.09	0.153	810.57	124.40
A_68_P25063531	chr7:38558593-38558648	NM_172385:-3849	Zfp536	PROMOTER	0.280	0.398	1341.66	534.25	0.111	1078.38	120.20
A_68_P23678471	chr5:49915727-49915771	ENSMUST00000087395:192		INSIDE	0.280	0.548	3283.95	1800.50	0.154	2382.03	365.68
A_68_P32698229	chrX:136813030-136813074	ENSMUST00000130153:-651		PROMOTER	0.280	1.345	3925.47	5279.46	0.376	1412.68	531.64
A_68_P23195467	chr4:108000626-108000670	NM_027250:-108	2010305A19Rik	PROMOTER	0.279	0.516	1602.85	827.23	0.144	1309.24	188.61
A_68_P26242184	chr8:126416045-126416089	NM_009606:2570	Acta1	INSIDE	0.279	0.610	4222.33	2574.56	0.170	3074.41	523.07
A_68_P31744347	chr18:58995833-58995877	NM_175506:-563	Adamts19	PROMOTER	0.279	0.496	1144.12	567.40	0.138	863.25	119.34
A_68_P21754298	chr2:153171422-153171466	NM_001039939:-430	Asxl1	PROMOTER	0.279	0.595	1114.15	663.06	0.166	835.84	138.76
A_68_P24056051	chr5:123959009-123959060	NM_198611:-1434	B3gnt4	PROMOTER	0.279	0.596	1020.64	608.48	0.166	712.01	118.30
A_68_P26132516	chr8:107778018-107778071	NM_178879:1007	B3gnt9-ps	INSIDE	0.279	0.618	863.99	533.71	0.172	713.52	122.82
A_68_P25503359	chr7:134120190-134120234	NM_138754:311	Cdipt	INSIDE	0.279	0.616	881.62	542.65	0.172	694.98	119.22
A_68_P25045781	chr7:35597428-35597472	NM_175140:280	Chst8	INSIDE	0.279	0.726	2068.81	1501.84	0.203	1430.67	290.07
A_68_P26016158	chr8:86239347-86239391	NM_197982:293	Ddx39	INSIDE	0.279	0.607	4677.60	2837.73	0.169	3307.24	559.31
A_68_P29011725	chr13:47201899-47201943	NM_025900:-331	Dek	PROMOTER	0.279	0.384	1550.14	595.33	0.107	1081.93	115.95
A_68_P23226799	chr4:115611753-115611802	NM_001025567:754	Dmbx1	INSIDE	0.279	0.640	982.15	628.68	0.179	665.18	118.81
A_68_P27849840	chr11:61498639-61498683	NM_178618:749	Fam83g	INSIDE	0.279	1.794	902.48	1619.19	0.500	636.82	318.52
A_68_P28463161	chr12:58640100-58640144	NM_008259:6986	Foxa1	DOWNSTREAM	0.279	0.579	959.17	555.42	0.162	804.71	130.17

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P22872581	chr4:43591992-43592036	NM_172692:-278	Gba2	PROMOTER	0.279	0.667	1750.32	1166.84	0.186	1386.88	258.22
A_68_P25362932	chr7:106774074-106774118	NM_001195529:1517	Gm4980	INSIDE	0.279	0.534	2137.54	1141.77	0.149	1580.08	235.53
A_68_P32401469	chrX:54756662-54756706	NM_001033360:250	Gpr101	INSIDE	0.279	1.503	1133.46	1703.26	0.419	530.24	222.05
A_68_P24979758	chr7:16705347-16705391	NM_133727:144	Kptn	INSIDE	0.279	0.601	1547.69	929.93	0.168	1213.70	203.83
A_68_P26192671	chr8:118229614-118229663	NM_001025577:1156	Maf	INSIDE	0.279	0.518	2078.13	1076.01	0.144	1552.88	224.28
A_68_P27787816	chr11:50105944-50105992	NM_175334:-130	Maml1	PROMOTER	0.279	0.611	864.37	528.36	0.171	704.18	120.09
A_68_P20826868	chr1:173177287-173177331	NM_153064:-65	Ndufs2	DIVERGENT_PROMOTER	0.279	0.570	910.55	519.24	0.159	736.87	117.21
A_68_P23720373	chr5:58111459-58111503	NM_018764:2221	Pcdh7	INSIDE	0.279	0.417	1401.92	583.99	0.116	1053.95	122.50
A_68_P29057257	chr13:55927883-55927927	NM_011097:4882	Pitx1	INSIDE	0.279	0.664	1735.85	1151.83	0.185	1409.77	261.10
A_68_P25017512	chr7:28271931-28271975	NM_018820:-19	Sertad1	PROMOTER	0.279	0.622	2163.16	1344.97	0.173	1769.61	306.95
A_68_P21986757	chr3:21974664-21974711	NM_030732:-886	Tbl1xr1	PROMOTER	0.279	0.374	1515.46	566.59	0.104	1158.01	120.71
A_68_P26706479	chr9:87634192-87634246	NM_023814:-8123	Tbx18	PROMOTER	0.279	0.466	1263.18	588.70	0.130	937.83	121.87
A_68_P23440601	chr4:155158362-155158406	NM_001033394:1599	Tmem88b	INSIDE	0.279	0.443	1265.33	560.57	0.124	941.84	116.58
A_68_P31259987	chr17:57226887-57226931	NM_009451:297	Tubb4	INSIDE	0.279	0.424	2760.55	1170.13	0.118	2071.49	245.36
A_68_P26470628	chr9:44773616-44773660	NM_145400:45	Ube4a	INSIDE	0.279	0.615	1197.04	736.45	0.172	834.72	143.46
A_68_P28072950	chr11:101126785-101126842	NM_175638:4933	Wnk4	INSIDE	0.279	0.449	1167.52	524.22	0.125	943.22	118.08
A_68_P27291280	chr10:81233564-81233608	NM_199062:301	Zfp781	INSIDE	0.279	0.672	3324.63	2233.59	0.187	2733.51	511.68
A_68_P23692830	chr5:52506763-52506822	AK076709:-1759		PROMOTER	0.279	0.501	1666.20	835.06	0.140	1348.90	188.51
A_68_P28181190	chr11:119803788-119803832	NM_001037754:-595	Baiap2	PROMOTER	0.278	0.531	3460.85	1837.20	0.148	2541.24	374.90
A_68_P31351851	chr17:74927352-74927396	NM_007566:-260	Birc6	PROMOTER	0.278	0.526	2662.66	1400.83	0.146	2001.97	292.52
A_68_P24114165	chr5:135462201-135462245	NM_009902:139	Cldn3	INSIDE	0.278	0.363	1646.86	597.77	0.101	1284.66	129.85
A_68_P26085422	chr8:98331940-98331984	NM_001205226:-600	Cnot1	PROMOTER	0.278	0.722	1947.02	1405.60	0.201	1396.11	280.41
A_68_P26016154	chr8:86238907-86238952	NM_197982:-146	Ddx39	PROMOTER	0.278	0.612	887.31	543.43	0.171	680.21	115.98
A_68_P25565217	chr7:144507254-144507298	NM_001113414:-1148	Ebf3	PROMOTER	0.278	0.689	1139.32	785.53	0.192	912.45	174.99
A_68_P26693192	chr9:85220596-85220642	NM_001160378:113	Fam46a	INSIDE	0.278	0.560	1460.86	818.73	0.156	1225.83	191.20
A_68_P28493836	chr12:66176491-66176538	NM_178912:-78	Fancm	DIVERGENT_PROMOTER	0.278	0.443	1198.26	530.99	0.123	978.67	120.62
A_68_P31093570	chr17:23908581-23908625	NM_153791:-44	Flywch1	PROMOTER	0.278	0.546	1754.60	957.21	0.152	1401.58	212.82
A_68_P22010769	chr3:27271192-27271236	NM_177330:942	Ghsr	INSIDE	0.278	0.629	1416.27	890.73	0.175	1126.14	197.20
A_68_P21099809	chr2:29701916-29701960	NR_029838:-691	Mir219-2	PROMOTER	0.278	0.609	2809.15	1711.19	0.169	1983.89	336.01
A_68_P30344754	chr15:75724482-75724526	NM_172607:407	Naprt1	INSIDE	0.278	0.655	1813.88	1187.79	0.182	1479.30	269.17
A_68_P23354482	chr4:139387475-139387522	NM_011039:1385	Pax7	INSIDE	0.278	0.520	1020.59	530.29	0.145	863.91	124.90
A_68_P29057249	chr13:55926961-55927005	NM_011097:5804	Pitx1	INSIDE	0.278	0.626	2167.75	1356.45	0.174	1561.70	271.78
A_68_P28614436	chr12:88488867-88488911	NM_153415:-36	Pomt2	PROMOTER	0.278	0.508	1893.67	961.70	0.141	1559.62	220.35
A_68_P28768145	chr12:117724630-117724674	NM_011215:460	Ptprn2	INSIDE	0.278	0.424	1564.92	664.12	0.118	1091.87	129.03
A_68_P25048761	chr7:36119403-36119447	NM_027897:169	Rhpn2	INSIDE	0.278	0.678	1219.41	826.55	0.188	828.80	156.00
A_68_P32075617	chr19:33466407-33466451	NM_001146342:357	Rnls	INSIDE	0.278	0.605	1223.58	740.14	0.168	977.74	164.39
A_68_P31138742	chr17:31413976-31414020	NM_025290:303	Rsph1	INSIDE	0.278	0.483	1230.30	594.82	0.135	968.81	130.39
A_68_P23312649	chr4:132066191-132066235	NM_144907:159	Sesn2	INSIDE	0.278	0.617	870.56	537.41	0.171	695.75	119.24
A_68_P21000515	chr2:10296432-10296476	NM_001198809:2392	Sfmbt2	INSIDE	0.278	0.559	1165.84	652.28	0.156	966.25	150.45
A_68_P31606709	chr18:33373631-33373675	NM_133774:-182	Stard4	PROMOTER	0.278	0.506	1136.21	575.08	0.141	878.34	123.59
A_68_P30652355	chr16:32420130-32420180	NM_025329:367	Tctex1d2	INSIDE	0.278	0.415	1761.15	730.98	0.115	1293.59	149.40
A_68_P31101668	chr17:25252658-25252702	NM_027880:170	Telo2	INSIDE	0.278	0.569	902.12	513.41	0.158	731.53	115.79
A_68_P31204667	chr17:46168826-46168870	NM_001110266:-6736	Vegfa	PROMOTER	0.278	0.407	1714.38	697.41	0.113	1245.65	140.94
A_68_P28573854	chr12:81216498-81216557	NM_007564:-2527	Zfp36l1	PROMOTER	0.278	0.613	903.02	553.40	0.171	697.81	119.01
A_68_P21124749	chr2:33822268-33822320			Unknown	0.278	0.485	1074.16	521.07	0.135	895.76	120.87
A_68_P21440136	chr2:94114022-94114066	ENSMUST00000167726:-9129		PROMOTER	0.278	0.476	4746.82	2259.25	0.132	3260.74	431.05
A_68_P24091117	chr5:130371504-130371553	NM_183088:-64	2410018M08Rik	DIVERGENT_PROMOTER	0.277	0.508	1104.46	561.61	0.141	859.59	121.15
A_68_P31149283	chr17:33661330-33661374	NM_172619:212	Adamts10	INSIDE	0.277	1.632	922.24	1505.21	0.452	739.29	334.16
A_68_P26888672	chr9:122203588-122203632	NM_133979:-118	Ano10	PROMOTER	0.277	0.602	3002.32	1807.81	0.167	2427.02	404.99
A_68_P30388929	chr15:83357855-83357899	NM_007546:585	Bik	INSIDE	0.277	0.586	880.06	515.70	0.163	715.98	116.36
A_68_P26467527	chr9:44226161-44226205	NM_201372:-92	Ccdc84	PROMOTER	0.277	0.654	1166.34	762.83	0.181	1031.60	186.87

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P30532562	chr16:8424938-8424982	NM_029070:269	Cldn26	INSIDE	0.277	0.705	2714.55	1914.14	0.196	2026.78	396.46
A_68_P21428538	chr2:92274073-92274117	NM_009963:132	Cry2	INSIDE	0.277	0.458	1293.82	591.94	0.127	926.38	117.21
A_68_P28396962	chr12:45311155-45311199	NM_013760:-121	Dnajb9	PROMOTER	0.277	0.394	1422.76	560.34	0.109	1067.66	116.53
A_68_P25095384	chr7:53087940-53087984	NM_008172:34089	Grin2d	INSIDE	0.277	0.679	1134.09	769.55	0.188	911.54	171.57
A_68_P31159075	chr17:35516634-35516678	NM_001143689:95	H2-Gs10	INSIDE	0.277	0.546	1820.45	993.97	0.151	1377.83	208.43
A_68_P23334048	chr4:136018725-136018769	NM_024452:-6929	Luzp1	PROMOTER	0.277	0.553	1038.17	573.81	0.153	789.09	120.97
A_68_P24302044	chr6:24477440-24477484	NM_026614:225	Ndufa5	INSIDE	0.277	0.567	3081.87	1747.08	0.157	2370.37	372.60
A_68_P25427824	chr7:120098233-120098277	NM_175279:779	Rassf10	INSIDE	0.277	0.501	2614.57	1308.78	0.139	2103.27	292.12
A_68_P28991172	chr13:43711132-43711176	NM_183204:-11	Rnf182	PROMOTER	0.277	0.583	891.90	519.95	0.161	742.80	119.85
A_68_P26948617	chr10:12728567-12728611	NM_175102:333	Sf3b5	INSIDE	0.277	0.474	1273.32	603.31	0.131	1126.82	147.89
A_68_P20353690	chr1:75385333-75385377	NM_001085370:3170	Speg	INSIDE	0.277	0.669	2015.09	1348.33	0.185	1596.50	296.11
A_68_P26426682	chr9:36575102-36575146	NM_008408:39	Stt3a	INSIDE	0.277	0.596	1931.40	1150.44	0.165	1437.89	237.04
A_68_P21875215	chr2:174241468-174241512	NM_020580:186	Th1l	INSIDE	0.277	0.694	1417.70	983.20	0.192	1072.06	206.01
A_68_P21070655	chr2:25080672-25080722	NM_146116:-474	Tubb2c	PROMOTER	0.277	0.375	1654.74	620.62	0.104	1188.67	123.65
A_68_P29240034	chr13:96094965-96095009	NM_028106:-205	Zbed3	PROMOTER	0.277	0.450	1360.48	611.58	0.124	1094.16	136.16
A_68_P25618386	chr8:4677981-4678025	ENSMUST00000058918:363		INSIDE	0.277	0.618	928.00	573.50	0.171	687.25	117.81
A_68_P25614137	chr8:3476402-3476449	NM_029598:5564	1700019B03Rik	INSIDE	0.276	2.077	1712.91	3558.55	0.574	1103.08	633.60
A_68_P22141947	chr3:53267624-53267668	NM_173382:-92	2810046L04Rik	DIVERGENT_PROMOTER	0.276	0.374	1367.28	511.93	0.103	1194.18	123.56
A_68_P25010199	chr7:26180658-26180710	NR_015569:252	4732471J01Rik	INSIDE	0.276	0.586	917.67	537.74	0.162	731.17	118.37
A_68_P25032018	chr7:31320141-31320185	NM_178252:-134	Arhgap33	PROMOTER	0.276	0.419	1337.10	559.89	0.116	1014.16	117.21
A_68_P24093836	chr5:130925066-130925110	NM_021371:427	Caln1	INSIDE	0.276	0.422	1512.80	638.21	0.117	1137.34	132.63
A_68_P20501014	chr1:106890387-106890439	NM_011800:225017	Cdh20	INSIDE	0.276	1.800	766.92	1380.67	0.497	673.52	334.64
A_68_P25272111	chr7:88599609-88599653	NM_007755:-68	Cpeb1	PROMOTER	0.276	0.444	2878.93	1277.00	0.123	2154.34	264.05
A_68_P22943680	chr4:57155729-57155773	NM_019427:278	Epb4.1l4b	INSIDE	0.276	0.484	1090.05	528.11	0.134	905.94	121.35
A_68_P23222368	chr4:114598578-114598622	NM_015758:18	Foxe3	INSIDE	0.276	0.630	2720.76	1714.30	0.174	2103.50	366.27
A_68_P29072412	chr13:58376159-58376204	NM_019832:-632	Gkap1	PROMOTER	0.276	1.706	2038.90	3477.83	0.471	1472.02	693.44
A_68_P27779978	chr11:48613766-48613813	NM_008143:-72	Gnb2l1	PROMOTER	0.276	0.433	1548.56	670.53	0.120	1016.21	121.67
A_68_P23978152	chr5:110605959-110606003	NM_008146:261	Golga3	INSIDE	0.276	0.742	3679.06	2728.70	0.205	2822.51	577.60
A_68_P21331226	chr2:73224914-73224958	NM_001190297:-481	Gpr155	PROMOTER	0.276	0.517	1051.40	543.58	0.143	819.19	116.82
A_68_P30621545	chr16:26581869-26581913	NM_134103:100	Il1rap	INSIDE	0.276	0.543	1535.69	834.13	0.150	1253.52	188.11
A_68_P27922757	chr11:74652026-74652070	NM_010813:7623	Mnt	INSIDE	0.276	0.595	1916.07	1140.92	0.164	1581.50	259.85
A_68_P28178576	chr11:119408102-119408146	NM_008730:1010	Nptx1	INSIDE	0.276	0.650	1013.18	658.50	0.179	666.32	119.32
A_68_P28052466	chr11:97606492-97606536	NM_054051:-496	Pip4k2b	PROMOTER	0.276	0.584	2592.54	1514.05	0.161	1842.31	297.34
A_68_P24538901	chr6:71859383-71859431	NM_009088:360	Polr1a	INSIDE	0.276	0.687	1229.99	844.63	0.189	871.66	165.02
A_68_P30426166	chr15:89421992-89422040	NM_026817:338	Rabl2	INSIDE	0.276	0.526	1238.52	651.34	0.145	816.93	118.47
A_68_P26766610	chr9:99771206-99771250	NM_011440:5361	Sox14	DOWNSTREAM	0.276	1.584	2458.98	3895.31	0.438	1555.38	681.07
A_68_P28100097	chr11:106055038-106055082	NM_028126:-198	Strada	PROMOTER	0.276	0.564	2868.73	1617.07	0.156	2206.11	343.13
A_68_P31197213	chr17:44914413-44914457	NM_178652:315	Supt3h	INSIDE	0.276	0.523	1541.87	807.13	0.145	1330.11	192.22
A_68_P22349233	chr3:96218809-96218853	NR_001579:-74	Terc	PROMOTER	0.276	0.669	2629.17	1759.65	0.185	2121.83	392.50
A_68_P24153541	chr5:143578202-143578246	NM_001122730:842	Tnrc18	INSIDE	0.276	0.445	1329.77	591.54	0.123	985.09	121.07
A_68_P22218907	chr3:68848966-68849010	NM_025863:-324	Trim59	PROMOTER	0.276	0.478	1197.29	571.94	0.132	927.40	122.43
A_68_P30572236	chr16:17147632-17147677	NM_026940:595	Ydjc	INSIDE	0.276	0.504	1137.45	573.08	0.139	826.87	115.16
A_68_P27992048	chr11:86806873-86806917	NM_001005341:370	Ypel2	INSIDE	0.276	0.558	1442.28	804.89	0.154	1067.92	164.24
A_68_P29053295	chr13:55206803-55206847	NM_012017:155	Zfp346	INSIDE	0.276	0.603	4070.91	2454.59	0.166	2887.16	480.19
A_68_P27269572	chr10:77127362-77127406			Unknown	0.276	1.694	1503.03	2546.41	0.468	1004.14	469.69
A_68_P26218683	chr8:122753604-122753648	ENSMUST00000127664:318886		INSIDE	0.276	0.628	1051.85	660.38	0.173	762.22	132.14
A_68_P26568902	chr9:61970547-61970591	mmu-mir-5133:-167		PROMOTER	0.276	0.439	1231.09	540.01	0.121	996.84	120.87
A_68_P31102483	chr17:25377069-25377113	NM_001163718:-24	0610007P22Rik	DIVERGENT_PROMOTER	0.275	0.365	1564.68	570.88	0.100	1276.81	127.95
A_68_P22958317	chr4:59796668-59796712	NM_001013577:37	1110054O05Rik	INSIDE	0.275	0.528	5380.06	2838.36	0.145	4209.44	611.65
A_68_P28788254	chr13:3477478-3477522	NR_015522:-48	2810429I04Rik	PROMOTER	0.275	0.649	3641.31	2362.40	0.178	2668.69	475.74
A_68_P27787096	chr11:49988189-49988233	NM_026543:-142	3010026O09Rik	PROMOTER	0.275	0.462	1569.17	725.65	0.127	1145.00	145.41

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P32180645	chr19:53217074-53217118	NM_001164100:-149	Add3	PROMOTER	0.275	0.597	1953.21	1166.94	0.164	1459.23	239.73
A_68_P26569949	chr9:62188962-62189006	NM_009672:-165	Anp32a	PROMOTER	0.275	0.481	3395.66	1634.79	0.132	2513.84	332.86
A_68_P23430519	chr4:153674176-153674220	NM_001112744:-194	Arhgef16	PROMOTER	0.275	0.426	3011.20	1283.74	0.117	2347.81	275.15
A_68_P26818137	chr9:108976539-108976583	NM_172774:78	Atrip	INSIDE	0.275	0.644	4735.75	3049.07	0.177	3476.43	615.89
A_68_P24055179	chr5:123794010-123794061	NM_029850:-421	Bcl7a	PROMOTER	0.275	0.488	1083.41	529.08	0.134	900.64	121.10
A_68_P32592614	chrX:106029534-106029578	NM_001081477:138	Brwd3	INSIDE	0.275	2.326	4733.30	11008.85	0.639	1847.91	1180.65
A_68_P26814949	chr9:108355021-108355065	NM_133744:-7806	Ccdc71	PROMOTER	0.275	0.418	1408.81	588.95	0.115	1134.04	130.56
A_68_P32099201	chr19:38129127-38129171	NM_028293:-366	Cep55	PROMOTER	0.275	1.940	12468.12	24188.29	0.533	7872.86	4194.58
A_68_P20551449	chr1:120285275-120285326	NM_001081276:-334	Clasp1	PROMOTER	0.275	0.560	1224.74	686.25	0.154	880.76	135.94
A_68_P31928179	chr19:5349318-5349363	NM_028623:234	Cst6	INSIDE	0.275	0.450	2286.28	1028.02	0.124	1811.51	223.91
A_68_P26135025	chr8:108159869-108159913	NM_181322:-547	Ctcf	PROMOTER	0.275	0.481	1876.65	902.22	0.132	1343.38	177.67
A_68_P26527199	chr9:54547693-54547737	NM_021422:349	Dnaja4	INSIDE	0.275	0.556	1005.14	558.46	0.153	768.88	117.48
A_68_P20383167	chr1:80754578-80754622	NM_175291:528	Dock10	INSIDE	0.275	0.671	3548.93	2381.70	0.185	2794.36	515.67
A_68_P29660083	chr14:63864272-63864316	NM_008092:-197	Gata4	PROMOTER	0.275	0.528	3707.11	1958.58	0.145	2991.53	434.68
A_68_P24078732	chr5:128112557-128112601	NM_177005:-53	Glt1d1	PROMOTER	0.275	0.655	2080.08	1363.22	0.180	1648.89	296.76
A_68_P25533778	chr7:139507346-139507390	NR_028578:22	Gm10584	INSIDE	0.275	0.483	3417.22	1651.74	0.133	2367.90	314.29
A_68_P25678155	chr8:15010976-15011020	NM_029116:-26	Kbtbd11	PROMOTER	0.275	0.533	1164.45	621.09	0.146	820.89	120.24
A_68_P31930911	chr19:5803095-5803139	NR_002847:-445	Malat1	PROMOTER	0.275	0.622	946.67	589.23	0.171	703.84	120.52
A_68_P26019014	chr8:86780727-86780772	NM_026423:474	Mri1	INSIDE	0.275	1.820	1382.34	2516.20	0.500	1033.50	516.86
A_68_P27553885	chr11:3661656-3661712	NM_152818:102222	Osbp2	INSIDE	0.275	0.462	1229.09	567.60	0.127	985.74	125.03
A_68_P24438209	chr6:50405431-50405477	NM_001163645:715	Osbpl3	INSIDE	0.275	0.562	1096.61	616.10	0.155	803.08	124.16
A_68_P28041006	chr11:95685266-95685311	NM_153104:-525	Phospho1	PROMOTER	0.275	0.550	939.14	516.98	0.152	796.29	120.65
A_68_P27230700	chr10:70061466-70061510	NM_001162846:-5928	Phyhipl	PROMOTER	0.275	0.519	1106.01	573.61	0.143	910.16	129.83
A_68_P24770498	chr6:115311955-115311999	NM_001127330:738	Pparg	INSIDE	0.275	0.496	1107.89	549.64	0.137	905.46	123.74
A_68_P21138680	chr2:36086050-36086094	NM_008969:127	Ptgs1	INSIDE	0.275	0.424	2870.32	1216.90	0.117	2218.77	258.87
A_68_P24040031	chr5:121099444-121099488	NM_013832:636	Rasal1	INSIDE	0.275	0.569	1124.74	640.49	0.157	921.54	144.51
A_68_P24054157	chr5:123592214-123592258	NM_175092:-9598	Rhof	PROMOTER	0.275	0.734	2218.10	1628.65	0.202	1766.95	357.29
A_68_P22864089	chr4:41687680-41687724	NM_011014:484	Sigmar1	INSIDE	0.275	0.517	2643.94	1365.98	0.142	1826.63	259.12
A_68_P22392363	chr3:104442146-104442191	NM_009196:-422	Slc16a1	PROMOTER	0.275	0.374	1638.66	613.26	0.103	1156.77	119.10
A_68_P26750963	chr9:97011708-97011752	NM_138756:-270	Slc25a36	PROMOTER	0.275	0.510	1489.71	759.94	0.140	1255.09	175.96
A_68_P28332015	chr12:32244658-32244702	NM_011867:154	Slc26a4	INSIDE	0.275	0.575	1918.56	1103.79	0.158	1386.50	219.63
A_68_P22963968	chr4:62021675-62021719	NM_175090:-38	Slc31a1	DIVERGENT_PROMOTER	0.275	0.486	2719.08	1322.52	0.134	1958.93	262.22
A_68_P25604004	chr7:151163627-151163676			Unknown	0.275	0.627	942.56	590.74	0.172	675.92	116.46
A_68_P25761251	chr8:33119625-33119669	ENSMUST00000080782:-65		PROMOTER	0.275	0.430	1262.48	543.12	0.118	984.62	116.55
A_68_P21341870	chr2:74975798-74975843	ENSMUST00000143898:35		INSIDE	0.275	0.394	1568.61	618.20	0.108	1315.17	142.51
A_68_P21626541	chr2:129626864-129626913	NR_029452:307	4932416H05Rik	INSIDE	0.274	0.558	1137.42	634.55	0.153	793.43	121.37
A_68_P23548816	chr5:25266039-25266083	NM_001004365:217	Actr3b	INSIDE	0.274	1.719	13031.31	22401.81	0.472	8506.81	4013.59
A_68_P25017993	chr7:28377186-28377230	NM_001110208:630	Akt2	INSIDE	0.274	0.697	2136.42	1489.41	0.191	1819.26	346.88
A_68_P25500902	chr7:133646038-133646082	NM_183020:756	Atxn2l	INSIDE	0.274	0.469	1481.07	695.32	0.128	1165.36	149.66
A_68_P23961352	chr5:106886727-106886771	NM_001005477:437	Barhl2	INSIDE	0.274	0.495	2262.70	1119.67	0.135	1646.56	222.88
A_68_P32260574	chrX:11705655-11705699	NM_001168321:31805	Bcor	INSIDE	0.274	1.667	5079.86	8467.01	0.456	1843.53	841.12
A_68_P32459814	chrX:70163539-70163583	NM_019405:123	Cetn2	INSIDE	0.274	1.811	1351.75	2447.48	0.496	519.22	257.64
A_68_P24994312	chr7:20189858-20189902	NM_016680:-63	Clasrp	PROMOTER	0.274	0.537	1872.87	1006.07	0.147	1489.84	219.38
A_68_P28525478	chr12:72411253-72411297	NM_001190466:404	Dact1	INSIDE	0.274	0.603	1095.25	660.89	0.165	781.86	129.22
A_68_P24118893	chr5:136470543-136470598	NM_023742:-176	Dtx2	PROMOTER	0.274	0.615	983.42	604.71	0.169	910.04	153.37
A_68_P25952515	chr8:73062683-73062729	NM_007924:-867	Ell	PROMOTER	0.274	1.486	2985.15	4436.35	0.407	1808.70	736.48
A_68_P22149161	chr3:54496698-54496742	NM_019995:-306	Fam48a	PROMOTER	0.274	0.725	1682.31	1220.29	0.199	1260.47	250.22
A_68_P29386050	chr14:8650925-8650970	NM_134080:477	Flnb	INSIDE	0.274	0.496	1103.67	547.52	0.136	868.91	117.93
A_68_P31876072	chr18:82575840-82575884	NM_008082:307	Galr1	INSIDE	0.274	0.550	2060.59	1133.84	0.151	1520.48	229.52
A_68_P28833514	chr13:12742271-12742315	NR_003568:370	Gpr137b-ps	INSIDE	0.274	0.479	1584.31	759.23	0.131	1308.74	171.55
A_68_P28883366	chr13:23853149-23853193	NM_178192:-144	Hist1h4a	PROMOTER	0.274	0.509	1158.81	589.30	0.140	857.37	119.61

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28748139	chr12:113383755-113383799	NM_001097621:-642	Kif26a	PROMOTER	0.274	0.645	1160.96	749.22	0.177	791.19	140.04
A_68_P26192682	chr8:118231333-118231382	NM_001025577:-563	Maf	PROMOTER	0.274	0.531	1446.93	768.66	0.146	1192.45	173.59
A_68_P24946853	chr7:3644138-3644182	NM_029934:967	Mboat7	INSIDE	0.274	0.511	1155.74	591.04	0.140	868.71	121.60
A_68_P25664801	chr8:12915981-12916035	NM_178076:116	Mcf2l	INSIDE	0.274	0.689	1297.83	894.77	0.189	959.41	181.19
A_68_P30082171	chr15:25552353-25552397	NM_019472:70	Myo10	INSIDE	0.274	0.499	2761.04	1376.67	0.137	1900.34	259.65
A_68_P32148153	chr19:47254029-47254073	NM_021360:741	Neurl1a	INSIDE	0.274	0.719	2005.46	1442.43	0.197	1556.76	307.34
A_68_P25144263	chr7:63217306-63217365	NM_023647:485	Nipa2	INSIDE	0.274	0.462	1255.49	580.62	0.127	952.08	120.51
A_68_P21089693	chr2:28061497-28061541	NM_001038612:310	Olfm1	INSIDE	0.274	0.276	2136.67	589.05	0.076	1666.45	125.96
A_68_P21769996	chr2:156022460-156022504	NM_172674:100	Phf20	INSIDE	0.274	0.405	1428.89	578.54	0.111	1123.25	124.64
A_68_P31162035	chr17:36116527-36116571	NM_145487:-136	Prr3	PROMOTER	0.274	0.516	2389.16	1231.91	0.141	1976.97	279.50
A_68_P21117413	chr2:32631242-32631286	NM_178595:-76	Ptrh1	DIVERGENT_PROMOTER	0.274	0.405	1300.18	526.14	0.111	1049.75	116.57
A_68_P30518123	chr16:5885155-5885211	NM_021477:297	Rbfox1	INSIDE	0.274	0.595	1352.88	805.35	0.163	1019.62	166.57
A_68_P27924775	chr11:75008355-75008401	NM_177708:884	Rtn4rl1	INSIDE	0.274	0.413	1547.24	638.93	0.113	1025.14	116.19
A_68_P20370950	chr1:78306691-78306735	NM_001004173:-208	Sgpp2	PROMOTER	0.274	0.506	2193.77	1109.05	0.139	1814.46	251.35
A_68_P28168285	chr11:117830022-117830066	NM_007707:636	Socs3	INSIDE	0.274	0.580	1701.31	987.33	0.159	1192.17	189.29
A_68_P31958015	chr19:11893696-11893748	NM_011502:-339	Stx3	PROMOTER	0.274	0.644	895.93	577.08	0.176	690.83	121.89
A_68_P28524523	chr12:72237247-72237292	NM_001024853:393	Timm9	INSIDE	0.274	0.417	1285.30	536.13	0.114	1046.67	119.56
A_68_P25469458	chr7:127779197-127779246	NM_025899:519	Uqcrc2	INSIDE	0.274	0.480	1509.41	723.99	0.131	1071.55	140.69
A_68_P21085240	chr2:27395797-27395841	NM_080848:25152	Wdr5	DOWNSTREAM	0.274	0.468	1597.32	747.42	0.128	1382.51	177.34
A_68_P23591880	chr5:34279319-34279363	NM_011914:-433	Whsc2	PROMOTER	0.274	0.496	1170.62	580.93	0.136	1024.26	139.05
A_68_P30476373	chr15:98603197-98603241	NM_011718:5363	Wnt10b	INSIDE	0.274	0.531	973.68	517.09	0.146	820.13	119.40
A_68_P30140507	chr15:36723784-36723828	NM_011740:487	Ywhaz	INSIDE	0.274	0.637	810.77	516.51	0.175	688.21	120.32
A_68_P25258775	chr7:86198137-86198181	NM_007424:-210	Acan	PROMOTER	0.273	0.563	2377.74	1339.81	0.154	1854.72	285.27
A_68_P21784026	chr2:158450747-158450791	NM_175419:120	Actr5	INSIDE	0.273	0.659	2060.57	1357.21	0.180	1368.50	246.22
A_68_P32186046	chr19:54119698-54119742	NM_007417:49	Adra2a	INSIDE	0.273	0.511	1098.89	561.95	0.140	866.41	120.92
A_68_P30421417	chr15:88649565-88649609	NM_001142357:162	Alg12	INSIDE	0.273	0.543	1595.05	866.27	0.148	1265.72	187.67
A_68_P26595212	chr9:66643626-66643670	NM_177583:-418	Aph1b	PROMOTER	0.273	0.575	2855.08	1642.69	0.157	2129.20	334.72
A_68_P28195046	chr12:3427021-3427065	NM_172421:159	Asxl2	INSIDE	0.273	0.518	1125.85	583.05	0.141	956.58	135.04
A_68_P30246252	chr15:57966703-57966747	NM_027435:-87	Atad2	DIVERGENT_PROMOTER	0.273	0.396	1933.52	766.20	0.108	1613.12	174.67
A_68_P31099851	chr17:24986997-24987041	NM_023480:229	Fahd1	INSIDE	0.273	0.608	945.82	575.36	0.166	731.33	121.44
A_68_P23979395	chr5:110815816-110815860	NM_028596:308	Fbrsl1	INSIDE	0.273	0.553	1392.97	770.15	0.151	1216.14	183.39
A_68_P23973155	chr5:109058342-109058386	NM_153569:394	Gak	INSIDE	0.273	0.621	1598.27	991.75	0.169	1173.02	198.75
A_68_P23438946	chr4:154866208-154866252	NM_001160016:761	Gnb1	INSIDE	0.273	0.489	2009.40	983.07	0.134	1514.53	202.52
A_68_P27581116	chr11:8911066-8911110	NM_008316:52	Hus1	INSIDE	0.273	0.739	2270.54	1677.16	0.201	1638.68	330.14
A_68_P23297601	chr4:129296491-129296543	NM_198026:-179	Iqcc	PROMOTER	0.273	0.658	823.66	542.29	0.180	657.74	118.15
A_68_P23752952	chr5:65195598-65195642	NM_008453:859	Klf3	INSIDE	0.273	0.420	1300.66	546.35	0.115	1043.43	119.55
A_68_P29842704	chr14:99698682-99698726	NM_009769:795	Klf5	INSIDE	0.273	0.515	1114.89	574.59	0.140	859.70	120.74
A_68_P30424716	chr15:89185877-89185921	NM_178919:192	Lmf2	INSIDE	0.273	0.364	1616.69	588.23	0.099	1185.44	117.79
A_68_P27855086	chr11:62462305-62462349	NM_175002:161	Mmgt2	INSIDE	0.273	0.670	1593.12	1067.87	0.183	1107.38	203.00
A_68_P26075855	chr8:96696139-96696185	NM_008630:-355	Mt2	PROMOTER	0.273	0.652	1159.31	755.79	0.178	994.54	177.13
A_68_P23057176	chr4:82151139-82151183	NM_001113209:52	Nfib	INSIDE	0.273	0.700	1996.42	1398.11	0.191	1418.21	271.28
A_68_P27900561	chr11:70223294-70223338	NM_029231:217	Pelp1	INSIDE	0.273	0.661	1311.25	866.90	0.180	1027.67	185.49
A_68_P23577162	chr5:31523190-31523234	NM_008014:-294	Ppm1g	PROMOTER	0.273	0.517	1770.88	914.90	0.141	1231.46	173.56
A_68_P23610087	chr5:37260107-37260152	NM_172994:321	Ppp2r2c	INSIDE	0.273	0.501	1025.47	514.19	0.137	886.49	121.48
A_68_P24170315	chr5:147644587-147644631	NM_019647:143	Rpl21	INSIDE	0.273	0.428	1357.42	580.44	0.117	1039.87	121.44
A_68_P28073901	chr11:101303846-101303890	NM_011289:310	Rpl27	INSIDE	0.273	0.501	1070.54	536.15	0.137	879.78	120.31
A_68_P25378792	chr7:109590509-109590553	NM_009103:322	Rrm1	INSIDE	0.273	0.658	1384.13	911.23	0.180	903.12	162.28
A_68_P32926581	chr13:93381448-93381492	NM_172588:378	Serinc5	INSIDE	0.273	0.505	1092.29	552.12	0.138	893.39	123.25
A_68_P20585379	chr1:127457276-127457320	NM_028787:-294	Slc35f5	PROMOTER	0.273	0.655	826.55	541.37	0.179	704.50	125.89
A_68_P20628459	chr1:135506499-135506543	NM_009227:337	Snrpe	INSIDE	0.273	0.660	4416.18	2913.10	0.180	3339.08	600.44
A_68_P29879699	chr14:106294307-106294351	NM_011897:1708	Spry2	INSIDE	0.273	0.616	3758.28	2313.71	0.168	2666.38	448.47

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P22200389	chr3:65332655-65332699	NM_178892:308	Tiparp	INSIDE	0.273	0.582	1856.08	1080.83	0.159	1515.63	241.15
A_68_P21574793	chr2:120178464-120178508	NM_147153:383	Vps39	INSIDE	0.273	0.459	1625.73	745.88	0.125	1311.91	164.56
A_68_P28119630	chr11:109472954-109472998	NM_145940:-273	Wipi1	PROMOTER	0.273	0.702	9981.09	7006.85	0.192	7927.89	1522.00
A_68_P30344507	chr15:75672464-75672508	NM_172121:-148	Zc3h3	PROMOTER	0.273	0.426	1350.14	574.93	0.116	1049.25	121.93
A_68_P30261318	chr15:60654478-60654526	NR_030696:-17	9930014A18Rik	PROMOTER	0.272	0.528	1085.91	572.91	0.144	840.37	120.70
A_68_P22410426	chr3:107889144-107889188	NM_028779:379	Ampd2	INSIDE	0.272	0.392	1509.32	590.95	0.106	1141.85	121.45
A_68_P23439689	chr4:154998937-154998981	NM_007661:-19	Cdk11b	PROMOTER	0.272	0.528	1003.84	529.90	0.144	872.08	125.29
A_68_P24818639	chr6:125046323-125046367	NM_145979:164	Chd4	INSIDE	0.272	0.298	2233.34	665.25	0.081	1657.90	134.33
A_68_P23254630	chr4:120712227-120712271	NM_007741:78	Col9a2	INSIDE	0.272	0.592	1082.22	640.95	0.161	890.79	143.52
A_68_P25588174	chr7:148513704-148513752	NM_016874:-104	Deaf1	DIVERGENT_PROMOTER	0.272	0.531	1000.56	531.62	0.145	805.47	116.56
A_68_P26584122	chr9:64659329-64659373	NM_001162917:533	Dennd4a	INSIDE	0.272	0.598	4331.66	2591.77	0.163	3237.48	527.72
A_68_P28332515	chr12:32339615-32339664	NM_028002:52	Dus4l	INSIDE	0.272	0.567	1352.00	766.46	0.154	1092.96	168.75
A_68_P26135514	chr8:108231844-108231888	NM_198299:202	E130303B06Rik	INSIDE	0.272	0.540	1060.09	572.21	0.147	789.68	115.78
A_68_P23981800	chr5:111199966-111200010	NM_029337:-252	Ep400	PROMOTER	0.272	0.306	1779.38	543.62	0.083	1446.64	120.14
A_68_P26693197	chr9:85221191-85221249	NM_001160379:-463	Fam46a	PROMOTER	0.272	0.409	1273.95	521.15	0.111	1062.68	118.15
A_68_P20294241	chr1:64781408-64781452	NM_001042659:2894	Fzd5	INSIDE	0.272	0.599	1039.29	622.94	0.163	784.86	127.76
A_68_P23787825	chr5:72092392-72092436	NM_008069:1160	Gabrb1	INSIDE	0.272	0.496	1200.92	595.31	0.135	904.97	121.84
A_68_P27286409	chr10:80393272-80393316	NM_008655:459	Gadd45b	INSIDE	0.272	0.492	3524.87	1733.92	0.134	2502.37	335.36
A_68_P28043171	chr11:96113156-96113200	NR_037977:205	Gm53	INSIDE	0.272	0.525	1062.94	557.89	0.143	813.18	116.18
A_68_P24611769	chr6:86683533-86683577	NM_011818:-182	Gmcl1	PROMOTER	0.272	0.645	819.39	528.22	0.175	687.12	120.47
A_68_P24142814	chr5:141178050-141178094	NM_028833:260	Iqce	INSIDE	0.272	0.508	2849.60	1446.95	0.138	2303.75	318.65
A_68_P23399815	chr4:148682002-148682046	NM_207682:-217	Kif1b	PROMOTER	0.272	0.665	4528.99	3012.98	0.181	3547.92	641.81
A_68_P21137823	chr2:35959065-35959110	NM_001083126:493	Lhx6	INSIDE	0.272	0.451	1462.87	659.90	0.123	981.61	120.30
A_68_P26227605	chr8:124109328-124109378	NM_026160:-5015	Map1lc3b	DIVERGENT_PROMOTER	0.272	0.591	995.82	588.63	0.161	733.41	118.12
A_68_P24946860	chr7:3645012-3645069	NM_029934:87	Mboat7	INSIDE	0.272	0.425	1259.44	535.12	0.116	1026.35	118.71
A_68_P23547782	chr5:25003584-25003633	NM_001081383:993	Mll3	INSIDE	0.272	0.448	1218.45	546.25	0.122	988.33	120.52
A_68_P28614145	chr12:88443030-88443074	NM_022414:437	Ngb	INSIDE	0.272	0.554	5083.73	2817.64	0.151	3776.37	570.08
A_68_P28057359	chr11:98448749-98448807	NM_025661:-219	Ormdl3	PROMOTER	0.272	0.380	1387.33	527.27	0.104	1146.88	118.76
A_68_P31619153	chr18:35758686-35758732	NM_026420:388	Paip2	INSIDE	0.272	0.448	1311.64	587.93	0.122	989.62	120.73
A_68_P28107246	chr11:107330411-107330455	NM_145823:1602	Pitpnc1	INSIDE	0.272	0.588	3975.75	2339.59	0.160	3186.82	509.66
A_68_P22518744	chr3:128917174-128917220	NM_001042502:342	Pitx2	INSIDE	0.272	0.664	1138.17	755.21	0.180	885.98	159.89
A_68_P27260808	chr10:75700481-75700530	NM_001077638:105	Prmt2	INSIDE	0.272	0.594	2200.79	1307.97	0.162	1495.66	242.19
A_68_P31306703	chr17:66868585-66868629	NM_024448:404	Rab12	INSIDE	0.272	0.538	1759.09	945.83	0.146	1430.87	209.26
A_68_P26747275	chr9:96378576-96378624	NM_011279:414	Rnf7	INSIDE	0.272	0.621	908.83	564.60	0.169	723.69	122.09
A_68_P24447788	chr6:51962397-51962441	NM_018773:130	Skap2	INSIDE	0.272	0.583	1040.59	606.93	0.159	746.70	118.55
A_68_P27841612	chr11:60024194-60024238	NM_011480:9890	Srebf1	INSIDE	0.272	0.365	1444.68	527.32	0.099	1170.03	116.38
A_68_P20885446	chr1:184055324-184055368	NM_012058:479	Srp9	INSIDE	0.272	0.440	2506.19	1103.56	0.120	2066.48	247.19
A_68_P21682255	chr2:139892211-139892255	NM_175225:264	Tasp1	INSIDE	0.272	0.556	1569.48	873.04	0.152	1259.13	190.81
A_68_P22336392	chr3:93247658-93247702	NM_001163098:1429	Tchh	INSIDE	0.272	0.510	1225.25	625.43	0.139	869.52	120.72
A_68_P21070914	chr2:25111268-25111312	NM_177344:332	Tmem203	INSIDE	0.272	0.607	3220.74	1954.68	0.165	2146.38	354.06
A_68_P31936614	chr19:6984396-6984443	NM_001166370:232	Trmt112	INSIDE	0.272	0.397	1504.42	597.01	0.108	1094.70	118.25
A_68_P21577444	chr2:120675934-120675978	NM_001024856:198	Ttbk2	INSIDE	0.272	0.591	955.67	564.61	0.161	771.32	124.01
A_68_P29952198	chr14:121229992-121230036			Unknown	0.272	0.589	1735.46	1022.59	0.160	1358.62	217.83
A_68_P28755046	chr12:114394157-114394201	NM_134041:-453	4930427A07Rik	PROMOTER	0.271	0.339	2445.69	827.90	0.092	1889.02	173.14
A_68_P28202319	chr12:4776061-4776106	NM_175431:-10	A830093I24Rik	DIVERGENT_PROMOTER	0.271	0.645	1217.67	785.47	0.175	1011.27	177.06
A_68_P27932045	chr11:76250435-76250479	NM_198018:72465	Abr	INSIDE	0.271	0.626	3404.65	2130.45	0.169	2601.46	440.86
A_68_P24925475	chr6:145812338-145812382	NM_024469:1500	Bhlhe41	INSIDE	0.271	0.434	1331.73	577.76	0.118	1030.57	121.35
A_68_P31323859	chr17:69767217-69767270	NR_026848:1457	C030034I22Rik	INSIDE	0.271	0.588	1073.03	630.54	0.159	817.56	130.24
A_68_P22874797	chr4:44025966-44026010	NM_001080384:474	Clta	INSIDE	0.271	0.611	872.51	533.24	0.165	728.24	120.40
A_68_P31679713	chr18:47118783-47118827	NM_178377:275	Commd10	INSIDE	0.271	0.626	1764.23	1104.33	0.170	1414.72	240.03
A_68_P23222365	chr4:114598324-114598368	NM_015758:272	Foxe3	INSIDE	0.271	0.530	1483.79	787.09	0.143	1185.89	170.17

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						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P24131920	chr5:139296987-139297031	NM_001195128:975	Gm5294	INSIDE	0.271	0.596	1815.72	1083.07	0.162	1460.19	235.83
A_68_P31162851	chr17:36304426-36304470	NM_001081032:1034	Gm8909	INSIDE	0.271	0.567	2648.62	1501.56	0.154	1891.47	291.08
A_68_P31151132	chr17:34077320-34077372	NM_010385:-58	H2-Ke2	DIVERGENT_PROMOTER	0.271	0.578	903.23	522.05	0.157	775.07	121.60
A_68_P23571066	chr5:30482087-30482136	NM_145558:250	Hadhb	INSIDE	0.271	0.517	1092.18	565.12	0.140	831.66	116.82
A_68_P21339318	chr2:74587859-74587910	NM_010468:37835	Hoxd3	DOWNSTREAM	0.271	0.535	990.54	530.01	0.145	835.08	121.03
A_68_P29657354	chr14:63379882-63379926	NM_008715:45	Ints6	INSIDE	0.271	0.529	1051.19	555.92	0.143	831.51	119.01
A_68_P28748138	chr12:113383612-113383656	NM_001097621:-784	Kif26a	PROMOTER	0.271	0.570	1017.07	579.61	0.154	743.14	114.67
A_68_P25484147	chr7:130521434-130521478	NM_025304:-39	Lcmt1	DIVERGENT_PROMOTER	0.271	0.411	1585.90	652.59	0.111	1099.91	122.53
A_68_P24796456	chr6:119988018-119988063	NR_030487:-3711	Mir706	PROMOTER	0.271	0.640	2373.74	1519.40	0.173	1878.18	325.82
A_68_P23567511	chr5:29761679-29761723	NM_001033457:494	Nom1	INSIDE	0.271	0.725	1879.56	1363.20	0.197	1471.14	289.57
A_68_P24164493	chr5:145900637-145900681	NM_001033313:300	Pdap1	INSIDE	0.271	0.483	1518.33	733.67	0.131	1248.49	163.74
A_68_P25953243	chr8:73183392-73183436	NM_023217:166	Pgpep1	INSIDE	0.271	0.620	1913.18	1185.96	0.168	1408.27	236.84
A_68_P29057250	chr13:55927065-55927109	NM_011097:5700	Pitx1	INSIDE	0.271	0.589	1041.08	612.90	0.160	760.85	121.46
A_68_P21870533	chr2:173411101-173411145	NR_027957:73918	Ppp4r1l-ps	INSIDE	0.271	0.517	1178.09	608.66	0.140	889.54	124.38
A_68_P28334786	chr12:32745694-32745738	NM_011158:428	Prkar2b	INSIDE	0.271	0.650	1100.48	715.17	0.176	804.41	141.51
A_68_P31097945	chr17:24670178-24670222	NM_177375:492	Rab26	INSIDE	0.271	0.509	1134.52	577.72	0.138	872.29	120.48
A_68_P27899668	chr11:70051980-70052024	NM_173742:1352	Rnasek	INSIDE	0.271	0.662	2107.64	1396.09	0.179	1454.29	260.82
A_68_P21227533	chr2:53937683-53937727	NM_023396:259	Rprm	INSIDE	0.271	0.421	1379.77	581.23	0.114	1078.45	123.26
A_68_P24950803	chr7:4795789-4795833	NM_172737:488	Shisa7	INSIDE	0.271	0.408	1569.89	641.13	0.110	1181.68	130.56
A_68_P28585128	chr12:83271163-83271207	NM_001167983:182	Sipa1l1	INSIDE	0.271	0.268	2096.62	562.41	0.073	1638.21	119.11
A_68_P31349752	chr17:74397147-74397191	NM_053188:88	Srd5a2	INSIDE	0.271	0.405	1263.86	512.28	0.110	1087.52	119.43
A_68_P27765165	chr11:45768563-45768620	NM_001080969:405	Thg1l	INSIDE	0.271	0.507	1104.46	559.49	0.138	839.87	115.48
A_68_P26579886	chr9:63908037-63908081	ENSMUST00000130862:10423		DOWNSTREAM	0.271	0.645	1340.94	864.55	0.175	1099.85	191.99
A_68_P27945544	chr11:78640263-78640307	NM_001076681:188	1810012P15Rik	INSIDE	0.270	0.607	862.96	523.41	0.164	763.48	124.95
A_68_P27279426	chr10:79337278-79337322	NM_001170935:79	BC005764	INSIDE	0.270	0.575	1006.84	578.86	0.155	765.90	118.75
A_68_P28078450	chr11:102110241-102110285	NM_153544:67	BC030867	INSIDE	0.270	0.529	1044.74	552.68	0.143	859.44	122.64
A_68_P27559363	chr11:4645990-4646034	NM_138948:769	Cabp7	INSIDE	0.270	0.621	1321.68	821.29	0.168	1083.20	182.06
A_68_P28685558	chr12:102267375-102267419	NM_026681:-203	Ccdc88c	PROMOTER	0.270	0.407	1691.89	689.44	0.110	1231.55	135.74
A_68_P30475237	chr15:98398586-98398630	NM_009833:-541	Ccnt1	PROMOTER	0.270	0.497	1171.00	581.59	0.134	878.82	117.85
A_68_P30405649	chr15:86015668-86015712	NM_145475:881	Cerk	INSIDE	0.270	0.611	952.62	582.38	0.165	733.58	121.17
A_68_P25948513	chr8:72410234-72410278	NM_026818:1035	Cilp2	INSIDE	0.270	0.530	1079.67	572.66	0.143	809.33	115.87
A_68_P30964660	chr16:91728640-91728684	NM_026994:385	Cryzl1	INSIDE	0.270	0.726	2596.26	1885.32	0.196	1729.11	338.75
A_68_P29659270	chr14:63741403-63741447	NM_007798:123	Ctsb	INSIDE	0.270	0.620	2316.59	1435.18	0.167	1751.69	293.15
A_68_P28079628	chr11:102308536-102308580	NM_199200:419	Fam171a2	INSIDE	0.270	0.556	4410.99	2451.56	0.150	3202.38	479.82
A_68_P29448410	chr14:21514889-21514933	NM_028428:721	Fut11	INSIDE	0.270	0.353	1663.01	586.40	0.095	1267.34	120.88
A_68_P24449041	chr6:52154245-52154298	NM_010453:315	Hoxa5	INSIDE	0.270	0.479	1220.24	584.92	0.129	921.20	119.11
A_68_P21683843	chr2:140221161-140221205	NM_028387:12	Macrod2	INSIDE	0.270	0.509	1963.27	1000.00	0.138	1607.61	221.42
A_68_P25193391	chr7:74516874-74516921	NM_001033713:847	Mef2a	INSIDE	0.270	0.382	1531.05	584.82	0.103	1173.78	120.84
A_68_P28457458	chr12:57637325-57637369	NM_001146198:-1253	Nkx2-1	PROMOTER	0.270	0.455	1415.43	644.37	0.123	970.61	119.24
A_68_P24816532	chr6:124662438-124662482	NM_007531:154	Phb2	INSIDE	0.270	0.649	854.19	554.53	0.175	692.18	121.25
A_68_P32555654	chrX:96665945-96665989	NM_001083110:108	Pja1	INSIDE	0.270	1.528	1401.52	2140.98	0.413	586.99	242.14
A_68_P24158565	chr5:144671053-144671097	NM_008886:205	Pms2	INSIDE	0.270	0.418	1317.53	550.65	0.113	1036.82	117.10
A_68_P22558734	chr3:136332458-136332502	NM_008913:-1253	Ppp3ca	PROMOTER	0.270	0.434	2000.90	867.72	0.117	1569.79	184.00
A_68_P30476737	chr15:98661589-98661633	NM_016781:329	Prkag1	INSIDE	0.270	0.494	1404.42	693.69	0.134	975.81	130.30
A_68_P21780562	chr2:157854036-157854080	NM_027434:-471	Rprd1b	PROMOTER	0.270	0.435	1452.64	632.44	0.118	1121.18	131.91
A_68_P31411656	chr17:86007613-86007657	NR_038085:10102	Six3os1	INSIDE	0.270	0.552	1036.40	571.73	0.149	835.90	124.37
A_68_P28118784	chr11:109333745-109333789	NM_134038:777	Slc16a6	INSIDE	0.270	0.454	1520.70	691.02	0.123	1224.16	150.33
A_68_P23973506	chr5:109106670-109106714	NM_174870:-2024	Slc26a1	PROMOTER	0.270	1.498	4716.65	7067.46	0.405	2790.84	1130.22
A_68_P22049518	chr3:34563441-34563498	NR_015580:104167	Sox2ot	INSIDE	0.270	0.425	1444.16	613.38	0.115	1024.52	117.35
A_68_P30595258	chr16:21947351-21947395	NM_025693:253	Tmem41a	INSIDE	0.270	0.710	4519.94	3208.62	0.192	3570.10	684.14
A_68_P22878935	chr4:44769408-44769452	NM_138590:0	Zcchc7	INSIDE	0.270	0.432	1307.13	564.76	0.117	1023.21	119.21

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26235836	chr8:125299500-125299544	NM_144932:118	Acsf3	INSIDE	0.269	1.433	3955.96	5667.01	0.386	2719.70	1048.79
A_68_P29223867	chr13:93195722-93195766	NM_175455:-179	Ankrd34b	PROMOTER	0.269	0.357	2515.33	897.35	0.096	2137.69	204.90
A_68_P22611615	chr3:145587665-145587709	NM_009740:345	Bcl10	INSIDE	0.269	0.620	1349.91	837.35	0.167	1077.79	179.79
A_68_P23240388	chr4:118109735-118109779	NM_023223:192	Cdc20	INSIDE	0.269	0.510	5179.82	2642.88	0.137	3749.47	514.66
A_68_P21639431	chr2:132089279-132089323	NM_138651:308	Cds2	INSIDE	0.269	0.471	2740.33	1290.68	0.127	2096.93	265.86
A_68_P27913314	chr11:72608834-72608878	NM_001024926:485	Cyb5d2	INSIDE	0.269	0.530	1076.15	570.73	0.142	841.16	119.81
A_68_P23797907	chr5:73882297-73882341	NM_001190733:54	Dcun1d4	INSIDE	0.269	0.510	1858.99	948.19	0.137	1504.47	206.78
A_68_P28744646	chr12:112776044-112776088	NM_173363:-245	Eif5	PROMOTER	0.269	0.663	2828.18	1875.34	0.178	2241.52	399.96
A_68_P25196760	chr7:75097984-75098028	NM_010513:864	Igf1r	INSIDE	0.269	0.593	1006.02	596.44	0.160	755.73	120.65
A_68_P26885525	chr9:121687219-121687263	NM_028202:516	Kbtbd5	INSIDE	0.269	0.493	1103.61	543.89	0.133	940.62	124.74
A_68_P28099138	chr11:105881660-105881704	NM_001037712:12166	Kcnh6	INSIDE	0.269	0.698	3544.63	2474.23	0.188	2626.04	493.34
A_68_P26346370	chr9:21092650-21092694	NM_145416:-259	Kri1	PROMOTER	0.269	0.549	2546.79	1398.83	0.148	1997.49	294.68
A_68_P27180700	chr10:60938374-60938418	NM_153542:-184	Lrrc20	PROMOTER	0.269	0.603	1258.02	758.07	0.162	994.79	161.06
A_68_P22028769	chr3:30407354-30407398	NM_021442:1033	Mecom	INSIDE	0.269	0.736	4058.31	2988.19	0.198	3247.42	643.40
A_68_P23226096	chr4:115511583-115511632	NM_021461:-243	Mknk1	PROMOTER	0.269	0.576	1032.04	594.16	0.155	752.72	116.63
A_68_P24055452	chr5:123845226-123845273	NM_177582:422	Mlxip	INSIDE	0.269	0.612	1275.11	780.85	0.165	976.05	161.01
A_68_P21044522	chr2:19293408-19293452	NM_029619:168	Msrb2	INSIDE	0.269	0.576	2781.09	1603.02	0.155	1989.46	308.99
A_68_P28052172	chr11:97560234-97560280	NM_001163307:442	Pcgf2	INSIDE	0.269	0.365	1830.49	668.55	0.098	1345.75	132.28
A_68_P20472798	chr1:99666127-99666173	NM_173760:519	Ppip5k2	INSIDE	0.269	0.477	1076.17	513.79	0.128	923.54	118.59
A_68_P24049493	chr5:122735201-122735245	NM_177242:816	Pptc7	INSIDE	0.269	0.579	3182.05	1842.25	0.156	2339.06	364.23
A_68_P23801766	chr5:74590964-74591008	NM_026878:-364	Rasl11b	PROMOTER	0.269	0.565	2245.94	1269.74	0.152	1672.29	254.39
A_68_P21634641	chr2:131178781-131178836	NM_178607:-180	Rnf24	PROMOTER	0.269	0.471	1229.72	579.43	0.127	936.00	118.59
A_68_P31003193	chr17:3114560-3114614	NM_134123:-385	Scaf8	PROMOTER	0.269	0.397	1860.62	738.51	0.107	1441.08	154.09
A_68_P20022048	chr1:9289699-9289746	NM_027671:89	Sntg1	INSIDE	0.269	0.571	937.05	534.97	0.154	776.36	119.29
A_68_P20616241	chr1:133423301-133423345	NM_001081011:616	Srgap2	INSIDE	0.269	0.467	1393.83	650.69	0.125	1000.15	125.44
A_68_P27943940	chr11:78349786-78349836	NM_001159392:-48	Tnfaip1	DIVERGENT_PROMOTER	0.269	0.604	1091.68	659.27	0.162	739.47	120.15
A_68_P26467466	chr9:44215609-44215655	NM_021789:-1	Trappc4	DIVERGENT_PROMOTER	0.269	0.448	1284.89	576.13	0.121	983.79	118.56
A_68_P26743634	chr9:95650227-95650271	NM_011643:529	Trpc1	INSIDE	0.269	0.644	1039.10	669.39	0.173	881.73	152.71
A_68_P28057144	chr11:98412585-98412629	NM_001166494:196	Zpbp2	INSIDE	0.269	0.457	2698.52	1233.87	0.123	2073.75	255.43
A_68_P28881179	chr13:23487667-23487711	BC160303:75810		INSIDE	0.269	0.535	2503.12	1338.96	0.144	1893.59	272.34
A_68_P24838569	chr6:128312716-128312760	NR_027360:102	5930416I19Rik	INSIDE	0.268	0.271	1924.42	521.64	0.073	1632.55	118.73
A_68_P20770261	chr1:163073112-163073156	NM_028664:292	Ankrd45	INSIDE	0.268	0.453	1294.84	586.81	0.121	972.84	118.12
A_68_P25352112	chr7:104886923-104886967	NM_175105:-187	Aqp11	PROMOTER	0.268	0.580	1006.01	583.48	0.155	776.88	120.66
A_68_P26797752	chr9:105396915-105396959	NM_175025:511	Atp2c1	INSIDE	0.268	0.689	1785.32	1230.42	0.184	1314.36	242.36
A_68_P28153130	chr11:115235797-115235841	NM_175454:-6785	C630004H02Rik	DIVERGENT_PROMOTER	0.268	0.693	1465.38	1015.15	0.185	1237.82	229.54
A_68_P21822534	chr2:165059212-165059256	NM_174988:1003	Cdh22	INSIDE	0.268	0.628	812.47	510.25	0.168	716.53	120.62
A_68_P31259432	chr17:57130046-57130090	NM_017393:382	Clpp	INSIDE	0.268	0.612	979.87	599.61	0.164	764.50	125.31
A_68_P22968884	chr4:62876409-62876457	NM_025685:-13	Col27a1	PROMOTER	0.268	0.551	1119.91	616.53	0.148	808.31	119.35
A_68_P25828056	chr8:46122297-46122344	NM_001081286:86759	Fat1	INSIDE	0.268	1.687	641.92	1082.79	0.453	567.83	257.12
A_68_P28924076	chr13:31718416-31718460	NM_010225:754	Foxf2	INSIDE	0.268	0.525	1141.36	599.10	0.141	950.70	133.64
A_68_P24819105	chr6:125115461-125115505	NM_008084:119	Gapdh	INSIDE	0.268	0.720	6768.06	4873.16	0.193	4535.51	873.94
A_68_P20417066	chr1:89223605-89223651	NM_001110212:25	Gigyf2	INSIDE	0.268	0.607	1552.15	942.01	0.163	1281.53	208.77
A_68_P25766297	chr8:33994011-33994055	NM_001177589:66466	Gm3985	DOWNSTREAM	0.268	0.596	969.08	577.10	0.160	761.22	121.61
A_68_P29138699	chr13:73405898-73405942	NM_018885:7976	Irx4	INSIDE	0.268	0.514	1100.44	565.73	0.138	856.73	118.21
A_68_P27543984	chr10:128371011-128371056	NM_008398:165	Itga7	INSIDE	0.268	0.318	1707.29	542.40	0.085	1374.66	116.90
A_68_P28997656	chr13:44825977-44826021	NM_001205044:-144	Jarid2	PROMOTER	0.268	0.506	1762.95	892.14	0.136	1405.33	190.89
A_68_P32137138	chr19:45298661-45298705	NM_010691:11044	Lbx1	DOWNSTREAM	0.268	0.588	1886.38	1108.70	0.158	1325.49	209.14
A_68_P26021275	chr8:87229477-87229521	NM_008535:4143	Lyl1	DOWNSTREAM	0.268	1.834	5704.28	10461.67	0.492	3414.91	1680.44
A_68_P27282871	chr10:79849463-79849507	NM_198615:912	Mex3d	INSIDE	0.268	0.520	1423.79	740.17	0.139	938.11	130.48
A_68_P23567756	chr5:29800752-29800798	NM_019944:4236	Mnx1	INSIDE	0.268	1.501	821.61	1232.99	0.402	556.60	223.56
A_68_P21070911	chr2:25110830-25110874	NM_001082476:82	Ndor1	INSIDE	0.268	0.703	1591.65	1119.44	0.188	1185.44	223.34

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26143994	chr8:109817474-109817518	NM_018823:127	Nfat5	INSIDE	0.268	0.602	904.00	544.53	0.161	757.62	122.26
A_68_P20010813	chr1:5906992-5907041	NM_010342:463	Npbwr1	INSIDE	0.268	0.595	1239.20	737.49	0.159	945.14	150.64
A_68_P21100057	chr2:29746300-29746344	NM_001177662:740	Odf2	INSIDE	0.268	0.593	962.80	571.25	0.159	767.46	122.15
A_68_P27638869	chr11:21896943-21896987	NM_011023:4690	Otx1	INSIDE	0.268	0.539	1447.03	779.37	0.144	1141.53	164.71
A_68_P26261064	chr8:129588848-129588893	NM_001122850:915	Pard3	INSIDE	0.268	0.728	3734.54	2719.01	0.195	2724.24	531.59
A_68_P21752417	chr2:152841063-152841107	NM_178939:35	Pdrg1	INSIDE	0.268	0.557	1741.01	969.95	0.149	1317.68	196.70
A_68_P32117863	chr19:41986389-41986433	NM_023418:50	Pgam1	INSIDE	0.268	0.485	2687.15	1302.79	0.130	2042.45	265.75
A_68_P20722065	chr1:154472108-154472163	NM_016846:106	Rgl1	INSIDE	0.268	0.398	1496.32	596.14	0.107	1195.18	127.54
A_68_P30572559	chr16:17210640-17210686	NM_001033338:2435	Rimbp3	INSIDE	0.268	0.627	1739.47	1091.01	0.168	1341.45	225.66
A_68_P24763849	chr6:114081414-114081459	NM_172890:202	Slc6a11	INSIDE	0.268	0.444	2197.67	974.80	0.119	1641.03	195.42
A_68_P27844725	chr11:60591042-60591086	NM_175491:38	Smcr8	INSIDE	0.268	0.531	1262.52	670.68	0.143	1045.08	148.93
A_68_P29937474	chr14:118634627-118634671	NM_177753:1604	Sox21	INSIDE	0.268	0.593	905.42	536.49	0.159	755.00	119.69
A_68_P30381700	chr15:81977560-81977604	NM_033218:-116	Srebf2	PROMOTER	0.268	0.552	1464.31	808.90	0.148	1024.78	151.75
A_68_P24760939	chr6:113646833-113646877	NM_001033463:-638	Tatdn2	PROMOTER	0.268	0.607	1884.49	1144.62	0.163	1714.85	278.69
A_68_P26239532	chr8:125898381-125898425	NM_001037877:668	Tcf25	INSIDE	0.268	2.679	2303.14	6169.57	0.719	1727.72	1241.70
A_68_P24593530	chr6:83391357-83391401	NM_183138:294	Tet3	INSIDE	0.268	0.553	2332.34	1290.74	0.148	1475.98	218.98
A_68_P27752129	chr11:43561327-43561371	NM_133795:127	Ttc1	INSIDE	0.268	0.579	1558.11	901.90	0.155	1154.64	179.09
A_68_P28712490	chr12:107248322-107248369	NM_001029843:-127	Vrk1	PROMOTER	0.268	0.492	1236.22	608.73	0.132	913.09	120.62
A_68_P21085075	chr2:27370596-27370640	NM_080848:-48	Wdr5	PROMOTER	0.268	0.704	5083.37	3577.92	0.189	3778.18	712.26
A_68_P22887518	chr4:46209177-46209222	NM_011728:-16	Xpa	PROMOTER	0.268	0.601	882.51	530.59	0.161	745.71	120.32
A_68_P24376841	chr6:38304658-38304702	NM_028421:-77	Zc3hav1	PROMOTER	0.268	0.419	1499.53	628.88	0.112	1192.29	134.02
A_68_P30506931	chr16:3872466-3872510	NM_001033159:-114	Zfp597	PROMOTER	0.268	0.594	2790.27	1656.08	0.159	2087.26	331.93
A_68_P27781838	chr11:49016880-49016924	NM_001024846:-99	Zfp62	PROMOTER	0.268	0.682	4759.34	3244.03	0.182	3846.82	701.43
A_68_P26822981	chr9:110207579-110207626	NM_001081381:-93	2610002I17Rik	PROMOTER	0.267	0.433	1295.83	560.67	0.116	1015.06	117.37
A_68_P26039918	chr8:90796247-90796291	NM_007406:-33	Adcy7	PROMOTER	0.267	0.574	965.93	554.35	0.153	780.81	119.53
A_68_P28175453	chr11:118902817-118902861	NM_013926:-611	Cbx8	PROMOTER	0.267	0.668	5932.39	3962.21	0.178	4121.47	734.38
A_68_P23601183	chr5:35868307-35868351	NM_153107:-53	Cpz	PROMOTER	0.267	0.577	2645.43	1527.42	0.154	1994.43	307.66
A_68_P31758331	chr18:61715432-61715480	NM_146087:221	Csnk1a1	INSIDE	0.267	0.536	1117.18	599.06	0.143	843.72	120.88
A_68_P22941963	chr4:56877865-56877909	NM_018761:197	Ctnnal1	INSIDE	0.267	0.673	3539.80	2381.13	0.180	2605.56	468.37
A_68_P21360374	chr2:77783936-77783980	NM_030560:452	Cwc22	INSIDE	0.267	0.466	2112.35	983.94	0.125	1760.28	219.18
A_68_P28100235	chr11:106078135-106078182	NM_028074:-81	Ddx42	DIVERGENT_PROMOTER	0.267	0.488	1267.69	618.10	0.130	900.17	117.27
A_68_P23226777	chr4:115609072-115609120	NM_001025567:3435	Dmbx1	INSIDE	0.267	0.588	1195.49	702.94	0.157	928.86	145.93
A_68_P27826023	chr11:57331958-57332002	NM_001168667:166	Fam114a2	INSIDE	0.267	0.523	3648.60	1906.86	0.140	2548.04	355.69
A_68_P27357059	chr10:93498957-93499001	NM_053072:233	Fgd6	INSIDE	0.267	0.491	1250.55	613.55	0.131	900.05	117.91
A_68_P21283785	chr2:64860691-64860735	NM_016719:111	Grb14	INSIDE	0.267	0.583	1408.09	820.40	0.156	1085.28	168.77
A_68_P23592734	chr5:34511815-34511865	NM_146159:233	Haus3	INSIDE	0.267	0.517	1113.92	576.21	0.138	872.87	120.52
A_68_P23231911	chr4:116668335-116668379	NM_175244:404	Hectd3	INSIDE	0.267	0.459	1858.83	853.81	0.123	1602.86	196.92
A_68_P27495358	chr10:119549908-119549958	NM_080446:89	Helb	INSIDE	0.267	0.615	969.27	596.28	0.164	731.87	120.14
A_68_P29613103	chr14:55196489-55196533	NM_010590:-12	Jub	PROMOTER	0.267	0.694	1422.73	986.66	0.185	1056.41	195.74
A_68_P31158189	chr17:35332625-35332669	NM_008518:1195	Ltb	INSIDE	0.267	0.396	1615.19	639.59	0.106	1192.92	126.15
A_68_P20551221	chr1:120218602-120218646	NM_026472:205	Mki67ip	INSIDE	0.267	0.557	987.20	550.06	0.149	789.50	117.28
A_68_P25948618	chr8:72426813-72426857	NM_023312:-377	Ndufa13	PROMOTER	0.267	0.444	2442.87	1083.58	0.118	1777.55	210.55
A_68_P23362017	chr4:140634100-140634144	NM_025383:138	Necap2	INSIDE	0.267	0.685	1299.10	890.49	0.183	962.95	176.55
A_68_P29288685	chr13:104899639-104899683	NM_029447:34	Nln	INSIDE	0.267	0.502	3750.88	1882.96	0.134	2717.95	364.88
A_68_P25377673	chr7:109358261-109358306	NM_022979:351	Nup98	INSIDE	0.267	0.374	1583.05	591.34	0.100	1224.31	121.96
A_68_P22484166	chr3:122432487-122432536	NM_153422:436	Pde5a	INSIDE	0.267	0.522	1141.46	595.92	0.140	846.25	118.12
A_68_P28941006	chr13:34967366-34967410	NM_013830:26	Prpf4b	INSIDE	0.267	0.446	1303.47	581.96	0.119	1031.54	123.01
A_68_P24980579	chr7:16858527-16858571	NM_001136270:493	Prr24	INSIDE	0.267	0.639	11345.83	7252.67	0.171	7850.37	1341.64
A_68_P20788006	chr1:166178784-166178828	NM_054087:-379	Slc19a2	PROMOTER	0.267	0.630	1163.80	733.02	0.168	891.55	150.13
A_68_P32240693	chrX:7461619-7461664	NM_001083937:272	Slc35a2	INSIDE	0.267	1.363	1457.12	1985.99	0.365	620.73	226.31
A_68_P21394884	chr2:84679887-84679931	NM_024497:-571	Slc43a1	PROMOTER	0.267	0.395	1482.17	585.71	0.105	1143.40	120.42

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P20024912	chr1:9934064-9934108	NR_004410:-1462	Snord87	PROMOTER	0.267	0.519	3610.77	1875.67	0.139	2681.81	371.53
A_68_P28555634	chr12:77811742-77811790	NM_013675:-232	Spnb1	PROMOTER	0.267	0.632	901.05	569.83	0.169	716.22	121.15
A_68_P30296506	chr15:67007655-67007699	NM_009177:768	St3gal1	INSIDE	0.267	0.461	1360.77	627.89	0.123	996.11	122.60
A_68_P32143397	chr19:46423267-46423311	NM_029186:-8081	Tmem180	PROMOTER	0.267	0.449	1558.92	699.81	0.120	1280.80	153.60
A_68_P27975818	chr11:83992769-83992817	ENSMUST00000136463:-520		PROMOTER	0.267	0.456	1222.65	557.05	0.121	963.12	117.01
A_68_P27851351	chr11:61770416-61770460	ENSMUST00000136971:127		INSIDE	0.267	0.548	950.77	520.75	0.146	830.11	121.23
A_68_P31465577	chr18:4921962-4922006	ENSMUST00000143254:261		INSIDE	0.267	0.674	1446.30	974.33	0.180	1089.49	196.12
A_68_P24325500	chr6:29222845-29222889	NM_023516:241	2310016C08Rik	INSIDE	0.266	0.519	1763.29	915.53	0.138	1391.52	191.86
A_68_P21418961	chr2:90623244-90623288	NM_178755:366	Agbl2	INSIDE	0.266	0.655	832.57	545.04	0.174	673.62	117.42
A_68_P27970639	chr11:83116144-83116188	NM_001035854:-32	Ap2b1	DIVERGENT_PROMOTER	0.266	0.337	1694.36	570.46	0.090	1348.12	120.78
A_68_P24050077	chr5:122841748-122841803	NM_019824:-161	Arpc3	PROMOTER	0.266	0.480	1637.78	786.52	0.128	1173.02	150.12
A_68_P22128529	chr3:51028612-51028656	NM_009834:266	Ccrn4l	INSIDE	0.266	0.692	4112.17	2845.24	0.184	3149.48	578.75
A_68_P29177663	chr13:81922129-81922187	NM_007684:-132	Cetn3	PROMOTER	0.266	0.526	1070.28	563.33	0.140	883.45	123.60
A_68_P26042572	chr8:91221405-91221449	NM_001128169:484	Cyld	INSIDE	0.266	0.527	1386.38	730.10	0.140	990.49	138.50
A_68_P21957442	chr3:14578468-14578519	NM_007892:-177	E2f5	PROMOTER	0.266	0.464	1625.94	754.46	0.123	1380.23	170.26
A_68_P28947128	chr13:36209814-36209858	NM_001039189:557	Fars2	INSIDE	0.266	0.634	945.14	599.59	0.169	815.97	137.83
A_68_P28067617	chr11:100217870-100217915	NM_010404:-437	Hap1	PROMOTER	0.266	0.581	1057.03	614.11	0.155	816.69	126.42
A_68_P30566358	chr16:15637618-15637664	NM_008565:-147	Mcm4	DIVERGENT_PROMOTER	0.266	0.442	1217.32	537.50	0.118	991.35	116.59
A_68_P26204801	chr8:120326174-120326218	NM_026758:-367	Mphosph6	PROMOTER	0.266	0.505	1151.05	581.37	0.135	911.11	122.60
A_68_P22278908	chr3:82162460-82162514	NM_001081230:493	Mtap9	INSIDE	0.266	0.442	1225.07	541.92	0.118	993.17	117.05
A_68_P20648914	chr1:138845211-138845255	NM_001159769:4975	Nr5a2	INSIDE	0.266	0.467	1245.99	581.75	0.124	956.08	118.87
A_68_P21839348	chr2:167905989-167906034	NM_021409:-492	Pard6b	PROMOTER	0.266	0.582	2128.01	1238.18	0.155	1636.37	253.01
A_68_P25957709	chr8:74120139-74120192	NM_025396:4083	Pgls	INSIDE	0.266	0.620	1070.78	664.12	0.165	861.19	142.27
A_68_P26079860	chr8:97381962-97382011	NM_009090:637	Polr2c	INSIDE	0.266	0.467	1201.30	560.87	0.124	927.62	115.20
A_68_P29568499	chr14:45609164-45609208	NM_008964:1401	Ptger2	INSIDE	0.266	0.518	1160.21	601.11	0.138	859.22	118.22
A_68_P26805684	chr9:106788066-106788110	NM_175402:1243	Rbm15b	INSIDE	0.266	0.639	849.13	542.77	0.170	678.03	115.28
A_68_P29982088	chr15:5066265-5066309	NM_026069:-326	Rpl37	DIVERGENT_PROMOTER	0.266	0.347	1734.07	602.29	0.092	1268.43	117.01
A_68_P30351093	chr15:76734840-76734884	NM_012053:362	Rpl8	INSIDE	0.266	0.623	1058.14	658.88	0.166	738.40	122.43
A_68_P20149048	chr1:36614178-36614222	NM_001126047:1026	Sema4c	INSIDE	0.266	0.466	1230.25	573.10	0.124	939.14	116.27
A_68_P26995733	chr10:21602269-21602313	NM_001161845:301	Sgk1	INSIDE	0.266	0.534	1247.06	666.50	0.142	1019.87	144.79
A_68_P21585949	chr2:122174591-122174635	NM_001013829:20042	Shf	DOWNSTREAM	0.266	0.532	1138.26	605.30	0.142	932.96	132.20
A_68_P23576445	chr5:31395426-31395470	NM_011773:452	Slc30a3	INSIDE	0.266	0.622	5256.90	3269.71	0.165	3941.63	652.25
A_68_P28466194	chr12:59314126-59314170	NM_009216:1358	Sstr1	INSIDE	0.266	0.523	1498.91	784.15	0.139	1114.45	155.35
A_68_P24922452	chr6:145289388-145289432			Unknown	0.266	0.684	1504.75	1028.72	0.182	1161.11	211.37
A_68_P23186776	chr4:106511986-106512035	ENSMUST00000151369:8515		DOWNSTREAM	0.266	0.539	1024.40	551.99	0.143	830.66	118.97
A_68_P24124950	chr5:137730313-137730357	NM_009599:830	Ache	INSIDE	0.265	0.678	2136.29	1447.55	0.179	1641.91	294.45
A_68_P21441211	chr2:94277500-94277544	NM_007466:782	Api5	INSIDE	0.265	0.417	1244.17	518.83	0.111	1103.43	121.96
A_68_P27900650	chr11:70245838-70245882	NM_145429:-294	Arrb2	PROMOTER	0.265	0.590	1112.28	656.73	0.156	1005.28	157.11
A_68_P27291405	chr10:81590620-81590664	NM_001163064:-115	AU041133	PROMOTER	0.265	0.641	887.31	568.78	0.170	709.54	120.48
A_68_P23295722	chr4:128916103-128916147	NM_001033189:9563	C77080	INSIDE	0.265	0.521	2413.50	1257.67	0.138	1941.47	268.53
A_68_P31140913	chr17:31773722-31773766	NM_178224:332	Cbs	INSIDE	0.265	0.493	1674.74	825.27	0.130	1345.15	175.42
A_68_P26236513	chr8:125394326-125394370	NM_007662:22075	Cdh15	DOWNSTREAM	0.265	1.798	1979.57	3559.51	0.477	1523.30	726.93
A_68_P27898423	chr11:69814128-69814172	NM_007888:23	Dvl2	INSIDE	0.265	0.528	2671.78	1409.79	0.140	1863.09	260.61
A_68_P25582341	chr7:147302455-147302502	NM_053119:-156	Echs1	DIVERGENT_PROMOTER	0.265	0.562	1003.74	563.95	0.149	816.93	121.63
A_68_P22729554	chr4:11314649-11314704	NM_194055:-746	Esrp1	PROMOTER	0.265	0.627	1378.65	864.11	0.166	1081.67	179.97
A_68_P31427927	chr17:88841025-88841069	NM_180974:995	Foxn2	INSIDE	0.265	0.520	3096.73	1609.43	0.138	2419.52	332.78
A_68_P22448216	chr3:115955553-115955597	NM_022427:828	Gpr88	INSIDE	0.265	0.697	1122.37	782.55	0.184	889.23	164.02
A_68_P25095368	chr7:53086086-53086130	NM_153419:51	Grwd1	INSIDE	0.265	0.603	866.65	522.86	0.160	750.00	119.92
A_68_P23596023	chr5:35104298-35104342	NM_010414:-68	Htt	PROMOTER	0.265	0.687	1410.34	968.64	0.182	1169.35	212.81
A_68_P25596366	chr7:149846243-149846296	NM_001122736:671	Igf2	INSIDE	0.265	0.565	1149.75	649.23	0.150	816.65	122.26
A_68_P32137135	chr19:45298271-45298326	NM_010691:11428	Lbx1	DOWNSTREAM	0.265	0.492	1426.47	701.76	0.130	962.12	125.49

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26227607	chr8:124109628-124109679	NM_026160:-4714	Map1lc3b	DIVERGENT_PROMOTER	0.265	0.620	943.16	584.78	0.164	724.21	118.92
A_68_P24623657	chr6:88674155-88674204	NM_001166249:-226	Mgll	PROMOTER	0.265	0.615	910.30	559.40	0.163	745.81	121.25
A_68_P27924623	chr11:74986635-74986679	NR_029794:-233	Mir212	DIVERGENT_PROMOTER	0.265	0.611	1122.06	685.33	0.162	738.36	119.43
A_68_P27922753	chr11:74651662-74651706	NM_010813:7259	Mnt	INSIDE	0.265	0.537	1150.75	617.92	0.142	851.75	121.25
A_68_P24009559	chr5:115886650-115886694	NM_008629:6979	Msi1	INSIDE	0.265	0.634	963.95	611.18	0.168	745.10	125.39
A_68_P24140929	chr5:140808002-140808046	NM_008637:149	Nudt1	INSIDE	0.265	1.402	1716.18	2405.38	0.371	1358.22	504.11
A_68_P22518619	chr3:128902745-128902789	NM_011098:-69	Pitx2	PROMOTER	0.265	0.629	896.46	563.85	0.167	737.64	122.95
A_68_P20412581	chr1:88421464-88421508	NM_008972:-1824	Ptma	PROMOTER	0.265	0.557	1663.73	927.10	0.148	1350.33	199.57
A_68_P28071212	chr11:100830764-100830808	NM_008986:1145	Ptrf	INSIDE	0.265	1.721	8144.08	14014.31	0.457	5451.22	2490.51
A_68_P27840876	chr11:59928639-59928683	NM_009021:10146	Rai1	INSIDE	0.265	0.523	2954.70	1544.03	0.138	2300.34	318.32
A_68_P30118694	chr15:32175744-32175788	NM_009154:1199	Sema5a	INSIDE	0.265	0.377	1639.40	618.15	0.100	1315.41	131.64
A_68_P24328153	chr6:29686461-29686505	NM_176996:986	Smo	INSIDE	0.265	0.565	1568.63	886.99	0.150	1095.05	163.87
A_68_P25840861	chr8:48373757-48373801	NM_001114311:978	Stox2	INSIDE	0.265	0.530	3849.13	2041.53	0.141	3167.91	445.20
A_68_P24521962	chr6:67485386-67485430	NM_020047:408	Tacstd2	INSIDE	0.265	0.563	1048.17	590.62	0.150	817.80	122.34
A_68_P29141046	chr13:73764254-73764302	NM_009354:-170	Tert	PROMOTER	0.265	1.714	4654.65	7976.14	0.454	2975.72	1350.69
A_68_P28170438	chr11:118151273-118151317	NM_001033528:264	Usp36	INSIDE	0.265	0.690	2983.32	2058.58	0.183	2067.49	377.70
A_68_P22963157	chr4:61869358-61869402	NM_009554:200	Zfp37	INSIDE	0.265	0.617	3214.07	1982.33	0.164	2353.55	384.85
A_68_P21426310	chr2:91900168-91900212	ENSMUST00000123840:-664		PROMOTER	0.265	0.430	2329.08	1002.63	0.114	1692.53	193.34
A_68_P27298723	chr10:83185538-83185582	NM_001145198:-49	1500009L16Rik	PROMOTER	0.264	0.633	3031.30	1917.79	0.167	2286.84	382.04
A_68_P20352243	chr1:75138899-75138957	NM_026977:14	1810031K17Rik	INSIDE	0.264	0.622	1005.25	625.04	0.164	715.96	117.57
A_68_P23601495	chr5:35917857-35917901	NM_030208:-159	2310079F23Rik	DIVERGENT_PROMOTER	0.264	0.467	1151.30	537.11	0.123	955.93	117.62
A_68_P21052780	chr2:20889683-20889727	NM_001081364:-356	Arhgap21	DIVERGENT_PROMOTER	0.264	0.377	1771.21	667.53	0.099	1252.59	124.43
A_68_P28788962	chr13:3610060-3610104	NM_134063:272	BC016423	INSIDE	0.264	0.552	1324.53	730.87	0.146	1111.58	161.92
A_68_P31100996	chr17:25150700-25150744	NM_020608:1453	Cramp1l	INSIDE	0.264	0.505	1505.33	760.87	0.133	1172.77	156.40
A_68_P26016155	chr8:86239004-86239050	NM_197982:-49	Ddx39	PROMOTER	0.264	0.436	1335.39	582.13	0.115	1047.94	120.51
A_68_P28075719	chr11:101646593-101646637	NM_008815:10	Etv4	INSIDE	0.264	0.387	1398.33	541.09	0.102	1162.02	118.63
A_68_P32023816	chr19:24551478-24551522	NM_026520:464	Fam122a	INSIDE	0.264	0.556	1049.22	583.33	0.147	820.35	120.62
A_68_P27800935	chr11:52578820-52578864	NM_177059:635	Fstl4	INSIDE	0.264	0.604	2257.04	1363.23	0.159	1817.90	289.88
A_68_P26200994	chr8:119681587-119681631	NM_001081151:-426	Gan	PROMOTER	0.264	0.514	1034.07	531.36	0.136	861.90	117.07
A_68_P29248565	chr13:97695108-97695152	NM_001166065:487	Gcnt4	INSIDE	0.264	0.497	2107.56	1047.39	0.131	1876.41	246.08
A_68_P31150611	chr17:33955093-33955137	NM_030697:7647	Kank3	INSIDE	0.264	0.566	1159.37	656.27	0.149	953.33	142.35
A_68_P30366911	chr15:79342352-79342396	NM_134090:-4463	Kdelr3	DIVERGENT_PROMOTER	0.264	0.657	3541.10	2327.67	0.173	2854.17	494.60
A_68_P27534886	chr10:126699975-126700019	NM_001039000:423	Kif5a	INSIDE	0.264	0.532	1181.40	628.45	0.140	850.79	119.49
A_68_P22934424	chr4:55544128-55544172	NM_010637:1197	Klf4	INSIDE	0.264	0.534	1468.63	784.65	0.141	1321.60	186.61
A_68_P20739604	chr1:157588731-157588781	NM_010712:401	Lhx4	INSIDE	0.264	0.577	1144.34	660.76	0.152	772.62	117.78
A_68_P24655997	chr6:94232874-94232918	NM_001029850:1002	Magi1	INSIDE	0.264	0.504	1466.14	739.50	0.133	1225.95	163.36
A_68_P22218630	chr3:68809433-68809477	NR_029529:-4239	Mir15b	PROMOTER	0.264	0.567	1025.55	580.98	0.150	802.95	120.16
A_68_P26716011	chr9:90009342-90009386	NM_001039147:294	Morf4l1	INSIDE	0.264	1.700	6468.15	10998.33	0.448	4107.86	1841.19
A_68_P29139136	chr13:73466105-73466159	NM_010888:-202	Ndufs6	DIVERGENT_PROMOTER	0.264	0.636	1318.25	838.33	0.168	1001.16	168.12
A_68_P24981708	chr7:17061429-17061473	NM_008718:679	Npas1	INSIDE	0.264	0.541	1054.92	570.50	0.143	813.15	116.19
A_68_P28600138	chr12:86114028-86114072	NM_023409:12	Npc2	INSIDE	0.264	0.361	2097.68	758.08	0.096	1556.27	148.71
A_68_P24192245	chr5:151476526-151476570	NM_175310:147	Pds5b	INSIDE	0.264	0.473	2267.39	1073.05	0.125	1818.86	227.40
A_68_P27900566	chr11:70223756-70223800	NM_029231:-245	Pelp1	PROMOTER	0.264	0.691	2541.05	1756.22	0.183	1812.48	330.89
A_68_P22778417	chr4:22404692-22404736	NM_008899:10564	Pou3f2	DOWNSTREAM	0.264	0.510	1777.13	906.10	0.135	1488.14	200.52
A_68_P32322125	chrX:34731608-34731653	NM_153503:293	Rnf113a1	INSIDE	0.264	1.436	1448.26	2079.46	0.379	565.57	214.43
A_68_P21747623	chr2:151921158-151921202	NM_001160410:13916	Scrt2	INSIDE	0.264	1.355	2032.50	2753.88	0.358	1383.66	495.61
A_68_P20005842	chr1:4487520-4487564	NM_011441:-1048	Sox17	PROMOTER	0.264	0.628	2618.18	1643.63	0.166	1927.02	319.87
A_68_P28615265	chr12:88640437-88640481	NM_011479:88722	Sptlc2	DOWNSTREAM	0.264	0.635	3336.21	2118.25	0.167	2605.01	436.06
A_68_P31415000	chr17:86544304-86544360	NM_030133:183	Srbd1	INSIDE	0.264	0.612	954.25	583.60	0.162	748.11	120.92
A_68_P31209391	chr17:47027623-47027667	NM_178385:75	Tbcc	INSIDE	0.264	0.514	1767.64	909.38	0.136	1393.69	189.26
A_68_P27044452	chr10:31165585-31165629	NM_009413:121	Tpd52l1	INSIDE	0.264	0.445	1375.58	611.90	0.118	1068.33	125.54

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25210208	chr7:77426309-77426353	AK148659:-1685		PROMOTER	0.264	0.564	1140.19	643.21	0.149	782.16	116.64
A_68_P21071706	chr2:25227652-25227698	NM_001081085:-166	2010317E24Rik	DIVERGENT_PROMOTER	0.263	0.408	1396.16	569.53	0.107	1148.30	123.05
A_68_P32226224	chr19:60656314-60656358	NM_001172096:590	2700078E11Rik	INSIDE	0.263	0.528	2263.29	1194.88	0.139	1593.13	220.91
A_68_P22900662	chr4:48552839-48552883	NM_001145924:-92	5730528L13Rik	PROMOTER	0.263	0.679	2390.51	1622.23	0.178	1855.54	330.55
A_68_P25956918	chr8:73987077-73987121	NM_022419:458	Abhd8	INSIDE	0.263	0.510	1074.65	548.49	0.134	913.13	122.63
A_68_P30512950	chr16:4964504-4964548	NM_028301:-196	Anks3	PROMOTER	0.263	0.484	3576.27	1730.55	0.127	2482.98	316.07
A_68_P30281417	chr15:64214477-64214523	NM_010026:-19	Asap1	PROMOTER	0.263	0.537	1075.83	577.34	0.141	854.13	120.74
A_68_P31485630	chr18:9450058-9450102	NM_026484:68	Ccny	INSIDE	0.263	0.645	1115.46	719.09	0.170	965.71	163.73
A_68_P22318571	chr3:89125906-89125950	NM_010108:873	Efna3	INSIDE	0.263	1.756	11254.09	19767.21	0.461	6990.29	3223.29
A_68_P23446277	chr5:3647175-3647234	NM_026033:732	Gatad1	INSIDE	0.263	0.480	1156.23	555.11	0.126	942.21	118.86
A_68_P32213510	chr19:58529067-58529111	NM_010279:-132	Gfra1	PROMOTER	0.263	0.492	1248.19	614.02	0.129	922.96	119.40
A_68_P26814363	chr9:108241800-108241844	NM_008160:412	Gpx1	INSIDE	0.263	0.526	1512.56	794.87	0.138	1164.10	160.62
A_68_P23807226	chr5:75471874-75471918	NM_133256:271	Gsx2	INSIDE	0.263	0.572	2189.19	1251.64	0.150	1679.14	252.11
A_68_P28269099	chr12:17183377-17183426	NM_201531:293	Kcnf1	INSIDE	0.263	0.449	1423.46	639.55	0.118	1023.25	121.10
A_68_P28069993	chr11:100620866-100620910	NM_001081194:204	Kcnh4	INSIDE	0.263	0.627	1564.29	980.36	0.165	1237.72	203.74
A_68_P27890038	chr11:68369674-68369718	NM_146004:9	Mfsd6l	INSIDE	0.263	0.598	1064.35	636.58	0.157	937.70	147.62
A_68_P22758679	chr4:17780394-17780442	NM_019724:-210	Mmp16	PROMOTER	0.263	1.556	704.55	1096.48	0.410	614.72	251.83
A_68_P29689076	chr14:68702020-68702064	NM_010910:102	Nefl	INSIDE	0.263	0.609	1345.69	819.39	0.160	980.66	156.81
A_68_P26282996	chr9:6168807-6168852	NM_027924:218	Pdgfd	INSIDE	0.263	0.506	1127.69	570.19	0.133	862.98	114.97
A_68_P24984097	chr7:17530264-17530308	NM_001099636:256	Pnmal2	INSIDE	0.263	0.483	1145.78	552.86	0.127	970.38	123.37
A_68_P23269520	chr4:124335988-124336032	NM_011141:1122	Pou3f1	INSIDE	0.263	0.410	1436.85	589.49	0.108	1120.14	120.65
A_68_P26260675	chr8:129494647-129494691	NM_172762:311	Rbm34	INSIDE	0.263	0.642	889.38	570.92	0.169	708.92	119.68
A_68_P31003198	chr17:3115122-3115166	NM_134123:173	Scaf8	INSIDE	0.263	0.617	1848.61	1141.12	0.162	1633.59	264.93
A_68_P27284239	chr10:80065786-80065830	NM_019575:182	Scamp4	INSIDE	0.263	0.374	1973.96	738.89	0.098	1545.77	152.22
A_68_P25957539	chr8:74093493-74093537	NM_011977:689	Slc27a1	INSIDE	0.263	0.656	965.00	633.10	0.173	689.33	118.92
A_68_P20464815	chr1:97564271-97564315	NM_009183:-121	St8sia4	PROMOTER	0.263	0.602	3080.86	1854.12	0.158	2195.52	347.78
A_68_P31150992	chr17:34056973-34057020	NM_001025313:574	Tapbp	INSIDE	0.263	0.458	1400.82	641.17	0.120	1005.80	120.94
A_68_P24053751	chr5:123526467-123526511	NM_001039723:205	Tmem120b	INSIDE	0.263	0.472	1791.91	846.46	0.124	1346.43	167.23
A_68_P24136194	chr5:140024878-140024927	NM_013702:5051	Uncx	DOWNSTREAM	0.263	0.366	1679.94	615.64	0.096	1316.56	126.70
A_68_P31879118	chr18:83079545-83079600	NM_183033:-698	Zfp516	PROMOTER	0.263	0.436	1472.32	642.13	0.115	1117.63	128.16
A_68_P24954290	chr7:6106969-6107013	NM_001013012:583	Zfp787	INSIDE	0.263	0.636	2127.44	1353.98	0.167	1612.30	269.57
A_68_P24039804	chr5:121062475-121062523	NM_029096:100	1110008J03Rik	INSIDE	0.262	0.569	1261.98	717.52	0.149	882.62	131.63
A_68_P25327110	chr7:100022539-100022587	NM_001080995:180	4632434I11Rik	INSIDE	0.262	0.488	1052.76	513.29	0.128	925.58	118.30
A_68_P22407412	chr3:107399505-107399559	NM_007441:1584	Alx3	INSIDE	0.262	0.590	1020.05	601.42	0.155	781.24	120.71
A_68_P26237608	chr8:125566474-125566518	NM_001081379:-312	Ankrd11	PROMOTER	0.262	0.647	2276.19	1472.92	0.170	1672.48	283.70
A_68_P20936658	chr1:193006394-193006440	NM_007498:796	Atf3	INSIDE	0.262	0.363	1570.51	570.60	0.095	1266.87	120.50
A_68_P27186920	chr10:62064870-62064914	NM_019553:154	Ddx21	INSIDE	0.262	0.630	1524.72	961.32	0.165	1259.10	207.79
A_68_P32030687	chr19:25680849-25680893	NM_177360:-4156	Dmrt3	PROMOTER	0.262	0.496	1556.60	772.47	0.130	1183.93	154.18
A_68_P30356910	chr15:77801656-77801700	NM_018749:-424	Eif3d	PROMOTER	0.262	0.709	1621.73	1149.04	0.186	1294.92	240.82
A_68_P29249242	chr13:97842053-97842097	NM_001100458:477	Fam169a	INSIDE	0.262	1.449	7529.40	10913.83	0.380	4994.78	1897.35
A_68_P26612681	chr9:69608333-69608380	NM_022378:391	Foxb1	INSIDE	0.262	0.575	1502.34	863.18	0.151	1310.12	197.56
A_68_P24449231	chr6:52176139-52176188	NM_010456:1206	Hoxa9	INSIDE	0.262	0.458	1245.49	570.57	0.120	974.02	116.97
A_68_P23237284	chr4:117587755-117587799	NM_146152:-172	Ipo13	PROMOTER	0.262	0.488	2105.90	1028.05	0.128	1536.08	196.84
A_68_P24759516	chr6:113392769-113392813	NM_026365:228	Jagn1	INSIDE	0.262	0.447	1223.78	546.49	0.117	1001.61	117.06
A_68_P24828015	chr6:126594566-126594610	NM_010595:1231	Kcna1	INSIDE	0.262	0.549	1578.22	866.29	0.144	1290.65	185.56
A_68_P20256314	chr1:58026706-58026750	NR_027630:-360	Kctd18	PROMOTER	0.262	0.497	1256.59	623.96	0.130	934.48	121.78
A_68_P24156414	chr5:144165340-144165384	NM_025841:-136	Kdelr2	PROMOTER	0.262	0.411	1449.80	595.41	0.108	1136.90	122.23
A_68_P26580975	chr9:64101634-64101678	NM_008927:-244	Map2k1	PROMOTER	0.262	0.690	1916.99	1322.23	0.181	1631.38	295.05
A_68_P32071016	chr19:32670611-32670655	NM_001201470:428	Papss2	INSIDE	0.262	0.565	905.97	511.93	0.148	817.77	121.14
A_68_P31701194	chr18:51277202-51277246	NM_001081224:-327	Prr16	PROMOTER	0.262	0.422	2592.04	1093.66	0.111	1981.48	219.32
A_68_P23062643	chr4:83131639-83131686	NM_133948:632	Psip1	INSIDE	0.262	0.465	1213.13	564.02	0.122	1010.70	123.17

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P24170393	chr5:147657202-147657261	NM_026864:585	Rasl11a	INSIDE	0.262	0.628	862.86	542.00	0.165	744.37	122.61
A_68_P25265202	chr7:87331967-87332011	NM_013659:262	Sema4b	INSIDE	0.262	0.668	1106.61	739.41	0.175	963.33	168.38
A_68_P32775571	chrX:156065929-156065973	NM_001135727:611	Sh3kbp1	INSIDE	0.262	2.135	1953.68	4170.95	0.559	864.18	482.74
A_68_P27569489	chr11:6525837-6525881	NR_034042:-5436	Snora5c	PROMOTER	0.262	0.498	3956.12	1972.10	0.131	2837.34	371.25
A_68_P29070327	chr13:58009211-58009255	NM_001166464:461	Spock1	INSIDE	0.262	0.611	949.70	580.03	0.160	775.08	124.21
A_68_P24125091	chr5:137748534-137748578	NM_001109909:346	Srrt	INSIDE	0.262	0.429	3285.78	1408.74	0.112	2266.19	254.16
A_68_P23616976	chr5:38430129-38430184	NM_026959:-317	Stx18	PROMOTER	0.262	0.520	1055.52	548.62	0.136	867.02	117.95
A_68_P30580630	chr16:18590465-18590509	NM_011532:-3424	Tbx1	PROMOTER	0.262	0.636	1959.90	1246.80	0.167	1509.33	251.50
A_68_P31468071	chr18:5334781-5334825	NM_178722:-365	Zfp438	PROMOTER	0.262	1.714	6621.53	11347.19	0.449	4557.49	2044.96
A_68_P31465564	chr18:4920657-4920701	ENSMUST00000138258:-24		PROMOTER	0.262	0.439	1286.82	564.99	0.115	1055.73	121.55
A_68_P23611135	chr5:37419493-37419537	ENSMUST00000165557:13371		DOWNSTREAM	0.262	0.463	2112.57	978.45	0.121	1495.76	181.64
A_68_P24908455	chr6:143048545-143048589	NM_001109688:61	5730419I09Rik	INSIDE	0.261	1.471	3034.78	4463.86	0.384	2078.50	798.52
A_68_P27404961	chr10:102491000-102491044	NM_172553:389	Alx1	INSIDE	0.261	0.510	1147.41	585.22	0.133	905.64	120.72
A_68_P23541721	chr5:23929534-23929578	NM_007668:-208	Cdk5	DIVERGENT_PROMOTER	0.261	0.398	1823.91	725.47	0.104	1213.29	125.79
A_68_P31678447	chr18:46887518-46887562	NM_033037:456	Cdo1	INSIDE	0.261	0.746	5411.06	4034.95	0.194	3873.70	753.00
A_68_P29098531	chr13:64471536-64471580	NM_009984:56	Ctsl	INSIDE	0.261	0.546	1591.37	869.53	0.142	1296.56	184.68
A_68_P31951638	chr19:10679902-10679946	NM_015735:-190	Ddb1	DIVERGENT_PROMOTER	0.261	0.460	2234.92	1027.13	0.120	1698.49	204.09
A_68_P21078047	chr2:26207480-26207524	NM_001139503:128	Dnlz	INSIDE	0.261	0.427	1395.73	596.10	0.111	1101.89	122.80
A_68_P22729160	chr4:11248943-11248991	NM_001081201:312	Dpy19l4	INSIDE	0.261	0.567	916.14	519.86	0.148	782.07	115.62
A_68_P28067422	chr11:100181743-100181787	NM_011508:455	Eif1	INSIDE	0.261	0.526	1833.83	964.85	0.137	1286.42	176.57
A_68_P23416731	chr4:151506130-151506174	NM_019585:-3118	Espn	PROMOTER	0.261	0.742	3064.47	2273.83	0.193	2069.66	400.14
A_68_P29726036	chr14:75530896-75530940	NM_027581:-228	Lrrc63	DIVERGENT_PROMOTER	0.261	0.612	1030.64	630.82	0.160	946.64	151.42
A_68_P28457455	chr12:57637056-57637100	NM_001146198:-985	Nkx2-1	PROMOTER	0.261	0.679	2448.65	1661.89	0.177	1953.15	346.47
A_68_P25934101	chr8:69212003-69212047	NM_016708:-31	Npy5r	DIVERGENT_PROMOTER	0.261	0.691	2268.25	1566.88	0.180	1775.21	319.68
A_68_P25256093	chr7:85723547-85723591	NM_008746:-844	Ntrk3	PROMOTER	0.261	0.650	1106.75	719.75	0.169	839.19	142.23
A_68_P25089408	chr7:52071427-52071471	NM_001171024:-291	Nup62-il4i1	DIVERGENT_PROMOTER	0.261	0.708	1442.12	1021.06	0.185	1029.63	190.19
A_68_P26742492	chr9:95459743-95459787	NM_198414:-471	Paqr9	PROMOTER	0.261	0.585	2114.75	1237.23	0.152	1786.35	272.26
A_68_P24808210	chr6:122289199-122289250	NM_001042623:-2191	Phc1	PROMOTER	0.261	0.615	853.00	524.41	0.161	758.78	121.84
A_68_P31093271	chr17:23863763-23863807	NM_023058:482	Pkmyt1	INSIDE	0.261	0.619	3258.03	2016.07	0.161	2439.27	393.82
A_68_P21019038	chr2:13976735-13976779	NM_001012396:906	Ptpla	INSIDE	0.261	0.441	1408.43	620.68	0.115	1048.47	120.55
A_68_P26811065	chr9:107673263-107673307	NM_148930:49	Rbm5	INSIDE	0.261	0.581	3298.25	1915.74	0.151	2540.08	384.63
A_68_P29152215	chr13:76080947-76080991	NM_028493:304	Rhobtb3	INSIDE	0.261	0.649	1542.39	1000.33	0.169	1357.99	229.92
A_68_P23523573	chr5:20457890-20457941	NM_001080977:-275	Rsbn1l	PROMOTER	0.261	0.601	951.08	571.17	0.157	736.57	115.32
A_68_P24464120	chr6:54516036-54516080	NM_027268:318	Scrn1	INSIDE	0.261	0.611	2879.70	1758.99	0.159	2081.78	331.40
A_68_P25961696	chr8:75015878-75015926	NM_177766:611	Slc35e1	INSIDE	0.261	0.406	1478.90	600.55	0.106	1216.53	128.73
A_68_P24773075	chr6:115758321-115758365	NR_028546:-221	Snora7a	PROMOTER	0.261	0.422	1285.48	542.41	0.110	1070.96	117.83
A_68_P30721030	chr16:44347912-44347958	NM_144550:421	Spice1	INSIDE	0.261	1.462	1597.91	2336.91	0.381	1233.66	470.42
A_68_P21101537	chr2:29989486-29989530	NM_146252:118	Tbc1d13	INSIDE	0.261	0.307	1950.56	598.97	0.080	1516.43	121.56
A_68_P24033990	chr5:120120273-120120317	NM_011535:-383	Tbx3	PROMOTER	0.261	0.394	1541.12	606.70	0.103	1242.43	127.87
A_68_P28261129	chr12:15821863-15821907	NM_144551:1707	Trib2	INSIDE	0.261	0.514	2868.64	1474.94	0.134	2134.33	286.42
A_68_P22485523	chr3:122686980-122687024	NM_133857:363	Usp53	INSIDE	0.261	0.520	1295.91	673.84	0.135	1054.22	142.82
A_68_P26467229	chr9:44169555-44169599	NM_027889:177	Vps11	INSIDE	0.261	0.687	2489.70	1710.48	0.180	1802.70	323.81
A_68_P25018706	chr7:28516596-28516644	NM_009560:193	Zfp60	INSIDE	0.261	0.635	947.15	601.13	0.166	751.37	124.48
A_68_P25735800	chr8:28087824-28087868	NM_001101502:39	Zfp703	INSIDE	0.261	0.608	2335.99	1420.43	0.159	1711.28	271.44
A_68_P23282963	chr4:126645533-126645577	NM_001114399:-387	Zmym4	PROMOTER	0.261	0.562	972.88	547.04	0.147	814.24	119.47
A_68_P31456431	chr17:95149568-95149616	NR_024720:153	2700099C18Rik	INSIDE	0.260	0.642	1050.61	674.32	0.167	722.30	120.75
A_68_P23545745	chr5:24606880-24606928	NR_027851:112	2900005J15Rik	INSIDE	0.260	0.644	954.35	614.72	0.167	713.29	119.41
A_68_P24865611	chr6:135148370-135148414	NM_028982:388	8430419L09Rik	INSIDE	0.260	0.604	1708.37	1032.67	0.157	1212.46	190.53
A_68_P26569951	chr9:62189186-62189230	NM_009672:59	Anp32a	INSIDE	0.260	0.687	1240.19	851.51	0.178	844.25	150.60
A_68_P27900654	chr11:70246223-70246267	NM_145429:90	Arrb2	INSIDE	0.260	0.482	1798.49	867.27	0.125	1423.92	178.46
A_68_P21072314	chr2:25316726-25316774	NM_153557:-136	BC029214	PROMOTER	0.260	0.557	1151.09	640.91	0.145	816.77	118.22

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P29530310	chr14:35316304-35316358	NM_009758:-598	Bmpr1a	PROMOTER	0.260	0.483	1204.06	581.45	0.126	927.24	116.61
A_68_P23094814	chr4:88941150-88941194	NM_009877:-649	Cdkn2a	PROMOTER	0.260	0.605	1710.14	1034.46	0.157	1371.20	215.88
A_68_P26846411	chr9:114690663-114690707	NM_133978:263	Cmtm7	INSIDE	0.260	0.610	3026.72	1847.42	0.159	2275.93	361.86
A_68_P23543724	chr5:24256980-24257024	NM_153076:6659	Crygn	INSIDE	0.260	0.620	921.89	571.35	0.161	754.76	121.85
A_68_P21421465	chr2:91076866-91076910	NM_028119:335	Ddb2	INSIDE	0.260	0.573	1487.24	852.56	0.149	1141.67	170.00
A_68_P29787828	chr14:87540919-87540963	NM_019670:-19	Diap3	PROMOTER	0.260	0.445	1272.45	566.38	0.116	1054.15	122.07
A_68_P20352840	chr1:75233023-75233067	NM_001159885:-232	Dnajb2	PROMOTER	0.260	0.555	1122.62	623.32	0.145	806.66	116.66
A_68_P21746892	chr2:151796494-151796538	NM_028666:3194	Fam110a	INSIDE	0.260	1.403	954.40	1339.09	0.364	679.62	247.63
A_68_P31947674	chr19:10056973-10057017	NM_010239:-198	Fth1	PROMOTER	0.260	0.530	1611.95	854.66	0.138	1292.12	178.30
A_68_P23977821	chr5:110536870-110536914	NM_145147:324	Gtpbp6	INSIDE	0.260	0.481	1316.34	632.71	0.125	935.37	116.70
A_68_P24444427	chr6:51419364-51419408	NM_016806:507	Hnrnpa2b1	INSIDE	0.260	0.495	7818.60	3872.52	0.129	5293.75	682.31
A_68_P20391713	chr1:82287149-82287194	NM_010570:843	Irs1	INSIDE	0.260	0.563	1174.25	661.49	0.146	876.78	128.25
A_68_P30991545	chr16:96413628-96413672	NM_001001492:214	Lca5l	INSIDE	0.260	0.598	1019.46	609.31	0.155	960.75	149.18
A_68_P28099907	chr11:106022041-106022085	NM_172397:-606	Limd2	PROMOTER	0.260	0.509	1120.65	570.89	0.133	885.89	117.42
A_68_P29453032	chr14:22319904-22319948	NM_017479:920	Myst4	INSIDE	0.260	0.602	1831.59	1101.96	0.156	1439.74	225.28
A_68_P27539158	chr10:127473288-127473332	NM_001113199:909	Naca	INSIDE	0.260	0.610	881.38	537.32	0.159	729.80	115.75
A_68_P24444195	chr6:51382942-51382986	NM_010903:296	Nfe2l3	INSIDE	0.260	0.527	1729.63	911.74	0.137	1332.69	182.34
A_68_P31774685	chr18:64499703-64499747	NM_194268:-293	Onecut2	PROMOTER	0.260	0.642	2246.19	1442.58	0.167	1660.70	277.03
A_68_P27892526	chr11:68821691-68821735	NM_001159519:250	Pfas	INSIDE	0.260	0.679	1985.15	1347.58	0.177	1438.44	253.91
A_68_P22350678	chr3:96500622-96500667	NM_001165949:-354	Pias3	PROMOTER	0.260	0.490	1885.22	923.57	0.127	1452.62	185.08
A_68_P21351698	chr2:76513834-76513878	NM_031256:485	Plekha3	INSIDE	0.260	0.603	1034.89	623.53	0.157	927.69	145.59
A_68_P29032313	chr13:51504178-51504222	NM_010101:214	S1pr3	INSIDE	0.260	0.719	3156.51	2268.83	0.187	2171.75	406.64
A_68_P31929913	chr19:5654718-5654762	NM_001164480:8967	Sipa1	INSIDE	0.260	0.609	1556.45	947.97	0.159	948.49	150.47
A_68_P31138855	chr17:31433416-31433460	NM_153062:1011	Slc37a1	INSIDE	0.260	0.535	1291.17	690.63	0.139	864.92	120.08
A_68_P28615264	chr12:88640362-88640406	NM_011479:88796	Sptlc2	DOWNSTREAM	0.260	0.742	4012.53	2977.58	0.193	2737.51	527.21
A_68_P20936015	chr1:192886699-192886743	NM_001163421:91	Tatdn3	INSIDE	0.260	0.715	1415.22	1011.79	0.186	1138.24	211.49
A_68_P32258642	chrX:11385042-11385086			Unknown	0.260	1.610	4746.81	7643.78	0.419	1923.65	806.44
A_68_P21747253	chr2:151855262-151855306			Unknown	0.260	0.487	1772.34	862.49	0.127	1317.40	166.97
A_68_P25068310	chr7:46807771-46807818	AK053739:-71		DIVERGENT_PROMOTER	0.260	0.634	1141.45	723.54	0.165	812.99	133.89
A_68_P23268973	chr4:124252578-124252622	ENSMUST00000164308:6168		INSIDE	0.260	0.541	2450.67	1324.64	0.141	1967.24	276.47
A_68_P25594223	chr7:149557894-149557939	NM_177265:248	6330512M04Rik	INSIDE	0.259	0.597	1039.87	621.10	0.155	751.83	116.47
A_68_P31108555	chr17:26275483-26275527	NM_001159598:-126	Axin1	PROMOTER	0.259	0.549	2182.74	1197.45	0.142	1680.47	238.80
A_68_P31423374	chr17:87846116-87846160	NM_007589:137	Calm2	INSIDE	0.259	0.559	3168.11	1772.10	0.145	2303.86	333.19
A_68_P24467403	chr6:55067907-55067951	NM_009953:15038	Crhr2	INSIDE	0.259	0.413	1531.70	633.35	0.107	1247.41	133.69
A_68_P28248079	chr12:13255873-13255917	NM_134040:86	Ddx1	INSIDE	0.259	0.410	1363.21	558.60	0.106	1130.66	120.11
A_68_P29651216	chr14:62268043-62268087	NR_028264:33146	Dleu2	INSIDE	0.259	0.665	1283.83	854.01	0.172	1162.00	200.09
A_68_P26129637	chr8:107165970-107166027	NM_026753:-370	Fam96b	PROMOTER	0.259	0.606	935.90	567.32	0.157	739.15	115.93
A_68_P27094090	chr10:41997470-41997514	NM_019740:-944	Foxo3	PROMOTER	0.259	0.371	3378.20	1254.08	0.096	2531.14	243.64
A_68_P24589798	chr6:82723620-82723664	NM_013820:806	Hk2	INSIDE	0.259	0.608	1041.30	633.02	0.157	861.69	135.63
A_68_P30366913	chr15:79342515-79342567	NM_134090:-4297	Kdelr3	DIVERGENT_PROMOTER	0.259	0.605	1135.05	686.84	0.157	791.57	124.14
A_68_P32560534	chrX:97821357-97821401	NM_008446:-25	Kif4	DIVERGENT_PROMOTER	0.259	1.624	1122.58	1823.48	0.422	487.74	205.59
A_68_P22793479	chr4:26273870-26273915	NM_172865:-93	Manea	PROMOTER	0.259	0.636	2350.69	1495.72	0.165	1838.38	302.63
A_68_P28605828	chr12:87087327-87087371	NM_145447:-140	Mfsd7c	PROMOTER	0.259	0.650	1866.08	1212.86	0.168	1477.13	248.37
A_68_P20224246	chr1:51972071-51972115	NM_001161817:726	Myo1b	INSIDE	0.259	0.508	1107.72	562.21	0.132	985.99	129.71
A_68_P29309818	chr13:108948386-108948430	NM_001127346:411	Ndufaf2	INSIDE	0.259	0.540	2197.54	1186.04	0.140	1671.17	233.20
A_68_P25092989	chr7:52671296-52671340	NM_198190:2254	Ntf5	INSIDE	0.259	1.361	2359.88	3212.89	0.352	1741.58	612.93
A_68_P31098617	chr17:24769589-24769637	NM_008743:-14	Nthl1	DIVERGENT_PROMOTER	0.259	0.438	1343.19	587.77	0.113	1033.40	116.93
A_68_P26727063	chr9:92437135-92437179	NM_001142916:96	Plod2	INSIDE	0.259	0.406	1465.54	595.12	0.105	1253.35	131.64
A_68_P20184679	chr1:42755285-42755329	NM_008900:1316	Pou3f3	INSIDE	0.259	0.342	1670.37	572.10	0.089	1297.84	115.19
A_68_P28035915	chr11:94852120-94852164	NM_172261:-383	Ppp1r9b	PROMOTER	0.259	0.656	2162.62	1419.34	0.170	1618.29	275.48
A_68_P24618289	chr6:87762138-87762182	NM_001039394:-387	Rab43	PROMOTER	0.259	1.426	4902.32	6989.80	0.369	3081.41	1138.39

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P23312646	chr4:132065845-132065889	NM_144907:505	Sesn2	INSIDE	0.259	0.589	985.42	580.54	0.153	759.13	116.03
A_68_P31138852	chr17:31433001-31433045	NM_153062:595	Slc37a1	INSIDE	0.259	0.647	1554.79	1006.32	0.167	1278.81	214.11
A_68_P30478329	chr15:98956569-98956613	NM_139140:-685	Spats2	PROMOTER	0.259	0.401	2401.18	963.44	0.104	1683.67	175.17
A_68_P25102496	chr7:54263191-54263240	NM_175318:569	Spty2d1	INSIDE	0.259	0.641	1605.62	1028.44	0.166	1192.96	197.82
A_68_P20833435	chr1:174430368-174430412	NM_178598:14	Tagln2	INSIDE	0.259	0.561	1076.93	604.25	0.145	856.45	124.37
A_68_P27290580	chr10:81033862-81033910	NM_019725:-4390	Tle2	PROMOTER	0.259	0.485	1276.90	619.11	0.125	922.00	115.67
A_68_P27947945	chr11:79068066-79068110	NM_019653:109	Wsb1	INSIDE	0.259	0.695	1869.44	1298.95	0.180	1284.56	231.41
A_68_P27288030	chr10:80657437-80657487	NR_015477:27	2310050B05Rik	INSIDE	0.258	0.577	951.66	548.79	0.149	792.99	117.91
A_68_P28081367	chr11:102635750-102635794	NM_001110778:13020	Adam11	INSIDE	0.258	0.657	858.17	564.16	0.169	742.98	125.83
A_68_P29269562	chr13:101439843-101439887	NM_001168386:429	Ccdc125	INSIDE	0.258	0.498	1358.06	676.80	0.129	1221.28	157.21
A_68_P26814948	chr9:108354920-108354964	NM_133744:-7906	Ccdc71	PROMOTER	0.258	0.682	2070.73	1412.54	0.176	1567.50	275.79
A_68_P28743716	chr12:112615206-112615250	NM_183016:701	Cdc42bpb	INSIDE	0.258	0.476	3007.78	1430.22	0.123	2145.77	263.65
A_68_P20613814	chr1:133034401-133034445	NM_145508:389	Dyrk3	INSIDE	0.258	0.521	1882.84	980.99	0.135	1552.70	208.88
A_68_P25582340	chr7:147302368-147302412	NM_053119:-68	Echs1	DIVERGENT_PROMOTER	0.258	0.566	3901.65	2206.87	0.146	3156.08	459.78
A_68_P22348573	chr3:96081761-96081812	NM_010186:16106	Fcgr1	DOWNSTREAM	0.258	0.428	1339.42	573.08	0.110	1067.05	117.67
A_68_P26761419	chr9:98855194-98855238	NR_003248:513	Foxl2os	INSIDE	0.258	0.554	995.23	551.29	0.143	826.08	117.92
A_68_P23510640	chr5:17865451-17865500	NM_010305:756	Gnai1	INSIDE	0.258	0.524	1027.11	538.29	0.135	882.05	119.26
A_68_P30497015	chr15:102110224-102110272	NM_134100:362	Mfsd5	INSIDE	0.258	0.596	913.35	544.77	0.154	766.22	117.76
A_68_P31222784	chr17:49567933-49567977	NM_020042:266	Mocs1	INSIDE	0.258	0.623	1012.45	631.16	0.161	833.11	134.07
A_68_P24643637	chr6:92133635-92133679	NM_025578:361	Mrps25	INSIDE	0.258	0.471	1218.06	574.11	0.121	998.31	121.24
A_68_P21579979	chr2:121115051-121115098	NM_032393:-263	Mtap1a	PROMOTER	0.258	0.454	1406.73	638.29	0.117	1024.38	119.88
A_68_P24302042	chr6:24477224-24477272	NM_026614:439	Ndufa5	INSIDE	0.258	0.498	1296.76	646.39	0.129	1005.79	129.36
A_68_P30365773	chr15:79158644-79158688	NM_001199023:135	Pla2g6	INSIDE	0.258	0.677	4985.11	3376.22	0.175	3564.43	622.24
A_68_P21078344	chr2:26245012-26245056	NM_173180:167	Pmpca	INSIDE	0.258	0.683	3723.02	2544.40	0.176	2491.77	439.28
A_68_P31936610	chr19:6984035-6984079	NM_012021:79	Prdx5	INSIDE	0.258	0.530	1234.11	654.53	0.137	872.43	119.46
A_68_P25090472	chr7:52242228-52242277	NM_019830:-550	Prmt1	PROMOTER	0.258	0.440	1220.67	536.62	0.114	1032.71	117.24
A_68_P24834758	chr6:127717838-127717882	NM_201371:887	Prmt8	INSIDE	0.258	0.454	1249.15	567.32	0.117	1041.14	121.95
A_68_P31000877	chr16:97985236-97985280	NM_023663:104	Ripk4	INSIDE	0.258	0.585	1650.93	965.70	0.151	1308.98	197.71
A_68_P26344889	chr9:20780299-20780343	NM_010333:917	S1pr2	INSIDE	0.258	0.333	1678.98	558.95	0.086	1407.01	121.05
A_68_P26645323	chr9:75531947-75531992	NM_001164790:-106	Scg3	PROMOTER	0.258	0.342	1926.36	658.56	0.088	1402.14	123.81
A_68_P25961699	chr8:75016300-75016344	NM_177766:191	Slc35e1	INSIDE	0.258	0.351	1716.66	603.10	0.091	1381.07	125.22
A_68_P20456743	chr1:95532366-95532410	NM_021537:-84	Stk25	PROMOTER	0.258	0.638	1464.50	934.08	0.165	1204.52	198.39
A_68_P32241630	chrX:7651107-7651151	NM_011514:758	Suv39h1	INSIDE	0.258	1.452	3468.64	5035.74	0.375	1484.14	556.46
A_68_P30887980	chr16:77014501-77014545	NM_013918:209	Usp25	INSIDE	0.258	0.617	1777.23	1096.07	0.159	1478.42	235.57
A_68_P23971891	chr5:108863299-108863343	NM_007507:77	Atp5k	INSIDE	0.257	0.700	3174.55	2223.18	0.180	2375.54	427.66
A_68_P25729004	chr8:26895328-26895372	NM_026121:331	Bag4	INSIDE	0.257	0.726	2088.94	1516.27	0.187	1593.79	297.73
A_68_P23314122	chr4:132352279-132352323	NM_001033308:-21	BC013712	PROMOTER	0.257	0.524	1021.92	535.19	0.134	881.43	118.45
A_68_P22338542	chr3:94168357-94168405	NM_001136117:2015	C2cd4d	INSIDE	0.257	0.585	989.64	579.24	0.150	779.66	117.12
A_68_P30588539	chr16:20621997-20622043	NM_028420:-669	Camk2n2	DIVERGENT_PROMOTER	0.257	0.384	1628.91	626.14	0.099	1210.12	119.78
A_68_P26140465	chr8:109127899-109127943	NM_009864:653	Cdh1	INSIDE	0.257	0.666	1669.23	1111.30	0.171	1176.17	201.07
A_68_P27281378	chr10:79622976-79623020	NM_007705:-7587	Cirbp	PROMOTER	0.257	0.342	1867.22	638.63	0.088	1413.73	124.08
A_68_P29455223	chr14:22666866-22666910	NM_026965:1244	Comtd1	INSIDE	0.257	0.664	2081.90	1383.19	0.171	1466.44	250.26
A_68_P28089251	chr11:103994664-103994708	NM_007762:491	Crhr1	INSIDE	0.257	0.456	2043.80	932.74	0.118	1551.33	182.30
A_68_P31933638	chr19:6277193-6277237	NM_010119:319	Ehd1	INSIDE	0.257	0.361	4704.13	1698.35	0.093	3546.43	328.91
A_68_P20618864	chr1:133904839-133904887	NM_007923:681	Elk4	INSIDE	0.257	0.515	1770.28	911.89	0.132	1351.53	179.07
A_68_P31053798	chr17:12962714-12962758	NM_010515:-164	Igf2r	PROMOTER	0.257	0.470	1654.62	777.03	0.121	1331.45	160.65
A_68_P26546341	chr9:58046993-58047037	NM_001161535:2508	Islr2	INSIDE	0.257	0.594	930.73	552.98	0.153	796.38	121.54
A_68_P32028430	chr19:25311947-25311991	NM_181404:277	Kank1	INSIDE	0.257	0.619	864.99	535.12	0.159	721.55	114.79
A_68_P30477339	chr15:98748465-98748509	NM_029098:43	Lmbr1l	INSIDE	0.257	0.535	1280.29	684.76	0.138	1047.75	144.24
A_68_P28084320	chr11:103128905-103128949	NM_016896:-211	Map3k14	PROMOTER	0.257	0.471	1406.35	662.20	0.121	996.05	120.57
A_68_P29512326	chr14:32307928-32307972	NM_025907:213	Mettl6	INSIDE	0.257	0.637	3846.95	2451.42	0.164	2876.98	472.03

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27788128	chr11:50172669-50172713	NR_030529:-1309	Mir804	PROMOTER	0.257	0.575	1876.93	1079.45	0.148	1315.86	194.80
A_68_P27835021	chr11:58948977-58949031	NM_001171512:873	Obscn	INSIDE	0.257	0.532	1261.38	670.51	0.137	870.24	118.93
A_68_P20506813	chr1:108069803-108069847	NM_133821:1379	Phlpp1	INSIDE	0.257	0.405	1464.44	592.73	0.104	1114.65	115.93
A_68_P26554636	chr9:59505260-59505304	NM_011099:868	Pkm2	INSIDE	0.257	0.623	1228.93	765.27	0.160	997.34	159.31
A_68_P27994099	chr11:87217797-87217841	NM_053269:179	Rad51c	INSIDE	0.257	0.544	949.30	516.49	0.140	860.86	120.27
A_68_P29618701	chr14:56210506-56210552	NM_194346:-98	Rnf31	DIVERGENT_PROMOTER	0.257	0.490	1201.07	588.59	0.126	969.33	122.31
A_68_P24604448	chr6:85282737-85282781	NM_178639:658	Sfxn5	INSIDE	0.257	0.485	1204.68	584.81	0.125	958.93	119.47
A_68_P31836532	chr18:75527265-75527309	NM_001042660:268	Smad7	INSIDE	0.257	0.355	2708.69	960.49	0.091	2229.45	203.56
A_68_P22858653	chr4:40704800-40704844	NM_021535:96	Smu1	INSIDE	0.257	0.522	2101.67	1097.71	0.134	1600.01	215.05
A_68_P29605233	chr14:52816767-52816813	NM_033618:124	Supt16h	INSIDE	0.257	0.546	1965.22	1073.44	0.140	1373.23	192.89
A_68_P29418914	chr14:14793253-14793298	NM_025435:464	Thoc7	INSIDE	0.257	1.810	1746.58	3161.01	0.465	1344.66	625.92
A_68_P24994882	chr7:20300214-20300266	NM_001109748:538	Tomm40	INSIDE	0.257	0.597	1233.87	737.16	0.154	810.04	124.51
A_68_P23317939	chr4:133054412-133054456	NM_001081156:31	Trnp1	INSIDE	0.257	0.640	2171.98	1389.98	0.164	1634.57	268.81
A_68_P25798745	chr8:40068907-40068951	NM_030254:8	Tusc3	INSIDE	0.257	0.501	2686.88	1347.04	0.129	2025.98	261.31
A_68_P23141221	chr4:98590064-98590123	NM_146144:-407	Usp1	PROMOTER	0.257	0.460	1246.18	573.60	0.118	1016.12	120.01
A_68_P29616217	chr14:55710378-55710422	NM_001039198:485	Zfhx2	INSIDE	0.257	0.671	3657.23	2453.69	0.173	2586.56	446.60
A_68_P27835440	chr11:59015809-59015853	NR_037964:103	2610507I01Rik	INSIDE	0.256	0.488	1229.36	599.64	0.125	976.08	121.97
A_68_P26569970	chr9:62191389-62191433	NM_009672:2261	Anp32a	INSIDE	0.256	0.376	1923.03	723.35	0.096	1579.92	151.98
A_68_P31380046	chr17:80294471-80294516	NM_019717:875	Atl2	INSIDE	0.256	0.423	1900.27	804.48	0.108	1656.10	179.57
A_68_P22859202	chr4:40801217-40801261	NM_022305:-207	B4galt1	PROMOTER	0.256	0.655	5248.09	3439.66	0.168	3734.72	626.73
A_68_P31125923	chr17:29231167-29231211	NM_007669:472	Cdkn1a	INSIDE	0.256	0.468	1219.23	570.02	0.120	1002.53	119.97
A_68_P26543677	chr9:57612772-57612816	NM_007713:873	Clk3	INSIDE	0.256	0.710	2611.59	1853.39	0.182	2075.87	377.17
A_68_P24780081	chr6:117118598-117118642	NM_021704:68	Cxcl12	INSIDE	0.256	0.527	3385.70	1785.81	0.135	2469.10	333.23
A_68_P26659608	chr9:78291066-78291110	NM_173386:-134	E330016A19Rik	DIVERGENT_PROMOTER	0.256	0.648	1462.04	948.02	0.166	1212.77	201.24
A_68_P20802627	chr1:168930921-168930965	NM_001160261:-605	Fam78b	DIVERGENT_PROMOTER	0.256	0.491	1108.28	544.22	0.126	962.92	121.06
A_68_P31484553	chr18:9213708-9213752	NM_008058:877	Fzd8	INSIDE	0.256	0.544	2788.80	1517.27	0.139	2149.47	299.46
A_68_P28083514	chr11:102993838-102993882	NM_001130516:-792	Hexim2	PROMOTER	0.256	1.534	1317.26	2021.04	0.394	917.91	361.20
A_68_P24798110	chr6:120313882-120313931	NM_145997:-210	Kdm5a	DIVERGENT_PROMOTER	0.256	0.411	1599.14	656.93	0.105	1153.34	121.36
A_68_P31708194	chr18:52689223-52689267	NM_010728:118	Lox	INSIDE	0.256	0.639	1116.91	714.20	0.164	922.54	151.29
A_68_P25956629	chr8:73904896-73904940	NM_010150:933	Nr2f6	INSIDE	0.256	0.680	2607.97	1773.22	0.174	1807.81	314.99
A_68_P31029179	chr17:8995332-8995389	NM_011866:751	Pde10a	INSIDE	0.256	0.381	1595.08	607.53	0.098	1245.60	121.50
A_68_P30670426	chr16:35490448-35490492	NM_028295:489	Pdia5	INSIDE	0.256	0.596	2155.10	1283.41	0.153	1781.12	272.00
A_68_P23415895	chr4:151370916-151370960	NM_172705:-650	Phf13	PROMOTER	0.256	0.546	1141.95	623.62	0.140	837.73	117.06
A_68_P20597392	chr1:129765401-129765445	NM_178690:73	Rab3gap1	INSIDE	0.256	0.626	1752.15	1097.06	0.160	1416.28	226.66
A_68_P20008180	chr1:5008925-5008969	NM_021374:561	Rgs20	INSIDE	0.256	0.312	1988.23	619.88	0.080	1559.71	124.60
A_68_P28938190	chr13:34436028-34436072	NM_001033167:1001	Slc22a23	INSIDE	0.256	0.619	1229.32	761.07	0.158	921.92	145.95
A_68_P31373355	chr17:79135650-79135694	NM_011500:228	Strn	INSIDE	0.256	0.648	2416.13	1566.20	0.166	1760.83	292.30
A_68_P31151041	chr17:34066176-34066220	NM_001025313:9776	Tapbp	INSIDE	0.256	1.682	1534.38	2580.59	0.431	1104.55	476.40
A_68_P26247722	chr8:127316654-127316700	NM_198632:-242	Trim67	PROMOTER	0.256	0.448	1189.03	533.27	0.115	1006.93	115.71
A_68_P25158152	chr7:66484943-66484987	NM_001033962:843	Ube3a	INSIDE	0.256	0.485	1627.14	789.31	0.124	1358.78	168.87
A_68_P30401588	chr15:85407657-85407702	NM_001163634:821	Wnt7b	INSIDE	0.256	0.407	1563.41	636.09	0.104	1152.95	120.14
A_68_P26744825	chr9:95854980-95855036	NM_011916:-170	Xrn1	PROMOTER	0.256	0.688	1726.58	1187.18	0.176	1312.62	231.39
A_68_P25411540	chr7:117204605-117204649	NM_009281:-589	Zfp143	PROMOTER	0.256	0.524	1155.24	605.15	0.134	899.50	120.40
A_68_P21382117	chr2:81893227-81893271	NM_175513:-566	Zfp804a	PROMOTER	0.256	0.626	4735.49	2962.82	0.160	3531.01	566.57
A_68_P29961928	chr14:122873448-122873492	NM_009574:-1135	Zic2	DIVERGENT_PROMOTER	0.256	0.512	2477.24	1268.52	0.131	1979.82	259.46
A_68_P20370555	chr1:78213280-78213324			Unknown	0.256	0.559	1833.86	1025.99	0.143	1329.44	190.55
A_68_P30693865	chr16:39984541-39984585	AK082117:-145		PROMOTER	0.256	0.611	950.57	580.47	0.157	830.70	130.05
A_68_P25537617	chr7:140122830-140122874	ENSMUST00000106157:28		INSIDE	0.256	0.471	3411.39	1606.56	0.121	2458.19	296.38
A_68_P27795275	chr11:51502704-51502761	NM_025319:-596	0610009B22Rik	PROMOTER	0.255	0.349	1652.35	576.76	0.089	1336.07	119.14
A_68_P21682771	chr2:139996347-139996391	NM_027093:-13	2310003L22Rik	DIVERGENT_PROMOTER	0.255	0.594	926.68	550.90	0.152	801.64	121.71
A_68_P28182972	chr11:120050647-120050697	NR_030682:498	2810410L24Rik	INSIDE	0.255	0.531	1271.45	674.60	0.135	863.83	116.90

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27661783	chr11:26110740-26110784	NR_027973:-186	5730522E02Rik	PROMOTER	0.255	0.552	2000.73	1104.89	0.141	1605.63	226.18
A_68_P25737280	chr8:28338452-28338496	NM_013462:1586	Adrb3	INSIDE	0.255	0.590	1032.95	609.49	0.150	815.87	122.62
A_68_P20411442	chr1:88199826-88199871	NM_145222:53	B3gnt7	INSIDE	0.255	0.510	1093.64	557.52	0.130	927.82	120.66
A_68_P25032103	chr7:31337454-31337505	NM_183321:-188	BC053749	DIVERGENT_PROMOTER	0.255	0.594	1222.36	725.97	0.152	829.22	125.79
A_68_P30977036	chr16:93683818-93683862	NM_173047:377	Cbr3	INSIDE	0.255	0.518	2863.07	1482.08	0.132	2135.60	281.40
A_68_P27894657	chr11:69181886-69181930	NM_146019:1020	Chd3	INSIDE	0.255	0.602	1082.25	651.85	0.154	781.56	120.11
A_68_P22829261	chr4:34010768-34010823	NM_007726:-811	Cnr1	PROMOTER	0.255	0.574	1125.72	646.46	0.147	878.96	128.87
A_68_P30113001	chr15:31153906-31153950	NM_146057:-211	Dap	PROMOTER	0.255	0.454	1495.20	678.79	0.116	1103.09	127.77
A_68_P29506061	chr14:31292780-31292824	NM_133761:52	Dcp1a	INSIDE	0.255	0.561	1187.63	666.14	0.143	937.02	134.17
A_68_P27896442	chr11:69485330-69485374	NM_001159375:573	Eif4a1	INSIDE	0.255	0.633	1529.93	969.07	0.161	1242.39	200.41
A_68_P23973612	chr5:109123736-109123780	NM_001164259:511	Fgfrl1	INSIDE	0.255	0.415	1763.84	732.32	0.106	1305.41	138.36
A_68_P22010772	chr3:27271476-27271522	NM_177330:1226	Ghsr	INSIDE	0.255	0.502	1159.36	581.81	0.128	899.87	114.94
A_68_P22010765	chr3:27270773-27270817	NM_177330:522	Ghsr	INSIDE	0.255	0.630	5161.96	3250.36	0.161	3663.81	589.33
A_68_P21569057	chr2:119151750-119151794	NR_030683:161	Gm14207	INSIDE	0.255	0.672	2166.85	1456.50	0.172	1612.44	276.87
A_68_P30490430	chr15:101055110-101055154	NM_019518:495	Grasp	INSIDE	0.255	0.420	1458.01	612.63	0.107	1122.94	120.32
A_68_P32016093	chr19:23217070-23217114	NR_035423:-6828	Mir1192	PROMOTER	0.255	0.536	1149.74	616.62	0.137	952.48	130.39
A_68_P21501826	chr2:106534164-106534208	NM_029837:-1571	Mpped2	PROMOTER	0.255	0.694	2711.45	1882.62	0.177	2027.49	358.99
A_68_P32774622	chrX:155853067-155853111	NM_001081124:579	Mtap7d2	INSIDE	0.255	1.575	2887.48	4549.12	0.401	1260.64	505.77
A_68_P31775848	chr18:64676151-64676195	NM_001142950:39	Nars	INSIDE	0.255	0.503	1203.13	605.41	0.129	921.01	118.39
A_68_P31099062	chr17:24833399-24833444	NM_027988:243	Noxo1	INSIDE	0.255	0.530	1205.75	639.44	0.135	910.91	123.16
A_68_P21634174	chr2:131087984-131088028	NM_153501:-229	Pank2	PROMOTER	0.255	0.605	979.32	592.66	0.154	756.60	116.58
A_68_P23720372	chr5:58111337-58111385	NM_018764:2101	Pcdh7	INSIDE	0.255	0.561	1135.39	637.20	0.143	856.38	122.59
A_68_P27898393	chr11:69810295-69810339	NM_030064:1044	Phf23	INSIDE	0.255	1.753	3199.51	5608.95	0.446	2134.93	952.71
A_68_P26815243	chr9:108420248-108420296	NM_001114119:855	Qrich1	INSIDE	0.255	0.546	1230.81	672.17	0.139	896.46	124.67
A_68_P21835806	chr2:167317742-167317786	NM_030743:-380	Rnf114	PROMOTER	0.255	0.540	1085.20	585.49	0.137	883.32	121.38
A_68_P31154750	chr17:34741259-34741304	NM_019403:-775	Rnf5	DIVERGENT_PROMOTER	0.255	0.651	2081.62	1354.46	0.166	1539.66	255.00
A_68_P23403479	chr4:149328561-149328605	NM_029035:533	Spsb1	INSIDE	0.255	0.493	1250.73	616.65	0.126	927.62	116.73
A_68_P23223132	chr4:114729449-114729493	NM_011527:-2661	Tal1	PROMOTER	0.255	0.725	4478.27	3247.27	0.185	3204.40	593.51
A_68_P30498347	chr15:102349032-102349076	NM_009319:378	Tarbp2	INSIDE	0.255	0.498	1317.88	656.61	0.127	1019.98	129.51
A_68_P27915635	chr11:72990099-72990143	NM_001168470:390	Tmem93	INSIDE	0.255	0.511	1762.61	901.27	0.131	1335.15	174.41
A_68_P21070651	chr2:25080168-25080218	NM_146116:30	Tubb2c	INSIDE	0.255	0.536	1514.11	810.85	0.137	1178.49	161.17
A_68_P31204666	chr17:46168644-46168688	NM_001110266:-6554	Vegfa	PROMOTER	0.255	0.501	1374.64	688.78	0.128	997.78	127.64
A_68_P29258380	chr13:99343921-99343965	AK135687:153807		INSIDE	0.255	0.664	960.40	637.94	0.169	747.60	126.54
A_68_P29445005	chr14:20902070-20902114	NM_026209:302	1810063B07Rik	INSIDE	0.254	0.388	1402.98	544.17	0.099	1187.66	117.17
A_68_P25090211	chr7:52184951-52185005	NM_001077264:-118	Ap2a1	PROMOTER	0.254	0.636	1021.77	649.55	0.162	733.63	118.69
A_68_P28183217	chr11:120094827-120094871	NM_198423:588	Bahcc1	INSIDE	0.254	0.580	1341.64	778.34	0.147	1091.17	160.66
A_68_P27899563	chr11:70040019-70040063	NM_007528:3260	Bcl6b	INSIDE	0.254	0.592	1588.96	941.28	0.150	1186.63	178.42
A_68_P24641803	chr6:91827853-91827908	NM_172730:-166	C130022K22Rik	PROMOTER	0.254	0.523	1199.69	627.78	0.133	911.33	120.90
A_68_P23396586	chr4:148180019-148180067	NM_027195:1542	Casz1	INSIDE	0.254	0.482	1461.78	704.77	0.122	1024.98	125.37
A_68_P26035015	chr8:89994889-89994933	NM_019626:1581	Cbln1	INSIDE	0.254	0.579	1616.71	935.56	0.147	1169.52	171.59
A_68_P27792932	chr11:51076708-51076752	NM_007714:58	Clk4	INSIDE	0.254	0.692	2234.37	1546.28	0.175	1465.41	257.09
A_68_P24600268	chr6:84534331-84534375	NM_175475:9452	Cyp26b1	INSIDE	0.254	0.403	1425.21	574.31	0.102	1140.45	116.76
A_68_P26612687	chr9:69609097-69609152	NM_022378:-377	Foxb1	PROMOTER	0.254	0.584	1028.12	600.77	0.149	776.19	115.31
A_68_P30020398	chr15:12135347-12135391	NM_172958:520	Mtmr12	INSIDE	0.254	0.433	1225.75	530.80	0.110	1062.33	116.77
A_68_P27539157	chr10:127473205-127473249	NM_001113199:825	Naca	INSIDE	0.254	0.470	1170.38	549.74	0.119	1011.14	120.70
A_68_P28105683	chr11:107050715-107050759	NM_001161329:-41	Nol11	PROMOTER	0.254	0.453	1295.12	586.91	0.115	1151.89	132.70
A_68_P21150007	chr2:38565998-38566044	NM_139051:4042	Nr5a1	INSIDE	0.254	0.572	1063.30	608.59	0.145	811.01	117.88
A_68_P32134814	chr19:44910682-44910726	NM_011037:78821	Pax2	INSIDE	0.254	0.557	1819.58	1012.69	0.141	1503.55	212.19
A_68_P21495906	chr2:105509202-105509246	NR_002867:1263	Pax6os1	INSIDE	0.254	0.687	1818.45	1249.49	0.175	1512.12	264.40
A_68_P31415134	chr17:86566646-86566690	NM_011104:-456	Prkce	PROMOTER	0.254	0.623	1912.25	1190.80	0.158	1313.18	207.50
A_68_P21629885	chr2:130276440-130276484	NM_001163688:449	Ptpra	INSIDE	0.254	0.453	1365.05	618.74	0.115	1192.92	137.52

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25669972	chr8:13677124-13677168	NM_009025:441	Rasa3	INSIDE	0.254	0.689	2615.30	1803.09	0.175	1884.79	329.83
A_68_P28174642	chr11:118771162-118771206	NM_001024931:-298	Rbfox3	PROMOTER	0.254	0.604	1069.81	646.22	0.154	769.17	118.08
A_68_P28429504	chr12:52478611-52478655	NM_029825:66	Scfd1	INSIDE	0.254	0.602	1313.85	791.57	0.153	910.79	139.23
A_68_P25950467	chr8:72736364-72736408	NM_001007570:-206	Slc25a42	PROMOTER	0.254	0.717	2209.13	1583.69	0.182	1728.52	314.58
A_68_P20870657	chr1:181448104-181448148	NM_027188:8	Smyd3	INSIDE	0.254	0.573	1056.77	605.15	0.146	806.52	117.39
A_68_P27569490	chr11:6525943-6525987	NR_034042:-5542	Snora5c	PROMOTER	0.254	0.385	2827.29	1088.72	0.098	2041.96	200.00
A_68_P32415806	chrX:58146341-58146385	NM_009237:243	Sox3	INSIDE	0.254	2.374	1679.56	3986.93	0.602	802.85	483.50
A_68_P31092273	chr17:23684002-23684046	NM_001033496:17169	Zfp213	DOWNSTREAM	0.254	0.524	1933.43	1012.25	0.133	1395.18	185.18
A_68_P25063497	chr7:38554739-38554783	NM_172385:11	Zfp536	INSIDE	0.254	0.366	1505.87	551.57	0.093	1250.12	116.48
A_68_P23611134	chr5:37419319-37419363	M30250:624167		INSIDE	0.254	0.638	859.27	548.15	0.162	728.30	117.99
A_68_P20304762	chr1:66863250-66863306	NM_001122738:891	1110028C15Rik	INSIDE	0.253	0.432	1501.38	648.86	0.109	1084.27	118.50
A_68_P27892798	chr11:68873155-68873199	NM_028005:-100	2310047M10Rik	PROMOTER	0.253	0.442	1362.85	602.21	0.112	1039.25	116.22
A_68_P31177904	chr17:41016953-41016997	NM_027834:533	9130008F23Rik	INSIDE	0.253	0.499	1212.22	604.69	0.126	944.15	119.26
A_68_P20947700	chr1:194999554-194999598	NM_001160360:-86	A130010J15Rik	PROMOTER	0.253	0.501	1101.04	551.61	0.127	906.35	114.75
A_68_P27083337	chr10:40022544-40022597	NM_009665:-576	Amd1	PROMOTER	0.253	0.449	1427.78	641.68	0.114	1062.36	120.88
A_68_P27508736	chr10:121886005-121886049	NM_016847:472	Avpr1a	INSIDE	0.253	0.633	4461.36	2822.08	0.160	3436.78	549.54
A_68_P28739140	chr12:111829834-111829881	NR_033340:274	B930059L03Rik	INSIDE	0.253	0.419	1487.94	622.74	0.106	1104.94	116.79
A_68_P27489860	chr10:118677501-118677545	NM_027994:-411	Cand1	PROMOTER	0.253	0.658	1529.32	1006.46	0.167	1147.21	191.22
A_68_P31625483	chr18:36885784-36885836	NM_009841:498	Cd14	INSIDE	0.253	0.719	1472.57	1059.13	0.182	1077.95	196.04
A_68_P27183507	chr10:61441706-61441750	NM_007731:128	Col13a1	INSIDE	0.253	0.649	1229.23	797.35	0.164	762.50	125.21
A_68_P31157712	chr17:35257797-35257841	NM_009975:574	Csnk2b	INSIDE	0.253	0.606	1049.24	635.32	0.153	839.51	128.42
A_68_P27903825	chr11:70817620-70817664	NM_178367:292	Dhx33	INSIDE	0.253	0.384	2082.91	800.73	0.097	1763.97	171.74
A_68_P23404989	chr4:149610705-149610749	NM_023119:-579	Eno1	PROMOTER	0.253	0.699	4196.06	2931.02	0.177	3037.00	536.56
A_68_P22666539	chr3:154756237-154756282	NM_029330:83	Fpgt	INSIDE	0.253	0.578	1023.23	591.59	0.146	824.71	120.69
A_68_P20556963	chr1:121316999-121317043	NM_008381:1805	Inhbb	INSIDE	0.253	0.588	1608.71	945.72	0.148	1229.97	182.62
A_68_P31516119	chr18:15309151-15309195	NM_134112:783	Kctd1	INSIDE	0.253	0.525	1732.70	909.46	0.133	1339.55	178.14
A_68_P30359737	chr15:78236916-78236960	NM_001162493:-203	Mpst	DIVERGENT_PROMOTER	0.253	0.601	1041.60	626.15	0.152	787.95	119.64
A_68_P31202532	chr17:45823669-45823714	NM_026732:371	Mrpl14	INSIDE	0.253	0.738	2348.99	1732.95	0.187	1638.74	306.16
A_68_P24591488	chr6:83059493-83059537	NM_026744:413	Mrpl53	INSIDE	0.253	0.554	992.61	550.16	0.140	842.28	117.95
A_68_P24385094	chr6:39760759-39760803	NM_001010930:155	Mrps33	INSIDE	0.253	0.499	1094.41	546.56	0.126	946.97	119.67
A_68_P25092691	chr7:52622936-52622980	NR_027802:356	Mtag2	INSIDE	0.253	0.565	1167.31	660.00	0.143	844.92	120.84
A_68_P32103772	chr19:38893658-38893702	NM_021315:47	Noc3l	INSIDE	0.253	0.551	3680.11	2025.94	0.139	2647.97	368.75
A_68_P27946028	chr11:78738513-78738557	NM_010927:4174	Nos2	INSIDE	0.253	0.622	1056.79	656.90	0.157	908.50	143.06
A_68_P26268777	chr8:130882335-130882384	NM_008737:-613	Nrp1	PROMOTER	0.253	0.610	995.81	607.04	0.154	779.14	119.94
A_68_P23819019	chr5:77380180-77380224	NM_025939:-233	Paics	PROMOTER	0.253	0.599	2057.85	1231.88	0.152	1576.69	238.91
A_68_P24624715	chr6:88824256-88824300	NM_176973:-240	Podxl2	PROMOTER	0.253	1.524	3710.00	5653.87	0.385	2664.39	1026.48
A_68_P27680413	chr11:30672528-30672572	NM_134013:776	Psme4	INSIDE	0.253	0.643	816.93	525.46	0.163	750.05	122.16
A_68_P24040029	chr5:121099253-121099297	NM_013832:444	Rasal1	INSIDE	0.253	0.361	1675.88	604.30	0.091	1277.89	116.66
A_68_P30546792	chr16:11203231-11203275	NM_025546:133	Rsl1d1	INSIDE	0.253	0.698	2707.74	1889.84	0.177	2152.81	380.38
A_68_P25265270	chr7:87343737-87343781	NM_013659:12032	Sema4b	INSIDE	0.253	0.604	1204.20	726.96	0.153	871.69	133.15
A_68_P21783925	chr2:158436516-158436560	NM_009508:45	Slc32a1	INSIDE	0.253	0.622	2370.41	1474.89	0.158	1913.02	301.52
A_68_P25232261	chr7:81157848-81157892	NM_009181:698	St8sia2	INSIDE	0.253	0.679	2235.50	1518.32	0.172	1503.65	257.94
A_68_P27682733	chr11:31271650-31271694	NM_011491:-1611	Stc2	PROMOTER	0.253	0.472	1361.46	642.53	0.120	1033.56	123.55
A_68_P25030456	chr7:31016600-31016644	NM_025548:426	Tbcb	INSIDE	0.253	0.602	1977.07	1191.00	0.152	1410.42	214.77
A_68_P21912031	chr2:181414879-181414923	NM_009326:-114	Tcea2	DIVERGENT_PROMOTER	0.253	0.574	1062.47	609.89	0.145	804.11	116.95
A_68_P24076583	chr5:127721966-127722010	NM_175432:-207	Tmem132c	PROMOTER	0.253	0.405	1679.29	680.32	0.102	1140.43	116.78
A_68_P23316764	chr4:132833345-132833389	NM_025667:339	Tmem222	INSIDE	0.253	0.501	1394.89	698.19	0.127	980.37	124.30
A_68_P23621602	chr5:38952317-38952368	NM_011715:492	Wdr1	INSIDE	0.253	0.362	1821.20	659.43	0.092	1336.12	122.32
A_68_P22164429	chr3:57379088-57379132	NM_133784:688	Wwtr1	INSIDE	0.253	0.664	947.44	629.49	0.168	774.59	130.00
A_68_P25028818	chr7:30645166-30645210	NM_172740:191	Zfp420	INSIDE	0.253	0.492	1317.60	648.40	0.124	990.70	123.34
A_68_P30402194	chr15:85500704-85500751	AK038224:-6444		PROMOTER	0.253	0.643	990.62	637.04	0.163	744.40	121.27

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27787098	chr11:49988398-49988442	NM_026543:68	3010026O09Rik	INSIDE	0.252	0.670	3617.47	2424.19	0.169	2600.39	438.38
A_68_P23312749	chr4:132089123-132089167	NM_007512:430	Atpif1	INSIDE	0.252	0.668	1867.63	1247.15	0.169	1405.01	236.85
A_68_P22859646	chr4:40894916-40894962	NM_001171739:389	Bag1	INSIDE	0.252	0.438	1370.07	600.23	0.110	1093.08	120.50
A_68_P28976946	chr13:41344925-41344972	NM_001135577:-264	BC024659	PROMOTER	0.252	0.491	1292.73	634.97	0.124	984.42	121.72
A_68_P27176087	chr10:60148828-60148872	NM_023370:10388	Cdh23	INSIDE	0.252	0.487	1481.03	721.42	0.123	1021.99	125.32
A_68_P21429513	chr2:92440608-92440652	NM_023850:767	Chst1	INSIDE	0.252	0.689	1515.97	1044.00	0.173	1107.85	192.14
A_68_P25470627	chr7:127987068-127987112	NM_007908:694	Eef2k	INSIDE	0.252	0.659	1620.71	1068.33	0.166	1275.93	211.57
A_68_P23400758	chr4:148859457-148859501	NM_026963:37	Lzic	INSIDE	0.252	0.559	1110.84	621.30	0.141	857.81	120.70
A_68_P26022619	chr8:87437298-87437343	NM_019945:23932	Mast1	INSIDE	0.252	0.612	1223.67	748.93	0.154	931.22	143.43
A_68_P31107425	chr17:26089202-26089246	NM_001039038:-7348	Nhlrc4	PROMOTER	0.252	0.645	1005.11	648.02	0.163	717.95	116.80
A_68_P27903591	chr11:70783309-70783353	NM_001083331:134	Nup88	INSIDE	0.252	0.561	1888.83	1060.44	0.142	1364.85	193.26
A_68_P23165462	chr4:102986330-102986374	NM_025909:-98	Oma1	PROMOTER	0.252	0.375	1524.11	571.70	0.094	1250.13	117.95
A_68_P20370404	chr1:78193792-78193836	NM_001159520:-103	Pax3	PROMOTER	0.252	0.338	2355.52	795.38	0.085	2047.23	173.97
A_68_P30349852	chr15:76501941-76501985	NM_033371:-147	Ppp1r16a	DIVERGENT_PROMOTER	0.252	0.572	917.75	525.14	0.144	815.00	117.53
A_68_P23575728	chr5:31262393-31262437	NM_016703:320	Preb	INSIDE	0.252	0.403	2398.80	967.07	0.102	1849.15	187.96
A_68_P26811064	chr9:107673153-107673200	NM_148930:157	Rbm5	INSIDE	0.252	0.666	1035.06	688.89	0.168	748.98	125.57
A_68_P29294057	chr13:105844812-105844856	NM_029879:176	Rgs7bp	INSIDE	0.252	0.459	1256.61	576.18	0.116	1031.29	119.37
A_68_P20348981	chr1:74552352-74552396	NM_021383:-259	Rqcd1	PROMOTER	0.252	0.664	2065.16	1371.79	0.168	1351.71	226.66
A_68_P20149045	chr1:36613770-36613814	NM_001126047:1434	Sema4c	INSIDE	0.252	0.701	1920.32	1346.18	0.176	1297.88	228.83
A_68_P20618601	chr1:133860103-133860147	NM_145977:-7061	Slc45a3	PROMOTER	0.252	0.605	1023.46	619.57	0.152	844.77	128.65
A_68_P28151701	chr11:115025012-115025056	NM_012030:380	Slc9a3r1	INSIDE	0.252	0.379	1605.23	608.54	0.095	1196.98	114.20
A_68_P32562915	chrX:98417474-98417518	NM_001110311:406	Snx12	INSIDE	0.252	2.320	2372.61	5505.41	0.585	1069.45	626.07
A_68_P28143023	chr11:113480461-113480507	NM_001042606:-5086	Sstr2	PROMOTER	0.252	0.400	1490.33	595.89	0.101	1226.66	123.47
A_68_P23332904	chr4:135804629-135804673	NM_011542:779	Tcea3	INSIDE	0.252	1.454	8931.15	12984.54	0.367	6266.69	2298.48
A_68_P21765246	chr2:155207391-155207435	NM_178111:-179	Trp53inp2	PROMOTER	0.252	0.659	3385.42	2231.52	0.166	2563.74	425.32
A_68_P20352742	chr1:75216148-75216195	NM_009447:-343	Tuba4a	PROMOTER	0.252	0.615	929.77	572.00	0.155	785.47	121.96
A_68_P30991292	chr16:96367120-96367164	NM_207301:117	Wrb	INSIDE	0.252	0.677	2934.92	1987.61	0.171	2052.27	350.11
A_68_P24129051	chr5:138596643-138596687	NM_019747:308	Zfp113	INSIDE	0.252	0.542	1896.16	1027.19	0.137	1377.73	188.16
A_68_P25604012	chr7:151164433-151164477			Unknown	0.252	0.555	3042.67	1689.02	0.140	2256.88	316.20
A_68_P26538531	chr9:56643513-56643557	AK155716:5534		DOWNSTREAM	0.252	0.550	1531.95	842.09	0.139	1185.03	164.35
A_68_P21866704	chr2:172765156-172765200	NM_007557:616	Bmp7	INSIDE	0.251	0.617	1113.69	687.29	0.155	799.62	123.96
A_68_P26659373	chr9:78243366-78243412	NM_001191044:-195	Ddx43	PROMOTER	0.251	0.644	883.18	569.18	0.162	723.28	117.06
A_68_P30261328	chr15:60655675-60655719	NM_001162926:939	Fam84b	INSIDE	0.251	0.662	860.65	569.47	0.166	705.49	117.12
A_68_P22791943	chr4:25726823-25726867	NM_010243:306	Fut9	INSIDE	0.251	0.613	3352.60	2053.88	0.154	2601.33	399.92
A_68_P24380022	chr6:38825884-38825928	NM_010433:283	Hipk2	INSIDE	0.251	0.613	909.00	556.86	0.154	797.67	122.74
A_68_P29134823	chr13:72768727-72768771	NM_010574:2323	Irx2	INSIDE	0.251	0.607	1084.09	658.22	0.152	791.69	120.70
A_68_P22683292	chr3:157699623-157699667	NM_024194:-22	Lrrc40	DIVERGENT_PROMOTER	0.251	0.412	2396.71	987.11	0.103	1828.22	188.88
A_68_P24127563	chr5:138227997-138228041	NM_144913:-89	Mepce	DIVERGENT_PROMOTER	0.251	0.520	1295.01	673.71	0.131	955.63	125.01
A_68_P27992598	chr11:86922877-86922926	NR_029652:-3604	Mir301	PROMOTER	0.251	0.671	913.85	613.08	0.168	698.71	117.62
A_68_P26021884	chr8:87308434-87308479	NM_001081982:15783	Nfix	INSIDE	0.251	0.402	1616.46	649.56	0.101	1163.98	117.58
A_68_P22422573	chr3:109946012-109946056	NM_001163348:356	Ntng1	INSIDE	0.251	0.544	1642.08	893.53	0.137	1231.93	168.45
A_68_P27970619	chr11:83112556-83112601	NM_134025:-99	Pex12	DIVERGENT_PROMOTER	0.251	0.482	1413.18	681.67	0.121	991.90	120.15
A_68_P32546910	chrX:94267800-94267844	NM_001033361:-112	Pgr15l	PROMOTER	0.251	1.589	842.15	1338.09	0.399	490.63	195.86
A_68_P31084400	chr17:21082518-21082562	NM_016891:123	Ppp2r1a	INSIDE	0.251	0.523	1275.90	667.73	0.131	953.66	125.31
A_68_P29982086	chr15:5066083-5066136	NM_026069:-503	Rpl37	DIVERGENT_PROMOTER	0.251	0.503	1450.34	729.04	0.126	1017.12	128.52
A_68_P26895475	chr9:123438639-123438695	NM_030692:-333	Sacm1l	PROMOTER	0.251	0.413	1389.88	574.54	0.104	1135.50	117.92
A_68_P25585438	chr7:148067601-148067645	NM_001127351:146	Sirt3	INSIDE	0.251	0.485	2710.95	1314.97	0.122	2100.29	255.63
A_68_P31926386	chr19:5024497-5024541	NM_007854:513	Slc29a2	INSIDE	0.251	0.647	910.24	589.06	0.162	715.85	116.11
A_68_P27779981	chr11:48614053-48614098	NR_028563:-1459	Snord96a	PROMOTER	0.251	0.560	1688.88	946.06	0.141	1321.04	185.84
A_68_P30234984	chr15:55738403-55738447	NM_016667:80	Sntb1	INSIDE	0.251	0.584	1983.17	1158.14	0.147	1406.89	206.35
A_68_P28050111	chr11:97223439-97223483	NM_138657:-404	Socs7	PROMOTER	0.251	0.486	1061.15	515.54	0.122	1010.41	123.40

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P23012918	chr4:71861537-71861581	NM_011599:395	Tle1	INSIDE	0.251	0.423	1877.73	793.71	0.106	1584.44	168.14
A_68_P31213635	chr17:47825554-47825598	NM_001164729:-241	Tomm6	DIVERGENT_PROMOTER	0.251	0.696	1225.87	852.85	0.175	968.48	169.39
A_68_P26685860	chr9:83728064-83728108	NM_001110265:-209	Ttk	PROMOTER	0.251	0.642	1466.07	941.56	0.161	1124.79	180.98
A_68_P26817225	chr9:108838988-108839032	NM_025407:350	Uqcrc1	INSIDE	0.251	0.665	1543.53	1026.21	0.167	1080.27	180.40
A_68_P21910759	chr2:181195175-181195219	NM_028125:-1065	Zbtb46	PROMOTER	0.251	0.383	1798.01	688.86	0.096	1403.35	135.02
A_68_P30019880	chr15:12047515-12047559	NM_011767:-69	Zfr	PROMOTER	0.251	0.641	961.01	615.57	0.161	749.52	120.32
A_68_P26451995	chr9:41698713-41698757			Unknown	0.251	0.666	920.33	613.30	0.167	714.16	119.56
A_68_P31402646	chr17:84496389-84496433	AK043195:199		INSIDE	0.251	0.497	1406.98	699.32	0.125	1048.85	130.86
A_68_P26871700	chr9:119230982-119231026	ENSMUST00000128880:436		INSIDE	0.251	0.448	2586.88	1160.14	0.112	1871.62	210.54
A_68_P23929548	chr5:100858327-100858371	NR_034038:206	5430416N02Rik	INSIDE	0.250	0.310	2096.69	649.23	0.077	1558.90	120.54
A_68_P31145426	chr17:32533638-32533682	NR_029458:-6298	A530088E08Rik	PROMOTER	0.250	0.616	890.06	548.63	0.154	770.84	118.86
A_68_P30092468	chr15:27396965-27397009	NM_020332:555	Ank	INSIDE	0.250	0.418	1669.18	698.02	0.104	1301.10	135.88
A_68_P22822463	chr4:32702764-32702814	NM_001122978:341	Casp8ap2	INSIDE	0.250	0.431	1458.07	627.89	0.108	1082.94	116.47
A_68_P21518697	chr2:109857970-109858014	NM_026613:19	Ccdc34	INSIDE	0.250	0.385	1651.79	636.17	0.096	1266.09	121.78
A_68_P26542211	chr9:57368765-57368824	NM_007747:-244	Cox5a	PROMOTER	0.250	0.550	940.51	517.00	0.137	876.65	120.48
A_68_P24131511	chr5:139231842-139231886	NM_030565:830	Fam20c	INSIDE	0.250	0.417	1683.12	702.67	0.104	1268.17	132.25
A_68_P28687868	chr12:103057400-103057444	NM_011812:-157	Fbln5	PROMOTER	0.250	0.451	1263.91	570.60	0.113	1050.30	118.38
A_68_P28563528	chr12:79327956-79328000	NM_145965:337	Gphn	INSIDE	0.250	0.623	931.00	579.71	0.156	749.76	116.75
A_68_P28154940	chr11:115569306-115569350	NM_008163:583	Grb2	INSIDE	0.250	0.475	1192.48	565.84	0.119	986.11	116.90
A_68_P24619081	chr6:87930736-87930780	NM_198622:718	H1fx	INSIDE	0.250	0.348	1708.96	594.22	0.087	1402.74	121.79
A_68_P26954160	chr10:13686535-13686580	NM_010437:373	Hivep2	INSIDE	0.250	0.364	1693.23	616.19	0.091	1290.86	117.38
A_68_P29614704	chr14:55483280-55483329	NM_001177705:-309	Homez	PROMOTER	0.250	0.504	1164.74	586.74	0.126	937.73	118.15
A_68_P27862287	chr11:63734368-63734412	NM_018805:1396	Hs3st3b1	INSIDE	0.250	0.540	1175.52	634.46	0.135	884.21	119.39
A_68_P22728834	chr4:11181339-11181383	NM_178112:46	Ints8	INSIDE	0.250	0.522	1918.88	1001.82	0.130	1572.92	205.05
A_68_P22403738	chr3:106839716-106839760	NM_008418:659	Kcna3	INSIDE	0.250	0.358	1902.64	680.64	0.089	1325.33	118.41
A_68_P30363244	chr15:78758585-78758629	NM_008495:1452	Lgals1	INSIDE	0.250	0.499	1257.39	627.81	0.125	961.17	120.08
A_68_P25535615	chr7:139802512-139802556	NM_029609:209	Lhpp	INSIDE	0.250	0.677	1632.46	1104.72	0.169	1279.92	216.22
A_68_P22661991	chr3:153992609-153992654	NM_010713:893	Lhx8	INSIDE	0.250	0.520	1089.44	566.10	0.130	925.76	120.41
A_68_P25376177	chr7:109082594-109082648	NM_001162973:-249	Lrrc51	PROMOTER	0.250	0.657	1623.44	1066.72	0.164	1236.97	202.92
A_68_P24137287	chr5:140212019-140212063	NM_174850:247	Micall2	INSIDE	0.250	0.440	2339.67	1029.16	0.110	1809.68	198.77
A_68_P26641837	chr9:74919720-74919769	NM_010864:732	Myo5a	INSIDE	0.250	0.452	1553.93	701.83	0.113	1136.12	128.18
A_68_P25144265	chr7:63217530-63217574	NM_023647:268	Nipa2	INSIDE	0.250	0.567	979.05	554.68	0.142	867.32	122.89
A_68_P22898179	chr4:48059988-48060034	NM_015743:-4109	Nr4a3	PROMOTER	0.250	0.586	1083.45	634.62	0.147	834.97	122.48
A_68_P26268785	chr8:130883347-130883403	NM_008737:402	Nrp1	INSIDE	0.250	0.516	1285.24	663.39	0.129	895.01	115.67
A_68_P25576662	chr7:146434859-146434912	NM_001033206:505	Pwwp2b	INSIDE	0.250	0.548	1233.31	676.32	0.137	886.07	121.68
A_68_P20378194	chr1:79855540-79855584	NM_009255:-322	Serpine2	PROMOTER	0.250	0.599	1703.55	1020.23	0.150	1455.57	218.36
A_68_P25994483	chr8:81923506-81923561	NM_008539:-166	Smad1	PROMOTER	0.250	0.535	1100.58	588.80	0.134	899.64	120.24
A_68_P26237919	chr8:125626230-125626274	NR_028128:-705	Snord68	PROMOTER	0.250	0.303	2213.47	670.78	0.076	1631.05	123.52
A_68_P22049389	chr3:34549058-34549109	NM_011443:157	Sox2	INSIDE	0.250	0.374	1498.19	560.90	0.094	1236.66	115.88
A_68_P24331348	chr6:30254521-30254565	NM_001169576:-3	Ube2h	PROMOTER	0.250	0.632	978.60	618.42	0.158	768.99	121.58
A_68_P25769987	chr8:34752626-34752684	NM_178648:-206	Ubxn8	PROMOTER	0.250	0.593	977.36	580.01	0.148	796.30	117.94
A_68_P20880189	chr1:183141032-183141076	NM_145514:1055	Wdr26	INSIDE	0.250	0.475	1247.65	593.23	0.119	978.33	116.08
A_68_P28084545	chr11:103173341-103173385			Unknown	0.250	0.687	1559.37	1071.09	0.172	1243.85	214.00
A_68_P24475723	chr6:56518661-56518705			Unknown	0.250	0.573	1022.89	585.65	0.143	813.71	116.49
A_68_P30138905	chr15:36426080-36426131	NM_175134:441	Ankrd46	INSIDE	0.249	0.446	1354.38	603.41	0.111	1065.59	118.07
A_68_P31380056	chr17:80295692-80295741	NM_178050:-253	Atl2	PROMOTER	0.249	0.670	1582.53	1060.85	0.167	1146.29	190.96
A_68_P25007799	chr7:25790496-25790540	NM_144921:396	Atp1a3	INSIDE	0.249	0.699	4545.61	3177.14	0.174	3043.34	530.46
A_68_P25011291	chr7:26466045-26466089	NM_172148:-110	B9d2	DIVERGENT_PROMOTER	0.249	0.494	1170.17	577.54	0.123	1002.37	123.37
A_68_P20408509	chr1:87690854-87690908	NM_133781:859	Cab39	INSIDE	0.249	0.498	1087.17	541.31	0.124	936.15	116.20
A_68_P27089717	chr10:41238672-41238716	NM_016898:-611	Cd164	PROMOTER	0.249	0.416	1409.04	586.62	0.104	1189.80	123.24
A_68_P22355189	chr3:97413826-97413870	NM_026539:265	Chd1l	INSIDE	0.249	0.549	1079.94	592.37	0.137	976.17	133.40

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P21320136	chr2:71384105-71384149	NM_010054:685	Dlx2	INSIDE	0.249	0.479	2446.96	1171.31	0.119	1782.62	212.75
A_68_P26659601	chr9:78290277-78290323	NM_173386:654	E330016A19Rik	INSIDE	0.249	0.541	1557.65	842.83	0.135	1237.15	166.67
A_68_P24123511	chr5:137358417-137358461	NM_024474:539	Emid2	INSIDE	0.249	1.441	6966.42	10040.89	0.358	4715.86	1690.59
A_68_P23440271	chr4:155109205-155109249	NM_001101506:314	Gm5151	INSIDE	0.249	0.664	1431.11	950.82	0.165	978.84	161.92
A_68_P20451403	chr1:94728878-94728922	NM_016696:638	Gpc1	INSIDE	0.249	0.530	1071.57	568.12	0.132	880.34	116.38
A_68_P20636647	chr1:136884516-136884560	NM_001033409:117315	Lgr6	INSIDE	0.249	0.558	1194.18	665.95	0.139	948.90	131.66
A_68_P31930913	chr19:5803254-5803298	NR_002847:-605	Malat1	PROMOTER	0.249	0.365	1861.18	679.93	0.091	1271.31	115.83
A_68_P20348304	chr1:74438995-74439039	NR_029743:-1867	Mir26b	PROMOTER	0.249	0.593	1025.19	607.94	0.148	823.03	121.73
A_68_P26075858	chr8:96696472-96696516	NM_008630:-23	Mt2	PROMOTER	0.249	0.518	1334.06	691.64	0.129	1082.89	139.77
A_68_P28566639	chr12:80013104-80013148	NM_013738:-5201	Plek2	PROMOTER	0.249	0.622	1004.53	624.80	0.155	860.67	133.32
A_68_P25089727	chr7:52112663-52112707	NM_021549:134	Pnkp	INSIDE	0.249	0.428	1476.56	631.94	0.106	1097.26	116.85
A_68_P24984112	chr7:17532039-17532083	NM_001099636:2030	Pnmal2	INSIDE	0.249	0.542	1291.60	700.57	0.135	1078.49	145.47
A_68_P25587466	chr7:148401511-148401555	NM_025886:-226	Rassf7	DIVERGENT_PROMOTER	0.249	0.482	3154.33	1521.92	0.120	1867.66	224.16
A_68_P21704900	chr2:143837439-143837493	NM_024281:-467	Rrbp1	PROMOTER	0.249	0.608	879.19	534.45	0.151	813.55	123.01
A_68_P27942191	chr11:78059485-78059537	NM_009143:263	Sdf2	INSIDE	0.249	0.519	1254.55	650.62	0.129	936.65	120.74
A_68_P28535273	chr12:74147578-74147622	NM_009189:99	Six1	INSIDE	0.249	0.691	1666.59	1152.26	0.172	1355.58	233.54
A_68_P31412149	chr17:86091406-86091450	NM_011380:-3834	Six2	PROMOTER	0.249	0.609	942.97	574.15	0.152	787.60	119.40
A_68_P22392373	chr3:104443206-104443250	NM_009196:638	Slc16a1	INSIDE	0.249	0.452	1320.86	596.50	0.112	1091.23	122.48
A_68_P28159860	chr11:116394577-116394621	NM_011451:-1455	Sphk1	PROMOTER	0.249	0.421	1380.55	581.67	0.105	1138.93	119.52
A_68_P20151298	chr1:36995764-36995812	NM_018872:584	Tmem131	INSIDE	0.249	0.669	936.42	626.07	0.166	709.28	117.87
A_68_P23928043	chr5:100587765-100587824	NM_182841:1033	Tmem150c	INSIDE	0.249	0.482	1184.56	570.70	0.120	965.70	115.97
A_68_P23141222	chr4:98590182-98590226	NM_146144:-296	Usp1	PROMOTER	0.249	0.389	2799.55	1088.64	0.097	1963.66	190.30
A_68_P25505911	chr7:134655737-134655781	NR_024331:625	1700008J07Rik	INSIDE	0.248	0.511	1287.65	658.42	0.127	1048.62	133.01
A_68_P30350785	chr15:76648219-76648263	NM_001168288:360	Arhgap39	INSIDE	0.248	1.361	6207.90	8446.78	0.337	4429.15	1492.51
A_68_P23440848	chr4:155205726-155205770	NM_025338:-6	Aurkaip1	PROMOTER	0.248	0.382	1957.60	747.37	0.095	1497.45	141.64
A_68_P29033454	chr13:51740459-51740503	NM_025415:-120	Cks2	PROMOTER	0.248	0.666	2797.00	1862.94	0.165	1960.06	323.12
A_68_P31157716	chr17:35258201-35258245	NM_009975:170	Csnk2b	INSIDE	0.248	0.679	3573.03	2425.02	0.168	2515.84	423.30
A_68_P23262660	chr4:123089459-123089503	NM_001167918:-326	D830031N03Rik	PROMOTER	0.248	0.563	1842.75	1037.08	0.140	1442.59	201.73
A_68_P25783726	chr8:37158263-37158317	NM_172911:409	D8Ertd82e	INSIDE	0.248	0.643	896.11	575.93	0.159	750.27	119.60
A_68_P23203726	chr4:109650077-109650121	NM_172296:-531	Dmrta2	PROMOTER	0.248	0.348	1771.24	616.01	0.086	1394.98	120.09
A_68_P25957394	chr8:74067191-74067235	NM_028617:384	Fam125a	INSIDE	0.248	1.361	4553.28	6199.19	0.337	2935.43	989.97
A_68_P23195773	chr4:108056312-108056356	NM_001099303:-380	Fam159a	PROMOTER	0.248	0.608	882.16	535.92	0.151	768.56	116.00
A_68_P27662609	chr11:26287534-26287589	NM_025923:478	Fancl	INSIDE	0.248	0.539	1119.39	603.35	0.134	880.25	117.62
A_68_P28157764	chr11:116029125-116029181	NM_172571:340	Fbf1	INSIDE	0.248	0.665	897.83	597.17	0.165	722.58	119.30
A_68_P23968407	chr5:108150057-108150101	NM_010278:3285	Gfi1	INSIDE	0.248	0.524	1114.27	583.38	0.130	902.75	117.05
A_68_P29856567	chr14:102128847-102128891	NM_201529:-276	Lmo7	PROMOTER	0.248	0.566	1138.18	644.40	0.140	966.86	135.63
A_68_P26159871	chr8:112472495-112472551	NM_212447:13583	Marveld3	INSIDE	0.248	0.444	1317.34	585.43	0.110	1064.82	117.42
A_68_P25092688	chr7:52622594-52622638	NR_027802:14	Mtag2	INSIDE	0.248	0.424	2052.66	870.38	0.105	1640.76	172.55
A_68_P25806929	chr8:41719873-41719917	NM_001040699:252	Mtmr7	INSIDE	0.248	0.666	1759.44	1172.43	0.166	1171.81	193.98
A_68_P30567338	chr16:15863650-15863696	NM_029354:-257	Mzt2	PROMOTER	0.248	0.550	1210.20	665.90	0.137	876.81	119.89
A_68_P20285508	chr1:63223074-63223120	NM_001160038:300	Ndufs1	INSIDE	0.248	0.586	1008.39	591.00	0.145	822.94	119.39
A_68_P31655264	chr18:42554220-42554264	NM_138945:-8	Pou4f3	PROMOTER	0.248	0.516	2157.75	1113.05	0.128	1627.84	208.28
A_68_P31921669	chr19:4192588-4192632	NM_031868:437	Ppp1ca	INSIDE	0.248	0.333	1914.53	638.15	0.083	1396.65	115.60
A_68_P24066363	chr5:125821560-125821604	NM_001205082:-118	Scarb1	PROMOTER	0.248	2.001	3253.79	6510.19	0.497	1989.18	988.87
A_68_P21749116	chr2:152222489-152222533	NM_011438:1272	Sox12	INSIDE	0.248	0.715	1820.46	1302.14	0.178	1253.43	222.55
A_68_P26421279	chr9:35018970-35019014	NM_026130:205	Srpr	INSIDE	0.248	0.458	1282.93	587.07	0.113	1084.90	123.11
A_68_P23322939	chr4:134024154-134024198	NM_019641:-58	Stmn1	PROMOTER	0.248	0.677	1098.48	743.38	0.168	909.59	152.39
A_68_P26921705	chr10:7675095-7675141	NM_138667:803	Tab2	INSIDE	0.248	0.490	1294.80	634.17	0.121	1001.60	121.49
A_68_P23223128	chr4:114729001-114729045	NM_011527:-3109	Tal1	PROMOTER	0.248	0.628	2838.27	1782.73	0.156	2026.60	315.49
A_68_P27693368	chr11:33104357-33104401	NM_019916:-790	Tlx3	PROMOTER	0.248	0.378	1811.26	684.73	0.094	1335.83	125.43
A_68_P24629441	chr6:89594015-89594059	NM_001178058:55	Txnrd3	INSIDE	0.248	0.656	1009.04	662.17	0.163	805.31	131.26

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P29052391	chr13:55057276-55057320	NM_153131:6506	Unc5a	INSIDE	0.248	0.494	1243.66	614.83	0.123	944.51	115.98
A_68_P30401593	chr15:85408317-85408361	NM_001163634:162	Wnt7b	INSIDE	0.248	0.484	1858.71	898.85	0.120	1460.05	174.80
A_68_P21721820	chr2:146839259-146839303	NM_011917:485	Xrn2	INSIDE	0.248	0.466	1205.21	562.07	0.116	1026.95	118.86
A_68_P26139674	chr8:108939165-108939209	NM_011764:-52	Zfp90	PROMOTER	0.248	0.631	2362.80	1491.34	0.157	1857.77	291.06
A_68_P30925087	chr16:84703818-84703862	ENSMUST00000164314:-9427		PROMOTER	0.248	0.742	2928.84	2174.37	0.184	2201.12	405.36
A_68_P23396591	chr4:148180645-148180689	NM_027195:2166	Casz1	INSIDE	0.247	0.605	1078.19	652.15	0.150	851.78	127.34
A_68_P25009415	chr7:26066798-26066842	NM_001110131:-377	Cic	PROMOTER	0.247	0.707	2165.51	1531.25	0.174	1462.29	255.03
A_68_P30431381	chr15:90509463-90509507	NM_025815:335	Cpne8	INSIDE	0.247	0.574	2229.14	1279.68	0.142	1778.65	251.86
A_68_P27564954	chr11:5688709-5688754	NM_001146308:246	Dbnl	INSIDE	0.247	0.504	2049.45	1033.33	0.124	1644.25	204.69
A_68_P23312760	chr4:132091448-132091492	NM_172400:-3	Dnajc8	DIVERGENT_PROMOTER	0.247	0.429	1410.70	604.57	0.106	1177.90	124.69
A_68_P22149159	chr3:54496467-54496512	NM_019995:-537	Fam48a	PROMOTER	0.247	0.598	930.57	556.52	0.148	797.22	117.81
A_68_P21374843	chr2:80287482-80287526	NM_011356:49	Frzb	INSIDE	0.247	0.517	1865.58	964.17	0.127	1511.34	192.69
A_68_P30655031	chr16:32877641-32877685	NM_001159349:-207	Fyttd1	DIVERGENT_PROMOTER	0.247	0.679	999.43	678.38	0.168	908.31	152.40
A_68_P24743884	chr6:110595643-110595687	NM_177328:73	Grm7	INSIDE	0.247	0.626	3444.15	2155.10	0.155	2719.05	420.72
A_68_P21489522	chr2:104333335-104333384	NM_001145824:1287	Hipk3	INSIDE	0.247	0.551	1078.04	593.61	0.136	855.10	116.07
A_68_P24449304	chr6:52184811-52184855	NM_008263:106	Hoxa10	INSIDE	0.247	0.543	1273.12	691.07	0.134	892.55	119.90
A_68_P23298316	chr4:129418783-129418827	NM_011317:722	Khdrbs1	INSIDE	0.247	0.445	1345.62	599.40	0.110	1156.77	127.12
A_68_P27284095	chr10:80039472-80039516	NM_078477:547	Klf16	INSIDE	0.247	0.599	1082.35	648.75	0.148	850.10	125.90
A_68_P28052727	chr11:97661201-97661245	NM_010688:237	Lasp1	INSIDE	0.247	0.663	921.86	611.42	0.164	725.01	118.93
A_68_P25972026	chr8:77633688-77633732	NM_008566:284	Mcm5	INSIDE	0.247	0.479	1134.94	543.88	0.118	977.78	115.69
A_68_P24129162	chr5:138612940-138612988	NR_029658:-5918	Mir106b	PROMOTER	0.247	0.478	1434.04	685.99	0.118	1050.23	124.18
A_68_P24591483	chr6:83058946-83058997	NM_026744:-130	Mrpl53	PROMOTER	0.247	0.554	1065.49	590.41	0.137	862.94	117.92
A_68_P27290096	chr10:80959275-80959319	NM_134009:-188	Ncln	PROMOTER	0.247	0.505	1653.89	834.60	0.125	1263.69	157.70
A_68_P23134317	chr4:97439073-97439121	NM_001122953:-5220	Nfia	PROMOTER	0.247	1.496	979.20	1464.48	0.370	748.59	276.95
A_68_P21351535	chr2:76485641-76485685	NM_011871:389	Prkra	INSIDE	0.247	0.492	1386.02	682.37	0.122	1100.87	134.11
A_68_P31107662	chr17:26122929-26122973	NM_153140:35855	Rab11fip3	DOWNSTREAM	0.247	0.499	1311.97	654.16	0.123	948.80	116.92
A_68_P31412111	chr17:86086474-86086527	NM_011380:1094	Six2	INSIDE	0.247	0.516	1216.26	627.03	0.127	937.53	119.16
A_68_P28186322	chr11:120575013-120575057	NM_016665:47	Stra13	INSIDE	0.247	0.477	2062.63	984.56	0.118	1300.03	153.53
A_68_P23223130	chr4:114729210-114729264	NM_011527:-2895	Tal1	PROMOTER	0.247	0.599	1091.58	653.85	0.148	812.11	120.04
A_68_P26082617	chr8:97844517-97844561	NM_028532:9026	Tepp	INSIDE	0.247	0.715	3769.19	2693.51	0.176	2829.49	499.21
A_68_P27854525	chr11:62364572-62364616	NM_011664:-411	Ubb	PROMOTER	0.247	0.331	1984.84	657.46	0.082	1445.63	118.38
A_68_P24973050	chr7:13388889-13388933	NM_026046:15299	Zfp329	DOWNSTREAM	0.247	0.691	1425.62	984.65	0.171	1036.10	176.71
A_68_P28736912	chr12:111426508-111426561	AK044800:749		INSIDE	0.247	0.649	1077.99	699.40	0.160	747.68	119.81
A_68_P24938724	chr6:148160617-148160668	NR_015615:-167	4732416N19Rik	PROMOTER	0.246	0.544	1132.18	616.32	0.134	902.71	120.87
A_68_P23693366	chr5:52581910-52581954	NR_015537:13	9230114K14Rik	INSIDE	0.246	0.669	895.12	599.22	0.164	748.74	123.07
A_68_P26074969	chr8:96535449-96535505	NM_011787:1064	Amfr	INSIDE	0.246	0.415	1454.74	603.24	0.102	1137.19	115.91
A_68_P24995363	chr7:20395100-20395149	NM_033601:12980	Bcl3	INSIDE	0.246	0.482	1232.37	593.66	0.118	1010.24	119.59
A_68_P28331590	chr12:32183836-32183892	NM_134048:541	Cbll1	INSIDE	0.246	0.561	1151.20	645.59	0.138	906.59	125.16
A_68_P30486141	chr15:100325298-100325342	NM_153407:350	Csrnp2	INSIDE	0.246	0.656	3590.26	2354.78	0.161	2892.42	466.83
A_68_P29659271	chr14:63741571-63741615	NM_007798:291	Ctsb	INSIDE	0.246	0.642	871.04	559.29	0.158	729.97	115.21
A_68_P26584123	chr9:64659420-64659464	NM_001162917:625	Dennd4a	INSIDE	0.246	0.637	3599.08	2292.08	0.157	2799.30	438.41
A_68_P23416686	chr4:151500208-151500252	NM_019585:2804	Espn	INSIDE	0.246	0.673	2026.10	1363.71	0.166	1552.55	257.45
A_68_P31615543	chr18:35091590-35091634	NM_144866:45	Etf1	INSIDE	0.246	0.471	1215.83	572.78	0.116	1023.61	118.81
A_68_P29712961	chr14:72932323-72932367	NM_207636:177466	Fndc3a	DOWNSTREAM	0.246	0.458	1223.38	559.76	0.113	1044.89	117.72
A_68_P27897193	chr11:69617732-69617776	NR_027913:584	G630025P09Rik	INSIDE	0.246	0.603	3433.80	2070.82	0.148	2527.28	374.87
A_68_P25011771	chr7:26540127-26540178	NM_144922:-413	Hnrnpul1	PROMOTER	0.246	0.490	1203.20	590.03	0.121	1059.53	127.76
A_68_P24284108	chr6:21165672-21165716	NM_019697:-414	Kcnd2	PROMOTER	0.246	0.424	1480.99	627.38	0.104	1327.55	138.59
A_68_P22201239	chr3:65462965-65463009	NM_001166659:-7163	Lekr1	PROMOTER	0.246	0.638	1854.25	1182.19	0.157	1453.43	228.11
A_68_P20440038	chr1:92949235-92949279	NM_001111311:-764	Lrrfip1	PROMOTER	0.246	0.534	1239.90	662.04	0.132	1002.65	131.96
A_68_P24119634	chr5:136612073-136612117	NM_027891:-150	Lrwd1	DIVERGENT_PROMOTER	0.246	0.500	1502.65	751.90	0.123	1087.69	133.96
A_68_P31055438	chr17:13108951-13108995	NM_026310:-15	Mrpl18	DIVERGENT_PROMOTER	0.246	0.555	2004.58	1111.78	0.137	1378.10	188.36

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P32471624	chrX:72661844-72661888	NM_010839:16	Mtcp1	INSIDE	0.246	1.875	2811.14	5270.45	0.461	1255.02	578.78
A_68_P31625589	chr18:36904175-36904219	NM_010885:6	Ndufa2	INSIDE	0.246	0.535	1190.46	637.10	0.132	897.44	118.28
A_68_P31499628	chr18:12394947-12394991	NM_008720:-73	Npc1	PROMOTER	0.246	0.446	1984.24	885.73	0.110	1492.97	163.80
A_68_P29057274	chr13:55929838-55929882	NM_011097:2926	Pitx1	INSIDE	0.246	0.515	1751.44	902.75	0.127	1017.60	129.18
A_68_P31863202	chr18:80453578-80453622	NM_001164423:556	Pqlc1	INSIDE	0.246	0.576	1681.61	968.09	0.142	1349.25	191.28
A_68_P22031195	chr3:30895073-30895117	NM_008857:402	Prkci	INSIDE	0.246	0.701	4152.45	2909.57	0.172	3217.84	554.14
A_68_P28079293	chr11:102255152-102255196	NM_016759:426	Rundc3a	INSIDE	0.246	0.585	1027.28	600.56	0.144	855.32	123.21
A_68_P30348901	chr15:76353383-76353427	NM_130893:-845	Scrt1	PROMOTER	0.246	0.440	1857.06	816.83	0.108	1307.90	141.70
A_68_P29982096	chr15:5067068-5067116	NR_028091:-1328	Snord72	PROMOTER	0.246	0.580	980.55	568.62	0.143	815.50	116.45
A_68_P25092884	chr7:52651057-52651101	NM_009224:-61	Snrnp70	PROMOTER	0.246	0.682	1805.87	1230.80	0.168	1483.35	248.75
A_68_P30544452	chr16:10784908-10784952	NM_009896:699	Socs1	INSIDE	0.246	0.522	4884.69	2550.00	0.129	3844.45	494.19
A_68_P31612300	chr18:34490731-34490775	NM_025527:-46	Srp19	PROMOTER	0.246	0.570	1033.65	589.20	0.140	865.75	121.36
A_68_P32196175	chr19:55817146-55817190	NM_001142918:869	Tcf7l2	INSIDE	0.246	0.608	2512.88	1527.96	0.150	1820.57	272.60
A_68_P24981572	chr7:17038213-17038257	NM_026938:107	Tmem160	INSIDE	0.246	0.522	1183.90	617.87	0.128	901.40	115.50
A_68_P24374366	chr6:37821755-37821801	NM_145076:968	Trim24	INSIDE	0.246	0.494	1248.19	616.73	0.122	990.00	120.32
A_68_P27836130	chr11:59119814-59119858	NM_139298:-595	Wnt9a	PROMOTER	0.246	0.582	1039.44	604.57	0.143	836.70	119.79
A_68_P30380963	chr15:81846798-81846842	NM_010247:22	Xrcc6	INSIDE	0.246	0.470	2002.64	941.12	0.116	1437.61	166.13
A_68_P28057143	chr11:98412469-98412513	NM_001166494:80	Zpbp2	INSIDE	0.246	0.505	1163.05	587.02	0.124	991.07	123.27
A_68_P29562138	chr14:42078358-42078402			Unknown	0.246	0.539	1206.31	650.61	0.133	922.79	122.37
A_68_P24760446	chr6:113554636-113554680	NM_133937:-107	6720456B07Rik	DIVERGENT_PROMOTER	0.245	0.601	951.85	572.19	0.147	792.84	116.55
A_68_P24067080	chr5:125956003-125956050	NM_030210:-216	Aacs	PROMOTER	0.245	0.484	1225.23	593.39	0.119	1006.51	119.61
A_68_P26716246	chr9:90058314-90058358	NM_001003911:521	Adamts7	INSIDE	0.245	0.578	1049.77	606.86	0.142	834.05	118.08
A_68_P31928608	chr19:5425407-5425451	NM_134149:285	AI837181	INSIDE	0.245	0.497	1252.93	622.27	0.122	994.39	121.10
A_68_P27129524	chr10:50312341-50312389	NM_001146089:-110	Ascc3	PROMOTER	0.245	0.369	1787.00	659.68	0.091	1316.22	119.18
A_68_P20936238	chr1:192922619-192922663	NM_030060:348	Batf3	INSIDE	0.245	0.611	1599.85	978.03	0.150	1215.48	182.03
A_68_P21067988	chr2:24617711-24617766	NM_001042528:829	Cacna1b	INSIDE	0.245	0.592	1501.68	889.57	0.145	1151.69	166.89
A_68_P23321458	chr4:133743204-133743248	NM_144527:-226	Ccdc21	PROMOTER	0.245	0.628	980.49	615.47	0.154	795.81	122.63
A_68_P25533790	chr7:139508854-139508902	NM_029935:-40	Chst15	PROMOTER	0.245	0.490	1193.59	585.00	0.120	1017.80	122.13
A_68_P20794594	chr1:167389733-167389777	NM_028759:840	Dcaf6	INSIDE	0.245	0.493	1247.80	615.17	0.121	999.50	120.48
A_68_P26426830	chr9:36604533-36604577	NM_007915:99	Ei24	INSIDE	0.245	0.560	1102.62	617.41	0.137	960.57	131.84
A_68_P22803176	chr4:28740507-28740557	NM_001122889:238	Epha7	INSIDE	0.245	0.609	1487.17	905.80	0.149	1091.94	162.87
A_68_P21339293	chr2:74585053-74585097	NM_010468:35025	Hoxd3	INSIDE	0.245	0.569	4052.26	2305.23	0.139	2746.45	382.56
A_68_P28036509	chr11:94937682-94937726	NM_013565:324	Itga3	INSIDE	0.245	0.446	1241.16	553.63	0.109	1125.20	122.77
A_68_P24112796	chr5:135164221-135164265	NM_010717:218	Limk1	INSIDE	0.245	0.638	1035.06	660.74	0.157	745.45	116.75
A_68_P30004453	chr15:9070451-9070495	NM_177178:147	Lmbrd2	INSIDE	0.245	0.418	1601.35	669.70	0.102	1191.30	121.89
A_68_P24655998	chr6:94232997-94233041	NM_001029850:880	Magi1	INSIDE	0.245	0.606	946.93	573.81	0.148	867.92	128.81
A_68_P24993423	chr7:20043402-20043446	NM_172279:419	Mark4	INSIDE	0.245	0.476	3301.16	1572.63	0.117	2516.76	293.36
A_68_P22028818	chr3:30413802-30413849	NM_021442:-5416	Mecom	PROMOTER	0.245	0.540	1131.26	610.42	0.132	897.32	118.46
A_68_P28054913	chr11:98054206-98054250	NM_013634:-8	Med1	PROMOTER	0.245	0.407	1488.16	606.27	0.100	1159.67	115.57
A_68_P23240178	chr4:118082173-118082217	NM_020000:253	Med8	INSIDE	0.245	1.336	7930.80	10595.11	0.327	4974.24	1627.96
A_68_P28037993	chr11:95170830-95170877	NM_001195003:707	Myst2	INSIDE	0.245	0.679	1249.80	848.64	0.166	987.41	163.98
A_68_P22081523	chr3:40604233-40604277	NM_011495:382	Plk4	INSIDE	0.245	0.572	2379.25	1360.46	0.140	2032.66	284.53
A_68_P31415145	chr17:86568034-86568078	NM_011104:932	Prkce	INSIDE	0.245	0.519	1143.65	593.22	0.127	926.35	117.61
A_68_P26983375	chr10:19570710-19570754	NM_029529:533	Slc35d3	INSIDE	0.245	0.632	2887.57	1824.08	0.155	2183.68	338.17
A_68_P26766655	chr9:99776052-99776096	NM_011440:515	Sox14	INSIDE	0.245	0.660	996.38	657.82	0.162	762.66	123.39
A_68_P27985579	chr11:85650619-85650663	NM_009324:4524	Tbx2	INSIDE	0.245	0.454	1767.83	802.03	0.111	1126.42	125.20
A_68_P31092979	chr17:23813505-23813549	NM_001161746:890	Tnfrsf12a	INSIDE	0.245	0.733	2153.76	1578.53	0.180	1562.27	281.07
A_68_P29051402	A_68_P29051402			Unknown	0.245	1.842	5836.03	10747.53	0.451	4088.25	1842.62
A_68_P30555519	A_68_P30555519			Unknown	0.245	0.325	1897.58	616.90	0.080	1502.99	119.59
A_68_P21571902	chr2:119698673-119698717	ENSMUST00000120952:5445		DOWNSTREAM	0.245	0.629	1584.29	996.08	0.154	1155.94	178.25
A_68_P21610826	chr2:126758946-126758990	NM_023220:3	2010106G01Rik	INSIDE	0.244	0.617	1130.54	697.54	0.151	890.64	134.16

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P24114260	chr5:135484941-135484991	NM_001190437:-55	Abhd11	DIVERGENT_PROMOTER	0.244	0.474	1464.32	694.49	0.116	1000.99	115.94
A_68_P28314431	chr12:29360343-29360387	NM_134052:293	Adi1	INSIDE	0.244	0.469	1350.01	633.68	0.115	1064.12	121.95
A_68_P27565299	chr11:5761759-5761803	NM_009636:-88	Aebp1	PROMOTER	0.244	0.742	2809.22	2083.64	0.181	1898.17	343.24
A_68_P26229676	chr8:124431860-124431904	NM_001033485:150	BC048644	INSIDE	0.244	0.520	1210.66	628.95	0.127	932.86	118.29
A_68_P27540747	chr10:127759432-127759482	NM_019953:-58	Cnpy2	PROMOTER	0.244	0.628	955.92	600.68	0.153	772.39	118.43
A_68_P25667343	chr8:13288388-13288432	NM_001024504:-284	Dcun1d2	PROMOTER	0.244	0.326	1894.86	616.97	0.079	1556.70	123.69
A_68_P27903933	chr11:70832700-70832744	NM_033562:43	Derl2	INSIDE	0.244	0.381	1754.26	668.50	0.093	1381.42	128.49
A_68_P27677368	chr11:29925763-29925807	NM_146016:249	Eml6	INSIDE	0.244	0.608	987.77	600.81	0.148	830.95	123.13
A_68_P23392754	chr4:147534489-147534533	NM_176848:-266	Fbxo2	DIVERGENT_PROMOTER	0.244	0.459	1456.48	667.93	0.112	1069.47	119.76
A_68_P24533909	chr6:70906592-70906636	NM_001101464:15	Foxi3	INSIDE	0.244	0.417	1622.51	676.55	0.102	1155.70	117.56
A_68_P27286406	chr10:80392969-80393019	NM_008655:159	Gadd45b	INSIDE	0.244	0.460	1472.03	677.22	0.112	1063.21	119.17
A_68_P26244130	chr8:126756129-126756173	NM_139272:857	Galnt2	INSIDE	0.244	0.534	1334.06	711.97	0.130	917.18	119.50
A_68_P23404232	chr4:149461503-149461547	NM_177366:-87	Gpr157	PROMOTER	0.244	1.620	10929.57	17710.04	0.396	7593.87	3007.82
A_68_P21576348	chr2:120454904-120454948	NM_025475:19755	Haus2	DOWNSTREAM	0.244	0.697	3304.90	2303.35	0.170	2438.74	414.22
A_68_P26546344	chr9:58047294-58047338	NM_001161535:2206	Islr2	INSIDE	0.244	0.661	1999.15	1322.25	0.162	1417.19	228.96
A_68_P24828016	chr6:126594679-126594723	NM_010595:1119	Kcna1	INSIDE	0.244	0.503	1603.48	807.19	0.123	1380.67	169.72
A_68_P31343005	chr17:73267359-73267403	NM_029999:-264	Lbh	PROMOTER	0.244	0.389	1741.25	676.88	0.095	1292.48	122.46
A_68_P26884588	chr9:121551071-121551115	NM_026915:-408	Lyzl4	DIVERGENT_PROMOTER	0.244	0.645	1522.36	981.64	0.158	1127.33	177.62
A_68_P27533650	chr10:126479347-126479401	NM_010792:387	Mettl1	INSIDE	0.244	0.591	1156.34	683.10	0.144	809.82	116.79
A_68_P26345185	chr9:20841278-20841322	NR_035438:-4528	Mir1900	PROMOTER	0.244	0.466	1128.85	526.57	0.114	1021.55	116.11
A_68_P27285700	chr10:80289932-80289982	NR_035503:-1585	Mir1982	PROMOTER	0.244	0.549	1267.57	695.71	0.134	870.10	116.62
A_68_P20454938	chr1:95239228-95239272	NM_080850:115	Pask	INSIDE	0.244	0.722	3157.92	2279.07	0.176	2475.54	436.55
A_68_P31937064	chr19:7050018-7050063	NM_008889:503	Ppp1r14b	INSIDE	0.244	0.593	1205.82	714.66	0.144	853.58	123.19
A_68_P31084397	chr17:21082131-21082175	NM_016891:-265	Ppp2r1a	PROMOTER	0.244	0.565	1103.92	623.25	0.138	871.77	120.28
A_68_P22182580	chr3:61168280-61168324	NM_028712:-126	Rap2b	PROMOTER	0.244	0.606	1397.27	846.36	0.148	1139.91	168.73
A_68_P32044142	chr19:28086118-28086162	NM_011265:-484	Rfx3	PROMOTER	0.244	0.695	3564.25	2477.90	0.170	2644.48	449.18
A_68_P30224201	chr15:53733924-53733974	NM_177225:43	Samd12	INSIDE	0.244	0.505	2498.86	1262.95	0.123	1701.81	209.48
A_68_P29116723	chr13:69750440-69750484	NM_175283:-121	Srd5a1	DIVERGENT_PROMOTER	0.244	0.533	2400.14	1279.76	0.130	1674.04	218.05
A_68_P26431943	chr9:37464781-37464825	NM_025289:95	Tbrg1	INSIDE	0.244	0.463	1252.33	580.45	0.113	1042.16	117.71
A_68_P30510784	chr16:4558577-4558621	NM_031182:1122	Tcfap4	INSIDE	0.244	0.518	1220.51	631.83	0.126	1044.20	131.77
A_68_P31936613	chr19:6984303-6984347	NM_001166370:137	Trmt112	INSIDE	0.244	0.473	2017.31	954.86	0.116	1482.48	171.54
A_68_P30476480	chr15:98622772-98622816	NM_021279:2507	Wnt1	INSIDE	0.244	2.247	1342.39	3015.79	0.547	940.63	514.86
A_68_P31840894	chr18:76219449-76219494	NM_145356:239640	Zbtb7c	INSIDE	0.244	0.543	1301.60	707.11	0.133	914.90	121.46
A_68_P31086419	chr17:21669765-21669813	NM_144515:-2714	Zfp52	PROMOTER	0.244	0.595	1120.49	666.87	0.145	853.51	124.17
A_68_P27809324	chr11:54117377-54117421	NM_001033597:-307	Acsl6	PROMOTER	0.243	0.597	2608.15	1556.32	0.145	1796.55	260.30
A_68_P31939553	chr19:7456891-7456935	NM_001033139:604	AI846148	INSIDE	0.243	0.574	1135.49	651.36	0.139	925.61	129.10
A_68_P25090207	chr7:52184463-52184510	NM_001077264:374	Ap2a1	INSIDE	0.243	0.639	1123.22	717.46	0.155	829.36	128.78
A_68_P26595210	chr9:66643453-66643497	NM_177583:-244	Aph1b	PROMOTER	0.243	0.391	1839.09	719.38	0.095	1408.54	133.93
A_68_P28836397	chr13:14046979-14047023	NM_178640:60	B3galnt2	INSIDE	0.243	0.301	2015.66	606.76	0.073	1578.47	115.55
A_68_P30369305	chr15:79764056-79764100	NM_144811:-1002	Cbx7	PROMOTER	0.243	0.517	1337.74	692.07	0.126	1058.17	133.11
A_68_P26822740	chr9:110148381-110148425	NM_001166273:2116	Cspg5	INSIDE	0.243	0.733	5820.68	4268.36	0.178	4139.87	736.45
A_68_P21629321	chr2:130188203-130188247	NM_001110513:66550	Ebf4	INSIDE	0.243	1.346	2219.49	2987.63	0.327	1802.35	589.92
A_68_P27034329	chr10:29033110-29033154	NM_025855:-173	Echdc1	PROMOTER	0.243	0.529	4172.73	2208.30	0.128	3208.55	412.26
A_68_P30221114	chr15:53176756-53176800	NM_010162:960	Ext1	INSIDE	0.243	0.723	3801.24	2749.66	0.176	2835.52	499.15
A_68_P20432979	chr1:91825300-91825344	NM_010262:2429	Gbx2	INSIDE	0.243	0.575	1071.25	616.12	0.140	893.18	124.67
A_68_P31205408	chr17:46297849-46297904	NM_001145979:-104	Gtpbp2	DIVERGENT_PROMOTER	0.243	0.545	1351.33	735.85	0.132	916.38	121.11
A_68_P24783942	chr6:117857933-117857977	NM_001166427:-9357	Hnrnpf	PROMOTER	0.243	0.508	1155.66	587.04	0.124	943.02	116.55
A_68_P24537471	chr6:71583335-71583379	NM_001038695:-457	Kdm3a	PROMOTER	0.243	0.635	2180.31	1384.48	0.154	1665.30	257.21
A_68_P24137290	chr5:140212320-140212364	NM_174850:-55	Micall2	PROMOTER	0.243	0.659	4096.08	2697.83	0.160	3099.99	496.06
A_68_P28833747	chr13:13530554-13530598	NM_010917:708	Nid1	INSIDE	0.243	0.598	969.85	579.59	0.145	838.52	121.56
A_68_P24754179	chr6:112439818-112439862	NM_001081147:-38	Oxtr	PROMOTER	0.243	0.504	1737.96	875.89	0.122	1551.07	189.66

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P22342239	chr3:94910572-94910617	NM_008847:186	Pip5k1a	INSIDE	0.243	0.663	904.30	599.63	0.161	732.92	118.25
A_68_P23820897	chr5:77739417-77739462	NM_153798:-69	Polr2b	DIVERGENT_PROMOTER	0.243	0.520	1813.02	943.61	0.127	1398.18	177.01
A_68_P26229672	chr8:124431324-124431368	NM_011404:240	Slc7a5	INSIDE	0.243	0.312	2401.66	749.30	0.076	1603.84	121.68
A_68_P25235396	chr7:81699348-81699401	NM_001038643:292	Slco3a1	INSIDE	0.243	0.664	1024.28	679.64	0.161	769.19	124.14
A_68_P27844727	chr11:60591282-60591326	NM_175491:278	Smcr8	INSIDE	0.243	0.570	1093.53	623.35	0.138	862.45	119.33
A_68_P24016052	chr5:117041312-117041356	NM_026886:492	Srrm4	INSIDE	0.243	0.597	1087.61	649.40	0.145	809.76	117.66
A_68_P25571660	chr7:145588945-145588989	NM_183289:447	Tcergl1	INSIDE	0.243	0.622	2394.00	1488.74	0.151	2010.74	303.62
A_68_P21864922	chr2:172376858-172376902	NM_001159696:390	Tcfap2c	INSIDE	0.243	0.596	1295.26	771.39	0.145	996.76	144.38
A_68_P20596473	chr1:129574700-129574744	NM_028135:-124	Tmem163	PROMOTER	0.243	0.480	1539.93	739.68	0.117	1033.16	120.45
A_68_P28157536	chr11:115992427-115992471	NM_178802:-6	Trim65	PROMOTER	0.243	0.472	1327.99	626.75	0.115	1088.63	124.89
A_68_P28712202	chr12:107201120-107201164	BC156654:163282		INSIDE	0.243	0.617	994.33	613.85	0.150	810.65	121.63
A_68_P28450735	chr12:56225735-56225781	NM_001100116:244	1700047I17Rik2	INSIDE	0.242	0.608	994.36	604.88	0.147	796.08	117.20
A_68_P25933302	chr8:69010455-69010506	NM_025465:-74	1810029B16Rik	PROMOTER	0.242	0.675	1746.74	1178.53	0.164	1330.58	217.58
A_68_P27899564	chr11:70040111-70040155	NM_007528:3168	Bcl6b	INSIDE	0.242	0.548	1105.14	605.71	0.133	906.96	120.48
A_68_P31351852	chr17:74927433-74927479	NM_007566:-178	Birc6	PROMOTER	0.242	0.596	962.59	573.43	0.144	805.36	116.00
A_68_P31152219	chr17:34257154-34257198	NR_037970:-331	Brd2	PROMOTER	0.242	0.558	2029.96	1132.29	0.135	1410.13	190.53
A_68_P24011279	chr5:116181126-116181170	NM_001080808:420	Ccdc64	INSIDE	0.242	0.452	2184.71	988.45	0.109	1684.64	184.15
A_68_P30362683	chr15:78673475-78673519	NM_027219:420	Cdc42ep1	INSIDE	0.242	0.635	881.58	559.83	0.154	802.19	123.46
A_68_P23807021	chr5:75440173-75440217	NM_028850:457	Chic2	INSIDE	0.242	0.641	857.81	549.48	0.155	792.60	122.78
A_68_P28754915	chr12:114378792-114378837	NM_024223:368	Crip2	INSIDE	0.242	0.632	945.68	598.03	0.153	758.98	116.00
A_68_P24058178	chr5:124356959-124357007	NM_026603:-301	Denr	PROMOTER	0.242	0.604	1267.63	766.02	0.146	1001.66	146.57
A_68_P20875116	chr1:182262065-182262109	NR_003623:-1406	Gm5069	PROMOTER	0.242	0.613	1056.39	648.05	0.149	815.81	121.22
A_68_P26807872	chr9:107240552-107240596	NM_133984:107	Hemk1	INSIDE	0.242	0.372	1849.45	687.29	0.090	1339.56	120.37
A_68_P21338756	chr2:74520344-74520390	NM_008273:-83	Hoxd11	PROMOTER	0.242	0.554	1053.33	583.16	0.134	864.65	115.70
A_68_P23231145	chr4:116497325-116497369	NM_146256:-3233	Hpdl	PROMOTER	0.242	0.438	1410.27	617.73	0.106	1110.21	117.57
A_68_P27765088	chr11:45757957-45758001	NM_028185:459	Lsm11	INSIDE	0.242	0.377	1609.20	606.79	0.091	1316.93	120.41
A_68_P30345342	chr15:75824398-75824446	NM_177922:224	Mapk15	INSIDE	0.242	0.550	1780.30	979.20	0.133	1385.91	184.43
A_68_P24191781	chr5:151396250-151396294	NM_133898:828	N4bp2l1	INSIDE	0.242	0.498	1290.90	642.22	0.120	982.44	118.33
A_68_P29620047	chr14:56442581-56442635	NM_001168346:-1023	Nfatc4	PROMOTER	0.242	0.553	1077.63	595.69	0.134	908.41	121.71
A_68_P25093530	chr7:52765419-52765466	NM_001163662:336	Nucb1	INSIDE	0.242	0.652	1067.29	695.72	0.158	768.33	121.05
A_68_P29962218	chr14:122933824-122933868	NM_144844:297	Pcca	INSIDE	0.242	0.347	1782.42	618.16	0.084	1398.41	117.43
A_68_P26700012	chr9:86465331-86465375	NM_001163746:97	Pgm3	INSIDE	0.242	0.436	1471.64	641.64	0.105	1155.40	121.71
A_68_P24048830	chr5:122607910-122607954	NM_013636:-355	Ppp1cc	PROMOTER	0.242	0.542	2194.06	1189.79	0.131	1630.19	214.19
A_68_P26463574	chr9:43553274-43553318	NM_021424:638	Pvrl1	INSIDE	0.242	0.476	1881.60	894.91	0.115	1558.53	179.03
A_68_P24604717	chr6:85324325-85324369	NM_001003955:282	Rab11fip5	INSIDE	0.242	0.368	1593.78	585.86	0.089	1316.00	117.27
A_68_P22906128	chr4:49645277-49645321	NM_001163263:367	Rnf20	INSIDE	0.242	0.440	1702.79	748.41	0.107	1139.29	121.41
A_68_P32464060	chrX:70918500-70918544	NM_001142809:51	Slc6a8	INSIDE	0.242	1.628	1115.81	1816.54	0.394	465.66	183.51
A_68_P29892688	chr14:109310708-109310754	NM_199065:2726	Slitrk1	INSIDE	0.242	0.479	1492.99	715.24	0.116	1061.43	122.83
A_68_P21628394	chr2:130004810-130004854	NM_009225:268	Snrpb	INSIDE	0.242	0.439	1231.64	540.40	0.106	1112.82	118.16
A_68_P26766651	chr9:99775638-99775682	NM_011440:929	Sox14	INSIDE	0.242	0.592	1159.00	686.08	0.143	996.97	142.58
A_68_P20962665	chr2:3391654-3391704	NM_022724:580	Suv39h2	INSIDE	0.242	0.594	1232.45	732.22	0.144	848.70	122.23
A_68_P22538545	chr3:132347325-132347369	NM_173032:239	Tbck	INSIDE	0.242	0.564	1141.22	644.05	0.137	872.71	119.33
A_68_P25589127	chr7:148667760-148667804	NM_053082:6644	Tspan4	INSIDE	0.242	1.392	4036.73	5617.31	0.337	2621.74	883.40
A_68_P22372359	chr3:100773528-100773572	NM_001013026:36	Ttf2	INSIDE	0.242	0.379	1562.60	591.71	0.092	1281.75	117.52
A_68_P24955196	chr7:6335606-6335650	NM_175247:-399	Zfp28	PROMOTER	0.242	0.734	4728.37	3468.38	0.177	3321.74	588.85
A_68_P20807989	chr1:169859876-169859920			Unknown	0.242	0.416	1495.89	622.72	0.101	1161.33	116.93
A_68_P25600978	chr7:150631111-150631170			Unknown	0.242	0.591	972.71	575.19	0.143	835.65	119.75
A_68_P25447473	chr7:123450914-123450958	ENSMUST00000106605:954		INSIDE	0.242	0.455	1224.62	556.85	0.110	1119.93	123.37
A_68_P21108247	chr2:31170255-31170299	ENSMUST00000113532:342		INSIDE	0.242	0.633	1447.25	916.49	0.153	1104.90	169.09
A_68_P31129446	chr17:29853826-29853870	NM_001163741:114	1110021J02Rik	INSIDE	0.241	1.895	2742.01	5195.22	0.457	1743.70	797.18
A_68_P29509884	chr14:31943948-31943992	NR_024069:-1854	2010107H07Rik	DIVERGENT_PROMOTER	0.241	0.517	1129.05	583.15	0.124	982.77	122.29

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25010196	chr7:26180415-26180459	NR_015569:4	4732471J01Rik	INSIDE	0.241	0.567	1132.31	641.65	0.136	846.53	115.51
A_68_P31833164	chr18:74938725-74938769	NM_177470:-119	Acaa2	DIVERGENT_PROMOTER	0.241	0.502	2606.13	1308.81	0.121	1781.96	215.91
A_68_P22682773	chr3:157611083-157611131	NM_001013806:677	Ankrd13c	INSIDE	0.241	0.612	1000.60	612.51	0.148	782.41	115.64
A_68_P28725222	chr12:109242213-109242257	NM_001079883:-610	Bcl11b	PROMOTER	0.241	0.588	1544.12	908.21	0.142	1218.37	172.55
A_68_P33005171	chr7:3366221-3366265	NM_133189:29558	Cacng7	INSIDE	0.241	0.708	1610.43	1139.90	0.170	1209.08	205.95
A_68_P22889569	chr4:46614182-46614226	NM_001164804:597	Coro2a	INSIDE	0.241	0.676	1630.99	1103.03	0.163	1072.11	174.96
A_68_P21103093	chr2:30270839-30270883	NM_007760:408	Crat	INSIDE	0.241	0.471	1612.70	759.28	0.114	1062.47	120.66
A_68_P21778674	chr2:157563392-157563436	NM_025680:278	Ctnnbl1	INSIDE	0.241	0.409	1607.35	657.19	0.098	1161.13	114.34
A_68_P25009061	chr7:26004576-26004627	NM_207677:277	Dedd2	INSIDE	0.241	0.694	1176.13	816.64	0.167	846.85	141.51
A_68_P27278867	chr10:79240093-79240137	NM_031380:96	Fstl3	INSIDE	0.241	1.481	8370.81	12393.22	0.357	5246.39	1873.49
A_68_P21609430	chr2:126501185-126501229	NM_010249:16	Gabpb1	INSIDE	0.241	0.665	1458.02	969.02	0.160	1358.39	217.26
A_68_P25274807	chr7:89078453-89078497	NM_013886:871	Hdgfrp3	INSIDE	0.241	0.657	1393.32	915.63	0.159	1078.97	171.14
A_68_P28918889	chr13:30842632-30842676	NM_013674:1528	Irf4	INSIDE	0.241	0.560	2493.13	1395.72	0.135	1806.47	243.41
A_68_P31296465	chr17:64951073-64951117	NM_008549:106	Man2a1	INSIDE	0.241	0.465	1684.05	783.28	0.112	1390.37	155.69
A_68_P22289192	chr3:83959834-83959879	NM_029797:-148	Mnd1	PROMOTER	0.241	0.577	1528.94	881.90	0.139	1204.95	167.29
A_68_P29368030	chr13:119176079-119176123	NM_021556:-41	Mrps30	PROMOTER	0.241	0.488	1388.29	677.38	0.118	1022.53	120.20
A_68_P27283558	chr10:79957724-79957768	NM_139226:96	Onecut3	INSIDE	0.241	0.669	1296.30	867.20	0.161	1054.45	169.95
A_68_P22484165	chr3:122432345-122432393	NM_153422:293	Pde5a	INSIDE	0.241	0.718	1869.49	1342.96	0.173	1351.58	233.54
A_68_P25375613	chr7:108970639-108970683	NM_008887:3834	Phox2a	INSIDE	0.241	0.595	947.93	564.05	0.143	821.31	117.77
A_68_P22342241	chr3:94910847-94910891	NM_008847:-88	Pip5k1a	DIVERGENT_PROMOTER	0.241	0.617	967.92	596.73	0.148	820.56	121.76
A_68_P32142306	chr19:46221925-46221969	NM_008852:869	Pitx3	INSIDE	0.241	0.402	4293.47	1727.85	0.097	3312.00	320.83
A_68_P27630333	chr11:20101414-20101458	NM_008996:-168	Rab1	PROMOTER	0.241	0.648	1231.38	797.88	0.156	941.83	146.80
A_68_P28038461	chr11:95245810-95245864	NM_016752:-399	Slc35b1	PROMOTER	0.241	0.677	948.26	642.06	0.163	735.47	120.24
A_68_P20596467	chr1:129573905-129573949	NM_028135:672	Tmem163	INSIDE	0.241	0.393	1527.15	600.07	0.095	1231.66	116.79
A_68_P28520554	chr12:71554239-71554283	NM_028339:120	Tmx1	INSIDE	0.241	0.426	1369.19	583.75	0.103	1131.56	116.17
A_68_P21099685	chr2:29682982-29683026	NM_026615:96	Urm1	INSIDE	0.241	0.515	1175.62	605.07	0.124	967.59	119.94
A_68_P30719353	chr16:44063345-44063389	AK153403:75766		INSIDE	0.241	0.589	1310.44	772.03	0.142	1124.33	159.32
A_68_P29964259	chr14:123312516-123312560	NM_145466:-151	A2ld1	PROMOTER	0.240	0.412	3027.30	1246.68	0.099	2385.40	236.01
A_68_P29342440	chr13:114584633-114584677	NM_172595:-61	Arl15	PROMOTER	0.240	0.709	2740.09	1942.55	0.170	1994.72	339.44
A_68_P22941606	chr4:56815104-56815148	NM_001081420:-74	BC026590	PROMOTER	0.240	0.624	2061.16	1286.76	0.150	1541.91	230.83
A_68_P23410166	chr4:150482290-150482334	NM_001081557:753565	Camta1	INSIDE	0.240	0.480	6637.68	3189.30	0.115	4849.80	559.19
A_68_P25782095	chr8:36889705-36889749	NM_027998:-113	Cldn23	PROMOTER	0.240	0.662	5066.24	3353.75	0.159	3789.35	601.43
A_68_P20412923	chr1:88483836-88483880	NM_172974:184	Cops7b	INSIDE	0.240	0.534	3097.12	1654.84	0.128	2250.29	288.46
A_68_P27284382	chr10:80085896-80085940	NM_001159591:-6482	Csnk1g2	PROMOTER	0.240	0.400	2767.12	1106.66	0.096	1963.51	188.81
A_68_P24600309	chr6:84539419-84539463	NM_175475:4364	Cyp26b1	INSIDE	0.240	0.514	1259.93	647.70	0.124	976.92	120.77
A_68_P21102297	chr2:30141550-30141594	NM_177648:302	Dolk	INSIDE	0.240	0.584	1091.43	637.59	0.140	871.46	122.24
A_68_P28038138	chr11:95198892-95198936	NM_172543:583	Fam117a	INSIDE	0.240	1.589	7638.24	12136.56	0.381	4870.98	1855.31
A_68_P26529950	chr9:55057294-55057339	NM_028049:575	Fbxo22	INSIDE	0.240	0.582	1123.23	654.00	0.140	848.96	118.67
A_68_P21107214	chr2:30996795-30996839	NM_001038700:712	Fnbp1	INSIDE	0.240	0.658	2276.84	1498.09	0.158	1765.69	278.45
A_68_P31484558	chr18:9214394-9214440	NM_008058:1563	Fzd8	INSIDE	0.240	0.683	1065.65	728.21	0.164	751.82	123.30
A_68_P28221292	chr12:8305005-8305049	NM_013527:3734	Gdf7	INSIDE	0.240	0.471	3100.53	1461.60	0.113	2033.55	230.54
A_68_P28059766	chr11:98844320-98844364	NM_178596:-12	Gjd3	PROMOTER	0.240	0.634	2659.07	1686.37	0.152	1969.80	299.66
A_68_P28153961	chr11:115375325-115375369	NM_008258:338	Hn1	INSIDE	0.240	0.667	868.25	579.30	0.160	744.49	119.08
A_68_P24632567	chr6:90413191-90413235	NM_023184:593	Klf15	INSIDE	0.240	0.525	2516.21	1320.70	0.126	1879.15	237.05
A_68_P28068271	chr11:100333552-100333596	NM_172565:522	Klhl11	INSIDE	0.240	0.560	1198.84	671.53	0.134	917.33	123.31
A_68_P24142214	chr5:141082926-141082970	NM_008494:-346	Lfng	PROMOTER	0.240	0.299	2280.33	682.81	0.072	1610.79	115.87
A_68_P21122321	chr2:33436455-33436499	NM_010725:59555	Lmx1b	INSIDE	0.240	0.472	1498.85	707.39	0.113	1062.56	120.34
A_68_P20624273	chr1:134776795-134776839	NM_010732:-115	Lrrn2	PROMOTER	0.240	0.656	1544.42	1013.26	0.157	1141.21	179.35
A_68_P28504589	chr12:68321801-68321851	NM_001193266:1710	Mdga2	INSIDE	0.240	0.598	1030.45	616.64	0.144	804.32	115.52
A_68_P30344756	chr15:75724658-75724702	NM_172607:231	Naprt1	INSIDE	0.240	0.606	3756.08	2274.42	0.145	2887.78	419.72
A_68_P25578925	chr7:146771094-146771138	NR_027857:-2420	Nkx6-2	PROMOTER	0.240	0.634	1013.49	642.24	0.152	773.00	117.77

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P30656618	chr16:33185004-33185048	NM_176840:-130	Osbpl11	PROMOTER	0.240	0.654	1195.62	782.21	0.157	877.80	137.67
A_68_P23618576	chr5:38668524-38668568	NM_172709:-96	Otop1	PROMOTER	0.240	0.573	2753.29	1577.43	0.137	2031.58	279.02
A_68_P24808212	chr6:122289513-122289557	NM_001042623:-2501	Phc1	PROMOTER	0.240	0.588	3941.43	2316.93	0.141	2493.67	351.46
A_68_P24992435	chr7:19864459-19864503	NM_177691:918	Ppm1n	INSIDE	0.240	0.634	2121.13	1345.56	0.152	1615.66	246.37
A_68_P24933419	chr6:147212900-147212944	NM_008970:-315	Pthlh	PROMOTER	0.240	0.597	1054.80	629.68	0.143	825.32	118.20
A_68_P21838403	chr2:167758113-167758157	NM_011201:308	Ptpn1	INSIDE	0.240	0.639	2010.74	1284.23	0.153	1447.22	221.38
A_68_P26595983	chr9:66767400-66767448	NM_173413:88	Rab8b	INSIDE	0.240	0.492	1447.64	712.61	0.118	997.94	117.73
A_68_P27926646	chr11:75344654-75344698	NM_001199284:-519	Slc43a2	PROMOTER	0.240	0.383	1726.94	661.76	0.092	1306.77	120.23
A_68_P28578880	chr12:82128213-82128257	NM_001146217:440	Smoc1	INSIDE	0.240	0.443	1418.74	628.52	0.106	1109.31	117.80
A_68_P27942517	chr11:78114890-78114934	NM_017407:-180	Spag5	PROMOTER	0.240	0.552	2688.70	1483.43	0.132	2027.92	268.46
A_68_P20456744	chr1:95532440-95532484	NM_021537:-158	Stk25	PROMOTER	0.240	0.551	2664.75	1468.30	0.132	1994.89	264.16
A_68_P24160097	chr5:144984259-144984304	NM_027410:166	Tecpr1	INSIDE	0.240	0.586	2682.15	1571.99	0.141	1836.21	258.47
A_68_P27188402	chr10:62350034-62350078	NM_027384:-7294	Tet1	PROMOTER	0.240	0.498	1184.98	590.54	0.119	979.41	116.97
A_68_P28326654	chr12:31269275-31269319	NM_172049:-11	Tmem18	PROMOTER	0.240	0.441	2546.94	1123.07	0.106	1977.26	209.37
A_68_P22168170	chr3:58220169-58220213	NM_001081229:580	Tsc22d2	INSIDE	0.240	0.426	1533.22	653.35	0.102	1154.07	117.94
A_68_P28356086	chr12:36768656-36768700	NM_025359:387	Tspan13	INSIDE	0.240	0.624	4176.37	2605.91	0.150	3185.85	477.85
A_68_P26232299	chr8:124808193-124808241	NM_009569:2176	Zfpm1	INSIDE	0.240	0.490	1186.44	581.57	0.118	988.73	116.35
A_68_P24641621	chr6:91793458-91793502			Unknown	0.240	0.443	1890.14	837.97	0.106	1569.51	166.74
A_68_P26710496	chr9:88417635-88417683	ENSMUST00000097243:-952		PROMOTER	0.240	0.625	993.59	621.25	0.150	811.46	121.80
A_68_P23754560	chr5:65499168-65499212	ENSMUST00000101192:384		INSIDE	0.240	0.489	1293.39	632.28	0.117	1090.80	128.00
A_68_P25952415	chr8:73046804-73046848	NM_029366:253	2810422J05Rik	INSIDE	0.239	0.593	3218.37	1908.33	0.142	2295.64	325.10
A_68_P26085412	chr8:98330809-98330853	NR_015574:101	4930513N10Rik	INSIDE	0.239	0.528	1077.22	569.02	0.126	955.36	120.83
A_68_P22900663	chr4:48552940-48552986	NM_028137:-408	5730528L13Rik	PROMOTER	0.239	0.632	924.22	584.41	0.151	784.92	118.41
A_68_P24455806	chr6:53237701-53237745	NR_015553:434	9430076C15Rik	INSIDE	0.239	0.670	2243.97	1503.01	0.160	1827.15	292.91
A_68_P24330604	chr6:30126170-30126214	NR_038124:-430	BB283400	DIVERGENT_PROMOTER	0.239	0.436	2105.06	916.86	0.104	1573.25	163.47
A_68_P27352991	chr10:92773177-92773221	NM_013508:706	Elk3	INSIDE	0.239	0.659	956.91	630.54	0.157	775.26	121.84
A_68_P21771129	chr2:156247015-156247059	NM_001003815:249	Epb4.1l1	INSIDE	0.239	0.591	3749.62	2215.37	0.141	2627.74	370.51
A_68_P31111041	chr17:26698638-26698682	NM_026170:204	Ergic1	INSIDE	0.239	0.443	1959.41	868.94	0.106	1422.68	150.48
A_68_P28340239	chr12:33832233-33832277	NR_015602:197	F730043M19Rik	INSIDE	0.239	0.626	1297.81	812.88	0.150	996.94	149.17
A_68_P25496221	chr7:132850823-132850867	NM_207239:358	Gtf3c1	INSIDE	0.239	0.572	4038.57	2311.41	0.137	2902.89	397.17
A_68_P27827764	chr11:57644954-57644998	NM_008213:673	Hand1	INSIDE	0.239	0.588	1092.67	642.27	0.140	841.67	118.22
A_68_P22348542	chr3:96073837-96073891	NM_175666:242	Hist2h2bb	INSIDE	0.239	0.591	1160.04	685.08	0.141	867.97	122.58
A_68_P21338806	chr2:74526046-74526090	NM_013554:-3936	Hoxd10	PROMOTER	0.239	0.685	2057.06	1409.00	0.164	1567.47	257.10
A_68_P32746463	chrX:148237989-148238033	NM_021523:186	Huwe1	INSIDE	0.239	1.935	1360.84	2633.43	0.463	563.26	260.79
A_68_P26695696	chr9:85642551-85642595	NM_001081282:369	Ibtk	INSIDE	0.239	0.442	1600.14	707.26	0.106	1319.07	139.30
A_68_P24182269	chr5:149740788-149740832	NM_153572:-587	Katnal1	PROMOTER	0.239	0.629	985.18	620.05	0.151	799.08	120.28
A_68_P30491859	chr15:101269185-101269229	NM_001003668:29	Krt83	INSIDE	0.239	0.535	2013.72	1078.12	0.128	1424.27	182.29
A_68_P25484148	chr7:130521551-130521596	NM_025304:78	Lcmt1	INSIDE	0.239	0.470	1227.30	577.17	0.112	1032.20	115.86
A_68_P24126717	chr5:138070748-138070792	NM_001168652:420	Lrch4	INSIDE	0.239	0.619	3670.65	2271.46	0.148	2544.93	377.02
A_68_P21794484	chr2:160191502-160191546	NM_010658:1277	Mafb	INSIDE	0.239	0.575	1209.16	695.07	0.137	908.40	124.75
A_68_P27835445	chr11:59016315-59016359	NM_026035:318	Mrpl55	INSIDE	0.239	0.638	825.75	526.60	0.153	794.02	121.16
A_68_P21419237	chr2:90687518-90687562	NM_019758:229	Mtch2	INSIDE	0.239	0.403	1534.02	617.76	0.096	1247.03	120.04
A_68_P20823476	chr1:172519433-172519477	NM_001109985:526	Nos1ap	INSIDE	0.239	0.668	1001.56	668.97	0.160	765.96	122.22
A_68_P32134211	chr19:44831069-44831120	NM_011037:-789	Pax2	PROMOTER	0.239	0.579	1189.72	689.32	0.138	867.34	120.06
A_68_P30397292	chr15:84684469-84684513	NM_001081166:2069	Phf21b	INSIDE	0.239	0.669	978.25	654.78	0.160	764.34	122.42
A_68_P27942688	chr11:78142334-78142378	NM_201406:433	Pigs	INSIDE	0.239	0.704	1187.31	835.77	0.168	891.88	149.88
A_68_P32142315	chr19:46223136-46223180	NM_008852:-343	Pitx3	DIVERGENT_PROMOTER	0.239	0.409	1947.09	796.59	0.098	1441.84	140.82
A_68_P27901225	chr11:70354037-70354081	NM_008876:393	Pld2	INSIDE	0.239	0.674	1192.74	803.98	0.161	959.31	154.27
A_68_P31415139	chr17:86567438-86567482	NM_011104:336	Prkce	INSIDE	0.239	0.696	1353.34	941.55	0.167	1035.38	172.52
A_68_P25017607	chr7:28293097-28293141	NM_019412:8776	Prx	INSIDE	0.239	0.704	2034.55	1431.90	0.168	1479.08	249.09
A_68_P23597153	chr5:35292578-35292624	NM_173402:504	Rgs12	INSIDE	0.239	1.933	751.95	1453.25	0.463	581.31	268.95

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P20391888	chr1:82313214-82313260	NM_029777:83	Rhbdd1	INSIDE	0.239	0.479	1322.67	633.46	0.115	1026.43	117.54
A_68_P25378791	chr7:109590355-109590403	NM_009103:170	Rrm1	INSIDE	0.239	0.573	1106.47	633.78	0.137	878.19	120.27
A_68_P23576446	chr5:31395554-31395598	NM_011773:324	Slc30a3	INSIDE	0.239	0.588	2122.58	1248.39	0.140	1595.07	224.02
A_68_P30653350	chr16:32609484-32609540	NM_011638:531	Tfrc	INSIDE	0.239	0.555	1029.36	571.46	0.132	871.59	115.44
A_68_P28536527	chr12:74387503-74387547	NM_029580:174	Trmt5	INSIDE	0.239	0.548	1058.22	579.94	0.131	899.35	117.74
A_68_P27056229	chr10:34017638-34017682	NM_030203:434	Tspyl4	INSIDE	0.239	0.614	1028.06	631.73	0.147	805.14	118.10
A_68_P26809576	chr9:107465904-107465952	NM_019742:343	Tusc2	INSIDE	0.239	0.642	1442.79	925.64	0.154	1125.52	172.87
A_68_P30147669	chr15:38007832-38007883	NM_001081359:751	Ubr5	INSIDE	0.239	0.477	1329.57	633.72	0.114	1067.81	121.71
A_68_P20935543	chr1:192802468-192802514	NM_144879:387	Vash2	INSIDE	0.239	0.557	1140.56	635.48	0.133	899.07	119.93
A_68_P24057208	chr5:124170620-124170665	NM_027494:411	Zcchc8	INSIDE	0.239	0.479	1258.50	602.59	0.115	1007.44	115.37
A_68_P27899662	chr11:70051263-70051307	NM_001177601:132	0610010K14Rik	INSIDE	0.238	0.356	1752.37	623.05	0.085	1486.63	125.86
A_68_P25089660	chr7:52104564-52104618	NM_026270:-6	Akt1s1	DIVERGENT_PROMOTER	0.238	0.600	1141.66	685.17	0.143	811.48	115.94
A_68_P21421623	chr2:91105084-91105140	NM_001166024:-159	Arfgap2	PROMOTER	0.238	0.543	1243.22	674.75	0.129	926.35	119.58
A_68_P27892699	chr11:68853816-68853860	NM_011496:-5306	Aurkb	PROMOTER	0.238	0.632	1137.73	718.78	0.150	817.33	122.66
A_68_P24330603	chr6:30126052-30126101	NR_038124:-546	BB283400	DIVERGENT_PROMOTER	0.238	0.596	1088.84	649.41	0.142	830.48	118.00
A_68_P27987617	chr11:86015036-86015080	NM_178309:-363	Brip1	PROMOTER	0.238	0.550	2619.06	1439.79	0.131	2060.48	270.07
A_68_P27902011	chr11:70483347-70483401	NM_001190376:18233	Camta2	INSIDE	0.238	1.484	1534.86	2277.19	0.353	1109.53	392.16
A_68_P27980571	chr11:84771814-84771858	NM_007607:581	Car4	INSIDE	0.238	0.464	1397.64	648.16	0.110	1205.84	132.91
A_68_P31125930	chr17:29232003-29232047	NM_007669:1308	Cdkn1a	INSIDE	0.238	0.614	2904.24	1782.82	0.146	2167.87	316.25
A_68_P32287120	chrX:19637562-19637606	NM_021715:889	Chst7	INSIDE	0.238	1.576	1428.99	2251.80	0.375	622.90	233.31
A_68_P25951454	chr8:72900470-72900514	NM_016685:3046	Comp	INSIDE	0.238	0.641	2556.74	1640.01	0.153	1812.97	277.27
A_68_P25776095	chr8:35872064-35872108	NM_176933:1423	Dusp4	INSIDE	0.238	0.666	1972.23	1312.54	0.158	1699.59	268.82
A_68_P27826627	chr11:57458543-57458587	NM_134189:-379	Galnt10	PROMOTER	0.238	0.571	1133.39	647.50	0.136	886.24	120.53
A_68_P25033089	chr7:31514898-31514944	NM_008085:9455	Gapdhs	INSIDE	0.238	0.571	1186.52	677.36	0.136	875.44	118.81
A_68_P25890515	chr8:59799750-59799801	NM_010402:-4	Hand2	PROMOTER	0.238	0.673	1746.30	1175.90	0.160	1357.53	217.41
A_68_P27497666	chr10:119912069-119912113	NM_010441:1901	Hmga2	INSIDE	0.238	0.459	2402.95	1102.85	0.109	1805.91	197.24
A_68_P21901451	chr2:179838159-179838203	NM_133849:747	Hrh3	INSIDE	0.238	0.507	1884.94	955.40	0.121	1411.15	170.36
A_68_P26809621	chr9:107471601-107471645	NM_010489:129	Hyal2	INSIDE	0.238	0.650	1680.29	1091.95	0.155	1121.80	173.51
A_68_P29484669	chr14:27852875-27852920	NM_134437:711	Il17rd	INSIDE	0.238	0.594	1284.13	763.21	0.142	940.23	133.05
A_68_P29134820	chr13:72768352-72768396	NM_010574:1949	Irx2	INSIDE	0.238	0.681	1921.84	1308.10	0.162	1670.26	270.98
A_68_P26531858	chr9:55388757-55388801	NM_027397:-177	Isl2	PROMOTER	0.238	0.401	1516.64	608.33	0.096	1249.83	119.39
A_68_P29630112	chr14:58445036-58445080	NM_026401:-17	Mrp63	DIVERGENT_PROMOTER	0.238	0.635	987.47	627.24	0.151	835.14	126.44
A_68_P27558533	chr11:4494164-4494208	NM_028860:632	Mtmr3	INSIDE	0.238	0.635	1033.93	656.51	0.151	815.70	123.39
A_68_P28052462	chr11:97605811-97605862	NM_054051:182	Pip4k2b	INSIDE	0.238	0.493	1477.68	728.81	0.117	1019.80	119.71
A_68_P27630334	chr11:20101506-20101552	NM_008996:-76	Rab1	PROMOTER	0.238	0.669	2440.74	1632.71	0.159	1960.15	312.42
A_68_P30496840	chr15:102077921-102077968	NM_001042727:-1161	Rarg	PROMOTER	0.238	0.454	1342.61	609.51	0.108	1082.86	116.92
A_68_P28149048	chr11:114530351-114530395	NM_001048058:278	Rpl38	INSIDE	0.238	0.607	1349.48	819.36	0.145	1087.82	157.45
A_68_P29620554	chr14:56519301-56519352	NM_001082975:-257	Sdr39u1	PROMOTER	0.238	0.523	1255.69	657.31	0.124	952.39	118.51
A_68_P23698174	chr5:53440423-53440467	NM_011402:-147	Slc34a2	PROMOTER	0.238	0.704	1995.35	1404.58	0.167	1649.27	276.23
A_68_P22032968	chr3:31208905-31208949	NM_172861:315	Slc7a14	INSIDE	0.238	0.438	1510.22	661.38	0.104	1201.77	125.33
A_68_P28042071	chr11:95896081-95896125	NM_033568:-128	Snf8	PROMOTER	0.238	0.480	1180.69	567.05	0.114	1023.13	117.03
A_68_P27365032	chr10:94878721-94878765	NM_001168656:-624	Socs2	PROMOTER	0.238	0.542	1075.34	582.41	0.129	951.34	122.87
A_68_P28137824	chr11:112643225-112643274	NM_011448:-274	Sox9	PROMOTER	0.238	0.598	1143.53	683.66	0.142	851.53	121.00
A_68_P27780097	chr11:48630503-48630547	NM_145377:369	Trim41	INSIDE	0.238	0.608	3970.23	2413.06	0.144	3080.04	444.73
A_68_P25358180	chr7:105983274-105983321	NM_009519:-4057	Wnt11	PROMOTER	0.238	0.690	1387.69	958.00	0.164	1012.62	166.19
A_68_P24057206	chr5:124170389-124170437	NM_027494:641	Zcchc8	INSIDE	0.238	0.470	1373.75	645.48	0.112	1055.47	117.79
A_68_P31323658	chr17:69731780-69731824	NM_009547:-1515	Zfp161	PROMOTER	0.238	0.587	1532.71	899.39	0.140	1122.30	156.80
A_68_P23577059	chr5:31504739-31504783	NM_175311:-84	Zfp513	PROMOTER	0.238	0.402	1702.97	685.42	0.096	1268.39	121.69
A_68_P25500990	chr7:133679747-133679791			Unknown	0.238	0.665	1417.85	943.47	0.159	1145.32	181.71
A_68_P30958535	chr16:90727405-90727449	NM_025642:190	2610039C10Rik	INSIDE	0.237	0.541	1226.40	663.48	0.128	955.47	122.43
A_68_P26171282	chr8:114516157-114516201	NM_013925:24	Adat1	INSIDE	0.237	0.667	1148.20	765.53	0.158	900.57	142.08

						Sham group			TiO$_2$-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25833743	chr8:47085442-47085486	NM_001039562:-260	Ankrd37	PROMOTER	0.237	0.688	2837.34	1953.45	0.163	2115.47	345.86
A_68_P26818135	chr9:108976311-108976355	NM_172774:306	Atrip	INSIDE	0.237	0.444	1435.34	637.57	0.105	1131.70	119.01
A_68_P31157811	chr17:35271987-35272046	NM_057171:-170	Bag6	DIVERGENT_PROMOTER	0.237	0.590	913.18	538.76	0.140	835.90	116.77
A_68_P30605853	chr16:23983382-23983426	NM_009744:5294	Bcl6	INSIDE	0.237	0.545	1598.52	870.94	0.129	1300.39	168.24
A_68_P23151263	chr4:100450587-100450631	NM_198037:1325	Cachd1	INSIDE	0.237	0.653	1046.97	683.68	0.155	777.29	120.27
A_68_P30588542	chr16:20622241-20622285	NM_028420:-911	Camk2n2	DIVERGENT_PROMOTER	0.237	0.583	1427.54	831.71	0.138	1042.94	143.75
A_68_P26139991	chr8:109031801-109031850	NM_007665:-2965	Cdh3	PROMOTER	0.237	0.584	1016.71	593.83	0.138	846.48	117.03
A_68_P23005998	chr4:70071674-70071724	NM_145990:-297	Cdk5rap2	PROMOTER	0.237	0.622	916.61	570.54	0.147	803.27	118.31
A_68_P30978142	chr16:93884445-93884489	NM_028083:321	Chaf1b	INSIDE	0.237	0.529	2334.30	1234.14	0.126	1707.44	214.36
A_68_P21569027	chr2:119148109-119148156	NM_019454:-3387	Dll4	PROMOTER	0.237	0.551	1196.58	659.25	0.131	921.33	120.35
A_68_P23226802	chr4:115612163-115612209	NM_001025567:345	Dmbx1	INSIDE	0.237	0.694	1164.16	808.42	0.164	882.65	145.18
A_68_P30378506	chr15:81416769-81416813	NM_177821:147	Ep300	INSIDE	0.237	0.499	2553.78	1274.79	0.118	1810.22	214.05
A_68_P29996485	chr15:7761244-7761297	NM_010275:260	Gdnf	INSIDE	0.237	0.607	1081.00	655.95	0.144	811.07	116.54
A_68_P21438070	chr2:93797249-93797293	NM_001145034:-13	Gm13889	PROMOTER	0.237	0.404	1890.71	763.41	0.096	1359.35	130.06
A_68_P21311538	chr2:69723596-69723640	NM_029280:43	Mettl5	INSIDE	0.237	0.361	1892.72	683.01	0.086	1449.82	124.08
A_68_P26082840	chr8:97877404-97877448	NM_008609:1190	Mmp15	INSIDE	0.237	0.581	1182.59	687.06	0.137	876.63	120.49
A_68_P26668158	chr9:80012869-80012913	NM_001039546:50	Myo6	INSIDE	0.237	0.485	1414.70	685.63	0.115	1096.58	125.96
A_68_P25535541	chr7:139791496-139791540	NM_009123:-198	Nkx1-2	PROMOTER	0.237	0.396	1501.30	595.07	0.094	1264.16	118.71
A_68_P22347475	chr3:95908828-95908872	NM_001025613:401	Otud7b	INSIDE	0.237	0.639	4257.97	2719.83	0.151	2976.07	449.84
A_68_P20474865	chr1:99991588-99991632	NM_013626:599	Pam	INSIDE	0.237	0.516	2373.73	1225.88	0.123	1819.31	222.91
A_68_P26573403	chr9:62828953-62828997	NM_019663:-288	Pias1	PROMOTER	0.237	0.442	2496.30	1103.02	0.105	2046.95	214.24
A_68_P30346979	chr15:76063160-76063204	NM_001163542:-1374	Plec	PROMOTER	0.237	0.575	1117.57	642.64	0.136	991.08	134.88
A_68_P25502251	chr7:133935372-133935418	NM_019674:591	Ppp4c	INSIDE	0.237	0.573	1612.56	924.09	0.136	1215.37	164.85
A_68_P26714905	chr9:89805194-89805241	NM_001039655:605	Rasgrf1	INSIDE	0.237	0.593	1021.30	605.32	0.141	834.71	117.30
A_68_P28291145	chr12:25393139-25393183	NM_009104:42	Rrm2	INSIDE	0.237	0.429	2583.12	1107.31	0.101	1970.28	199.87
A_68_P20632245	chr1:136131391-136131435	NM_001008533:592	Adora1	INSIDE	0.236	0.724	3114.22	2255.32	0.171	2208.47	377.27
A_68_P27257133	chr10:75023101-75023145	NM_198860:-47	AI646023	PROMOTER	0.236	0.516	1623.55	837.00	0.122	1313.90	160.10
A_68_P22346233	chr3:95698306-95698355	NM_146134:353	Aph1a	INSIDE	0.236	0.541	1344.79	728.00	0.128	960.83	122.67
A_68_P22695195	chr4:3866261-3866305	NM_001190322:222	Chchd7	INSIDE	0.236	0.518	3915.50	2027.86	0.122	2828.14	344.95
A_68_P23401329	chr4:148961308-148961352	NM_023051:584	Clstn1	INSIDE	0.236	1.777	8284.43	14721.64	0.420	5276.83	2216.45
A_68_P23270838	chr4:124558750-124558797	NM_177671:-255	Epha10	PROMOTER	0.236	0.601	981.03	589.78	0.142	821.39	116.53
A_68_P24397654	chr6:42274034-42274078	NM_001113327:583	Fam131b	INSIDE	0.236	0.478	2129.41	1016.84	0.112	1648.23	185.38
A_68_P24991622	chr7:19717039-19717083	NM_175530:11853	Fbxo46	INSIDE	0.236	0.705	1814.17	1279.23	0.167	1475.60	245.86
A_68_P31677416	chr18:46685866-46685910	NM_173423:-263	Fem1c	PROMOTER	0.236	0.603	997.57	601.92	0.142	856.38	121.70
A_68_P20644875	chr1:138156699-138156743	NM_001101516:730	Gpr25	INSIDE	0.236	0.409	2461.74	1005.72	0.096	1911.15	184.04
A_68_P28684630	chr12:102137196-102137240	NM_001177674:516	Gpr68	INSIDE	0.236	0.446	1366.00	609.35	0.105	1112.33	117.31
A_68_P24449350	chr6:52190240-52190299	NM_008263:-5331	Hoxa10	PROMOTER	0.236	0.485	1311.09	636.18	0.114	1053.10	120.41
A_68_P24448784	chr6:52122568-52122612	NM_010452:40476	Hoxa3	INSIDE	0.236	0.633	1727.18	1093.31	0.149	1299.10	193.89
A_68_P26528146	chr9:54711666-54711710	NM_022655:127	Ireb2	INSIDE	0.236	0.537	2123.00	1139.14	0.127	1638.59	207.48
A_68_P26022960	chr8:87502192-87502236	NM_008416:433	Junb	INSIDE	0.236	0.503	1916.97	964.93	0.119	1434.02	170.04
A_68_P24038702	chr5:120885755-120885799	NM_008499:3882	Lhx5	INSIDE	0.236	0.574	2246.26	1288.75	0.135	1720.35	232.70
A_68_P21767513	chr2:155601572-155601616	NM_010808:515	Mmp24	INSIDE	0.236	1.833	7977.50	14624.27	0.433	5165.28	2239.08
A_68_P30784592	chr16:57167576-57167629	NM_023175:-157	Nit2	PROMOTER	0.236	0.637	1034.90	659.23	0.150	801.68	120.37
A_68_P23637424	chr5:42155415-42155459	NM_007524:23	Nkx3-2	INSIDE	0.236	0.668	5005.43	3344.39	0.158	3885.17	612.69
A_68_P30961642	chr16:91220360-91220404	NM_016967:-5412	Olig2	PROMOTER	0.236	0.632	1864.85	1177.71	0.149	1449.49	215.84
A_68_P23184553	chr4:106136681-106136725	NM_153565:228	Pcsk9	INSIDE	0.236	0.585	2619.25	1531.96	0.138	1790.12	246.69
A_68_P22405711	chr3:107135861-107135907	NM_001045807:323	Rbm15	INSIDE	0.236	0.524	1429.53	748.48	0.123	1113.74	137.33
A_68_P22215791	chr3:68298276-68298322	NR_036665:184	Schip1	INSIDE	0.236	0.512	1328.75	680.03	0.121	1000.96	121.08
A_68_P27940380	chr11:77744288-77744332	NM_021286:-134	Sez6	DIVERGENT_PROMOTER	0.236	0.644	2433.21	1565.98	0.152	1867.18	283.94
A_68_P30550103	chr16:11983989-11984033	NM_001174086:-195	Shisa9	PROMOTER	0.236	0.466	1546.59	721.02	0.110	1081.69	118.95
A_68_P23668871	chr5:48377683-48377731	NM_178804:3313	Slit2	INSIDE	0.236	0.450	1498.39	673.99	0.106	1081.97	114.74

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P32401092	chrX:54645722-54645768	NR_002903:-1058	Snord61	PROMOTER	0.236	1.548	1608.93	2491.29	0.365	688.02	251.46
A_68_P28307260	chr12:28026977-28027021	NM_009234:585	Sox11	INSIDE	0.236	0.492	2068.26	1018.46	0.116	1588.87	184.55
A_68_P21330516	chr2:73110924-73110977	NM_001005343:968	Sp9	INSIDE	0.236	0.599	1160.10	694.45	0.142	946.97	134.01
A_68_P25952997	chr8:73135574-73135625	NM_133772:-3386	Ssbp4	DIVERGENT_PROMOTER	0.236	0.521	1205.98	627.73	0.123	1006.37	123.76
A_68_P23616979	chr5:38430477-38430521	NM_026959:25	Stx18	INSIDE	0.236	0.529	2805.20	1483.16	0.125	2117.72	264.34
A_68_P25091864	chr7:52471284-52471328	NM_011565:184	Tead2	INSIDE	0.236	1.385	3920.49	5428.73	0.327	2823.33	923.91
A_68_P25777210	chr8:36028138-36028182	NM_175091:584	Tnks	INSIDE	0.236	0.523	3263.36	1707.65	0.123	2635.24	324.98
A_68_P24974296	chr7:13623790-13623834	NM_001168469:-193	Ube2m	PROMOTER	0.236	0.505	1239.19	625.40	0.119	1003.09	119.35
A_68_P25241766	chr7:82927030-82927082			Unknown	0.236	0.604	1072.24	647.36	0.143	842.83	120.17
A_68_P24034670	chr5:120246491-120246535	AK006202:11366		DOWNSTREAM	0.236	0.689	2481.64	1710.16	0.163	1890.26	307.36
A_68_P22349551	chr3:96279198-96279254	AK136676:11232		DOWNSTREAM	0.236	2.570	1808.56	4648.15	0.607	1306.08	792.58
A_68_P28595538	chr12:85292535-85292579	NM_023633:999	2410016O06Rik	INSIDE	0.235	0.678	1223.41	829.37	0.159	965.04	153.78
A_68_P30421419	chr15:88649879-88649923	NM_001142357:-152	Alg12	DIVERGENT_PROMOTER	0.235	0.665	2666.42	1773.58	0.156	1891.08	295.64
A_68_P26764913	chr9:99469012-99469056	NM_028768:284	Armc8	INSIDE	0.235	0.503	1708.02	858.31	0.118	1403.53	165.42
A_68_P20837653	chr1:175297800-175297844	NM_053199:4	Cadm3	INSIDE	0.235	0.486	3872.79	1882.95	0.114	2816.07	322.23
A_68_P25458768	chr7:125676881-125676932	NM_009940:-79	Coq7	PROMOTER	0.235	0.623	973.65	606.34	0.147	802.68	117.65
A_68_P21863931	chr2:172196546-172196590	NM_024199:66	Cstf1	INSIDE	0.235	0.721	2329.05	1678.69	0.169	1783.98	302.07
A_68_P28186829	chr11:120657297-120657341	NM_026824:391	Dus1l	INSIDE	0.235	0.603	1173.52	707.97	0.142	821.66	116.66
A_68_P31982703	chr19:16947053-16947097	NM_008023:1246	Foxb2	INSIDE	0.235	0.394	1598.16	629.53	0.093	1266.31	117.41
A_68_P22351744	chr3:96708735-96708782	NM_026229:463	Gpr89	INSIDE	0.235	0.518	1322.86	685.78	0.122	1099.69	133.83
A_68_P28290830	chr12:25336784-25336828	NM_178357:571	Klf11	INSIDE	0.235	1.611	1105.43	1781.36	0.379	863.67	326.94
A_68_P24057384	chr5:124199713-124199761	NM_001042421:2	Kntc1	INSIDE	0.235	0.650	1032.62	671.61	0.153	791.13	120.72
A_68_P24946855	chr7:3644343-3644387	NM_029934:763	Mboat7	INSIDE	0.235	0.516	2454.88	1266.28	0.121	2005.03	243.01
A_68_P28338223	chr12:33504900-33504944	NM_021524:-277	Nampt	PROMOTER	0.235	0.713	1627.55	1160.45	0.168	1281.67	214.98
A_68_P21345538	chr2:75542631-75542675	NM_010902:46	Nfe2l2	INSIDE	0.235	1.890	1017.95	1923.79	0.445	717.11	318.98
A_68_P26039502	chr8:90722771-90722830	NM_001164497:-311	Papd5	PROMOTER	0.235	0.596	1067.36	635.66	0.140	879.73	123.07
A_68_P21867220	chr2:172847673-172847717	NM_019547:292	Rbm38	INSIDE	0.235	0.365	2237.16	817.21	0.086	1560.60	134.19
A_68_P23234667	chr4:117156923-117156969	NM_025739:12574	Rnf220	INSIDE	0.235	0.434	1231.67	533.99	0.102	1145.56	116.51
A_68_P23313958	chr4:132324242-132324286	NM_011284:-10	Rpa2	PROMOTER	0.235	0.623	1899.16	1182.91	0.146	1397.23	204.59
A_68_P30351090	chr15:76734597-76734641	NM_012053:118	Rpl8	INSIDE	0.235	1.752	3291.12	5766.71	0.412	2381.31	980.56
A_68_P23080556	chr4:86221599-86221643	NM_178376:44	Rraga	INSIDE	0.235	0.491	1057.19	518.78	0.115	995.50	114.97
A_68_P23997436	chr5:113739937-113739981	NM_172718:-152	Sgsm1	PROMOTER	0.235	0.668	1154.23	770.79	0.157	1014.52	158.92
A_68_P28938203	chr13:34437339-34437383	NM_001033167:-309	Slc22a23	PROMOTER	0.235	0.671	944.05	633.18	0.158	787.18	124.33
A_68_P30496207	chr15:101966685-101966729	NM_001033277:-60	Spryd3	DIVERGENT_PROMOTER	0.235	0.490	1236.78	605.57	0.115	1013.36	116.77
A_68_P21266386	chr2:61643664-61643708	NM_009322:1177	Tbr1	INSIDE	0.235	0.370	1751.30	648.82	0.087	1354.19	118.14
A_68_P24946865	chr7:3645526-3645571	NM_024168:-561	Tsen34	PROMOTER	0.235	0.434	1474.09	640.26	0.102	1181.30	120.83
A_68_P28170440	chr11:118151534-118151578	NM_001033528:2	Usp36	INSIDE	0.235	0.345	1889.19	652.00	0.081	1482.46	120.12
A_68_P30476457	chr15:98620052-98620096	NM_021279:-213	Wnt1	PROMOTER	0.235	0.743	3250.75	2414.27	0.175	2345.77	409.61
A_68_P22963156	chr4:61869252-61869305	NM_009554:302	Zfp37	INSIDE	0.235	1.663	3280.03	5454.28	0.390	2359.03	920.14
A_68_P32601448	chrX:109008982-109009026			Unknown	0.235	1.575	1741.53	2743.17	0.370	745.40	276.00
A_68_P26065837	chr8:94984139-94984189			Unknown	0.235	0.506	1155.92	585.01	0.119	988.15	117.29
A_68_P28182973	chr11:120050796-120050840	NR_030682:352	2810410L24Rik	INSIDE	0.234	0.512	1211.69	620.02	0.120	1017.97	121.81
A_68_P28612795	chr12:88232987-88233039	NM_145836:-7248	6430527G18Rik	PROMOTER	0.234	0.631	1574.07	993.66	0.148	1198.97	177.21
A_68_P22353007	chr3:96962730-96962774	NM_019800:53	Acp6	INSIDE	0.234	0.698	1586.71	1107.81	0.164	1317.97	215.73
A_68_P22408053	chr3:107498878-107498922	NM_145542:566	Ahcyl1	INSIDE	0.234	0.588	2456.61	1443.28	0.138	1764.56	243.08
A_68_P28743035	chr12:112509516-112509560	NM_033603:217	Amn	INSIDE	0.234	2.192	2467.95	5408.97	0.512	1719.17	880.66
A_68_P22860480	chr4:41045173-41045217	NM_016689:22	Aqp3	INSIDE	0.234	0.480	1320.46	633.38	0.112	1077.59	120.80
A_68_P27083518	chr10:40068868-40068914	NM_001168304:-223	Cdk19	PROMOTER	0.234	0.416	1580.29	658.15	0.097	1201.49	116.90
A_68_P27543290	chr10:128242192-128242236	NM_028873:-517	Dnajc14	DIVERGENT_PROMOTER	0.234	0.612	1036.99	634.30	0.143	890.24	127.51
A_68_P31106871	chr17:26005229-26005273	NM_026633:433	Fam195a	INSIDE	0.234	0.400	2342.18	936.32	0.094	1823.49	170.70
A_68_P21345230	chr2:75498077-75498131	NR_033513:758	Gm6793	INSIDE	0.234	0.519	1346.23	698.49	0.121	1003.81	121.69

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P23417743	chr4:151660802-151660846	NM_008237:4947	Hes3	INSIDE	0.234	0.655	1545.32	1011.76	0.153	1151.32	176.17
A_68_P28042990	chr11:96064768-96064813	NM_008267:9116	Hoxb13	DOWNSTREAM	0.234	0.726	4266.44	3097.35	0.170	3090.64	523.99
A_68_P21339411	chr2:74601129-74601173	NM_010467:114	Hoxd1	INSIDE	0.234	0.471	3599.67	1695.18	0.110	2829.54	311.74
A_68_P28670942	chr12:99812802-99812846	NM_029911:3326	Kcnk10	INSIDE	0.234	0.699	4832.58	3376.41	0.163	3451.33	563.71
A_68_P24137625	chr5:140267376-140267420	NM_010757:-91	Mafk	PROMOTER	0.234	0.548	8056.66	4414.12	0.128	5679.47	727.79
A_68_P28089839	chr11:104092302-104092349	NM_001038609:-424	Mapt	PROMOTER	0.234	0.649	848.16	550.81	0.152	767.68	116.83
A_68_P28089849	chr11:104093607-104093651	NM_001038609:879	Mapt	INSIDE	0.234	0.384	1552.58	596.49	0.090	1337.82	120.28
A_68_P27935699	chr11:76891803-76891847	NR_030756:-150	Mir423	PROMOTER	0.234	0.649	2118.19	1374.49	0.152	1754.69	266.12
A_68_P27998475	chr11:88018009-88018053	NM_024174:111	Mrps23	INSIDE	0.234	0.715	2166.43	1548.72	0.167	1692.33	282.84
A_68_P25092692	chr7:52623070-52623114	NR_027802:490	Mtag2	INSIDE	0.234	0.589	1156.52	681.03	0.138	914.46	126.01
A_68_P22157975	chr3:55986717-55986761	NM_030595:885	Nbea	INSIDE	0.234	0.481	1636.72	786.77	0.112	1228.86	138.21
A_68_P26021885	chr8:87308549-87308593	NM_001081982:15669	Nfix	INSIDE	0.234	0.667	3124.48	2083.98	0.156	2177.25	340.14
A_68_P21240002	chr2:56966945-56966989	NM_013613:483	Nr4a2	INSIDE	0.234	0.598	3165.16	1891.41	0.140	2717.55	380.54
A_68_P25587561	chr7:148414503-148414549	NM_001081118:-160	Phrf1	DIVERGENT_PROMOTER	0.234	0.675	1003.84	677.39	0.158	746.82	117.88
A_68_P22825899	chr4:33334854-33334898	NM_001033225:886	Pnrc1	INSIDE	0.234	0.334	2113.96	707.02	0.078	1737.46	136.20
A_68_P27311090	chr10:85379118-85379174	NM_181650:544	Prdm4	INSIDE	0.234	0.624	1012.52	631.82	0.146	816.68	119.27
A_68_P20085267	chr1:22813048-22813092	NM_001012623:-507	Rims1	PROMOTER	0.234	0.714	2083.88	1488.27	0.167	1498.07	250.84
A_68_P25090673	chr7:52271610-52271654	NM_001008422:-13	Scaf1	DIVERGENT_PROMOTER	0.234	0.503	1312.83	660.29	0.118	1005.47	118.24
A_68_P24078667	chr5:128097745-128097789	NM_133895:-4	Slc15a4	PROMOTER	0.234	0.396	1600.03	634.00	0.093	1259.71	117.05
A_68_P28154497	chr11:115489343-115489387	NM_026071:89	Slc25a19	INSIDE	0.234	0.519	2614.44	1356.14	0.122	1961.26	238.46
A_68_P30296519	chr15:67008963-67009007	NM_009177:-540	St3gal1	PROMOTER	0.234	1.397	6262.09	8746.16	0.327	3972.83	1297.23
A_68_P21612443	chr2:127096615-127096659	NM_139308:672	Stard7	INSIDE	0.234	0.575	2492.29	1433.71	0.135	2089.87	281.79
A_68_P29855885	chr14:102007169-102007213	NM_001081278:1218	Tbc1d4	INSIDE	0.234	0.626	2309.75	1445.57	0.146	1716.71	251.11
A_68_P26696146	chr9:85737161-85737205	NM_001164792:724	Tpbg	INSIDE	0.234	0.718	8510.89	6108.73	0.168	5688.51	954.17
A_68_P23311786	chr4:131885241-131885285	NM_027925:191	Trnau1ap	INSIDE	0.234	0.647	1547.09	1000.95	0.151	1252.65	189.76
A_68_P21117412	chr2:32631071-32631115	NM_177384:-189	Ttc16	DIVERGENT_PROMOTER	0.234	0.368	1711.38	628.97	0.086	1341.61	115.48
A_68_P32791135	chrX:159266933-159266977	NM_178935:377	Txlng	INSIDE	0.234	2.256	4704.49	10614.11	0.527	2013.52	1061.48
A_68_P29531325	chr14:35487686-35487738	NM_001004436:599	Wapal	INSIDE	0.234	0.416	1647.16	684.76	0.097	1240.23	120.52
A_68_P31879121	chr18:83079861-83079905	NM_183033:-388	Zfp516	PROMOTER	0.234	0.632	975.37	616.53	0.148	821.38	121.34
A_68_P28746257	chr12:113052309-113052356	NM_026752:-48	Zfyve21	DIVERGENT_PROMOTER	0.234	0.514	3051.94	1568.17	0.120	2361.82	284.15
A_68_P20877757	chr1:182708574-182708623	AK013590:626		INSIDE	0.234	0.677	1003.11	678.65	0.158	763.77	120.90
A_68_P23588842	chr5:33775723-33775772	ENSMUST00000030994:-1903		PROMOTER	0.234	0.478	1263.06	604.05	0.112	1034.77	115.76
A_68_P21101976	chr2:30093104-30093148	NR_028299:25	1700084E18Rik	INSIDE	0.233	0.511	1287.13	657.70	0.119	1021.28	121.43
A_68_P25933301	chr8:69010356-69010400	NM_025465:28	1810029B16Rik	INSIDE	0.233	0.708	3416.36	2418.37	0.165	2503.84	413.15
A_68_P25097406	chr7:53435172-53435216	NM_011510:209	Abcc8	INSIDE	0.233	1.709	815.63	1393.61	0.397	472.43	187.76
A_68_P28081370	chr11:102636075-102636119	NM_001110778:13344	Adam11	INSIDE	0.233	0.526	1296.45	681.48	0.122	980.89	120.04
A_68_P21635701	chr2:131387590-131387634	NM_013460:409	Adra1d	INSIDE	0.233	0.736	10680.82	7860.54	0.172	7030.56	1207.73
A_68_P27896074	chr11:69419192-69419236	NM_013415:248	Atp1b2	INSIDE	0.233	0.617	1655.94	1021.30	0.144	1303.26	187.19
A_68_P22592103	chr3:142364167-142364211	NM_173763:145	Ccbl2	INSIDE	0.233	0.573	2890.94	1655.59	0.133	2268.19	302.15
A_68_P21822531	chr2:165058849-165058897	NM_174988:1365	Cdh22	INSIDE	0.233	0.655	964.16	631.37	0.152	775.00	118.13
A_68_P31259845	chr17:57201740-57201784	NM_177638:63	Crb3	INSIDE	0.233	0.557	1288.48	718.25	0.130	950.80	123.39
A_68_P23448648	chr5:4104578-4104622	NM_020010:97	Cyp51	INSIDE	0.233	0.382	1575.88	602.63	0.089	1302.24	115.83
A_68_P23262654	chr4:123088662-123088706	NM_001167918:470	D830031N03Rik	INSIDE	0.233	0.439	1564.50	686.89	0.102	1135.67	116.27
A_68_P27259217	chr10:75355978-75356022	NM_024440:-142	Derl3	PROMOTER	0.233	1.510	6147.63	9284.02	0.353	4088.95	1441.76
A_68_P31065304	chr17:15517920-15517964	NM_007865:-5155	Dll1	PROMOTER	0.233	0.429	2393.26	1026.31	0.100	1839.54	183.79
A_68_P29699002	chr14:70475220-70475264	NM_018781:-2009	Egr3	PROMOTER	0.233	0.626	1024.73	641.53	0.146	798.27	116.46
A_68_P31418980	chr17:87152677-87152727	NM_010137:-501	Epas1	PROMOTER	0.233	0.437	1621.88	708.25	0.102	1324.91	134.92
A_68_P25025744	chr7:29956908-29956952	NM_182696:1522	Ggn	INSIDE	0.233	0.510	1654.80	844.00	0.119	1331.23	158.23
A_68_P26220482	chr8:123011851-123011906	NM_198671:-887	Gse1	PROMOTER	0.233	0.659	1206.07	794.68	0.154	959.89	147.68
A_68_P23977818	chr5:110536465-110536509	NM_145147:730	Gtpbp6	INSIDE	0.233	1.433	6337.49	9079.31	0.334	4296.42	1435.34
A_68_P24038703	chr5:120885821-120885873	NM_008499:3952	Lhx5	INSIDE	0.233	0.532	1193.21	635.22	0.124	972.07	120.79

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28077443	chr11:101949878-101949922	NM_016695:-71	Mpp2	PROMOTER	0.233	0.589	3476.25	2048.62	0.138	2582.86	355.15
A_68_P30126800	chr15:34012857-34012901	NM_026002:405	Mtdh	INSIDE	0.233	0.566	1116.12	632.15	0.132	971.16	128.37
A_68_P27555611	chr11:3996953-3997010	NM_026443:-1547	Mtfp1	PROMOTER	0.233	0.678	934.18	633.01	0.158	748.48	118.13
A_68_P23392000	chr4:147413032-147413076	NM_010840:-131	Mthfr	DIVERGENT_PROMOTER	0.233	0.683	2292.33	1565.34	0.159	1870.54	297.44
A_68_P28958208	chr13:38129074-38129118	NM_024242:239	Riok1	INSIDE	0.233	0.718	3482.16	2499.46	0.168	2431.95	407.54
A_68_P30465139	chr15:96539817-96539861	NM_175121:-9709	Slc38a2	PROMOTER	0.233	0.578	1594.16	920.82	0.135	1284.27	173.18
A_68_P24114434	chr5:135517995-135518039	NM_016801:18575	Stx1a	INSIDE	0.233	2.067	2582.59	5339.45	0.482	1589.18	766.62
A_68_P24333613	chr6:30643690-30643734	NM_031998:-30	Tsga14	PROMOTER	0.233	0.486	1368.04	664.28	0.113	1098.58	124.28
A_68_P21848231	chr2:169459132-169459176	NM_080455:9	Tshz2	INSIDE	0.233	0.442	1443.67	638.70	0.103	1160.36	119.75
A_68_P20002775	chr1:3662278-3662322	NM_001011874:-721	Xkr4	PROMOTER	0.233	0.536	1206.69	647.03	0.125	940.71	117.56
A_68_P26342787	chr9:20326238-20326285	NM_001082485:-398	Zfp266	PROMOTER	0.233	0.635	1069.12	678.69	0.148	807.82	119.60
A_68_P24951572	chr7:4966899-4966945	NM_025324:-187	Zfp524	DIVERGENT_PROMOTER	0.233	0.450	1318.63	593.58	0.105	1108.13	116.21
A_68_P24954796	chr7:6237873-6237917	NM_001024928:-287	Zfp667	PROMOTER	0.233	0.626	982.30	614.46	0.146	794.62	115.95
A_68_P22360090	chr3:98231396-98231440	NM_172863:45015	Zfp697	INSIDE	0.233	0.571	1128.96	644.47	0.133	894.34	118.88
A_68_P25358042	chr7:105963755-105963799			Unknown	0.233	0.599	5371.82	3215.15	0.139	3624.26	504.82
A_68_P22283285	chr3:82931474-82931533	ENSMUST00000047876:1665		INSIDE	0.233	0.645	1220.09	787.32	0.150	817.90	122.85
A_68_P21810971	chr2:163029162-163029206	ENSMUST00000128999:-1104		PROMOTER	0.233	0.671	1963.89	1317.26	0.157	1476.06	231.09
A_68_P30371088	chr15:80086012-80086056	NM_009716:421	Atf4	INSIDE	0.232	0.672	1019.51	685.55	0.156	773.57	120.87
A_68_P30588540	chr16:20622060-20622119	NM_028420:-738	Camk2n2	DIVERGENT_PROMOTER	0.232	0.667	992.97	662.42	0.155	753.11	116.79
A_68_P31140916	chr17:31774060-31774104	NM_178224:-6	Cbs	PROMOTER	0.232	0.365	1673.06	610.58	0.085	1378.49	116.65
A_68_P27280212	chr10:79451564-79451608	NM_007725:242	Cnn2	INSIDE	0.232	0.650	3682.96	2393.12	0.151	2593.38	391.22
A_68_P27793111	chr11:51103960-51104004	NM_153393:561	Col23a1	INSIDE	0.232	0.666	2226.32	1483.60	0.154	1682.83	259.68
A_68_P22609986	chr3:145316237-145316281	NM_010516:-3309	Cyr61	PROMOTER	0.232	2.130	5851.95	12467.31	0.494	3845.62	1900.72
A_68_P30244838	chr15:57723989-57724033	NM_024207:-37	Derl1	PROMOTER	0.232	0.450	1669.72	750.80	0.104	1165.30	121.68
A_68_P26136484	chr8:108404850-108404894	NM_181594:22	Edc4	INSIDE	0.232	1.482	3712.53	5500.23	0.344	2542.61	874.56
A_68_P26657026	chr9:77765571-77765615	NM_134255:421	Elovl5	INSIDE	0.232	0.545	2279.31	1242.80	0.127	1766.07	223.49
A_68_P28609997	chr12:87763078-87763133	NM_011934:512	Esrrb	INSIDE	0.232	0.539	1254.47	675.77	0.125	972.41	121.42
A_68_P22649280	chr3:151873415-151873459	NM_057172:15	Fubp1	INSIDE	0.232	0.596	2909.92	1734.84	0.138	1925.74	266.55
A_68_P24126250	chr5:137972865-137972909	NM_010312:1571	Gnb2	INSIDE	0.232	0.470	1789.81	841.55	0.109	1339.94	146.17
A_68_P23270089	chr4:124428703-124428747	NM_008385:9603	Inpp5b	INSIDE	0.232	0.511	2225.93	1136.63	0.118	1843.02	218.23
A_68_P32028428	chr19:25311817-25311861	NM_181404:147	Kank1	INSIDE	0.232	0.545	1629.53	887.99	0.126	1274.83	161.15
A_68_P22281944	chr3:82708169-82708225	NM_023624:-300	Lrat	PROMOTER	0.232	0.448	1438.07	644.30	0.104	1180.35	122.71
A_68_P31253992	chr17:56260257-56260301	NM_029796:1091	Lrg1	INSIDE	0.232	0.475	1515.77	720.31	0.110	1143.42	125.89
A_68_P30480289	chr15:99288589-99288642	NM_001001884:-436	Nckap5l	PROMOTER	0.232	0.587	1160.68	681.02	0.136	876.01	119.15
A_68_P29031122	chr13:51266973-51267017	NM_029173:601	Nxnl2	INSIDE	0.232	0.644	2163.55	1392.28	0.149	1691.08	252.45
A_68_P21818228	chr2:164323274-164323322	NM_133779:274	Pigt	INSIDE	0.232	0.474	1533.57	726.45	0.110	1144.52	125.71
A_68_P27982135	chr11:85124644-85124688	NM_016910:-89	Ppm1d	PROMOTER	0.232	0.470	1328.03	624.62	0.109	1120.50	122.48
A_68_P32479506	chrX:75041133-75041177	NM_016979:145	Prkx	INSIDE	0.232	1.361	2009.54	2735.05	0.316	788.05	249.02
A_68_P25508223	chr7:135079560-135079608	NM_001081374:10655	Prss36	INSIDE	0.232	0.516	1289.27	665.11	0.120	976.47	116.85
A_68_P21044977	chr2:19367764-19367808	NM_018809:497	Ptf1a	INSIDE	0.232	0.402	3542.83	1422.71	0.093	2799.56	261.23
A_68_P29405444	chr14:12386788-12386841	NM_008981:748	Ptprg	INSIDE	0.232	0.674	1055.50	711.71	0.157	757.52	118.69
A_68_P22615131	chr3:146184129-146184173	NM_027371:237	Rpf1	INSIDE	0.232	0.683	1735.20	1185.85	0.159	1443.96	229.10
A_68_P28429502	chr12:52478398-52478449	NM_029825:-143	Scfd1	PROMOTER	0.232	0.411	1649.56	678.52	0.095	1260.64	120.27
A_68_P27091228	chr10:41530095-41530139	NM_001162908:-263	Sesn1	DIVERGENT_PROMOTER	0.232	0.568	2939.31	1670.16	0.132	2179.70	287.93
A_68_P27176493	chr10:60215697-60215744	NM_023596:-190	Slc29a3	PROMOTER	0.232	0.573	1256.27	719.52	0.133	891.49	118.71
A_68_P20254931	chr1:57831531-57831575	NM_144882:-152	Spats2l	PROMOTER	0.232	0.580	2911.19	1689.19	0.135	2333.82	314.72
A_68_P23607899	chr5:36826309-36826353	NM_001170454:604	Tada2b	INSIDE	0.232	0.687	2737.89	1879.93	0.159	1874.62	298.03
A_68_P31006135	chr17:3557579-3557623	NM_146074:113	Tfb1m	INSIDE	0.232	0.563	1307.09	735.85	0.131	902.22	117.79
A_68_P29506485	chr14:31362134-31362189	NM_009388:-173	Tkt	PROMOTER	0.232	0.524	1355.15	709.45	0.122	979.44	119.11
A_68_P26469618	chr9:44607091-44607135	NM_027865:187	Tmem25	INSIDE	0.232	0.566	6036.59	3415.64	0.131	4438.21	582.03
A_68_P28520552	chr12:71554055-71554099	NM_028339:-64	Tmx1	PROMOTER	0.232	0.645	936.06	603.94	0.150	787.49	117.81

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P22168178	chr3:58221125-58221170	NM_001081229:1537	Tsc22d2	INSIDE	0.232	0.391	1634.68	639.56	0.091	1344.83	121.81
A_68_P32749010	chrX:148776690-148776734	NM_029836:315	Tspyl2	INSIDE	0.232	1.354	4174.90	5653.56	0.315	1736.77	546.61
A_68_P27332828	chr10:89208416-89208468	NM_029166:707	Uhrf1bp1l	INSIDE	0.232	0.575	1160.00	667.26	0.133	881.77	117.45
A_68_P23183545	chr4:105988267-105988311	NM_183225:-529	Usp24	PROMOTER	0.232	1.519	1236.60	1878.81	0.353	961.88	339.71
A_68_P23872778	chr5:88983098-88983142	NM_023054:-387	Utp3	PROMOTER	0.232	0.583	1209.59	705.76	0.135	960.89	130.11
A_68_P29478593	chr14:26426711-26426755	NM_183208:148062	Zmiz1	INSIDE	0.232	0.562	1087.34	611.02	0.131	894.35	116.79
A_68_P29059927	chr13:56323524-56323570	ENSMUST00000127754:21755		DOWNSTREAM	0.232	0.573	1211.01	693.96	0.133	912.40	121.44
A_68_P30633252	chr16:28929399-28929443	NM_177718:364	1600021P15Rik	INSIDE	0.231	1.334	3525.37	4702.95	0.309	2392.68	738.53
A_68_P22552058	chr3:135101385-135101433	NR_030689:221	4930539J05Rik	INSIDE	0.231	0.462	1382.80	638.29	0.107	1089.09	116.36
A_68_P25645837	chr8:9978074-9978118	NM_001081119:380	Abhd13	INSIDE	0.231	0.627	931.50	584.18	0.145	819.22	118.56
A_68_P22862464	chr4:41445752-41445802	NM_001085515:4333	AI464131	INSIDE	0.231	0.610	1138.17	694.28	0.141	833.82	117.44
A_68_P31625260	chr18:36839170-36839214	NM_146085:-172	Apbb3	PROMOTER	0.231	1.575	1739.12	2739.35	0.364	1216.07	442.92
A_68_P24330605	chr6:30126242-30126286	NR_038124:-358	BB283400	DIVERGENT_PROMOTER	0.231	0.510	2454.40	1251.63	0.118	1994.97	234.89
A_68_P27927584	chr11:75493253-75493297	NM_133656:463	Crk	INSIDE	0.231	0.688	2841.10	1953.86	0.159	2229.42	354.73
A_68_P25501142	chr7:133709848-133709892	NM_146200:10	Eif3c	INSIDE	0.231	0.669	1853.08	1239.80	0.155	1422.48	219.90
A_68_P26779719	chr9:102255984-102256028	NM_001168296:1017	Ephb1	INSIDE	0.231	0.492	1373.43	676.13	0.114	1048.05	119.08
A_68_P29518106	chr14:33327086-33327130	NM_001081221:402	Ercc6	INSIDE	0.231	0.598	2380.00	1422.77	0.138	1768.56	244.24
A_68_P25724987	chr8:26149339-26149383	NM_001081187:74	Htra4	INSIDE	0.231	0.672	1954.50	1313.09	0.155	1484.86	230.09
A_68_P30366869	chr15:79335593-79335637	NM_008427:57	Kcnj4	INSIDE	0.231	0.476	1403.09	668.18	0.110	1117.27	122.75
A_68_P23657076	chr5:45911955-45911999	NM_025895:509	Med28	INSIDE	0.231	0.478	1401.70	669.62	0.110	1080.19	119.27
A_68_P21038121	chr2:17986435-17986479	NM_010804:9559	Mllt10	INSIDE	0.231	0.529	2055.16	1088.18	0.122	1603.82	196.13
A_68_P28077432	chr11:101948559-101948603	NM_016695:1249	Mpp2	INSIDE	0.231	0.591	1080.73	639.08	0.137	843.37	115.31
A_68_P23657846	chr5:46060767-46060811	NM_019438:-375	Ncapg	PROMOTER	0.231	0.607	2072.32	1257.71	0.140	1388.98	194.68
A_68_P28047030	chr11:96690616-96690669	NM_001130451:-5201	Nfe2l1	PROMOTER	0.231	0.568	1541.58	875.05	0.131	1166.96	152.97
A_68_P20642548	chr1:137815415-137815459	NM_019645:165	Pkp1	INSIDE	0.231	0.496	1469.62	729.61	0.115	1129.56	129.38
A_68_P29322934	chr13:111185727-111185771	NM_152804:497	Plk2	INSIDE	0.231	0.658	2584.00	1700.99	0.152	1944.48	295.33
A_68_P23545731	chr5:24605464-24605510	NM_145401:974	Prkag2	INSIDE	0.231	1.809	2890.53	5229.58	0.418	1905.40	795.52
A_68_P27543378	chr10:128259182-128259239	NM_025364:384	Sarnp	INSIDE	0.231	0.497	1334.36	662.70	0.115	1044.10	120.03
A_68_P21117852	chr2:32701638-32701686	NM_009295:1090	Stxbp1	INSIDE	0.231	0.465	1469.55	683.45	0.108	1104.27	118.87
A_68_P26958516	chr10:14425277-14425321	NM_025418:-3	Vta1	PROMOTER	0.231	0.633	1890.19	1195.71	0.146	1397.50	204.00
A_68_P23296886	chr4:129168678-129168722	NM_001085491:267	1700125D06Rik	INSIDE	0.230	0.414	1808.23	748.83	0.095	1441.27	137.45
A_68_P20878147	chr1:182781059-182781103	NM_145943:-201	BC031781	PROMOTER	0.230	0.459	2994.02	1372.79	0.105	2437.79	256.85
A_68_P21615856	chr2:127657274-127657318	NM_001113179:299	Bub1	INSIDE	0.230	0.398	1552.78	617.92	0.091	1339.09	122.33
A_68_P23345839	chr4:138009933-138009977	NM_025451:-1108	Camk2n1	PROMOTER	0.230	0.499	1350.39	673.19	0.114	1018.54	116.58
A_68_P21325834	chr2:72314810-72314854	NM_025866:557	Cdca7	INSIDE	0.230	0.559	1315.79	734.89	0.128	934.23	119.79
A_68_P27542787	chr10:128142015-128142063	NM_016756:69	Cdk2	INSIDE	0.230	0.446	1582.07	705.57	0.102	1206.47	123.58
A_68_P25843135	chr8:48798585-48798629	NM_172407:679	Cdkn2aip	INSIDE	0.230	0.618	1365.36	844.39	0.142	989.25	140.46
A_68_P26785468	chr9:103266904-103266948	NM_001134427:383	Cdv3	INSIDE	0.230	0.644	2629.97	1694.11	0.148	1895.91	280.58
A_68_P31666410	chr18:44540001-44540048	NM_027490:-129	Dcp2	PROMOTER	0.230	0.612	1102.95	674.76	0.141	869.71	122.60
A_68_P21568394	chr2:119034600-119034644	NM_139139:-91	Dnajc17	PROMOTER	0.230	0.469	1812.04	850.67	0.108	1319.29	142.16
A_68_P25310575	chr7:97128573-97128627	NM_021876:886	Eed	INSIDE	0.230	0.560	1210.82	678.16	0.129	895.85	115.59
A_68_P25952518	chr8:73062911-73062958	NM_007924:-639	Ell	PROMOTER	0.230	0.477	1401.11	667.69	0.109	1136.48	124.39
A_68_P20827965	chr1:173367690-173367734	NM_172647:21	F11r	INSIDE	0.230	0.607	1412.46	858.03	0.139	1210.79	168.87
A_68_P31253725	chr17:56218817-56218862	NM_008233:-240	Hdgfrp2	DIVERGENT_PROMOTER	0.230	2.071	10447.06	21635.33	0.476	6921.80	3296.94
A_68_P23598367	chr5:35448339-35448383	NM_013587:-14	Lrpap1	PROMOTER	0.230	0.573	1196.14	685.54	0.132	920.87	121.64
A_68_P23547781	chr5:25003445-25003504	NM_001081383:1127	Mll3	INSIDE	0.230	0.613	1029.87	631.36	0.141	825.57	116.54
A_68_P30463776	chr15:96291913-96291959	NM_028148:-662	Scaf11	PROMOTER	0.230	0.690	1041.08	718.10	0.158	769.02	121.80
A_68_P20038598	chr1:12982722-12982766	NM_172841:-1528	Slco5a1	PROMOTER	0.230	0.707	2334.38	1649.89	0.162	1690.97	274.48
A_68_P23281723	chr4:126412326-126412376	NM_198960:1163	Tcfap2e	INSIDE	0.230	0.514	1321.82	679.86	0.119	1017.52	120.60
A_68_P22168171	chr3:58220304-58220348	NM_001081229:716	Tsc22d2	INSIDE	0.230	0.512	2654.64	1358.59	0.118	1937.31	228.40
A_68_P31118858	chr17:27993704-27993749	NM_001080769:275	Uhrf1bp1	INSIDE	0.230	0.517	1782.60	921.56	0.119	1305.18	155.06

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P24136133	chr5:140016708-140016752	NM_013702:-3121	Uncx	PROMOTER	0.230	0.701	1942.94	1362.01	0.161	1361.68	219.39
A_68_P23340748	chr4:137150166-137150210	NM_130879:85	Usp48	INSIDE	0.230	0.638	1200.76	765.53	0.147	1080.33	158.73
A_68_P30476474	chr15:98622103-98622147	NM_021279:1837	Wnt1	INSIDE	0.230	0.554	1776.70	984.99	0.127	1383.80	176.20
A_68_P24385314	chr6:39822837-39822881			Unknown	0.230	0.703	1373.49	965.48	0.161	1176.89	190.03
A_68_P23255468	chr4:120887443-120887487	ENSMUST00000056635:225		INSIDE	0.230	0.591	3483.66	2059.02	0.136	2540.34	344.63
A_68_P26422484	chr9:35229611-35229655	ENSMUST00000154652:-1540		PROMOTER	0.230	0.359	1934.75	695.19	0.083	1457.55	120.50
A_68_P23996379	chr5:113567220-113567264	NM_172884:25091	2900026A02Rik	INSIDE	0.229	0.720	1688.07	1214.90	0.165	1308.43	215.28
A_68_P30647299	chr16:31430033-31430077	NM_001122683:1216	Bdh1	INSIDE	0.229	0.646	983.74	635.74	0.148	846.49	125.33
A_68_P30588538	chr16:20621896-20621940	NM_028420:-567	Camk2n2	DIVERGENT_PROMOTER	0.229	0.430	2415.28	1037.65	0.099	1723.21	169.85
A_68_P23362366	chr4:140695171-140695215	NM_001025608:519	D4Ertd22e	INSIDE	0.229	0.487	2705.91	1319.03	0.112	2048.62	229.04
A_68_P20842586	chr1:176432169-176432213	NM_019445:235	Fmn2	INSIDE	0.229	0.618	1096.30	677.62	0.141	846.06	119.63
A_68_P24126253	chr5:137973169-137973213	NM_010312:1267	Gnb2	INSIDE	0.229	0.518	3088.52	1599.67	0.118	2325.88	275.27
A_68_P24501234	chr6:63206775-63206826	NM_008167:-50	Grid2	PROMOTER	0.229	0.614	1104.05	677.98	0.141	870.04	122.35
A_68_P27127190	chr10:49503177-49503221	NM_001111268:5362	Grik2	INSIDE	0.229	0.713	1333.07	950.48	0.163	1153.25	188.08
A_68_P26560493	chr9:60561252-60561296	NM_026235:347	Larp6	INSIDE	0.229	0.463	1618.21	749.42	0.106	1254.34	133.27
A_68_P24563520	chr6:77194801-77194845	NM_028880:2112	Lrrtm1	INSIDE	0.229	0.567	1769.99	1003.29	0.130	1170.13	152.11
A_68_P22133753	chr3:51907587-51907631	NM_001004176:1320	Maml3	INSIDE	0.229	0.492	2548.76	1253.29	0.112	1797.82	202.21
A_68_P31151558	chr17:34162154-34162198	NR_029800:-139	Mir219-1	PROMOTER	0.229	0.552	3826.60	2112.13	0.126	2635.08	333.09
A_68_P31475749	chr18:7002345-7002389	NM_177595:2411	Mkx	INSIDE	0.229	0.503	1655.81	832.28	0.115	1285.05	148.23
A_68_P31112749	chr17:26981132-26981187	NM_008700:-2649	Nkx2-5	PROMOTER	0.229	0.613	1091.76	668.73	0.140	865.35	121.26
A_68_P32319271	chrX:34138375-34138419	NM_016783:177	Pgrmc1	INSIDE	0.229	2.513	5728.76	14398.84	0.576	2272.59	1309.61
A_68_P27921014	chr11:74336964-74337008	NM_001015046:66674	Rap1gap2	INSIDE	0.229	0.567	1792.23	1016.13	0.130	1253.56	162.62
A_68_P32790792	chrX:159198218-159198262	NM_009031:-63	Rbbp7	PROMOTER	0.229	2.049	3263.63	6685.96	0.469	1471.76	690.26
A_68_P22345833	chr3:95622982-95623029	NM_001081293:-129	Rprd2	PROMOTER	0.229	0.515	2375.11	1222.59	0.118	1766.61	208.20
A_68_P28224314	chr12:8777965-8778009	NM_011519:-215	Sdc1	PROMOTER	0.229	0.578	2685.91	1552.20	0.132	2166.00	286.47
A_68_P20427310	chr1:90967840-90967891	NM_133816:829	Sh3bp4	INSIDE	0.229	0.686	1010.05	693.00	0.157	747.24	117.40
A_68_P20788007	chr1:166178862-166178906	NM_054087:-301	Slc19a2	PROMOTER	0.229	0.623	2213.34	1379.14	0.143	1587.80	227.00
A_68_P26229668	chr8:124430812-124430856	NM_011404:752	Slc7a5	INSIDE	0.229	0.475	2550.79	1211.51	0.109	1869.54	203.48
A_68_P21626535	chr2:129626154-129626199	NM_001038635:-76	Stk35	PROMOTER	0.229	0.638	1788.07	1140.54	0.146	1277.63	186.81
A_68_P26239528	chr8:125898007-125898051	NM_001037877:294	Tcf25	INSIDE	0.229	0.415	1480.75	613.93	0.095	1293.94	122.71
A_68_P24117665	chr5:136219665-136219716	NM_172541:352	Tmem120a	INSIDE	0.229	0.419	1817.89	762.17	0.096	1454.78	139.72
A_68_P25393401	chr7:112781612-112781656	NM_018880:379	Trim3	INSIDE	0.229	2.580	12493.00	32226.47	0.591	7813.22	4616.60
A_68_P32791133	chrX:159266782-159266826	NM_178935:527	Txlng	INSIDE	0.229	2.150	4533.73	9746.57	0.493	1915.65	945.02
A_68_P26494988	chr9:48793866-48793910	NM_175482:399	Usp28	INSIDE	0.229	0.611	2573.08	1571.55	0.140	1976.90	276.95
A_68_P26815581	chr9:108480573-108480617	NM_031392:407	Wdr6	INSIDE	0.229	1.755	3847.46	6751.21	0.402	2617.85	1051.32
A_68_P28765737	chr12:117285901-117285952	NM_001004066:-8	Zfp386	PROMOTER	0.229	0.483	1357.82	655.37	0.110	1100.32	121.55
A_68_P32795837	chrX:160396347-160396391	NM_009453:230	Zrsr2	INSIDE	0.229	1.434	1335.87	1915.14	0.328	616.79	202.08
A_68_P20395056	chr1:82835794-82835840	NM_010472:-241	Agfg1	PROMOTER	0.228	0.582	1367.22	795.85	0.132	1049.33	139.00
A_68_P26351650	chr9:22193454-22193498	NM_028390:174	Anln	INSIDE	0.228	0.582	1163.79	677.46	0.132	892.77	118.28
A_68_P28836955	chr13:14156050-14156094	NM_194262:14	Arid4b	INSIDE	0.228	0.499	1692.12	844.59	0.114	1468.23	166.81
A_68_P25288544	chr7:91558102-91558146	NM_007488:345	Arnt2	INSIDE	0.228	0.557	1228.88	683.88	0.127	943.46	119.77
A_68_P31213160	chr17:47747908-47747952	NM_016859:511	Bysl	INSIDE	0.228	0.669	1659.15	1110.35	0.153	1158.95	177.21
A_68_P31921020	chr19:4097226-4097270	NM_026373:-102	Cdk2ap2	PROMOTER	0.228	0.505	3118.73	1573.89	0.115	2145.91	246.50
A_68_P31374517	chr17:79336211-79336255	NM_001024806:178	Cebpz	INSIDE	0.228	0.527	1260.97	664.02	0.120	1009.35	121.04
A_68_P28890408	chr13:25147877-25147921	NM_001195617:26	Dcdc2a	INSIDE	0.228	0.634	1612.26	1022.62	0.145	1252.37	181.08
A_68_P29787827	chr14:87540778-87540822	NM_019670:121	Diap3	INSIDE	0.228	0.321	2073.67	665.05	0.073	1605.15	117.38
A_68_P21584024	chr2:121854878-121854922	NM_144545:542	Eif3j	INSIDE	0.228	0.531	1199.32	636.98	0.121	976.93	118.55
A_68_P25328172	chr7:100228249-100228299	NM_021427:-114	Fam181b	PROMOTER	0.228	0.622	1141.45	709.95	0.142	869.60	123.51
A_68_P21007905	chr2:11699155-11699199	NM_015792:-22	Fbxo18	DIVERGENT_PROMOTER	0.228	0.687	6451.61	4434.24	0.157	4539.72	711.85
A_68_P21010261	chr2:12223501-12223545	NM_001001309:25	Itga8	INSIDE	0.228	0.609	1016.91	618.98	0.139	853.94	118.60
A_68_P25044857	chr7:35438615-35438659	NM_146188:-776	Kctd15	PROMOTER	0.228	0.466	3075.38	1431.70	0.106	2089.06	221.55

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P32252886	chrX:10294260-10294304	NM_001166635:-208	Mid1ip1	PROMOTER	0.228	1.749	3300.16	5771.56	0.400	1260.09	503.43
A_68_P21141629	chr2:37214726-37214772	NM_026176:104	Pdcl	INSIDE	0.228	0.656	929.43	609.90	0.150	810.06	121.39
A_68_P27857781	chr11:62946689-62946733	NM_008885:1699	Pmp22	INSIDE	0.228	0.715	2391.88	1709.08	0.163	1719.60	280.20
A_68_P29618605	chr14:56197304-56197348	NM_011189:-4	Psme1	PROMOTER	0.228	0.455	2276.43	1036.04	0.104	1636.18	170.03
A_68_P20557410	chr1:121400955-121400999	NM_022327:383	Ralb	INSIDE	0.228	0.470	1289.95	606.52	0.107	1098.83	117.85
A_68_P20722064	chr1:154472045-154472089	NM_016846:175	Rgl1	INSIDE	0.228	0.518	2141.40	1108.91	0.118	1617.76	190.72
A_68_P26809960	chr9:107515313-107515362	NM_001042779:-3765	Sema3b	PROMOTER	0.228	0.430	1862.68	801.38	0.098	1275.80	125.33
A_68_P23436702	chr4:154524641-154524685	NM_011385:71982	Ski	DOWNSTREAM	0.228	0.707	2730.88	1930.75	0.161	1921.47	309.69
A_68_P25016046	chr7:27981095-27981139	NM_001046637:-337	Snrpa	PROMOTER	0.228	0.556	2592.11	1441.01	0.127	1811.49	230.09
A_68_P21612309	chr2:127074111-127074155	NM_175145:422	Tmem127	INSIDE	0.228	0.615	2264.80	1391.86	0.140	2102.52	294.53
A_68_P22372021	chr3:100726069-100726113	NM_001165953:-325	Trim45	PROMOTER	0.228	0.724	3143.26	2274.43	0.165	2238.33	369.09
A_68_P20778488	chr1:164500535-164500579	NM_016796:-402	Vamp4	PROMOTER	0.228	0.611	1052.93	643.04	0.139	869.56	120.86
A_68_P25026079	chr7:30023546-30023590	NM_001110201:227	Yif1b	INSIDE	0.228	0.623	1092.98	680.64	0.142	863.65	122.69
A_68_P20914304	chr1:189432802-189432861	ENSMUST00000110939:-76		PROMOTER	0.228	0.647	1454.05	941.09	0.148	1143.24	168.99
A_68_P26132765	chr8:107813703-107813757	NM_001166394:-302	4931428F04Rik	PROMOTER	0.227	0.493	1401.74	691.31	0.112	1099.34	123.31
A_68_P31549440	chr18:22503476-22503523	NM_001167777:-90	Asxl3	PROMOTER	0.227	1.545	1348.28	2083.47	0.350	980.71	343.59
A_68_P28725223	chr12:109242384-109242437	NM_001079883:-786	Bcl11b	PROMOTER	0.227	0.611	1322.10	807.96	0.139	977.03	135.75
A_68_P27308091	chr10:84849925-84849970	NM_028709:389	Btbd11	INSIDE	0.227	0.598	1118.31	668.60	0.136	904.39	122.55
A_68_P27702677	chr11:34647134-34647181	NM_027411:-14	Ccdc99	PROMOTER	0.227	0.567	1373.61	779.00	0.129	949.47	122.32
A_68_P28555790	chr12:77866473-77866523	NM_206534:-61	Churc1	PROMOTER	0.227	0.538	1321.97	711.28	0.122	1081.85	132.15
A_68_P25693340	chr8:17534794-17534838	NM_053171:569	Csmd1	INSIDE	0.227	0.643	1476.56	950.06	0.146	1076.95	157.17
A_68_P23203752	chr4:109652831-109652875	NM_172296:2223	Dmrta2	INSIDE	0.227	0.473	1258.70	594.89	0.107	1156.24	123.89
A_68_P29615091	chr14:55545244-55545288	NM_010112:359	Efs	INSIDE	0.227	0.697	2996.73	2088.62	0.158	2246.55	354.71
A_68_P25307424	chr7:96553350-96553394	NM_008055:497	Fzd4	INSIDE	0.227	0.603	1060.52	639.19	0.137	849.41	116.30
A_68_P20875120	chr1:182262437-182262486	NR_003623:-1781	Gm5069	PROMOTER	0.227	0.471	1415.53	667.34	0.107	1133.67	121.35
A_68_P25957090	chr8:74012768-74012812	NM_032544:789	Gtpbp3	INSIDE	0.227	0.615	1880.96	1156.69	0.140	1471.00	205.56
A_68_P23560507	chr5:28398167-28398211	NM_153526:237	Insig1	INSIDE	0.227	0.447	2884.31	1288.71	0.102	2063.02	209.57
A_68_P22612825	chr3:145812772-145812816	NM_026656:-2	Mcoln2	PROMOTER	0.227	0.553	1541.66	852.82	0.125	1200.17	150.48
A_68_P29020009	chr13:48641246-48641290	NR_029725:-7627	Mirlet7a-1	PROMOTER	0.227	0.342	1970.65	673.30	0.078	1617.68	125.47
A_68_P25031432	chr7:31206971-31207015	NM_172142:-1330	Nfkbid	DIVERGENT_PROMOTER	0.227	0.654	1051.60	688.17	0.148	792.05	117.47
A_68_P23894275	chr5:92864051-92864096	NM_183392:152	Nup54	INSIDE	0.227	0.635	5751.09	3654.74	0.144	4115.74	592.88
A_68_P31849787	chr18:78033303-78033347	NM_013831:36	Pstpip2	INSIDE	0.227	0.557	3770.04	2098.95	0.126	2881.75	364.01
A_68_P31375198	chr17:79451766-79451811	NM_027455:543	Qpct	INSIDE	0.227	0.551	1256.17	692.22	0.125	989.53	123.97
A_68_P23313959	chr4:132324309-132324353	NM_011284:56	Rpa2	INSIDE	0.227	1.401	2229.35	3122.60	0.318	1580.26	503.03
A_68_P27005216	chr10:23507028-23507072	NM_011295:-35	Rps12	DIVERGENT_PROMOTER	0.227	0.325	1968.49	640.42	0.074	1604.57	118.75
A_68_P26873361	chr9:119488531-119488575	NM_021544:-418	Scn5a	PROMOTER	0.227	0.637	1505.63	959.34	0.145	1164.02	168.23
A_68_P22342533	chr3:94964490-94964535	NM_011351:-3783	Sema6c	PROMOTER	0.227	0.645	1517.74	979.46	0.146	1204.60	176.39
A_68_P30979328	chr16:94087095-94087143	NM_011377:1614	Sim2	INSIDE	0.227	0.487	1307.82	636.43	0.110	1033.86	114.14
A_68_P28689579	chr12:103367433-103367477	NM_172152:-174	Slc24a4	PROMOTER	0.227	0.522	2343.86	1222.49	0.118	1721.88	203.96
A_68_P31836541	chr18:75528547-75528591	NM_001042660:1550	Smad7	INSIDE	0.227	0.433	1579.90	684.75	0.098	1186.66	116.88
A_68_P27687371	chr11:32105349-32105400	NM_030093:-40	Snrnp25	DIVERGENT_PROMOTER	0.227	0.697	1684.48	1174.71	0.158	1181.82	186.84
A_68_P25016043	chr7:27980751-27980801	NM_001046637:3	Snrpa	INSIDE	0.227	0.682	976.34	666.12	0.155	786.18	121.56
A_68_P32143669	chr19:46471505-46471549	NM_001025391:119	Sufu	INSIDE	0.227	0.568	3769.01	2140.86	0.129	2680.27	344.84
A_68_P30405824	chr15:86045163-86045207	NM_145476:296	Tbc1d22a	INSIDE	0.227	1.886	5680.44	10712.98	0.428	3911.71	1672.61
A_68_P25618380	chr8:4677371-4677415	ENSMUST00000058918:973		DOWNSTREAM	0.227	0.570	2730.49	1557.32	0.130	1877.95	243.39
A_68_P25087380	chr7:51684809-51684853	ENSMUST00000127790:443		INSIDE	0.227	1.595	1141.73	1821.11	0.362	850.97	308.14
A_68_P27921678	chr11:74462698-74462742	NM_001081158:-276	1300001I01Rik	PROMOTER	0.226	0.460	1396.56	643.09	0.104	1256.78	130.76
A_68_P30403116	chr15:85641498-85641553	NM_001164625:602	2210021J22Rik	INSIDE	0.226	0.701	2134.13	1496.30	0.158	1606.59	254.60
A_68_P29699593	chr14:70553524-70553568	NM_146055:52	2610301G19Rik	INSIDE	0.226	0.660	2993.10	1974.52	0.149	2377.12	354.63
A_68_P26595209	chr9:66643358-66643402	NM_177583:-150	Aph1b	PROMOTER	0.226	0.460	1352.03	621.39	0.104	1192.41	123.65
A_68_P29482769	chr14:27457424-27457468	NM_007479:-236	Arf4	PROMOTER	0.226	0.645	3679.84	2373.45	0.146	2565.68	374.55

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31112417	chr17:26918235-26918282	NM_172149:235	Bnip1	INSIDE	0.226	0.574	1232.99	707.88	0.130	894.82	116.33
A_68_P26809310	chr9:107429107-107429155	NM_001174047:126920	Cacna2d2	INSIDE	0.226	0.430	1548.14	665.56	0.097	1204.64	117.14
A_68_P28688780	chr12:103213637-103213681	NM_016856:-525	Cpsf2	PROMOTER	0.226	0.477	1300.12	619.67	0.108	1093.07	117.81
A_68_P23146396	chr4:99496193-99496248	NM_145549:30	Efcab7	INSIDE	0.226	0.593	1339.13	793.48	0.134	923.42	123.66
A_68_P23232034	chr4:116691797-116691854	NM_175135:-187	Eif2b3	PROMOTER	0.226	0.465	1277.46	593.48	0.105	1150.60	120.98
A_68_P20900748	chr1:187186729-187186773	NM_029735:-223	Eprs	PROMOTER	0.226	0.542	1199.24	649.65	0.122	981.95	120.28
A_68_P21240630	chr2:57090894-57090938	NM_010274:124	Gpd2	INSIDE	0.226	0.409	1920.58	784.94	0.092	1393.48	128.66
A_68_P29942855	chr14:119537625-119537669	NM_015820:160	Hs6st3	INSIDE	0.226	0.665	2929.87	1949.12	0.151	2206.34	332.32
A_68_P31257378	chr17:56765895-56765939	NM_028782:410	Lonp1	INSIDE	0.226	0.533	1370.49	730.40	0.121	1002.40	120.89
A_68_P25979818	chr8:79426066-79426110	NM_001083906:-318	Nr3c2	DIVERGENT_PROMOTER	0.226	0.646	2683.35	1734.08	0.146	1859.18	271.02
A_68_P27211072	chr10:66748247-66748295	NM_001036293:-241	Nrbf2	PROMOTER	0.226	0.496	1248.05	618.48	0.112	1043.39	116.87
A_68_P32552413	chrX:96086058-96086102	NM_052976:244	Ophn1	INSIDE	0.226	1.785	1041.69	1858.89	0.403	475.40	191.68
A_68_P31621133	chr18:36124466-36124510	NM_028707:0	Psd2	INSIDE	0.226	0.673	1959.00	1317.70	0.152	1477.38	224.43
A_68_P22413314	chr3:108357099-108357143	NR_028538:200	Scarna2	DOWNSTREAM	0.226	0.642	1098.59	705.00	0.145	833.93	120.84
A_68_P20976256	chr2:5816062-5816106	NM_021305:315	Sec61a2	INSIDE	0.226	0.459	1341.45	615.26	0.104	1155.91	120.02
A_68_P20240053	chr1:55084178-55084222	NM_031179:122	Sf3b1	INSIDE	0.226	0.444	1384.17	614.65	0.100	1143.74	114.79
A_68_P24134132	chr5:139676747-139676791	NM_024451:145	Sun1	INSIDE	0.226	0.529	4932.70	2610.57	0.120	3774.58	451.15
A_68_P23608243	chr5:36872903-36872947	NM_001113364:348	Tbc1d14	INSIDE	0.226	0.564	1122.37	633.34	0.128	919.62	117.39
A_68_P30508110	chr16:4077547-4077591	NM_026508:242	Trap1	INSIDE	0.226	0.516	4083.99	2108.96	0.116	3328.19	387.58
A_68_P22372357	chr3:100773219-100773269	NM_001013026:342	Ttf2	INSIDE	0.226	0.574	1209.86	695.00	0.130	914.88	118.99
A_68_P25505329	chr7:134507375-134507419	NM_175560:12168	Zfp747	DOWNSTREAM	0.226	0.581	2164.11	1257.35	0.131	1676.62	220.09
A_68_P28613115	chr12:88288746-88288790	NM_173735:476	2310044G17Rik	INSIDE	0.225	1.409	2822.27	3976.08	0.317	1969.41	624.83
A_68_P30927982	chr16:85173354-85173398	NM_001198823:576	App	INSIDE	0.225	0.442	1681.20	742.41	0.100	1203.18	119.72
A_68_P30476330	chr15:98593656-98593700	NM_007478:-129	Arf3	PROMOTER	0.225	0.595	1091.17	649.54	0.134	882.99	118.50
A_68_P32208210	chr19:57684728-57684772	NM_181415:-773	Atrnl1	PROMOTER	0.225	0.598	1168.08	698.32	0.135	866.06	116.62
A_68_P27360780	chr10:94151776-94151822	NM_029852:264	Ccdc41	INSIDE	0.225	0.510	1519.35	774.16	0.114	1119.43	128.11
A_68_P26543684	chr9:57613558-57613602	NM_007713:87	Clk3	INSIDE	0.225	0.523	1385.99	724.53	0.118	1029.36	121.22
A_68_P31420723	chr17:87424816-87424860	NM_019936:-62	Cript	DIVERGENT_PROMOTER	0.225	0.716	1836.76	1314.24	0.161	1325.06	213.69
A_68_P28697531	chr12:104664203-104664252	NM_020494:-150	Ddx24	DIVERGENT_PROMOTER	0.225	0.454	1592.75	723.07	0.102	1138.88	116.34
A_68_P25672259	chr8:14096757-14096801	NM_001145965:904	Dlgap2	INSIDE	0.225	0.657	984.04	646.62	0.148	783.35	115.74
A_68_P20558188	chr1:121545438-121545482	NM_145506:117	Epb4.1l5	INSIDE	0.225	0.421	2282.47	960.48	0.095	1827.99	173.00
A_68_P22803177	chr4:28740631-28740686	NM_001122889:364	Epha7	INSIDE	0.225	0.622	1204.78	749.81	0.140	860.74	120.32
A_68_P29529255	chr14:35124395-35124439	NM_008133:504	Glud1	INSIDE	0.225	0.419	1938.13	811.39	0.094	1549.72	146.20
A_68_P27067366	chr10:36694758-36694802	NM_008229:431	Hdac2	INSIDE	0.225	0.338	1989.68	672.65	0.076	1573.38	119.47
A_68_P22957172	chr4:59594608-59594652	NM_024255:196	Hsdl2	INSIDE	0.225	0.569	1682.05	957.35	0.128	1278.50	164.03
A_68_P28556955	chr12:78063502-78063546	NM_001146176:-289	Max	PROMOTER	0.225	0.632	1880.31	1187.61	0.142	1410.83	200.35
A_68_P23245808	chr4:119165389-119165433	NM_177572:-207	Rimkla	PROMOTER	0.225	0.712	1299.82	924.89	0.160	1104.98	177.24
A_68_P21212081	chr2:51003539-51003583	NM_028810:1071	Rnd3	INSIDE	0.225	0.673	4864.49	3271.81	0.151	3367.42	509.13
A_68_P21095247	chr2:28980444-28980489	NM_198033:-45	Setx	PROMOTER	0.225	0.478	3232.84	1546.02	0.108	2561.81	276.11
A_68_P27285561	chr10:80261463-80261507	NM_013651:5	Sf3a2	INSIDE	0.225	0.461	1503.32	692.75	0.104	1146.08	118.93
A_68_P28161646	chr11:116714298-116714343	NM_011358:88	Srsf2	INSIDE	0.225	0.417	1703.04	710.00	0.094	1296.28	121.79
A_68_P24134129	chr5:139676494-139676538	NM_024451:-107	Sun1	PROMOTER	0.225	0.479	2168.67	1039.52	0.108	1474.69	159.26
A_68_P28974118	chr13:40818211-40818255	NM_001122948:7580	Tcfap2a	INSIDE	0.225	0.595	1079.99	642.85	0.134	889.72	119.32
A_68_P24459352	chr6:53770524-53770568	NM_025817:273	Tril	INSIDE	0.225	0.675	1095.07	739.25	0.152	870.73	132.26
A_68_P30140504	chr15:36723408-36723452	NM_011740:863	Ywhaz	INSIDE	0.225	0.498	2368.50	1179.93	0.112	1691.16	189.74
A_68_P27892804	chr11:68873951-68873999	NM_028005:698	2310047M10Rik	INSIDE	0.224	0.393	1791.71	703.54	0.088	1346.38	118.62
A_68_P32759042	chrX:151697320-151697364	NM_019736:300	Acot9	INSIDE	0.224	1.545	1448.06	2236.73	0.347	587.84	203.70
A_68_P25960288	chr8:74763954-74763998	NM_007456:-54	Ap1m1	PROMOTER	0.224	0.419	1594.49	668.04	0.094	1274.85	119.73
A_68_P28191918	chr11:121533998-121534047	NM_178664:443	B3gntl1	INSIDE	0.224	1.567	1903.51	2983.37	0.351	1321.69	464.28
A_68_P26846738	chr9:114752895-114752940	NM_027294:353	Cmtm8	INSIDE	0.224	0.402	2429.36	977.79	0.090	1935.55	174.75
A_68_P21784861	chr2:158594102-158594146	NM_027975:290	Fam83d	INSIDE	0.224	0.294	3051.25	896.00	0.066	2377.29	156.69

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P24839025	chr6:128388883-128388942	NR_028592:138	Gm10069	INSIDE	0.224	0.491	1224.64	600.76	0.110	1049.15	115.49
A_68_P24118365	chr5:136364296-136364340	NM_013560:530	Hspb1	INSIDE	0.224	0.692	2438.28	1688.50	0.155	1753.64	272.50
A_68_P27943941	chr11:78349868-78349912	NM_018854:-47	Ift20	DIVERGENT_PROMOTER	0.224	0.677	994.15	672.98	0.152	774.97	117.66
A_68_P26065134	chr8:94881423-94881467	NM_018826:-250	Irx5	DIVERGENT_PROMOTER	0.224	0.710	2622.75	1860.87	0.159	1783.03	282.91
A_68_P28679266	chr12:101203176-101203220	NM_001164426:490	Kcnk13	INSIDE	0.224	0.548	1392.85	763.65	0.123	1007.56	123.49
A_68_P28206067	chr12:5381571-5381617	NM_001164493:894	Klhl29	INSIDE	0.224	0.386	1891.09	730.58	0.086	1389.97	120.09
A_68_P28291795	chr12:25515888-25515932	NM_001083341:-553	Mboat2	PROMOTER	0.224	0.425	1799.10	765.28	0.095	1226.85	116.65
A_68_P29162321	chr13:78342782-78342832	NM_010151:-4563	Nr2f1	PROMOTER	0.224	0.582	1214.72	707.18	0.130	912.49	119.04
A_68_P25979819	chr8:79426229-79426273	NM_001083906:-156	Nr3c2	DIVERGENT_PROMOTER	0.224	0.633	1069.13	676.55	0.142	853.53	121.06
A_68_P29269014	chr13:101322735-101322779	NM_008756:-303	Ocln	PROMOTER	0.224	1.359	5204.64	7074.70	0.305	3479.69	1059.69
A_68_P32142236	chr19:46211273-46211317	NM_008852:11521	Pitx3	INSIDE	0.224	1.389	2293.90	3186.51	0.311	1545.80	480.40
A_68_P23308590	chr4:131393615-131393659	NM_001083119:557	Ptpru	INSIDE	0.224	1.430	2572.74	3680.22	0.321	1833.59	587.85
A_68_P21783924	chr2:158436419-158436463	NM_009508:-53	Slc32a1	PROMOTER	0.224	0.451	2642.45	1192.06	0.101	2041.59	205.90
A_68_P32150751	chr19:47654747-47654794	NM_001164639:262	Slk	INSIDE	0.224	0.664	1068.65	709.14	0.149	886.09	131.91
A_68_P27673288	chr11:29073469-29073513	NM_134034:584	Smek2	INSIDE	0.224	0.563	2869.12	1616.49	0.126	2088.09	263.61
A_68_P28160910	chr11:116555525-116555569	NM_009180:428	St6galnac2	INSIDE	0.224	0.553	1129.88	624.68	0.124	965.65	119.80
A_68_P30510783	chr16:4558483-4558531	NM_031182:1214	Tcfap4	INSIDE	0.224	0.644	1002.74	645.57	0.144	820.88	118.54
A_68_P30510788	chr16:4558960-4559004	NM_031182:738	Tcfap4	INSIDE	0.224	0.646	4333.57	2798.33	0.145	3231.19	467.51
A_68_P26564391	chr9:61221577-61221621	NM_001083927:1426	Tle3	INSIDE	0.224	0.561	1189.27	667.05	0.126	919.45	115.66
A_68_P27845263	chr11:60691958-60692002	NM_001168507:560	Tmem11	INSIDE	0.224	0.273	5352.00	1462.81	0.061	4513.81	276.73
A_68_P31992848	chr19:18824278-18824322	NM_153417:-172	Trpm6	PROMOTER	0.224	0.525	1331.08	698.30	0.118	1033.08	121.53
A_68_P31509666	chr18:14129064-14129108	NM_145492:2156	Zfp521	INSIDE	0.224	1.826	1431.31	2614.02	0.409	1103.50	451.41
A_68_P28140558	chr11:113062660-113062712	NR_015556:466	2610035D17Rik	INSIDE	0.223	0.458	1392.18	637.90	0.102	1134.67	115.94
A_68_P22350131	chr3:96402359-96402403	NM_001024851:1822	Ankrd34a	INSIDE	0.223	0.644	1039.90	669.76	0.144	816.36	117.23
A_68_P26234301	chr8:125100388-125100432	NM_009698:397	Aprt	INSIDE	0.223	0.607	2351.89	1427.00	0.135	1568.82	211.96
A_68_P24330585	chr6:30124034-30124078	NR_038124:-2566	BB283400	DIVERGENT_PROMOTER	0.223	0.446	1567.77	698.75	0.099	1168.43	116.05
A_68_P24004707	chr5:115021632-115021676	NM_001004180:3395	BC057022	INSIDE	0.223	0.650	3315.15	2155.60	0.145	2225.50	322.35
A_68_P27649060	chr11:23977147-23977191	NM_001159289:-887	Bcl11a	PROMOTER	0.223	0.636	1174.52	746.71	0.142	836.81	118.72
A_68_P20631265	chr1:135975492-135975536	NM_007570:218	Btg2	INSIDE	0.223	0.494	1402.73	693.60	0.110	1049.13	115.80
A_68_P27902141	chr11:70501579-70501623	NM_001190376:7	Camta2	INSIDE	0.223	0.408	1899.04	774.26	0.091	1384.81	125.96
A_68_P21101913	chr2:30061520-30061564	NM_172404:-323	Ccbl1	PROMOTER	0.223	0.406	3242.53	1316.38	0.091	2507.03	227.35
A_68_P24009178	chr5:115799183-115799231	NM_007748:-242	Cox6a1	PROMOTER	0.223	0.642	1190.71	764.41	0.143	831.42	118.85
A_68_P26016160	chr8:86239497-86239541	NM_197982:443	Ddx39	INSIDE	0.223	0.669	3311.86	2216.78	0.149	2072.39	309.11
A_68_P32087893	chr19:36131475-36131520	NM_008315:353	Htr7	INSIDE	0.223	0.528	1413.08	746.73	0.118	997.15	117.36
A_68_P25084097	chr7:51052779-51052823	NM_008940:-146	Klk8	PROMOTER	0.223	0.654	1079.39	705.65	0.146	821.74	119.64
A_68_P22082254	chr3:40753323-40753367	NM_001040399:-1208	Larp1b	PROMOTER	0.223	0.727	2704.73	1966.74	0.162	2073.35	336.45
A_68_P30501455	chr15:102844938-102844988	NR_030526:-378	Mir615	PROMOTER	0.223	0.682	1955.63	1334.50	0.152	1482.50	225.64
A_68_P25360744	chr7:106416416-106416460	NM_001043355:-417	Mtap6	PROMOTER	0.223	0.511	2418.34	1236.69	0.114	1740.19	198.36
A_68_P22674486	chr3:156225270-156225314	NM_177274:370	Negr1	INSIDE	0.223	0.573	2338.36	1338.93	0.128	1657.76	212.05
A_68_P32697227	chrX:136596984-136597028	NM_001081668:101	Nup62cl	INSIDE	0.223	1.655	1194.86	1977.34	0.370	551.75	203.93
A_68_P22207931	chr3:66789980-66790024	NM_025822:409	Rsrc1	INSIDE	0.223	0.484	1667.13	806.64	0.108	1515.52	163.79
A_68_P32049530	chr19:28909696-28909740	NM_009199:63	Slc1a1	INSIDE	0.223	0.399	2660.52	1061.46	0.089	1677.45	149.03
A_68_P27327921	chr10:88349290-88349347	NM_145423:582	Slc5a8	INSIDE	0.223	0.641	1035.31	663.66	0.143	815.56	116.52
A_68_P28402110	chr12:46174903-46174947	NM_144552:546	Stxbp6	INSIDE	0.223	0.691	2217.95	1531.70	0.154	1492.17	229.35
A_68_P31187140	chr17:43154341-43154385	NM_178589:859	Tnfrsf21	INSIDE	0.223	1.504	3996.57	6010.79	0.335	2823.24	946.31
A_68_P31501878	chr18:12802774-12802818	NM_028341:755	Ttc39c	INSIDE	0.223	0.558	1396.43	778.72	0.124	992.46	123.39
A_68_P30579666	chr16:18426377-18426421	NM_013711:-111	Txnrd2	PROMOTER	0.223	0.561	1220.57	684.81	0.125	1009.17	126.49
A_68_P31255135	chr17:56442788-56442838	NM_001111078:-923	Uhrf1	PROMOTER	0.223	0.671	1245.67	835.51	0.150	764.21	114.41
A_68_P26874902	chr9:119804502-119804546	NM_026236:512	Wdr48	INSIDE	0.223	0.440	1385.24	609.24	0.098	1180.24	115.63
A_68_P30421093	chr15:88582624-88582670	NM_181412:506	Zbed4	INSIDE	0.223	0.526	1384.33	728.62	0.117	1044.77	122.49
A_68_P24195533	chr5:152036016-152036060	ENSMUST00000129088:311		INSIDE	0.223	0.453	1941.21	879.85	0.101	1559.84	157.49

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P21341868	chr2:74975538-74975582	ENSMUST00000143898:295		INSIDE	0.223	0.550	1113.90	613.12	0.123	975.05	119.72
A_68_P29157707	chr13:77274878-77274925	NM_001081353:105	2210408I21Rik	INSIDE	0.222	0.579	1285.00	743.45	0.129	909.28	116.89
A_68_P28155138	chr11:115626737-115626781	NM_028014:12	2310067B10Rik	INSIDE	0.222	0.657	1110.69	729.25	0.146	842.23	122.66
A_68_P31809744	chr18:70631379-70631435	NM_172967:728	4930503L19Rik	INSIDE	0.222	0.629	1113.79	700.24	0.139	864.49	120.41
A_68_P30778447	chr16:55933919-55933975	NM_028815:1015	Cep97	INSIDE	0.222	0.440	1614.04	710.87	0.098	1224.26	119.86
A_68_P23904976	chr5:96591506-96591557	NM_144910:-522	Cnot6l	PROMOTER	0.222	1.477	2018.15	2981.57	0.329	1455.09	478.23
A_68_P28593010	chr12:84827335-84827379	NM_058212:1302	Dpf3	INSIDE	0.222	2.186	3502.32	7657.51	0.486	2189.41	1063.70
A_68_P25776082	chr8:35870564-35870608	NM_176933:-77	Dusp4	PROMOTER	0.222	0.683	2338.94	1597.35	0.151	1536.62	232.66
A_68_P22128830	chr3:51080151-51080198	NM_023502:49735	Elf2	INSIDE	0.222	0.707	1359.74	961.45	0.157	893.64	140.22
A_68_P32219507	chr19:59526323-59526367	NR_002863:6781	Emx2os	INSIDE	0.222	0.539	1342.15	723.59	0.120	1009.85	120.74
A_68_P24175503	chr5:148537797-148537841	NM_010228:-254	Flt1	PROMOTER	0.222	0.456	2386.15	1088.41	0.101	1826.77	185.09
A_68_P25531562	chr7:139158754-139158798	NM_173410:634	Gpr26	INSIDE	0.222	0.404	1661.87	671.82	0.090	1302.92	117.10
A_68_P28149601	chr11:114626740-114626784	NM_001102615:60	Kif19a	INSIDE	0.222	0.615	3182.32	1958.20	0.137	2326.78	318.00
A_68_P32016038	chr19:23209873-23209917	NM_010638:-5821	Klf9	PROMOTER	0.222	0.618	1116.76	690.02	0.137	856.02	117.19
A_68_P24946854	chr7:3644206-3644250	NM_029934:899	Mboat7	INSIDE	0.222	0.523	2317.38	1211.72	0.116	1868.31	216.60
A_68_P30567336	chr16:15863446-15863492	NM_029354:-53	Mzt2	PROMOTER	0.222	0.549	1337.26	734.18	0.122	990.04	120.68
A_68_P25031675	chr7:31250465-31250509	NR_004443:124	Nphs1as	INSIDE	0.222	0.708	2299.80	1628.55	0.157	1832.80	287.65
A_68_P25375584	chr7:108967279-108967328	NM_008887:477	Phox2a	INSIDE	0.222	3.232	2387.91	7718.57	0.718	1716.21	1232.01
A_68_P29841642	chr14:99498547-99498591	NM_029454:-83	Pibf1	PROMOTER	0.222	0.601	1780.94	1070.43	0.133	1437.93	191.69
A_68_P32238975	chrX:7151016-7151060	NM_138605:208	Ppp1r3f	INSIDE	0.222	2.207	5680.18	12533.80	0.491	2241.81	1100.11
A_68_P23433031	chr4:154008979-154009030	NM_001177995:1978	Prdm16	INSIDE	0.222	0.463	1534.85	710.42	0.103	1160.07	119.40
A_68_P21417952	chr2:90419722-90419766	NM_008982:1060	Ptprj	INSIDE	0.222	0.464	1393.67	646.07	0.103	1167.97	120.06
A_68_P22730294	chr4:11486345-11486389	NM_001039556:248	Rad54b	INSIDE	0.222	0.604	2029.09	1225.36	0.134	1473.31	197.23
A_68_P20149057	chr1:36615326-36615370	NM_001126047:-122	Sema4c	PROMOTER	0.222	0.600	1039.55	624.11	0.133	895.19	119.36
A_68_P32427553	chrX:61530261-61530305	NM_178740:-111	Slitrk4	PROMOTER	0.222	2.360	6864.58	16201.24	0.523	2553.62	1336.04
A_68_P21081137	chr2:26772296-26772346	NM_013677:-270	Surf1	PROMOTER	0.222	0.469	1525.77	716.25	0.104	1092.17	113.86
A_68_P25957479	chr8:74082789-74082840	NM_001100462:-44	Tmem221	PROMOTER	0.222	0.678	1055.74	715.89	0.150	820.15	123.37
A_68_P23429475	chr4:153535140-153535184	NM_026388:-369	Tprgl	DIVERGENT_PROMOTER	0.222	0.693	3013.74	2088.44	0.154	2198.31	338.44
A_68_P26247724	chr8:127316847-127316891	NM_198632:-50	Trim67	PROMOTER	0.222	0.629	2976.08	1871.69	0.140	2437.95	340.98
A_68_P28155496	chr11:115676513-115676557	NM_029557:482	Tsen54	INSIDE	0.222	0.409	1575.38	644.19	0.091	1320.59	120.08
A_68_P22372358	chr3:100773375-100773419	NM_001013026:190	Ttf2	INSIDE	0.222	0.456	1603.65	731.80	0.101	1212.38	122.64
A_68_P25108145	chr7:56044314-56044358	NM_028031:-36	Zdhhc13	PROMOTER	0.222	0.662	2869.26	1900.27	0.147	2287.55	336.69
A_68_P27902560	chr11:70577738-70577782	NM_177565:-188	Zfp3	PROMOTER	0.222	0.618	2629.42	1625.00	0.137	1961.89	268.95
A_68_P25008231	chr7:25862140-25862187	NM_001168506:-60	Zfp574	DIVERGENT_PROMOTER	0.222	0.680	1118.80	760.76	0.151	820.12	123.60
A_68_P20530742	chr1:114313443-114313487			Unknown	0.222	0.492	2444.72	1203.45	0.110	1809.50	198.19
A_68_P22717330	chr4:8838562-8838606			Unknown	0.222	0.519	3686.74	1913.30	0.115	2999.59	346.21
A_68_P28183969	chr11:120210906-120210950	NR_038126:937	0610009L18Rik	INSIDE	0.221	0.653	1539.12	1004.95	0.145	1088.27	157.27
A_68_P21105254	chr2:30650269-30650313	NM_198000:6937	1700001O22Rik	DOWNSTREAM	0.221	0.462	1621.13	748.23	0.102	1197.51	122.03
A_68_P28612794	chr12:88232860-88232910	NM_145836:-7120	6430527G18Rik	PROMOTER	0.221	0.481	4579.19	2202.59	0.106	3103.89	330.53
A_68_P26595474	chr9:66683005-66683049	NM_026674:-513	Aph1c	PROMOTER	0.221	0.571	2018.53	1153.26	0.126	1774.12	223.63
A_68_P25810709	chr8:42460188-42460232	NM_019734:-159	Asah1	PROMOTER	0.221	0.564	2228.79	1257.40	0.124	1636.78	203.73
A_68_P20872964	chr1:181889645-181889689	NM_001033285:-1553	Cdc42bpa	PROMOTER	0.221	0.579	1329.05	769.35	0.128	1181.58	151.12
A_68_P28555792	chr12:77866643-77866687	NM_206534:105	Churc1	INSIDE	0.221	0.540	1305.10	705.30	0.119	1024.00	122.33
A_68_P26586898	chr9:65142471-65142515	NM_001044389:391	Clpx	INSIDE	0.221	0.483	1308.51	632.29	0.107	1136.13	121.45
A_68_P28581229	chr12:82585711-82585766	NM_025461:359	Cox16	INSIDE	0.221	0.487	1436.61	699.30	0.107	1130.79	121.39
A_68_P31065263	chr17:15513198-15513242	NM_007865:-433	Dll1	PROMOTER	0.221	0.505	1418.02	716.55	0.112	1091.38	121.76
A_68_P22903299	chr4:49072794-49072838	NM_178756:483	E130309F12Rik	INSIDE	0.221	0.469	1377.16	646.06	0.104	1128.47	116.80
A_68_P21767285	chr2:155555051-155555095	NM_145537:139	Edem2	INSIDE	0.221	0.422	1513.77	638.13	0.093	1302.04	121.37
A_68_P31933631	chr19:6276479-6276524	NM_010119:-394	Ehd1	PROMOTER	0.221	0.476	1612.19	767.36	0.105	1143.85	120.40
A_68_P20562764	chr1:122500570-122500618	NM_010133:1531	En1	INSIDE	0.221	0.507	1330.92	674.70	0.112	1069.33	120.02
A_68_P30651586	chr16:32246480-32246526	NM_173439:609	Fbxo45	INSIDE	0.221	0.664	938.83	623.10	0.147	791.97	116.26

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P29631507	chr14:58695104-58695149	NM_013518:3604	Fgf9	INSIDE	0.221	0.553	1110.80	614.03	0.122	940.82	114.94
A_68_P25362945	chr7:106775610-106775654	NM_001195529:-19	Gm4980	PROMOTER	0.221	0.596	1216.15	725.10	0.132	903.27	119.17
A_68_P23417749	chr4:151661314-151661358	NM_008237:4435	Hes3	INSIDE	0.221	0.659	1411.08	929.33	0.145	1140.56	165.80
A_68_P26228504	chr8:124254834-124254878	NM_020605:398	Jph3	INSIDE	0.221	0.624	5034.56	3142.71	0.138	3573.54	492.61
A_68_P21665425	chr2:136717109-136717162	NM_001141946:7	Mkks	INSIDE	0.221	0.647	1087.20	703.64	0.143	819.68	117.01
A_68_P23536417	chr5:22940364-22940408	NM_026984:140	Mll5	INSIDE	0.221	0.425	3661.06	1556.77	0.094	2883.92	270.88
A_68_P29348446	chr13:115608303-115608349	NM_001113374:-118	Mocs2	PROMOTER	0.221	0.625	1209.20	755.22	0.138	874.37	120.87
A_68_P26742491	chr9:95459602-95459646	NM_198414:-611	Paqr9	PROMOTER	0.221	0.494	3459.56	1710.48	0.109	2436.14	266.52
A_68_P23523572	chr5:20457823-20457867	NM_001080977:-204	Rsbn1l	PROMOTER	0.221	0.564	1162.73	655.66	0.124	995.22	123.80
A_68_P31682228	chr18:47526263-47526314	NM_018744:2234	Sema6a	INSIDE	0.221	0.401	1677.78	672.30	0.089	1322.60	117.19
A_68_P32796352	chrX:160514293-160514337	NM_009173:-333	Siah1b	PROMOTER	0.221	1.672	1531.25	2560.23	0.369	718.98	265.23
A_68_P29729987	chr14:76186477-76186521	NM_026232:346	Slc25a30	INSIDE	0.221	0.461	2324.93	1071.35	0.102	1708.26	174.13
A_68_P25094689	chr7:52973005-52973055	NM_020011:-2453	Sphk2	PROMOTER	0.221	0.394	1649.80	650.58	0.087	1387.81	120.90
A_68_P29570219	chr14:45970863-45970907	NM_019637:24	Styx	INSIDE	0.221	0.507	3184.68	1614.61	0.112	2349.79	263.33
A_68_P27985638	chr11:85657554-85657604	NM_009324:11462	Tbx2	DOWNSTREAM	0.221	0.635	2955.37	1878.11	0.141	2099.88	295.11
A_68_P27693363	chr11:33103831-33103878	NM_019916:-266	Tlx3	PROMOTER	0.221	0.453	1492.55	676.80	0.100	1176.29	117.83
A_68_P29428727	chr14:17197508-17197553	NM_009409:-189	Top2b	PROMOTER	0.221	0.554	1431.70	792.82	0.123	1177.86	144.42
A_68_P31962499	chr19:12870892-12870947	NR_024093:-306	U05342	DIVERGENT_PROMOTER	0.221	0.665	1256.85	835.66	0.147	878.84	129.33
A_68_P32257888	chrX:11242196-11242240			Unknown	0.221	1.506	892.23	1343.34	0.332	417.66	138.86
A_68_P30142411	chr15:37065165-37065209			Unknown	0.221	0.605	1668.75	1009.26	0.134	1246.12	166.87
A_68_P25952418	chr8:73047097-73047144	NM_029366:-41	2810422J05Rik	DIVERGENT_PROMOTER	0.220	0.459	1642.77	754.01	0.101	1173.97	118.38
A_68_P24624507	chr6:88792017-88792061	NM_030251:-109	Abtb1	PROMOTER	0.220	1.629	9945.62	16204.31	0.358	6894.62	2468.28
A_68_P21862266	chr2:171868455-171868499	NM_175631:490	Cbln4	INSIDE	0.220	0.476	1245.34	593.24	0.105	1123.41	117.97
A_68_P20578314	chr1:125942313-125942357	NM_199021:-198	Dpp10	PROMOTER	0.220	0.698	2018.23	1408.33	0.153	1557.90	238.78
A_68_P32128057	chr19:43764144-43764188	NM_053103:-12	Entpd7	PROMOTER	0.220	0.437	1708.33	746.86	0.096	1331.71	128.00
A_68_P20012308	chr1:6349244-6349288	NM_001195732:-145	Fam150a	PROMOTER	0.220	0.552	1876.32	1035.36	0.122	1483.36	180.38
A_68_P32127031	chr19:43599236-43599283	NM_010324:-164	Got1	PROMOTER	0.220	0.351	2021.86	709.33	0.077	1499.30	115.49
A_68_P32141593	chr19:46078116-46078160	NM_176785:171	Hps6	INSIDE	0.220	0.376	1648.90	619.58	0.082	1429.07	117.87
A_68_P23312413	chr4:132019816-132019860	NM_026039:-2	Med18	PROMOTER	0.220	0.510	1309.51	667.85	0.112	1033.51	116.04
A_68_P20877310	chr1:182626954-182626998	NM_013729:189	Mixl1	INSIDE	0.220	0.511	2298.80	1175.44	0.112	1768.12	198.67
A_68_P22039663	chr3:32635419-32635463	NM_029017:237	Mrpl47	INSIDE	0.220	0.602	1443.47	868.54	0.132	1078.72	142.90
A_68_P32774623	chrX:155853132-155853176	NM_001081124:645	Mtap7d2	INSIDE	0.220	1.352	4018.89	5431.73	0.298	1763.61	525.16
A_68_P22310997	chr3:87774900-87774944	NM_016701:-92	Nes	PROMOTER	0.220	0.611	1215.89	743.21	0.134	933.88	125.51
A_68_P27897808	chr11:69715226-69715270	NM_001013414:-131	Neurl4	DIVERGENT_PROMOTER	0.220	0.490	1412.54	692.69	0.108	1118.73	120.59
A_68_P20010816	chr1:5907329-5907377	NM_010342:127	Npbwr1	INSIDE	0.220	0.567	1229.17	697.00	0.124	966.44	120.31
A_68_P22752865	chr4:15941230-15941274	NM_145950:-228	Osgin2	PROMOTER	0.220	0.591	1076.26	635.82	0.130	910.26	118.49
A_68_P21639372	chr2:132078905-132078949	NM_011045:-10	Pcna	PROMOTER	0.220	0.479	1561.67	748.74	0.105	1221.16	128.56
A_68_P21073068	chr2:25430283-25430334	NM_029293:83	Phpt1	INSIDE	0.220	0.705	2050.79	1446.58	0.155	1397.62	216.77
A_68_P28055832	chr11:98209796-98209843	NM_144828:-232	Ppp1r1b	PROMOTER	0.220	1.502	2044.06	3070.04	0.330	1364.32	449.94
A_68_P31158044	chr17:35302111-35302155	NM_001199044:-310	Prrc2a	PROMOTER	0.220	0.658	2606.73	1714.01	0.145	1756.43	253.85
A_68_P23393508	chr4:147661631-147661675	NM_001083342:422	Ptchd2	INSIDE	0.220	0.525	1671.57	877.18	0.116	1087.12	125.78
A_68_P28163122	chr11:116976258-116976302	NR_029459:-205	Sec14l1	PROMOTER	0.220	0.621	2834.40	1759.68	0.136	2013.85	274.88
A_68_P31421207	chr17:87507571-87507615	NM_019654:574	Socs5	INSIDE	0.220	0.603	1102.86	664.52	0.133	865.96	114.97
A_68_P27995859	chr11:87550663-87550719	NM_009296:-376	Supt4h1	PROMOTER	0.220	0.549	1312.14	719.86	0.120	981.68	118.25
A_68_P31752323	chr18:60755666-60755710	NM_177340:28271	Synpo	INSIDE	0.220	0.694	2519.68	1747.97	0.153	2012.45	306.92
A_68_P25465170	chr7:126863806-126863854	NM_145585:449	Thumpd1	INSIDE	0.220	0.546	1174.82	641.66	0.120	972.79	116.95
A_68_P21578169	chr2:120802714-120802767	NM_175285:-57	Tmem62	DIVERGENT_PROMOTER	0.220	0.468	1291.18	604.77	0.103	1148.64	118.44
A_68_P28314942	chr12:29436931-29436975	NM_201357:260	Tssc1	INSIDE	0.220	0.577	1189.84	686.99	0.127	895.52	113.69
A_68_P26469621	chr9:44607463-44607507	NM_138951:3550	Ttc36	INSIDE	0.220	0.554	2445.69	1355.52	0.122	1759.58	214.34
A_68_P30651942	chr16:32332504-32332548	NM_177633:189	Ubxn7	INSIDE	0.220	0.435	1879.98	816.89	0.096	1483.41	141.93
A_68_P22774764	chr4:21703668-21703712	NM_152825:274	Usp45	INSIDE	0.220	0.416	1567.03	651.39	0.092	1257.44	115.25

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31801894	chr18:69357768-69357812	AK080553:16		INSIDE	0.220	1.557	1118.87	1742.24	0.343	839.72	287.67
A_68_P23699553	chr5:53658148-53658198	NM_001145433:-172	1810013D10Rik	PROMOTER	0.219	0.673	1273.30	857.06	0.147	1110.20	163.35
A_68_P29050148	chr13:54676323-54676367	NM_019968:-29	Arl10	DIVERGENT_PROMOTER	0.219	0.331	2013.17	665.54	0.072	1613.11	116.60
A_68_P23971892	chr5:108863393-108863437	NM_007507:-17	Atp5k	PROMOTER	0.219	0.542	1340.39	726.27	0.119	982.53	116.49
A_68_P29480509	chr14:26746634-26746678	NM_025311:80	D14Ertd449e	INSIDE	0.219	0.513	3717.51	1907.51	0.112	2996.38	336.38
A_68_P32121689	chr19:42593058-42593107	NM_177464:-212	D19Ertd386e	PROMOTER	0.219	0.463	1829.26	847.56	0.101	1380.23	139.96
A_68_P26543334	chr9:57556210-57556266	NM_153799:-137	Edc3	PROMOTER	0.219	0.668	1038.76	694.08	0.146	788.01	115.20
A_68_P29061785	chr13:56623742-56623786	NM_178674:-104	Fbxl21	PROMOTER	0.219	0.471	5436.07	2558.92	0.103	4378.98	451.91
A_68_P26171001	chr8:114464407-114464460	NM_026693:-184	Gabarapl2	DIVERGENT_PROMOTER	0.219	0.643	984.49	632.93	0.141	828.49	116.56
A_68_P23968445	chr5:108154656-108154700	NM_010278:-1315	Gfi1	PROMOTER	0.219	0.620	1078.97	668.62	0.136	848.09	115.35
A_68_P20945388	chr1:194597149-194597193	NM_144881:243	Hhat	INSIDE	0.219	0.555	1192.89	661.67	0.122	1010.54	122.83
A_68_P29247521	chr13:97440411-97440457	NM_008255:457	Hmgcr	INSIDE	0.219	0.510	1283.20	654.55	0.112	1052.96	117.56
A_68_P24119630	chr5:136611720-136611770	NM_027891:200	Lrwd1	INSIDE	0.219	0.670	2503.87	1678.03	0.147	1750.50	256.69
A_68_P32742984	chrX:147247606-147247650	NM_001199246:618	Maged2	INSIDE	0.219	2.249	3314.50	7454.73	0.492	1228.13	604.81
A_68_P31130218	chr17:29989237-29989281	NM_001081160:35569	Mdga1	INSIDE	0.219	1.358	2278.29	3093.88	0.297	1689.65	501.92
A_68_P21345540	chr2:75542919-75542963	NM_010902:-242	Nfe2l2	PROMOTER	0.219	1.443	9326.85	13462.96	0.317	5986.99	1895.76
A_68_P29702205	chr14:70977218-70977273	NM_153136:-408	Nudt18	PROMOTER	0.219	0.494	1447.28	714.31	0.108	1079.99	116.63
A_68_P26460519	chr9:43047271-43047315	NM_178644:607	Oaf	INSIDE	0.219	0.536	1851.00	991.97	0.118	1439.47	169.19
A_68_P21110358	chr2:31492494-31492545	NM_001123362:-3037	Prdm12	PROMOTER	0.219	0.655	1499.15	981.63	0.143	1196.84	171.26
A_68_P29007689	chr13:46513571-46513615	NM_001081425:-76	Rbm24	PROMOTER	0.219	0.535	1288.04	689.07	0.117	1001.11	117.15
A_68_P26017900	chr8:86590423-86590471	NM_009055:-288	Rfx1	PROMOTER	0.219	0.467	1542.89	720.55	0.102	1141.34	116.58
A_68_P26926728	chr10:8606159-8606207	NM_175155:-314	Sash1	PROMOTER	0.219	0.538	1448.43	778.96	0.118	1026.36	121.00
A_68_P29645527	chr14:61253344-61253393	NM_001033272:-197	Spata13	PROMOTER	0.219	1.637	789.50	1292.71	0.358	597.57	214.18
A_68_P25510944	chr7:135603768-135603821	NM_009383:1233	Tial1	INSIDE	0.219	0.551	1134.54	625.30	0.120	977.11	117.70
A_68_P31465566	chr18:4920932-4920979	ENSMUST00000143254:-768		PROMOTER	0.219	0.634	1092.37	693.08	0.139	836.16	116.34
A_68_P23186773	chr4:106511533-106511577	ENSMUST00000151369:8971		DOWNSTREAM	0.219	0.645	1593.54	1027.15	0.141	1159.51	163.84
A_68_P21754949	chr2:153269590-153269634	NM_001001986:603	8430427H17Rik	INSIDE	0.218	0.518	3142.39	1629.16	0.113	2335.58	264.12
A_68_P32364048	chrX:45696786-45696830	NM_178782:2274	Bcorl1	INSIDE	0.218	1.818	2008.87	3651.17	0.397	794.03	315.28
A_68_P26313776	chr9:13631112-13631156	NR_037622:363	Cep57	INSIDE	0.218	0.455	1704.09	774.90	0.099	1190.57	118.27
A_68_P24091083	chr5:130363235-130363294	NM_024166:76	Chchd2	INSIDE	0.218	0.527	1457.36	767.87	0.115	1093.40	125.35
A_68_P28175184	chr11:118860828-118860872	NM_001030291:11349	Enpp7	DOWNSTREAM	0.218	0.673	1798.49	1209.95	0.147	1236.34	181.69
A_68_P23323333	chr4:134090414-134090464	NM_029759:-1771	Fam54b	PROMOTER	0.218	0.419	1983.79	832.15	0.092	1316.62	120.50
A_68_P27845563	chr11:60744900-60744958	NR_027800:441	Gm16516	INSIDE	0.218	0.557	1399.94	779.86	0.121	958.84	116.18
A_68_P29296002	chr13:106234796-106234840	NM_008308:1046	Htr1a	INSIDE	0.218	0.643	948.61	609.97	0.140	855.18	119.97
A_68_P24427997	chr6:48504680-48504727	NM_001110160:-94	Lrrc61	PROMOTER	0.218	0.455	1528.41	695.21	0.099	1205.06	119.72
A_68_P30499098	chr15:102502893-102502944	NR_030460:-621	Mir688	PROMOTER	0.218	0.642	2372.14	1523.12	0.140	1712.84	239.71
A_68_P26542420	chr9:57400417-57400461	NM_025837:121	Mpi	INSIDE	0.218	0.632	1306.03	824.99	0.138	889.75	122.52
A_68_P20412903	chr1:88479253-88479300	NM_008801:-200	Pde6d	DIVERGENT_PROMOTER	0.218	0.585	1102.76	644.58	0.127	917.18	116.84
A_68_P24123992	chr5:137463167-137463211	NM_011962:300	Plod3	INSIDE	0.218	0.530	1554.59	824.02	0.115	1028.86	118.78
A_68_P31252243	chr17:55851934-55851978	NM_028370:-30	Pot1b	PROMOTER	0.218	0.671	919.36	616.51	0.146	846.60	123.75
A_68_P23433035	chr4:154009415-154009459	NM_001177995:1546	Prdm16	INSIDE	0.218	0.516	1439.28	742.62	0.112	1070.32	120.25
A_68_P27027630	chr10:27794848-27794893	NM_008983:245	Ptprk	INSIDE	0.218	0.474	1775.42	841.13	0.103	1262.62	130.46
A_68_P21395229	chr2:84728472-84728517	NM_199223:-1645	Rtn4rl2	PROMOTER	0.218	0.511	1371.91	700.70	0.111	1068.19	118.67
A_68_P20427307	chr1:90967569-90967615	NM_133816:556	Sh3bp4	INSIDE	0.218	0.556	2192.39	1219.94	0.121	1649.27	199.62
A_68_P29033147	chr13:51663043-51663087	NM_009167:-611	Shc3	PROMOTER	0.218	0.502	1396.09	701.39	0.109	1078.14	117.96
A_68_P21081132	chr2:26771837-26771881	NM_013678:-82	Surf2	PROMOTER	0.218	0.581	1757.38	1021.63	0.127	1228.82	155.81
A_68_P26082618	chr8:97844602-97844646	NM_028532:9112	Tepp	INSIDE	0.218	0.488	1408.76	687.38	0.106	1097.57	116.57
A_68_P26023335	chr8:87561478-87561522	NM_001122843:434	Tnpo2	INSIDE	0.218	2.482	6585.83	16344.37	0.540	4234.41	2286.58
A_68_P24319967	chr6:28347629-28347673	ENSMUST00000035930:355		INSIDE	0.218	0.477	1398.99	667.09	0.104	1125.26	116.82
A_68_P28091093	chr11:104304028-104304074	NM_001081045:-445	1700081L11Rik	PROMOTER	0.217	0.441	1552.06	684.41	0.096	1209.75	115.88
A_68_P23296723	chr4:129138984-129139028	NM_133889:84	Bsdc1	INSIDE	0.217	1.938	4850.53	9399.00	0.420	3306.54	1388.52

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27266461	chr10:76628282-76628326	NM_009929:971	Col18a1	INSIDE	0.217	0.628	2195.41	1377.63	0.136	1733.46	235.82
A_68_P31101000	chr17:25151186-25151230	NM_020608:967	Cramp1l	INSIDE	0.217	0.571	8431.38	4816.82	0.124	5935.64	736.09
A_68_P27535081	chr10:126727643-126727687	NM_007837:-184	Ddit3	DIVERGENT_PROMOTER	0.217	0.702	2155.36	1513.65	0.152	1507.48	229.87
A_68_P30478224	chr15:98928096-98928143	NM_176835:-1795	Dnajc22	DIVERGENT_PROMOTER	0.217	2.356	920.59	2169.23	0.510	625.86	319.42
A_68_P29702478	chr14:71018216-71018260	NM_013514:11723	Epb4.9	INSIDE	0.217	0.546	1416.88	774.30	0.118	1084.92	128.50
A_68_P24994093	chr7:20158292-20158342	NM_027189:376	Gemin7	INSIDE	0.217	0.433	1744.46	755.51	0.094	1311.11	123.25
A_68_P21133753	chr2:35317703-35317754	NM_001145821:-783	Ggta1	PROMOTER	0.217	0.610	1035.25	631.88	0.133	870.24	115.39
A_68_P21874764	chr2:174156135-174156179	NM_001077510:567	Gnas	INSIDE	0.217	0.691	2930.84	2026.36	0.150	2257.92	339.15
A_68_P20962883	chr2:3429988-3430032	NM_015765:76	Hspa14	INSIDE	0.217	0.456	1304.03	594.09	0.099	1207.04	119.60
A_68_P24538443	chr6:71781629-71781673	NM_029673:326	Immt	INSIDE	0.217	0.595	1774.79	1056.80	0.129	1573.85	203.49
A_68_P31074422	chr17:17761131-17761175	NM_172827:301	Lnpep	INSIDE	0.217	0.675	3437.73	2320.19	0.147	2441.17	357.67
A_68_P31112801	chr17:26987616-26987660	NM_008700:-9128	Nkx2-5	PROMOTER	0.217	0.583	1235.25	719.91	0.126	966.81	122.03
A_68_P21112482	chr2:31830089-31830133	NM_172268:141	Nup214	INSIDE	0.217	0.462	1430.40	660.43	0.100	1205.86	120.66
A_68_P24172758	chr5:148081815-148081859	NM_008814:130	Pdx1	INSIDE	0.217	0.637	2676.54	1705.06	0.138	1822.81	251.55
A_68_P26951868	chr10:13272953-13272998	NM_001164195:-27	Pex3	PROMOTER	0.217	0.613	1178.92	723.07	0.133	901.64	119.76
A_68_P24123988	chr5:137462758-137462802	NM_011962:-108	Plod3	PROMOTER	0.217	0.741	3574.70	2648.17	0.161	2601.49	418.05
A_68_P22880642	chr4:45031769-45031813	NM_022811:294	Polr1e	INSIDE	0.217	0.562	1262.24	709.54	0.122	958.42	116.91
A_68_P24008582	chr5:115688344-115688391	NM_026398:2508	Pop5	INSIDE	0.217	0.659	1079.88	711.64	0.143	833.10	118.98
A_68_P20138943	chr1:34516740-34516784	NM_011206:172	Ptpn18	INSIDE	0.217	0.471	3441.33	1619.67	0.102	2469.09	252.00
A_68_P26630337	chr9:72772909-72772953	NM_028116:-526	Pygo1	PROMOTER	0.217	0.746	4817.15	3595.57	0.162	3665.08	593.01
A_68_P22405706	chr3:107135381-107135431	NM_001045807:801	Rbm15	INSIDE	0.217	0.465	1542.54	716.97	0.101	1153.45	116.49
A_68_P27278806	chr10:79229855-79229899	NR_027505:-190	Rnf126	PROMOTER	0.217	0.677	3395.37	2299.16	0.147	2693.21	396.10
A_68_P24089364	chr5:130007431-130007475	NM_172276:347	Sfswap	INSIDE	0.217	0.422	1659.11	700.53	0.091	1319.24	120.65
A_68_P27807567	chr11:53793320-53793364	NM_019723:187	Slc22a21	INSIDE	0.217	0.558	1200.61	669.52	0.121	1023.84	123.87
A_68_P23439556	chr4:154976380-154976427	NM_177186:879	Slc35e2	INSIDE	0.217	0.497	1428.41	710.37	0.108	1090.57	117.81
A_68_P26578199	chr9:63605284-63605328	NM_016769:495	Smad3	INSIDE	0.217	0.487	1865.39	909.37	0.106	1437.25	151.98
A_68_P21626534	chr2:129626071-129626115	NM_001038635:-160	Stk35	PROMOTER	0.217	0.676	1252.10	846.38	0.146	905.72	132.61
A_68_P23891540	chr5:92391970-92392018	NR_028429:87	Thap6	INSIDE	0.217	0.598	1218.87	728.40	0.130	950.96	123.28
A_68_P22319099	chr3:89196394-89196438	NM_009565:709	Zbtb7b	INSIDE	0.217	0.461	1592.61	734.56	0.100	1281.94	128.06
A_68_P30351004	chr15:76709899-76709943	NM_145916:215	Zfp7	INSIDE	0.217	0.596	1210.58	721.99	0.130	900.39	116.73
A_68_P28680481	chr12:101425433-101425477	ENSMUST00000146364:-723		PROMOTER	0.217	0.663	2268.07	1503.49	0.144	1587.82	228.01
A_68_P31918873	chr19:3708527-3708572	NM_028077:217	1810055G02Rik	INSIDE	0.216	0.664	9223.46	6124.10	0.144	6444.52	925.99
A_68_P21665424	chr2:136717006-136717053	NM_028201:76	2210009G21Rik	INSIDE	0.216	0.475	1486.99	705.78	0.103	1146.17	117.69
A_68_P24641805	chr6:91828146-91828192	NM_172730:122	C130022K22Rik	INSIDE	0.216	0.569	1374.82	781.83	0.123	998.05	122.84
A_68_P27702675	chr11:34646901-34646945	NM_027411:221	Ccdc99	INSIDE	0.216	0.342	1771.09	606.24	0.074	1558.20	114.97
A_68_P29957981	chr14:122196637-122196681	NM_134074:298	Dock9	INSIDE	0.216	0.504	2447.64	1233.96	0.109	1897.75	206.32
A_68_P25528905	chr7:138686558-138686602	NM_008257:104	Hmx3	INSIDE	0.216	0.356	2359.46	839.52	0.077	1880.21	144.42
A_68_P21339173	chr2:74570711-74570762	NM_010468:20687	Hoxd3	INSIDE	0.216	0.642	1038.19	666.11	0.139	849.83	117.73
A_68_P20351509	chr1:74997858-74997902	NM_010544:345	Ihh	INSIDE	0.216	0.535	4688.95	2509.03	0.115	3681.84	425.12
A_68_P21428210	chr2:92229536-92229580	NM_001202445:3282	Mapk8ip1	INSIDE	0.216	0.541	1363.25	737.44	0.117	1008.86	117.90
A_68_P20394350	chr1:82721424-82721468	NM_029409:-46	Mff	PROMOTER	0.216	0.666	1563.58	1041.16	0.144	1171.41	168.60
A_68_P26991374	chr10:20878723-20878777	NM_001198914:2040	Myb	INSIDE	0.216	0.623	1126.09	702.08	0.134	896.91	120.53
A_68_P20224252	chr1:51972666-51972710	NM_001161817:130	Myo1b	INSIDE	0.216	0.425	3979.41	1689.63	0.092	3162.87	289.48
A_68_P31943410	chr19:8831910-8831954	NM_016813:340	Nxf1	INSIDE	0.216	0.419	1761.24	738.39	0.091	1322.43	119.97
A_68_P21490982	chr2:104657364-104657415	NM_001123327:-536	Qser1	PROMOTER	0.216	0.577	1357.06	782.79	0.124	942.23	117.13
A_68_P30351089	chr15:76734484-76734528	NM_012053:6	Rpl8	INSIDE	0.216	2.013	4053.37	8160.62	0.434	2534.05	1100.09
A_68_P22207872	chr3:66782957-66783001	NM_013665:2715	Shox2	INSIDE	0.216	0.639	1015.17	648.97	0.138	890.26	122.84
A_68_P26998900	chr10:22365258-22365302	NM_178934:464	Slc2a12	INSIDE	0.216	0.713	3308.36	2358.11	0.154	2497.69	384.56
A_68_P25091293	chr7:52383927-52383971	NR_000002:-1115	Snord32a	PROMOTER	0.216	0.496	2853.82	1416.27	0.107	2008.95	215.02
A_68_P21081016	chr2:26758519-26758565	NM_009298:-209	Surf6	PROMOTER	0.216	0.444	1587.69	705.71	0.096	1208.72	115.86
A_68_P30374041	chr15:80542355-80542399	NM_144812:634	Tnrc6b	INSIDE	0.216	0.675	2383.47	1608.99	0.146	1698.77	247.47

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P21433080	chr2:93028458-93028502	NM_001025246:740	Trp53i11	INSIDE	0.216	0.666	1377.28	917.76	0.144	1043.00	149.90
A_68_P29473058	chr14:25598908-25598952			Unknown	0.216	0.603	1367.18	824.35	0.130	927.42	120.68
A_68_P27291139	chr10:81167549-81167593	BC064812:1		INSIDE	0.216	0.534	3162.18	1687.25	0.115	2542.55	293.39
A_68_P29050102	chr13:54666387-54666431	NM_133797:335	4833439L19Rik	INSIDE	0.215	0.664	3256.05	2160.82	0.143	2139.99	305.26
A_68_P30587615	chr16:20426603-20426647	NM_013790:-157	Abcc5	PROMOTER	0.215	0.631	1192.94	752.32	0.136	911.87	123.67
A_68_P26078867	chr8:97190919-97190966	NM_024269:-63	Arl2bp	PROMOTER	0.215	0.562	2225.49	1250.55	0.121	1533.88	185.36
A_68_P20898010	chr1:186706559-186706603	NM_178692:335	C130074G19Rik	INSIDE	0.215	0.629	1120.27	705.20	0.135	946.14	128.04
A_68_P24818072	chr6:124946958-124947002	NM_001145927:-1474	C530028O21Rik	PROMOTER	0.215	0.679	5799.59	3935.88	0.146	4114.28	599.34
A_68_P20551458	chr1:120286341-120286385	NM_001081276:728	Clasp1	INSIDE	0.215	0.601	1367.14	821.79	0.129	1065.48	137.92
A_68_P31259431	chr17:57129908-57129952	NM_017393:244	Clpp	INSIDE	0.215	0.600	1560.12	935.58	0.129	1124.24	144.91
A_68_P23401325	chr4:148960914-148960958	NM_023051:190	Clstn1	INSIDE	0.215	0.624	4047.49	2524.53	0.134	3361.42	450.60
A_68_P32121140	chr19:42505908-42505952	NM_145123:343	Crtac1	INSIDE	0.215	0.612	2052.70	1256.73	0.131	1546.30	203.26
A_68_P27287961	chr10:80645653-80645705	NM_001190474:-73	Dapk3	PROMOTER	0.215	0.593	1201.87	712.63	0.127	965.21	122.92
A_68_P21629724	chr2:130250001-130250045	NM_178762:2	Fam113a	INSIDE	0.215	0.452	1530.22	692.37	0.097	1217.98	118.45
A_68_P25549532	chr7:142129376-142129420	NM_001143802:715	Fam196a	INSIDE	0.215	0.438	1618.87	708.29	0.094	1238.96	116.41
A_68_P31260715	chr17:57387144-57387195	NM_030084:-105	Gpr108	DIVERGENT_PROMOTER	0.215	0.558	1245.72	695.29	0.120	974.77	117.10
A_68_P23333862	chr4:135980297-135980341	NM_008309:880	Htr1d	INSIDE	0.215	0.525	2722.47	1430.04	0.113	2013.17	227.22
A_68_P28041932	chr11:95868837-95868881	NM_009951:-1600	Igf2bp1	PROMOTER	0.215	0.678	3053.63	2071.81	0.146	2236.41	326.97
A_68_P24325220	chr6:29161862-29161906	NM_011829:387	Impdh1	INSIDE	0.215	0.573	1491.16	854.85	0.123	969.70	119.71
A_68_P27927256	chr11:75444673-75444717	NM_008916:173	Inpp5k	INSIDE	0.215	0.604	2194.17	1324.53	0.130	1601.96	207.50
A_68_P23297039	chr4:129191585-129191629	NM_010807:782	Marcksl1	INSIDE	0.215	0.451	2018.76	909.69	0.097	1618.42	156.86
A_68_P27924617	chr11:74985774-74985818	NR_029794:-1093	Mir212	DIVERGENT_PROMOTER	0.215	0.495	2420.60	1198.01	0.106	1753.87	186.61
A_68_P25578888	chr7:146767137-146767194	NR_027857:1531	Nkx6-2	INSIDE	0.215	1.487	770.38	1145.54	0.320	626.56	200.61
A_68_P27796178	chr11:51669754-51669800	NM_199299:1207	Phf15	INSIDE	0.215	1.880	904.15	1700.07	0.404	548.44	221.76
A_68_P21820163	chr2:164683274-164683318	NM_011125:-88	Pltp	PROMOTER	0.215	0.543	2459.64	1334.68	0.117	1895.58	221.18
A_68_P28197876	chr12:3960172-3960216	NM_008895:5244	Pomc	INSIDE	0.215	0.617	1693.45	1044.97	0.132	1304.22	172.63
A_68_P21909033	chr2:180922121-180922165	NM_025598:95	Ppdpf	INSIDE	0.215	0.683	2411.20	1648.05	0.147	1744.28	256.12
A_68_P23230433	chr4:116358143-116358188	NM_011034:-38	Prdx1	PROMOTER	0.215	0.514	1789.23	919.01	0.110	1275.88	140.81
A_68_P32054982	chr19:29887617-29887661	NM_177721:-174	Ranbp6	PROMOTER	0.215	0.635	1252.81	794.95	0.136	978.17	133.14
A_68_P25091294	chr7:52384091-52384135	NM_009438:-7	Rpl13a	PROMOTER	0.215	0.508	1412.29	716.96	0.109	1088.05	118.93
A_68_P23768841	chr5:67998640-67998694	NM_001033415:-455	Shisa3	PROMOTER	0.215	0.548	1358.69	745.24	0.118	1042.23	123.18
A_68_P25023456	chr7:29551693-29551750	NM_001122765:-49	Sirt2	DIVERGENT_PROMOTER	0.215	0.529	1418.61	750.93	0.114	1041.82	118.62
A_68_P24134127	chr5:139676250-139676294	NM_024451:-351	Sun1	PROMOTER	0.215	0.545	3313.35	1806.29	0.117	2218.98	259.55
A_68_P25502831	chr7:134028530-134028574	NM_001163774:-71	Taok2	PROMOTER	0.215	0.532	1210.85	643.63	0.114	1093.88	124.80
A_68_P28974207	chr13:40829034-40829090	NM_001122948:-3250	Tcfap2a	PROMOTER	0.215	0.599	1215.48	727.99	0.129	918.48	118.31
A_68_P24431873	chr6:49213588-49213632	NM_198102:441	Tra2a	INSIDE	0.215	0.626	2953.52	1847.72	0.134	2091.01	280.83
A_68_P29982442	chr15:5135931-5135975	NM_026213:393	Ttc33	INSIDE	0.215	0.512	2213.53	1132.96	0.110	1641.21	180.60
A_68_P29056625	chr13:55816369-55816420	NM_175150:384	Txndc15	INSIDE	0.215	0.578	1333.07	770.55	0.124	943.04	117.21
A_68_P26345605	chr9:20935853-20935897	NM_001205312:-155	Tyk2	PROMOTER	0.215	0.430	1723.99	740.76	0.092	1306.52	120.43
A_68_P31092406	chr17:23701243-23701288	NM_001033496:-72	Zfp213	PROMOTER	0.215	0.467	1510.69	705.92	0.100	1222.53	122.54
A_68_P29961931	chr14:122873762-122873806	NM_009574:-821	Zic2	DIVERGENT_PROMOTER	0.215	0.639	1897.42	1212.25	0.137	1310.39	179.67
A_68_P24329524	chr6:29935157-29935209	ENSMUST00000124522:-146		PROMOTER	0.215	1.545	1914.40	2958.60	0.332	1385.72	459.46
A_68_P30413825	chr15:87375567-87375611	ENSMUST00000169110:685		INSIDE	0.215	0.395	2089.00	824.78	0.085	1382.39	117.45
A_68_P23424431	chr4:152748069-152748119	NM_001099299:108845	Ajap1	INSIDE	0.214	2.353	842.68	1982.91	0.504	619.09	311.99
A_68_P26818139	chr9:108976760-108976804	NM_172774:-144	Atrip	PROMOTER	0.214	0.492	1577.61	775.75	0.105	1148.62	120.80
A_68_P20827006	chr1:173200478-173200522	NM_020579:42	B4galt3	INSIDE	0.214	0.567	1207.57	684.57	0.122	980.32	119.18
A_68_P32139026	chr19:45616482-45616535	NM_001037758:178285	Btrc	DOWNSTREAM	0.214	0.665	1005.56	668.88	0.142	866.88	123.16
A_68_P20887292	chr1:184447385-184447429	NM_009794:208	Capn2	INSIDE	0.214	0.529	1722.29	911.49	0.113	1424.86	161.52
A_68_P25313622	chr7:97591232-97591276	NM_145151:-36	Crebzf	PROMOTER	0.214	0.476	1463.37	697.12	0.102	1187.97	121.08
A_68_P30356903	chr15:77800770-77800814	NM_018749:462	Eif3d	INSIDE	0.214	0.401	1814.73	726.86	0.086	1402.05	120.45
A_68_P26531721	chr9:55359505-55359549	NM_145615:524	Etfa	INSIDE	0.214	0.669	924.00	618.42	0.144	808.91	116.11

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25273842	chr7:88907926-88907970	NM_025997:110	Fam103a1	INSIDE	0.214	0.506	1396.06	705.75	0.108	1135.26	122.96
A_68_P28080441	chr11:102467523-102467567	NM_020510:1800	Fzd2	INSIDE	0.214	0.443	1719.82	762.55	0.095	1281.40	121.74
A_68_P21147620	chr2:38204034-38204078	NM_010710:-2771	Lhx2	PROMOTER	0.214	0.698	1219.42	850.76	0.149	904.37	134.90
A_68_P24639527	chr6:91466074-91466119	NM_026309:68	Lsm3	INSIDE	0.214	0.481	1591.63	765.80	0.103	1182.52	121.51
A_68_P32539363	chrX:91786834-91786878	NM_019791:557	Maged1	INSIDE	0.214	1.969	2039.95	4016.39	0.422	861.74	363.89
A_68_P22793477	chr4:26273660-26273704	NM_172865:117	Manea	INSIDE	0.214	0.522	2042.56	1066.96	0.112	1569.08	175.51
A_68_P31930244	chr19:5696279-5696323	NM_022012:7170	Map3k11	INSIDE	0.214	0.664	1221.58	811.28	0.142	884.26	125.39
A_68_P27535216	chr10:126748924-126748968	NM_001003913:-104	Mars	PROMOTER	0.214	0.513	1570.58	806.44	0.110	1103.63	121.01
A_68_P28556954	chr12:78063431-78063475	NM_001146176:-217	Max	PROMOTER	0.214	0.552	1344.60	742.55	0.118	1011.22	119.36
A_68_P23394433	chr4:147822470-147822515	NM_020009:-198	Mtor	DIVERGENT_PROMOTER	0.214	0.631	1215.94	767.22	0.135	861.85	116.54
A_68_P27184376	chr10:61596437-61596481	NM_009719:621	Neurog3	INSIDE	0.214	0.611	4051.69	2475.51	0.131	2544.56	332.73
A_68_P21740960	chr2:150612370-150612414	NM_153781:-139	Pygb	PROMOTER	0.214	0.551	1328.47	731.88	0.118	995.95	117.64
A_68_P32672688	chrX:131120583-131120633	NM_019865:416	Rpl36a	INSIDE	0.214	1.483	1086.35	1610.71	0.317	406.96	128.91
A_68_P29879718	chr14:106296554-106296598	NM_011897:-540	Spry2	PROMOTER	0.214	0.522	1234.23	643.73	0.111	1053.87	117.43
A_68_P30546421	chr16:11134214-11134258	NM_029582:389	Txndc11	INSIDE	0.214	0.540	1251.05	675.46	0.116	1053.64	121.97
A_68_P31620975	chr18:36092956-36093005			Unknown	0.214	0.546	1390.76	759.12	0.117	1021.83	119.28
A_68_P27095871	chr10:42333813-42333861	ENSMUST00000144806:30193		INSIDE	0.214	1.679	726.43	1219.37	0.360	492.51	177.25
A_68_P27992495	chr11:86900155-86900199	NM_024262:103	1200011M11Rik	INSIDE	0.213	0.674	1512.21	1018.51	0.143	1136.18	162.92
A_68_P28607941	chr12:87423506-87423550	NM_001199843:18	1700019E19Rik	INSIDE	0.213	0.647	1038.30	672.16	0.138	855.70	118.19
A_68_P23189064	chr4:106850847-106850891	NM_025617:103	2210012G02Rik	INSIDE	0.213	0.526	2225.36	1170.43	0.112	1595.14	178.77
A_68_P21487320	chr2:103963515-103963559	NM_026634:611	A930018P22Rik	INSIDE	0.213	0.547	1711.64	936.35	0.116	1350.53	157.27
A_68_P31144953	chr17:32457424-32457468	NM_019774:652	Akap8	INSIDE	0.213	0.556	1507.99	838.82	0.118	1145.46	135.54
A_68_P23237065	chr4:117559612-117559656	NM_033617:300	Atp6v0b	INSIDE	0.213	0.361	1985.78	716.44	0.077	1563.17	120.25
A_68_P31921523	chr19:4169744-4169788	NM_134148:5713	Carns1	INSIDE	0.213	0.718	2056.57	1476.48	0.153	1352.51	206.71
A_68_P31126793	chr17:29375333-29375377	NM_153166:-619	Cpne5	PROMOTER	0.213	0.657	4373.03	2873.01	0.140	3311.27	463.04
A_68_P25504836	chr7:134404187-134404231	NM_023203:-27	Dctpp1	PROMOTER	0.213	0.634	1960.28	1242.27	0.135	1478.54	199.20
A_68_P32117991	chr19:42007492-42007537	NM_001164561:290	Exosc1	INSIDE	0.213	0.591	3443.25	2036.05	0.126	2579.87	324.38
A_68_P31162043	chr17:36117444-36117488	NM_008136:567	Gnl1	INSIDE	0.213	0.639	2631.89	1682.19	0.136	1877.78	255.71
A_68_P28266912	chr12:16807246-16807296	NM_015764:422	Greb1	INSIDE	0.213	0.662	1020.75	676.17	0.141	843.42	119.20
A_68_P32454250	chrX:68809345-68809389	NM_008253:199	Hmgb3	INSIDE	0.213	1.632	1137.69	1856.64	0.348	554.51	193.12
A_68_P20391709	chr1:82286790-82286834	NM_010570:1202	Irs1	INSIDE	0.213	0.607	1052.84	638.66	0.129	882.24	114.25
A_68_P26016964	chr8:86423687-86423732	NM_181039:-287	Lphn1	PROMOTER	0.213	0.567	3680.21	2085.07	0.121	2727.19	329.79
A_68_P23955793	chr5:105948778-105948822	NM_133897:311	Lrrc8c	INSIDE	0.213	0.481	1484.06	714.32	0.103	1271.43	130.44
A_68_P30356226	chr15:77672472-77672516	NM_022410:51	Myh9	INSIDE	0.213	0.556	1149.55	638.58	0.118	1012.00	119.81
A_68_P27542070	chr10:128002461-128002505	NM_011119:508	Pa2g4	INSIDE	0.213	0.622	1273.81	792.64	0.133	907.46	120.41
A_68_P28145837	chr11:113927724-113927772	NM_172800:-483	Sdk2	PROMOTER	0.213	0.457	1717.83	785.36	0.097	1261.79	122.97
A_68_P27167591	chr10:58684147-58684191	NM_001024910:427	Septin10	INSIDE	0.213	0.481	1967.67	946.89	0.102	1442.77	147.74
A_68_P29033148	chr13:51663167-51663218	NM_009167:-739	Shc3	PROMOTER	0.213	0.559	1402.04	784.25	0.119	985.98	117.27
A_68_P20723689	chr1:154750745-154750789	NM_001005507:-990	Smg7	PROMOTER	0.213	0.560	1196.19	669.59	0.119	1019.43	121.35
A_68_P31958008	chr19:11892927-11892972	NM_011502:434	Stx3	INSIDE	0.213	0.548	1367.45	749.55	0.117	1038.29	121.12
A_68_P31092955	chr17:23810698-23810747	NM_001008425:15	Thoc6	INSIDE	0.213	0.505	1823.42	921.40	0.108	1354.68	145.90
A_68_P27981396	chr11:84953706-84953750	NM_001029934:-271	Usp32	PROMOTER	0.213	0.477	1455.31	694.32	0.102	1174.14	119.28
A_68_P30572235	chr16:17147510-17147562	NM_026940:477	Ydjc	INSIDE	0.213	0.470	1873.92	880.30	0.100	1217.96	121.97
A_68_P25183344	chr7:72672119-72672163			Unknown	0.213	0.686	2290.43	1570.94	0.146	1821.55	265.88
A_68_P31753363	chr18:60908551-60908595	ENSMUST00000066785:-268		PROMOTER	0.213	0.356	2170.57	772.65	0.076	1784.29	135.44
A_68_P28155137	chr11:115626646-115626697	NM_028014:-75	2310067B10Rik	PROMOTER	0.212	0.619	3676.80	2274.87	0.131	2447.94	321.31
A_68_P31921206	chr19:4121378-4121422	NM_016666:4427	Aip	INSIDE	0.212	0.356	2112.87	751.28	0.075	1614.89	121.80
A_68_P27281231	chr10:79604257-79604301	NM_025313:-781	Atp5d	DIVERGENT_PROMOTER	0.212	0.398	2124.86	845.47	0.084	1462.53	123.55
A_68_P32262593	chrX:12164837-12164881	NM_027439:-26	Atp6ap2	PROMOTER	0.212	1.548	1788.61	2768.02	0.328	654.60	214.96
A_68_P27278359	chr10:79167367-79167411	NM_001077184:286	Bsg	INSIDE	0.212	0.438	1665.67	728.83	0.093	1262.70	117.39
A_68_P30588528	chr16:20620501-20620545	NM_028420:829	Camk2n2	INSIDE	0.212	2.275	5785.35	13159.28	0.483	3595.98	1735.95

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P30247880	chr15:58247520-58247564	NM_145959:520	D15Ertd621e	INSIDE	0.212	0.584	1212.14	707.47	0.124	937.07	116.08
A_68_P27281213	chr10:79601565-79601609	NM_001195268:-1454	Dos	PROMOTER	0.212	0.720	2801.43	2016.59	0.152	1810.65	275.80
A_68_P21573667	chr2:119980437-119980486	NM_133838:-150	Ehd4	PROMOTER	0.212	0.650	1219.61	792.90	0.138	907.55	125.04
A_68_P22128828	chr3:51079948-51080002	NM_023502:49935	Elf2	INSIDE	0.212	0.543	1349.36	732.60	0.115	1059.90	121.80
A_68_P21727910	chr2:147871145-147871199	NM_010446:1533	Foxa2	INSIDE	0.212	0.488	1554.78	758.55	0.104	1116.50	115.72
A_68_P28925105	chr13:31899742-31899786	NM_008592:1250	Foxc1	INSIDE	0.212	0.352	2137.96	753.60	0.075	1619.39	121.05
A_68_P32337350	chrX:38754572-38754616	NM_016886:114	Gria3	INSIDE	0.212	10.544	7878.95	83076.23	2.233	3793.06	8470.29
A_68_P21475553	chr2:102026602-102026646	NM_178886:-90	Ldlrad3	PROMOTER	0.212	0.633	1564.80	990.89	0.134	1390.68	186.51
A_68_P31669146	chr18:44972023-44972067	NM_001085373:-208	Mcc	PROMOTER	0.212	0.680	1072.62	729.22	0.144	950.32	136.99
A_68_P28177556	chr11:119251329-119251373	NR_035453:-435	Mir1932	PROMOTER	0.212	0.618	1251.20	773.13	0.131	1163.40	152.46
A_68_P23088441	chr4:87677667-87677717	NM_027326:1619	Mllt3	INSIDE	0.212	0.534	1325.92	708.62	0.113	1058.65	120.07
A_68_P26772694	chr9:100979083-100979130	NM_001100451:656	Msl2	INSIDE	0.212	0.570	1325.78	756.27	0.121	1057.20	127.87
A_68_P25360738	chr7:106415893-106415949	NM_001048167:-36	Mtap6	PROMOTER	0.212	0.709	1944.04	1378.28	0.151	1326.39	199.73
A_68_P28004913	chr11:89163892-89163940	NM_008711:-43	Nog	PROMOTER	0.212	0.658	1124.21	740.24	0.139	882.21	122.93
A_68_P22898162	chr4:48057954-48057998	NM_015743:-6143	Nr4a3	PROMOTER	0.212	0.645	2007.57	1293.93	0.137	1556.05	212.88
A_68_P23261316	chr4:122878552-122878598	NM_001085502:-221	Nt5c1a	PROMOTER	0.212	0.667	1290.84	860.65	0.141	883.84	125.03
A_68_P31117522	chr17:27759599-27759649	NM_019837:773	Nudt3	INSIDE	0.212	0.571	1376.47	786.56	0.121	952.80	115.26
A_68_P29589384	chr14:49284797-49284844	NM_144841:-2273	Otx2	DIVERGENT_PROMOTER	0.212	0.442	1758.34	776.68	0.094	1301.11	121.78
A_68_P30463768	chr15:96290631-96290675	NM_028148:622	Scaf11	INSIDE	0.212	0.646	1225.33	792.11	0.137	899.46	123.32
A_68_P25585439	chr7:148067707-148067751	NM_001127351:40	Sirt3	INSIDE	0.212	0.648	4502.68	2916.34	0.137	3126.92	429.10
A_68_P27926647	chr11:75344750-75344794	NM_001199284:-423	Slc43a2	PROMOTER	0.212	0.614	3844.62	2361.91	0.130	2777.15	361.76
A_68_P30132016	chr15:35085389-35085433	NM_019635:151	Stk3	INSIDE	0.212	0.427	2475.64	1056.78	0.091	1865.54	168.98
A_68_P25581339	chr7:147130322-147130366	NM_009482:590	Utf1	INSIDE	0.212	0.737	3285.27	2420.71	0.156	2239.97	350.38
A_68_P22413527	chr3:108395008-108395052	NM_181400:835	Wdr47	INSIDE	0.212	0.674	1234.98	832.66	0.143	958.45	137.22
A_68_P29493861	chr14:29319923-29319970	NM_009524:1288	Wnt5a	INSIDE	0.212	0.649	1142.28	740.90	0.138	884.44	121.88
A_68_P27873629	chr11:65620598-65620642	NM_026107:-125	Zkscan6	PROMOTER	0.212	0.473	1604.04	758.35	0.100	1386.18	138.84
A_68_P23276155	chr4:125406755-125406803			Unknown	0.212	0.598	1119.36	669.61	0.127	917.61	116.46
A_68_P28712204	chr12:107201277-107201321	BC156654:163438		INSIDE	0.212	0.671	1583.27	1061.75	0.142	1215.43	172.53
A_68_P25032100	chr7:31337206-31337250	NM_183321:63	BC053749	INSIDE	0.211	0.678	1287.72	873.66	0.143	968.38	138.38
A_68_P21866705	chr2:172765232-172765276	NM_007557:540	Bmp7	INSIDE	0.211	0.607	1805.03	1094.84	0.128	1376.69	175.80
A_68_P31616442	chr18:35278972-35279016	NM_009818:429	Ctnna1	INSIDE	0.211	0.530	2167.37	1148.16	0.112	1700.53	189.95
A_68_P27010235	chr10:24431971-24432016	NM_008813:-85	Enpp1	PROMOTER	0.211	1.551	4773.09	7404.26	0.328	3283.83	1077.11
A_68_P31105766	chr17:25854648-25854692	NM_022422:554	Gng13	INSIDE	0.211	0.607	1896.77	1151.03	0.128	1384.17	177.16
A_68_P30349000	chr15:76369261-76369305	NM_029643:-90	Gpr172b	DIVERGENT_PROMOTER	0.211	0.610	1310.06	798.80	0.128	921.05	118.29
A_68_P27894382	chr11:69145803-69145849	NM_010599:6067	Kcnab3	INSIDE	0.211	0.615	1137.58	699.65	0.130	919.99	119.25
A_68_P20864285	chr1:180457620-180457665	NM_001161665:-1613	Kif26b	PROMOTER	0.211	0.685	1043.38	714.81	0.145	828.04	119.70
A_68_P20739602	chr1:157588540-157588584	NM_010712:595	Lhx4	INSIDE	0.211	0.559	1290.80	721.36	0.118	1000.12	118.05
A_68_P26016963	chr8:86423548-86423592	NM_181039:-426	Lphn1	PROMOTER	0.211	1.819	1385.72	2520.14	0.384	862.35	330.90
A_68_P23955160	chr5:105845255-105845299	NM_001033550:483	Lrrc8b	INSIDE	0.211	0.721	3690.54	2661.87	0.152	2789.03	423.94
A_68_P31156878	chr17:35119267-35119311	NM_001204273:214	Lsm2	INSIDE	0.211	0.426	2163.90	921.01	0.090	1727.66	155.21
A_68_P20625164	chr1:134921568-134921624	NM_008575:329	Mdm4	INSIDE	0.211	0.476	1535.53	731.06	0.100	1151.70	115.67
A_68_P23547790	chr5:25005052-25005096	NM_001081383:-473	Mll3	DIVERGENT_PROMOTER	0.211	0.431	1689.66	727.94	0.091	1313.71	119.23
A_68_P23760679	chr5:66651534-66651578	NM_027602:193	Nsun7	INSIDE	0.211	2.423	3500.23	8481.48	0.510	2272.03	1159.24
A_68_P25090923	chr7:52309399-52309443	NM_022999:7602	Prrg2	INSIDE	0.211	0.414	2016.49	834.08	0.087	1331.76	116.05
A_68_P31151620	chr17:34169430-34169477	NM_001205215:159	Rxrb	INSIDE	0.211	0.635	1134.78	720.41	0.134	909.88	121.64
A_68_P21420761	chr2:90955447-90955493	NM_011355:18517	Sfpi1	INSIDE	0.211	0.616	2220.61	1367.15	0.130	1646.00	213.32
A_68_P30720961	chr16:44332811-44332855	NM_001159419:119	Sidt1	INSIDE	0.211	0.514	1403.51	721.28	0.108	1057.45	114.47
A_68_P28963696	chr13:39052204-39052248	NM_001170430:180	Slc35b3	INSIDE	0.211	0.424	2156.19	914.27	0.089	1634.57	146.09
A_68_P20285517	chr1:63224065-63224115	NR_028558:-1506	Snora41	PROMOTER	0.211	0.661	1079.27	713.94	0.140	870.30	121.74
A_68_P21729944	chr2:148221334-148221378	NM_009219:244	Sstr4	INSIDE	0.211	0.419	1936.96	811.30	0.088	1419.29	125.50
A_68_P20833437	chr1:174430507-174430560	NM_178598:157	Tagln2	INSIDE	0.211	0.632	1185.26	748.97	0.133	872.30	116.31

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P24591244	chr6:83019585-83019631	NM_009392:611	Tlx2	INSIDE	0.211	1.357	2903.42	3939.31	0.287	2041.11	585.21
A_68_P28077838	chr11:102017610-102017654	NM_029649:89	Tmem101	INSIDE	0.211	0.537	1320.23	708.54	0.113	1019.49	115.32
A_68_P28740679	chr12:112088312-112088356	NM_001199785:-154	Zfp839	DIVERGENT_PROMOTER	0.211	0.522	1567.46	818.57	0.110	1114.40	122.80
A_68_P24951608	chr7:4971880-4971924	NM_001033383:-75	Zfp865	PROMOTER	0.211	0.610	1354.54	825.75	0.128	1101.01	141.39
A_68_P25352333	chr7:104936712-104936764	ENSMUST00000172423:-312		PROMOTER	0.211	0.525	1305.14	684.58	0.111	1057.60	117.01
A_68_P31162735	chr17:36282108-36282152	NR_033517:168	2410017I17Rik	INSIDE	0.210	0.339	2071.48	702.04	0.071	1698.86	121.17
A_68_P27554557	chr11:3794614-3794660	NM_026150:493	4921536K21Rik	INSIDE	0.210	0.685	1094.46	750.24	0.144	853.87	122.70
A_68_P24056045	chr5:123958382-123958426	NM_198611:-2064	B3gnt4	PROMOTER	0.210	0.724	2214.58	1603.82	0.152	1378.04	209.88
A_68_P25093327	chr7:52722315-52722359	NM_007527:-68	Bax	PROMOTER	0.210	0.440	1677.04	737.35	0.092	1334.59	123.19
A_68_P21075525	chr2:25837701-25837745	NM_001115076:1080	Camsap1	INSIDE	0.210	0.619	5224.55	3234.22	0.130	3672.23	476.80
A_68_P24164623	chr5:145928226-145928276	NM_178576:158	Cpsf4	INSIDE	0.210	0.495	1597.11	791.11	0.104	1135.02	118.17
A_68_P23363729	chr4:140938544-140938588	NM_001085513:14432	Fam131c	INSIDE	0.210	0.349	2605.47	909.22	0.073	2026.32	148.37
A_68_P22342883	chr3:95021867-95021911	NM_029885:-24	Gabpb2	PROMOTER	0.210	0.533	2194.14	1168.55	0.112	1552.65	173.45
A_68_P27327040	chr10:88193638-88193682	NM_001037166:186	Gm4925	INSIDE	0.210	0.682	1158.20	790.22	0.144	860.64	123.59
A_68_P31929497	chr19:5567328-5567372	NM_001033448:-723	Gm962	DIVERGENT_PROMOTER	0.210	0.396	1771.28	701.58	0.083	1400.99	116.79
A_68_P32743828	chrX:147451859-147451906	NM_198110:-17	Gnl3l	PROMOTER	0.210	1.520	1249.25	1899.02	0.320	439.86	140.58
A_68_P24783934	chr6:117857089-117857136	NM_001166428:-709	Hnrnpf	PROMOTER	0.210	0.593	1355.27	803.51	0.124	947.50	117.90
A_68_P24773305	chr6:115803441-115803485	NM_001167763:-83	Ift122	DIVERGENT_PROMOTER	0.210	0.521	4045.60	2107.25	0.110	2545.14	279.03
A_68_P32682200	chrX:133276451-133276498	NM_019768:-326	Morf4l2	PROMOTER	0.210	2.160	1277.76	2760.01	0.454	556.76	252.51
A_68_P29448045	chr14:21460170-21460214	NM_021508:15570	Myoz1	DOWNSTREAM	0.210	0.570	1308.25	746.19	0.120	1075.45	129.03
A_68_P27180398	chr10:60881315-60881364	NM_013611:620	Nodal	INSIDE	0.210	0.553	1653.01	914.21	0.116	1045.46	121.46
A_68_P31958766	chr19:12040692-12040739	NM_001033174:382	Osbp	INSIDE	0.210	0.549	2021.86	1109.81	0.115	1485.17	171.21
A_68_P22282900	chr3:82859514-82859558	NM_016784:77	Plrg1	INSIDE	0.210	0.651	1292.96	841.12	0.136	912.32	124.39
A_68_P22778525	chr4:22417373-22417424	NM_008899:-2120	Pou3f2	PROMOTER	0.210	0.693	1839.83	1275.14	0.145	1322.69	192.24
A_68_P21110359	chr2:31492659-31492703	NM_001123362:-2876	Prdm12	PROMOTER	0.210	0.527	1536.65	809.63	0.110	1149.29	126.98
A_68_P31108129	chr17:26205895-26205939	NM_001162868:206	Rab11fip3	INSIDE	0.210	0.412	1898.53	782.04	0.087	1363.38	118.20
A_68_P27943646	chr11:78304705-78304749	NM_001168521:6530	Sarm1	INSIDE	0.210	0.508	1438.88	731.17	0.107	1130.88	120.88
A_68_P28051144	chr11:97393113-97393157	NM_018873:43306	Srcin1	INSIDE	0.210	0.620	1230.03	762.31	0.130	902.66	117.54
A_68_P27841685	chr11:60033832-60033876	NM_011480:252	Srebf1	INSIDE	0.210	0.430	1969.99	846.79	0.090	1551.22	139.74
A_68_P25949498	chr8:72567097-72567141	NM_027481:407	Sugp1	INSIDE	0.210	0.674	1080.25	727.73	0.141	883.59	124.97
A_68_P23440545	chr4:155148332-155148376	NM_147776:316	Vwa1	INSIDE	0.210	0.618	1236.84	764.72	0.130	912.07	118.50
A_68_P29613709	chr14:55305052-55305096	NM_021437:67	1700123O20Rik	INSIDE	0.209	0.597	1182.48	705.82	0.125	972.83	121.36
A_68_P27306489	chr10:84565593-84565637	NM_001013028:243	AI597468	INSIDE	0.209	0.401	1986.43	796.55	0.084	1449.41	121.45
A_68_P27083331	chr10:40021980-40022028	NM_009665:-10	Amd1	PROMOTER	0.209	0.490	1556.69	763.54	0.103	1316.87	135.25
A_68_P30498879	chr15:102456094-102456138	NM_146065:-264	Atf7	PROMOTER	0.209	0.676	1260.49	851.60	0.141	942.59	133.37
A_68_P25007800	chr7:25790566-25790610	NM_144921:326	Atp1a3	INSIDE	0.209	0.658	5992.61	3945.69	0.138	4462.89	613.87
A_68_P29575961	chr14:47008247-47008291	NM_007554:2006	Bmp4	INSIDE	0.209	0.677	1030.31	697.63	0.142	852.97	120.73
A_68_P22348132	chr3:96001190-96001234	NM_026975:297	Bola1	INSIDE	0.209	0.545	1434.53	782.45	0.114	1022.17	116.65
A_68_P30475794	chr15:98493006-98493053	NM_001080981:291	Ddx23	INSIDE	0.209	0.639	2285.80	1460.93	0.134	1669.03	222.94
A_68_P28729567	chr12:109940312-109940358	NM_001171002:182	Degs2	INSIDE	0.209	1.574	1344.99	2117.06	0.329	1051.35	345.38
A_68_P26659810	chr9:78328608-78328655	NM_010106:900	Eef1a1	INSIDE	0.209	0.441	1641.13	723.39	0.092	1262.23	116.02
A_68_P22318559	chr3:89124527-89124571	NM_010108:2253	Efna3	INSIDE	0.209	0.569	1246.80	709.24	0.119	1012.21	120.11
A_68_P20863273	chr1:180248534-180248578	NM_025511:-727	Fam36a	PROMOTER	0.209	0.411	3704.05	1521.18	0.086	2683.04	230.25
A_68_P22963965	chr4:62021291-62021335	NM_001045528:270	Fkbp15	INSIDE	0.209	0.417	1761.10	734.52	0.087	1367.87	119.46
A_68_P29055023	chr13:55546318-55546369	NM_011938:-351	Grk6	PROMOTER	0.209	0.531	1579.54	838.79	0.111	1085.71	120.68
A_68_P22964786	chr4:62163240-62163284	NM_024257:-28	Hdhd3	PROMOTER	0.209	0.526	4534.31	2384.03	0.110	3319.07	364.93
A_68_P23931498	chr5:101227159-101227203	NM_001081107:439	Helq	INSIDE	0.209	0.449	1418.54	637.57	0.094	1225.39	115.33
A_68_P26022961	chr8:87502281-87502328	NM_008416:343	Junb	INSIDE	0.209	0.546	1447.23	789.73	0.114	1027.33	117.18
A_68_P27894955	chr11:69225357-69225401	NM_001017426:1799	Kdm6b	INSIDE	0.209	0.460	1724.87	792.89	0.096	1266.95	121.57
A_68_P26896522	chr9:123626490-123626534	NM_033322:163	Lztfl1	INSIDE	0.209	0.509	1557.42	793.18	0.106	1194.78	127.24
A_68_P32119295	chr19:42222796-42222840	NM_183195:940	Marveld1	INSIDE	0.209	0.625	1289.12	805.26	0.131	991.06	129.49

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P23936330	chr5:102092926-102092970	NM_144955:782	Nkx6-1	INSIDE	0.209	0.313	2159.98	675.14	0.065	1813.16	118.67
A_68_P26567746	chr9:61762612-61762656	NM_018853:-317	Rplp1	PROMOTER	0.209	0.563	2224.76	1252.02	0.118	1738.35	204.80
A_68_P31923329	chr19:4476649-4476693	NM_134164:473	Syt12	INSIDE	0.209	0.584	1908.85	1114.19	0.122	1492.52	181.69
A_68_P20634930	chr1:136605441-136605485	NM_009307:62205	Syt2	INSIDE	0.209	0.623	1887.85	1177.05	0.130	1439.02	187.36
A_68_P27845268	chr11:60692459-60692503	NM_001168507:60	Tmem11	INSIDE	0.209	0.462	1528.73	705.52	0.096	1235.84	118.93
A_68_P32118296	chr19:42056888-42056932	NM_145500:658	Ubtd1	INSIDE	0.209	0.569	1433.39	815.35	0.119	1000.59	118.92
A_68_P22038452	chr3:32409336-32409380	NM_001161818:-113	Zfp639	PROMOTER	0.209	0.497	1877.11	932.54	0.104	1464.39	151.70
A_68_P26158503	chr8:112229246-112229291	NM_001167946:-180	Zfp821	PROMOTER	0.209	0.587	1375.93	808.02	0.123	967.55	118.73
A_68_P24336406	chr6:31166272-31166316	ENSMUST00000115107:2139		INSIDE	0.209	0.665	1921.71	1278.28	0.139	1373.14	191.27
A_68_P21528941	chr2:112295418-112295462	NM_133749:259	2900064A13Rik	INSIDE	0.208	0.657	1184.08	778.36	0.137	868.83	119.05
A_68_P23720349	chr5:58108780-58108824	NR_015588:356	4932441J04Rik	INSIDE	0.208	0.355	2032.39	722.34	0.074	1583.11	116.77
A_68_P28836390	chr13:14046166-14046215	NM_178640:-750	B3galnt2	PROMOTER	0.208	0.471	1662.08	782.80	0.098	1194.51	117.01
A_68_P22859648	chr4:40895242-40895286	NM_001171739:63	Bag1	INSIDE	0.208	0.672	1045.28	702.02	0.139	870.47	121.42
A_68_P30599073	chr16:22656907-22656951	NM_138650:376	Dgkg	INSIDE	0.208	0.398	1936.43	771.09	0.083	1520.32	125.83
A_68_P26572470	chr9:62659765-62659809	NM_010193:-331	Fem1b	PROMOTER	0.208	0.734	3215.67	2361.11	0.153	2271.39	347.13
A_68_P21536545	chr2:113597825-113597869	NM_011824:959	Grem1	INSIDE	0.208	0.495	1505.72	745.64	0.103	1194.34	123.19
A_68_P25656209	chr8:11555685-11555729	NM_011919:-359	Ing1	DIVERGENT_PROMOTER	0.208	1.456	5723.71	8334.47	0.302	3509.69	1061.17
A_68_P23226467	chr4:115563355-115563399	NM_001039124:6372	Kncn	DOWNSTREAM	0.208	0.282	2582.53	729.15	0.059	2030.85	119.09
A_68_P24624871	chr6:88848565-88848609	NM_008564:188	Mcm2	INSIDE	0.208	0.552	1909.73	1053.30	0.115	1419.60	162.77
A_68_P25256094	chr7:85723616-85723660	NM_008746:-914	Ntrk3	PROMOTER	0.208	0.471	1632.25	768.13	0.098	1205.76	117.77
A_68_P21496012	chr2:105522220-105522268	NM_013627:5643	Pax6	INSIDE	0.208	0.658	989.65	651.41	0.137	886.93	121.32
A_68_P30346763	chr15:76028781-76028825	NM_201393:-163	Plec	PROMOTER	0.208	0.582	1177.22	685.59	0.121	1012.57	122.73
A_68_P29033515	chr13:51747268-51747312	NM_029279:208	Secisbp2	INSIDE	0.208	0.435	1823.23	793.52	0.091	1354.61	122.85
A_68_P31411739	chr17:86017697-86017743	NR_038085:16	Six3os1	INSIDE	0.208	0.478	1661.34	794.86	0.099	1227.89	122.08
A_68_P31926383	chr19:5024065-5024109	NM_007854:81	Slc29a2	INSIDE	0.208	0.736	4823.55	3549.49	0.153	3181.33	487.98
A_68_P23236666	chr4:117508743-117508787	NM_008135:902	Slc6a9	INSIDE	0.208	1.603	1739.84	2789.62	0.333	1369.60	455.94
A_68_P20833440	chr1:174430851-174430895	NM_178598:496	Tagln2	INSIDE	0.208	1.526	3322.33	5068.85	0.318	2115.33	672.02
A_68_P22871719	chr4:43455836-43455880	NM_011571:710	Tesk1	INSIDE	0.208	0.547	1291.16	706.00	0.114	1078.75	122.79
A_68_P22015871	chr3:28161528-28161576	NM_001163009:-583	Tnik	PROMOTER	0.208	0.685	1661.47	1138.35	0.142	1103.60	157.16
A_68_P27833860	chr11:58791364-58791408	NM_053168:-231	Trim11	PROMOTER	0.208	0.587	1611.99	946.59	0.122	1170.48	142.80
A_68_P28344357	chr12:34643155-34643199	NM_011658:641	Twist1	INSIDE	0.208	0.519	2328.00	1207.52	0.108	1817.89	196.54
A_68_P27241482	chr10:72117682-72117727	NM_025635:62	Zwint	INSIDE	0.208	0.550	2538.04	1397.16	0.114	1784.68	203.97
A_68_P30501993	chr15:102916820-102916864	AF216290:299276		INSIDE	0.208	0.679	2967.95	2015.11	0.141	2264.43	320.17
A_68_P26219857	chr8:122923797-122923841	ENSMUST00000127664:489078		INSIDE	0.208	0.661	1229.77	813.15	0.137	987.87	135.61
A_68_P23349878	chr4:138686042-138686091	NR_033745:886	2310028O11Rik	INSIDE	0.207	0.647	2238.73	1447.58	0.134	1701.77	227.33
A_68_P33012177	chr9_random:57060-57104	NR_027950:2390	4930526I15Rik	DOWNSTREAM	0.207	0.426	2559.74	1089.63	0.088	1905.00	167.60
A_68_P28612738	chr12:88225828-88225872	NM_145836:-86	6430527G18Rik	PROMOTER	0.207	0.417	1685.17	702.72	0.086	1393.89	120.26
A_68_P21061195	chr2:22895595-22895639	NM_001077190:144	Abi1	INSIDE	0.207	0.689	1127.46	777.11	0.143	843.87	120.53
A_68_P22411287	chr3:108013581-108013625	NM_175183:250	Atxn7l2	INSIDE	0.207	0.553	1489.46	824.29	0.115	1006.84	115.32
A_68_P21578342	chr2:120834147-120834191	NM_010761:25	Ccndbp1	INSIDE	0.207	0.497	1474.35	732.77	0.103	1131.62	116.70
A_68_P29639453	chr14:60216909-60216959	NM_001168535:-138	Cdadc1	PROMOTER	0.207	0.705	1290.49	909.87	0.146	858.38	125.57
A_68_P22394781	chr3:104855923-104855967	NM_001163332:-73	Cttnbp2nl	PROMOTER	0.207	0.640	1291.37	826.03	0.133	925.04	122.58
A_68_P23363728	chr4:140938466-140938511	NM_001085513:14354	Fam131c	INSIDE	0.207	0.668	2729.78	1822.27	0.138	1996.94	275.52
A_68_P20405972	chr1:84836507-84836554	NM_025386:115	Fbxo36	INSIDE	0.207	0.611	1513.41	924.52	0.126	1158.18	146.33
A_68_P20967779	chr2:4322142-4322186	NM_001177843:143	Frmd4a	INSIDE	0.207	0.513	1447.52	742.55	0.106	1134.20	120.21
A_68_P24798580	chr6:120413892-120413937	NM_008359:700	Il17ra	INSIDE	0.207	0.566	1714.17	969.72	0.117	1354.93	158.53
A_68_P28225282	chr12:8929275-8929319	NM_008640:1184	Laptm4a	INSIDE	0.207	0.455	2872.67	1306.34	0.094	2023.07	190.15
A_68_P22028766	chr3:30407046-30407090	NM_021442:1341	Mecom	INSIDE	0.207	0.554	1358.36	752.35	0.114	1029.61	117.86
A_68_P24818881	chr6:125082179-125082232	NM_138747:305	Nop2	INSIDE	0.207	0.648	1343.94	871.34	0.134	892.32	120.00
A_68_P32134817	chr19:44911075-44911119	NM_011037:79213	Pax2	INSIDE	0.207	0.665	3155.10	2098.20	0.137	2086.37	286.87
A_68_P23445966	chr5:3596177-3596221	NM_027777:133	Pex1	INSIDE	0.207	0.601	1327.02	798.14	0.125	969.34	120.85

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P20642549	chr1:137815494-137815538	NM_019645:85	Pkp1	INSIDE	0.207	0.556	1379.07	766.37	0.115	1012.58	116.56
A_68_P32598390	chrX:108010197-108010241	NM_008901:415	Pou3f4	INSIDE	0.207	1.766	1988.11	3511.50	0.366	770.87	282.44
A_68_P28781843	chr12:120081478-120081528	NM_177082:-3299	Sp8	PROMOTER	0.207	0.633	1141.75	722.26	0.131	945.26	123.88
A_68_P23364637	chr4:141092753-141092798	NM_019763:1737	Spen	INSIDE	0.207	0.516	2508.16	1294.92	0.107	1890.18	201.74
A_68_P26770646	chr9:100543212-100543261	NM_009282:-805	Stag1	PROMOTER	0.207	0.547	1360.75	744.75	0.113	1029.76	116.60
A_68_P29243709	chr13:96731427-96731477	NM_029210:171080	Sv2c	INSIDE	0.207	0.697	1088.88	758.67	0.144	842.99	121.36
A_68_P25617013	chr8:4275737-4275784	NM_011592:145	Timm44	INSIDE	0.207	1.605	1445.75	2321.02	0.333	1021.57	339.75
A_68_P32010023	chr19:22213713-22213757	NM_001035239:128	Trpm3	INSIDE	0.207	0.633	1092.36	691.78	0.131	890.32	116.73
A_68_P22964621	chr4:62131699-62131744	NM_023597:185	Wdr31	INSIDE	0.207	1.446	1591.49	2301.38	0.299	1144.37	341.99
A_68_P21910191	chr2:181100855-181100899	NM_001048148:749	Zgpat	INSIDE	0.207	0.519	2327.42	1208.76	0.108	1971.85	212.37
A_68_P25509652	chr7:135381090-135381137	NM_146205:243	Armc5	INSIDE	0.206	0.625	1325.94	828.76	0.129	959.78	123.47
A_68_P27534362	chr10:126607844-126607888	NM_027739:4980	B4galnt1	INSIDE	0.206	1.623	5915.14	9597.99	0.335	4256.99	1425.98
A_68_P31102616	chr17:25393043-25393087	NM_001163270:245	Baiap3	INSIDE	0.206	0.484	1772.69	858.10	0.100	1298.53	129.50
A_68_P21425382	chr2:91763987-91764031	NM_007699:1663	Chrm4	INSIDE	0.206	0.561	1302.41	730.67	0.116	1165.03	134.91
A_68_P27540983	chr10:127805581-127805626	NM_001081040:1490	Coq10a	INSIDE	0.206	0.541	3351.38	1813.28	0.111	2483.56	276.82
A_68_P28581231	chr12:82586058-82586102	NM_025461:17	Cox16	INSIDE	0.206	0.430	1631.91	701.37	0.088	1341.97	118.54
A_68_P24600267	chr6:84534196-84534247	NM_175475:9583	Cyp26b1	INSIDE	0.206	0.512	1498.50	766.72	0.105	1165.31	122.64
A_68_P30791338	chr16:58408465-58408509	NM_028523:-161	Dcbld2	PROMOTER	0.206	0.524	3810.82	1998.41	0.108	2860.03	308.87
A_68_P29150854	chr13:75845732-75845776	NM_138953:823	Ell2	INSIDE	0.206	0.632	2950.51	1864.78	0.130	2282.07	297.40
A_68_P29309821	chr13:108948883-108948927	NM_028042:-27	Ercc8	DIVERGENT_PROMOTER	0.206	0.464	2242.55	1041.49	0.095	1640.73	156.61
A_68_P31544266	chr18:21458217-21458261	NM_001033445:402	Fam59a	INSIDE	0.206	0.338	2077.35	702.95	0.070	1666.76	116.30
A_68_P23591970	chr5:34326722-34326766	NM_001033458:622	Gm1673	INSIDE	0.206	0.640	1317.32	843.64	0.132	919.47	121.41
A_68_P23571063	chr5:30481709-30481753	NM_145558:-131	Hadhb	DIVERGENT_PROMOTER	0.206	0.550	1400.06	770.27	0.114	1102.29	125.21
A_68_P28036515	chr11:94938400-94938444	NM_013565:-394	Itga3	PROMOTER	0.206	0.532	1481.29	788.74	0.110	1079.50	118.57
A_68_P30423458	chr15:88977331-88977375	NM_011161:2684	Mapk11	INSIDE	0.206	0.627	1094.51	686.24	0.129	926.20	119.72
A_68_P30344675	chr15:75714543-75714587	NM_172607:10347	Naprt1	DOWNSTREAM	0.206	0.704	1351.77	951.47	0.145	1014.95	146.84
A_68_P22378546	chr3:101816277-101816321	NM_178777:2231	Nhlh2	INSIDE	0.206	0.441	1622.57	715.38	0.091	1330.59	121.14
A_68_P28041049	chr11:95691702-95691746	NM_153104:5911	Phospho1	INSIDE	0.206	0.379	1814.12	687.98	0.078	1469.47	114.85
A_68_P31937065	chr19:7050107-7050153	NM_008889:593	Ppp1r14b	INSIDE	0.206	0.620	1412.19	875.28	0.128	955.26	121.88
A_68_P22933513	chr4:55363588-55363632	NM_009011:697	Rad23b	INSIDE	0.206	0.722	3535.60	2554.47	0.149	2988.87	444.07
A_68_P24040026	chr5:121098911-121098955	NM_013832:102	Rasal1	INSIDE	0.206	1.637	3219.68	5269.97	0.338	2523.31	851.68
A_68_P30670707	chr16:35542109-35542153	NM_013661:683	Sema5b	INSIDE	0.206	0.690	5977.77	4122.35	0.142	4231.33	601.94
A_68_P23997299	chr5:113716482-113716526	NR_027934:-6883	Sgsm1	PROMOTER	0.206	0.632	1542.14	974.42	0.130	1093.21	142.15
A_68_P28963695	chr13:39052121-39052165	NM_001170430:264	Slc35b3	INSIDE	0.206	0.352	2444.68	861.62	0.073	1875.39	136.47
A_68_P31247137	chr17:54437878-54437922	NM_022025:459	Slc5a7	INSIDE	0.206	0.676	1031.82	697.71	0.139	837.54	116.66
A_68_P21911961	chr2:181405887-181405931	NM_009236:437	Sox18	INSIDE	0.206	0.419	1844.05	773.02	0.086	1340.17	115.64
A_68_P21835810	chr2:167318513-167318557	NM_170756:-160	Spata2	PROMOTER	0.206	0.443	2442.29	1082.11	0.091	1742.88	158.77
A_68_P24907674	chr6:142912449-142912500	NM_011374:498	St8sia1	INSIDE	0.206	0.641	1077.96	690.69	0.132	910.95	120.33
A_68_P30255508	chr15:59479606-59479650	NM_144549:-580	Trib1	PROMOTER	0.206	0.566	1128.83	638.86	0.117	1002.69	117.03
A_68_P27854526	chr11:62364648-62364692	NM_011664:-335	Ubb	PROMOTER	0.206	0.344	2463.59	847.60	0.071	1806.92	128.23
A_68_P30660865	chr16:33967049-33967093	NM_009471:19	Umps	INSIDE	0.206	0.507	2569.49	1301.49	0.104	2231.05	232.45
A_68_P25447480	chr7:123451642-123451686	ENSMUST00000106605:226		INSIDE	0.206	0.473	1486.39	703.19	0.098	1230.35	120.17
A_68_P21071433	chr2:25187978-25188029	NR_027448:88	AA543186	INSIDE	0.205	0.617	1139.84	703.03	0.127	937.15	118.60
A_68_P24600305	chr6:84538923-84538970	NM_175475:4858	Cyp26b1	INSIDE	0.205	0.731	2470.27	1804.54	0.149	1827.62	273.18
A_68_P26239891	chr8:125967011-125967055	NM_054046:147	Def8	INSIDE	0.205	0.738	3573.26	2635.91	0.151	2702.48	408.50
A_68_P28003586	chr11:88921355-88921399	NM_019505:686	Dgke	INSIDE	0.205	0.488	1550.72	756.41	0.100	1202.65	120.29
A_68_P26347068	chr9:21229822-21229866	NM_001039520:456	Dnm2	INSIDE	0.205	0.679	3523.93	2394.24	0.139	2488.52	346.23
A_68_P22071618	chr3:38787168-38787212	NM_183221:1329	Fat4	INSIDE	0.205	0.479	1581.88	758.06	0.098	1187.12	116.78
A_68_P25034759	chr7:31837288-31837332	NM_052991:2562	Fxyd1	INSIDE	0.205	0.516	1508.92	778.84	0.106	1191.40	126.36
A_68_P31484554	chr18:9213845-9213889	NM_008058:1013	Fzd8	INSIDE	0.205	0.504	1373.75	691.81	0.103	1130.15	116.60
A_68_P24449398	chr6:52195787-52195837	NM_010450:-46	Hoxa11	PROMOTER	0.205	0.417	1997.63	832.36	0.086	1403.88	120.15

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P24591138	chr6:83004321-83004365	NM_019752:223	Htra2	INSIDE	0.205	0.536	1358.99	728.89	0.110	1125.58	123.95
A_68_P32746462	chrX:148237878-148237922	NM_021523:76	Huwe1	INSIDE	0.205	1.411	1026.71	1449.13	0.289	400.33	115.65
A_68_P27281295	chr10:79612639-79612683	NM_021565:1626	Midn	INSIDE	0.205	0.381	2238.43	853.50	0.078	1564.83	122.55
A_68_P30499097	chr15:102502826-102502874	NR_030460:-553	Mir688	PROMOTER	0.205	0.601	1299.35	780.72	0.123	981.98	120.95
A_68_P24796460	chr6:119988597-119988641	NR_030487:-4289	Mir706	PROMOTER	0.205	0.575	1994.68	1147.28	0.118	1485.86	175.52
A_68_P24932172	chr6:146991149-146991196	NM_145573:-119	Mrps35	PROMOTER	0.205	0.650	968.71	629.59	0.133	916.27	122.09
A_68_P24112020	chr5:134697723-134697767	NM_010876:7751	Ncf1	INSIDE	0.205	1.742	3557.52	6197.13	0.357	2328.54	831.60
A_68_P20370345	chr1:78186294-78186338	NM_001159520:7395	Pax3	INSIDE	0.205	0.389	2393.57	931.76	0.080	2085.41	166.70
A_68_P24119913	chr5:136674484-136674528	NM_025774:318	Prkrip1	INSIDE	0.205	0.674	2938.19	1979.41	0.138	2100.59	290.08
A_68_P21473125	chr2:101636609-101636660	NM_001083810:1230	Prr5l	INSIDE	0.205	0.639	1193.94	763.32	0.131	910.97	119.39
A_68_P26044789	chr8:91567168-91567212	NM_021390:871	Sall1	INSIDE	0.205	0.554	1453.85	805.70	0.114	1052.79	119.57
A_68_P22982499	chr4:65266160-65266204	NM_001161782:163	Trim32	INSIDE	0.205	2.166	12466.27	26998.36	0.443	8254.48	3659.90
A_68_P29143148	chr13:74074758-74074802	NM_027182:435	Trip13	INSIDE	0.205	2.800	7233.64	20250.81	0.575	4920.66	2830.36
A_68_P20820926	chr1:172105452-172105507	NM_133806:-402	Uap1	PROMOTER	0.205	0.535	1269.42	679.15	0.110	1086.78	119.01
A_68_P24136136	chr5:140017148-140017192	NM_013702:-2681	Uncx	PROMOTER	0.205	0.410	1855.71	761.57	0.084	1437.44	121.11
A_68_P30546657	chr16:11175989-11176033	NM_145931:476	Zc3h7a	INSIDE	0.205	0.644	2402.16	1546.32	0.132	1818.70	240.31
A_68_P22287008	chr3:83593973-83594017	ENSMUST00000149626:-116		PROMOTER	0.205	0.360	2166.55	780.64	0.074	1577.98	116.62
A_68_P28182937	chr11:120046685-120046736	NR_030682:4460	2810410L24Rik	DOWNSTREAM	0.204	0.708	1312.95	929.89	0.144	990.91	143.01
A_68_P23320947	chr4:133637971-133638015	NM_001162970:13626	Aim1l	INSIDE	0.204	0.553	1238.36	685.15	0.113	1041.24	117.48
A_68_P28185537	chr11:120460129-120460181	NM_001038230:309	Anapc11	INSIDE	0.204	0.523	1413.86	738.97	0.106	1145.06	121.88
A_68_P31095793	chr17:24306024-24306068	NR_037854:294	Atp6v0c-ps2	INSIDE	0.204	1.458	5335.23	7779.95	0.298	3518.06	1048.64
A_68_P25392269	chr7:112574333-112574377	NM_007627:21	Cckbr	INSIDE	0.204	0.744	3037.40	2261.06	0.152	2333.85	354.73
A_68_P25422972	chr7:119301935-119301979	NM_015814:615	Dkk3	INSIDE	0.204	2.165	9130.25	19767.68	0.443	5681.27	2514.80
A_68_P21573664	chr2:119979962-119980006	NM_133838:327	Ehd4	INSIDE	0.204	0.507	1361.52	690.49	0.104	1120.93	116.07
A_68_P20842587	chr1:176432270-176432314	NM_019445:337	Fmn2	INSIDE	0.204	0.704	4111.06	2893.75	0.144	2781.22	399.20
A_68_P26761442	chr9:98857658-98857702	NM_012020:1655	Foxl2	INSIDE	0.204	0.615	1224.55	752.82	0.125	962.15	120.56
A_68_P29660138	chr14:63870620-63870670	NM_008092:-6547	Gata4	PROMOTER	0.204	0.546	1439.97	785.91	0.111	1087.14	120.86
A_68_P24466586	chr6:54942741-54942785	NM_026637:99	Ggct	INSIDE	0.204	0.428	1823.74	781.34	0.088	1331.71	116.65
A_68_P24116813	chr5:136021029-136021073	NM_146001:-58	Hip1	PROMOTER	0.204	0.560	1404.69	786.06	0.114	1097.20	125.40
A_68_P23331344	chr4:135502377-135502421	NM_008254:31	Hmgcl	INSIDE	0.204	0.594	1240.26	736.22	0.121	952.96	115.63
A_68_P26586063	chr9:64989672-64989716	NM_008988:699	Igdcc3	INSIDE	0.204	0.657	1706.16	1121.37	0.134	1289.38	173.05
A_68_P31516120	chr18:15309236-15309280	NM_134112:697	Kctd1	INSIDE	0.204	0.585	2412.99	1412.22	0.120	1891.21	226.24
A_68_P32752567	chrX:149672709-149672753	NM_173780:143	Klf8	INSIDE	0.204	1.586	2576.06	4085.29	0.323	1015.29	328.05
A_68_P25279951	chr7:90016308-90016352	NM_175366:488	Mex3b	INSIDE	0.204	0.519	1451.64	753.75	0.106	1151.48	121.92
A_68_P28055687	chr11:98188542-98188588	NM_010895:2395	Neurod2	INSIDE	0.204	0.561	1453.35	815.91	0.115	1156.57	132.64
A_68_P31926194	chr19:4989799-4989843	NM_153553:151	Npas4	INSIDE	0.204	0.494	1799.08	889.29	0.101	1230.56	124.04
A_68_P26980662	chr10:19077212-19077256	NM_053008:890	Olig3	INSIDE	0.204	0.493	1482.76	731.55	0.101	1131.98	114.07
A_68_P25948238	chr8:72356673-72356717	NM_001024954:92	Pbx4	INSIDE	0.204	0.486	1389.65	675.11	0.099	1155.72	114.80
A_68_P23176982	chr4:104830286-104830330	NM_080555:357	Ppap2b	INSIDE	0.204	0.588	2653.85	1560.48	0.120	1893.15	226.67
A_68_P27478501	chr10:116386814-116386861	NM_001003950:599	Rab3ip	INSIDE	0.204	0.670	1135.79	761.11	0.137	870.62	119.07
A_68_P31934220	chr19:6363615-6363659	NM_001110791:-53	Sf1	PROMOTER	0.204	0.566	2062.29	1168.25	0.115	1363.93	157.53
A_68_P28070587	chr11:100721732-100721776	NM_001164062:-43	Stat5a	PROMOTER	0.204	0.531	1426.91	758.02	0.108	1076.18	116.36
A_68_P25959798	chr8:74659599-74659643	NM_001001491:430	Tpm4	INSIDE	0.204	0.518	3464.10	1794.52	0.105	2558.82	269.81
A_68_P24951867	chr7:5013463-5013510	NM_001205231:-258	U2af2	PROMOTER	0.204	0.628	1088.31	683.19	0.128	913.11	117.03
A_68_P27981394	chr11:84953213-84953257	NM_001029934:223	Usp32	INSIDE	0.204	0.729	5481.35	3997.05	0.149	4000.64	594.10
A_68_P31204657	chr17:46167697-46167741	NM_001110266:-5606	Vegfa	PROMOTER	0.204	0.642	2436.41	1563.93	0.131	1890.76	247.36
A_68_P31054974	chr17:13185825-13185876	NM_175394:-445	Wtap	PROMOTER	0.204	0.600	1131.54	679.26	0.122	997.11	122.05
A_68_P26744827	chr9:95855160-95855204	NM_011916:4	Xrn1	INSIDE	0.204	0.648	1124.55	728.52	0.132	905.68	119.45
A_68_P27833210	chr11:58680690-58680734	NM_172403:-29	2810021J22Rik	PROMOTER	0.203	0.471	1495.18	704.17	0.095	1292.19	123.35
A_68_P27897804	chr11:69714837-69714881	NM_027419:-370	2810408A11Rik	DIVERGENT_PROMOTER	0.203	0.623	2830.13	1763.22	0.127	2153.95	272.76
A_68_P27554558	chr11:3794697-3794745	NM_026150:409	4921536K21Rik	INSIDE	0.203	0.615	1690.84	1039.26	0.125	1225.11	153.16

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31624566	chr18:36720188-36720232	NM_175375:-46	Ankhd1	PROMOTER	0.203	0.676	1116.52	754.30	0.137	874.25	119.67
A_68_P26883806	chr9:121403762-121403806	NM_031161:1023	Cck	INSIDE	0.203	0.591	2642.63	1560.77	0.120	1986.84	238.69
A_68_P32097109	chr19:37773781-37773827	NM_007811:1507	Cyp26a1	INSIDE	0.203	0.472	2573.06	1214.84	0.096	2008.95	192.74
A_68_P23226797	chr4:115611470-115611514	NM_001025567:1039	Dmbx1	INSIDE	0.203	0.604	2027.15	1225.38	0.123	1562.01	191.89
A_68_P32030685	chr19:25680631-25680675	NM_177360:-4374	Dmrt3	PROMOTER	0.203	0.698	1697.10	1184.90	0.141	1261.40	178.39
A_68_P28602892	chr12:86560540-86560584	NM_145445:100	Eif2b2	INSIDE	0.203	0.534	1407.50	751.37	0.108	1091.84	118.30
A_68_P23270915	chr4:124572399-124572443	NM_177671:13392	Epha10	DOWNSTREAM	0.203	0.637	3074.52	1957.06	0.129	2382.37	307.28
A_68_P22874562	chr4:43970796-43970840	NM_027450:245	Glipr2	INSIDE	0.203	0.687	2370.98	1629.69	0.139	1874.53	261.24
A_68_P26020979	chr8:87186333-87186377	NM_010499:397	Ier2	INSIDE	0.203	0.426	1628.62	694.60	0.086	1404.48	121.32
A_68_P29618998	chr14:56254267-56254311	NM_024267:227	Ipo4	INSIDE	0.203	0.579	1225.27	709.22	0.117	1024.29	120.17
A_68_P26227629	chr8:124114089-124114133	NM_026160:-257	Map1lc3b	PROMOTER	0.203	0.467	1645.46	768.07	0.095	1245.84	117.86
A_68_P22317890	chr3:89017814-89017858	NM_001161824:421	Mtx1	INSIDE	0.203	0.737	4415.74	3253.73	0.150	2917.74	437.03
A_68_P28246294	chr12:12947123-12947167	NM_008709:1498	Mycn	INSIDE	0.203	0.485	3235.04	1570.37	0.099	2055.94	203.09
A_68_P23543337	chr5:24191628-24191672	NM_016736:18	Nub1	INSIDE	0.203	1.600	4781.80	7649.06	0.324	3187.57	1034.03
A_68_P26142834	chr8:109572130-109572174	NM_026513:362	Pdf	INSIDE	0.203	0.667	2418.04	1612.21	0.135	1921.62	260.15
A_68_P29275481	chr13:102538276-102538320	NM_001077495:-126	Pik3r1	PROMOTER	0.203	0.522	2880.19	1503.99	0.106	2349.49	248.86
A_68_P31207971	chr17:46765981-46766025	NM_175168:451	Ptk7	INSIDE	0.203	0.523	2923.74	1528.13	0.106	2021.64	214.17
A_68_P31257591	chr17:56812887-56812931	NM_027933:229	Ranbp3	INSIDE	0.203	0.329	2100.47	690.05	0.067	1813.72	120.85
A_68_P26809513	chr9:107456377-107456421	NM_019713:-588	Rassf1	PROMOTER	0.203	0.686	1131.58	775.79	0.139	839.72	116.60
A_68_P23359686	chr4:140258987-140259035	NM_173867:1623	Rcc2	INSIDE	0.203	0.601	1281.87	770.88	0.122	962.24	117.72
A_68_P26143093	chr8:109619905-109619949	NM_009353:519	Terf2	INSIDE	0.203	0.656	2194.17	1440.32	0.133	1586.25	211.56
A_68_P23367601	chr4:141640480-141640524	NM_145402:-283	Tmem51	PROMOTER	0.203	0.504	1862.95	939.53	0.102	1420.14	145.43
A_68_P27273026	chr10:77707095-77707139	NM_001081055:271	Trappc10	INSIDE	0.203	0.411	2015.47	827.41	0.083	1647.53	137.20
A_68_P20405961	chr1:84835228-84835272	NM_133975:629	Trip12	INSIDE	0.203	1.596	6729.40	10740.45	0.324	4499.56	1458.85
A_68_P31118859	chr17:27993828-27993872	NM_001080769:399	Uhrf1bp1	INSIDE	0.203	0.657	3498.82	2298.77	0.133	2559.01	340.95
A_68_P24002090	chr5:114580992-114581036	NM_011677:-150	Ung	PROMOTER	0.203	0.552	1463.58	808.59	0.112	1104.62	123.89
A_68_P28931386	chr13:32894845-32894889	NM_030215:968	Wrnip1	INSIDE	0.203	0.404	2034.57	821.24	0.082	1543.77	126.66
A_68_P21810975	chr2:163029586-163029630	ENSMUST00000128999:-680		PROMOTER	0.203	1.334	9188.32	12258.04	0.270	6087.24	1645.52
A_68_P27933163	chr11:76435980-76436032	ENSMUST00000155035:-190		PROMOTER	0.203	0.655	1146.82	750.91	0.133	903.75	120.10
A_68_P21615858	chr2:127657441-127657493	NM_001113179:129	Bub1	INSIDE	0.202	0.694	1119.43	776.42	0.140	852.83	119.77
A_68_P26080248	chr8:97441798-97441842	NM_001033533:178	Ccdc102a	INSIDE	0.202	0.696	1400.12	974.39	0.141	1161.98	163.33
A_68_P24990418	chr7:19495547-19495597	NM_001033314:181	Ccdc61	INSIDE	0.202	0.598	1461.41	873.69	0.121	1130.10	136.73
A_68_P27937691	chr11:77275964-77276008	NM_139128:-1428	Coro6	PROMOTER	0.202	0.539	4893.39	2636.77	0.109	3266.74	356.09
A_68_P26665915	chr9:79607435-79607480	NM_009945:203	Cox7a2	INSIDE	0.202	0.652	1853.07	1208.60	0.132	1468.04	193.66
A_68_P26585437	chr9:64880753-64880797	NM_028906:510	Dpp8	INSIDE	0.202	0.730	2641.78	1929.15	0.148	1885.44	278.25
A_68_P27845568	chr11:60745336-60745380	NR_027800:11	Gm16516	INSIDE	0.202	0.424	1765.82	749.44	0.086	1337.97	114.76
A_68_P27327041	chr10:88193707-88193757	NM_001037166:114	Gm4925	INSIDE	0.202	0.712	2460.09	1751.05	0.143	1849.12	265.29
A_68_P20739601	chr1:157588425-157588469	NM_010712:711	Lhx4	INSIDE	0.202	0.494	1652.57	816.53	0.100	1243.00	123.79
A_68_P21137726	chr2:35946774-35946818	NM_001083126:12784	Lhx6	INSIDE	0.202	0.448	2055.55	920.94	0.091	1429.55	129.42
A_68_P21137822	chr2:35958973-35959017	NM_001083126:586	Lhx6	INSIDE	0.202	0.429	2004.19	860.63	0.087	1632.53	141.74
A_68_P21122747	chr2:33495004-33495053	NM_010725:1003	Lmx1b	INSIDE	0.202	0.543	1509.64	820.36	0.110	1078.16	118.27
A_68_P26827665	chr9:111020395-111020439	NM_001164838:-198	Lrrfip2	PROMOTER	0.202	0.716	2023.28	1449.50	0.144	1379.14	199.20
A_68_P23524106	chr5:20561482-20561526	NM_011203:111	Ptpn12	INSIDE	0.202	0.431	2473.67	1066.31	0.087	1985.19	172.77
A_68_P26706396	chr9:87624611-87624655	NM_023814:1463	Tbx18	INSIDE	0.202	0.428	1771.06	757.16	0.086	1387.00	119.78
A_68_P27892867	chr11:68884346-68884390	NM_025838:58	Tmem107	INSIDE	0.202	0.364	2524.41	919.11	0.074	1745.29	128.44
A_68_P25588179	chr7:148514181-148514225	NR_024509:174	Tmem80	INSIDE	0.202	0.369	1949.27	719.31	0.075	1554.11	115.81
A_68_P23296884	chr4:129168378-129168422	NM_001085491:-33	1700125D06Rik	DIVERGENT_PROMOTER	0.201	0.683	1197.36	817.50	0.137	877.02	120.53
A_68_P32180644	chr19:53216958-53217002	NM_001164100:-265	Add3	PROMOTER	0.201	0.580	4243.47	2462.55	0.117	3297.27	384.65
A_68_P26818138	chr9:108976646-108976690	NM_172774:-30	Atrip	PROMOTER	0.201	0.688	2069.91	1423.61	0.139	1605.61	222.50
A_68_P23440041	chr4:155069180-155069224	NM_178699:752	B930041F14Rik	INSIDE	0.201	0.433	2290.82	992.66	0.087	1698.61	147.58
A_68_P31202232	chr17:45767295-45767346	NM_001013767:28938	Capn11	INSIDE	0.201	0.545	1439.37	784.15	0.109	1084.88	118.51

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27187842	chr10:62254957-62255001	NM_026201:138	Ccar1	INSIDE	0.201	0.465	1658.33	771.11	0.093	1248.31	116.57
A_68_P26590186	chr9:65757328-65757375	NM_173185:535	Csnk1g1	INSIDE	0.201	0.555	1332.98	739.79	0.112	1041.20	116.32
A_68_P22609958	chr3:145312902-145312946	NM_010516:25	Cyr61	INSIDE	0.201	0.534	1382.71	737.81	0.107	1107.28	118.96
A_68_P23262655	chr4:123088845-123088889	NM_001167918:288	D830031N03Rik	INSIDE	0.201	0.680	2105.68	1432.35	0.137	1569.54	214.32
A_68_P29310804	chr13:109106277-109106321	NM_178683:-232	Depdc1b	PROMOTER	0.201	0.653	1030.65	673.28	0.131	890.20	116.69
A_68_P29681795	chr14:67487454-67487502	NM_009955:-41	Dpysl2	DIVERGENT_PROMOTER	0.201	0.617	1264.24	780.41	0.124	974.26	120.62
A_68_P29204944	chr13:88961571-88961615	NM_001037987:516	Edil3	INSIDE	0.201	0.629	1172.78	738.12	0.126	911.57	115.06
A_68_P29292940	chr13:105653878-105653922	NM_029984:73	Fam159b	INSIDE	0.201	0.551	1329.81	732.42	0.111	1074.31	119.08
A_68_P29578549	chr14:47442107-47442163	NM_022023:-217	Gmfb	DIVERGENT_PROMOTER	0.201	0.504	1458.55	734.90	0.101	1152.78	116.58
A_68_P25082509	chr7:50721683-50721727	NM_001164518:23689	Iglon5	DOWNSTREAM	0.201	1.425	2700.72	3849.50	0.286	1906.16	544.92
A_68_P27812424	chr11:54674270-54674317	NM_029327:-200	Lyrm7	DIVERGENT_PROMOTER	0.201	0.614	1145.31	703.43	0.123	973.58	120.06
A_68_P20337462	chr1:72582708-72582752	NM_001045533:408	Marchf4	INSIDE	0.201	0.683	1949.89	1331.51	0.137	1454.01	199.79
A_68_P23265181	chr4:123582007-123582051	NM_019660:-227	Mycbp	PROMOTER	0.201	0.384	1828.94	702.29	0.077	1497.45	115.71
A_68_P25494916	chr7:132635012-132635056	NM_026330:22	Nsmce1	INSIDE	0.201	0.540	2314.21	1249.49	0.109	1645.48	178.56
A_68_P26242536	chr8:126473255-126473299	NM_172288:-111	Nup133	PROMOTER	0.201	0.322	2254.66	726.10	0.065	1823.86	117.95
A_68_P21100055	chr2:29745964-29746008	NM_001177662:404	Odf2	INSIDE	0.201	0.609	1174.99	715.00	0.122	987.70	120.84
A_68_P26640631	chr9:74711117-74711161	NM_008262:1411	Onecut1	INSIDE	0.201	0.644	1047.88	674.85	0.129	900.21	116.27
A_68_P28458297	chr12:57797636-57797681	NM_011041:1033	Pax9	INSIDE	0.201	0.481	1608.53	774.33	0.097	1229.54	118.93
A_68_P25326019	chr7:99818550-99818594	NM_029078:-150	Pcf11	PROMOTER	0.201	0.433	1873.39	811.66	0.087	1358.15	118.48
A_68_P30578587	chr16:18248121-18248165	NM_011239:645	Ranbp1	INSIDE	0.201	0.579	1146.06	664.12	0.117	1005.90	117.32
A_68_P28534667	chr12:74041473-74041517	NM_011384:563	Six6	INSIDE	0.201	0.707	1249.09	883.01	0.142	1026.02	145.52
A_68_P28307269	chr12:28028213-28028257	NM_009234:-651	Sox11	PROMOTER	0.201	0.597	2510.47	1499.70	0.120	1675.13	200.76
A_68_P32103865	chr19:38911994-38912038	NM_145952:948	Tbc1d12	INSIDE	0.201	0.409	1826.24	746.26	0.082	1472.60	120.68
A_68_P24608768	chr6:86145664-86145708	NM_031199:442	Tgfa	INSIDE	0.201	0.461	1548.42	713.33	0.092	1238.73	114.54
A_68_P23575088	chr5:31172158-31172203	NM_144525:161	Tmem214	INSIDE	0.201	0.602	2368.37	1425.35	0.121	1444.20	174.87
A_68_P24113930	chr5:135408345-135408389	NM_024479:124	Wbscr27	INSIDE	0.201	0.706	2367.41	1671.21	0.142	1727.80	244.89
A_68_P31879129	chr18:83080856-83080900	NM_001177464:-3145	Zfp516	PROMOTER	0.201	1.487	1836.25	2730.14	0.298	1301.81	388.17
A_68_P30284263	chr15:64753735-64753779	NM_009623:102	Adcy8	INSIDE	0.200	0.386	2013.85	777.96	0.077	1477.48	114.23
A_68_P32200577	chr19:56471803-56471847	NM_007611:206	Casp7	INSIDE	0.200	0.544	2040.89	1110.40	0.109	1849.95	200.84
A_68_P29651431	chr14:62305946-62306001	NR_028264:-4763	Dleu2	PROMOTER	0.200	0.623	1314.06	819.32	0.125	978.36	122.26
A_68_P29699021	chr14:70477881-70477925	NM_018781:651	Egr3	INSIDE	0.200	0.651	2839.06	1848.43	0.130	2319.54	301.92
A_68_P26685697	chr9:83699258-83699303	NM_001145974:569	Elovl4	INSIDE	0.200	1.549	758.58	1174.68	0.310	595.79	184.95
A_68_P29050431	chr13:54723325-54723369	NM_178397:202	Faf2	INSIDE	0.200	0.592	1357.03	803.83	0.118	992.95	117.46
A_68_P30279146	chr15:63891463-63891507	NM_144846:526	Fam49b	INSIDE	0.200	0.702	1470.92	1032.91	0.141	1240.59	174.59
A_68_P31093565	chr17:23908024-23908068	NM_153791:512	Flywch1	INSIDE	0.200	0.580	1344.49	779.38	0.116	1002.94	116.44
A_68_P28246315	chr12:12949549-12949593	NM_008709:-928	Mycn	PROMOTER	0.200	0.464	1639.65	760.27	0.093	1287.97	119.40
A_68_P27926998	chr11:75401820-75401864	NM_008850:233	Pitpna	INSIDE	0.200	0.663	1335.14	885.01	0.133	1121.74	148.86
A_68_P24984115	chr7:17532440-17532484	NM_001099636:2432	Pnmal2	INSIDE	0.200	0.503	1456.66	732.44	0.101	1171.19	117.94
A_68_P23542951	chr5:24104726-24104770	NM_025891:3072	Smarcd3	INSIDE	0.200	0.603	2177.16	1312.59	0.121	1575.82	190.31
A_68_P25950579	chr8:72758186-72758230	NM_001168290:84	Sugp2	INSIDE	0.200	0.491	1547.57	759.29	0.098	1268.99	124.75
A_68_P30572946	chr16:17277489-17277533	NM_177473:1118	Tmem191c	INSIDE	0.200	0.586	1278.86	749.53	0.117	1042.69	122.32
A_68_P27287608	chr10:80598003-80598047	NM_010731:-991	Zbtb7a	PROMOTER	0.200	0.470	1658.99	779.85	0.094	1258.52	118.28
A_68_P21823563	chr2:165213394-165213441	NM_178411:342	Zfp334	INSIDE	0.200	0.484	2097.41	1015.15	0.097	1669.03	161.23
A_68_P26552549	chr9:59138886-59138933	NM_028121:-469	Adpgk	PROMOTER	0.199	1.569	699.77	1097.66	0.312	432.76	135.16
A_68_P26816846	chr9:108729372-108729416	NM_080437:744	Celsr3	INSIDE	0.199	0.521	3449.92	1796.89	0.104	2478.45	257.31
A_68_P28143423	chr11:113544774-113544818	NM_138598:669	D11Wsu99e	INSIDE	0.199	0.623	1170.45	729.50	0.124	947.60	117.73
A_68_P27543295	chr10:128242767-128242811	NM_028873:57	Dnajc14	INSIDE	0.199	0.511	1583.52	809.79	0.102	1222.92	124.16
A_68_P21933404	chr3:8665074-8665126	NM_010423:1938	Hey1	INSIDE	0.199	0.690	1111.30	766.70	0.138	884.71	121.66
A_68_P21037807	chr2:17949322-17949366	NR_028378:469	LOC100034739	INSIDE	0.199	0.653	1963.96	1282.65	0.130	1479.02	192.21
A_68_P31734233	chr18:57292628-57292672	NM_001001979:-93	Megf10	PROMOTER	0.199	0.624	2747.69	1713.88	0.124	2036.81	252.76
A_68_P23609669	chr5:37187204-37187251	NM_026242:766	Mrfap1	INSIDE	0.199	0.677	1172.98	794.28	0.135	880.28	118.67

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P21115162	chr2:32252222-32252274	NM_133783:839	Ptges2	INSIDE	0.199	0.677	1509.10	1021.34	0.135	1036.54	139.73
A_68_P26825587	chr9:110645381-110645425	NM_001083936:-288	Pth1r	PROMOTER	0.199	0.714	2429.62	1735.16	0.142	1721.31	244.66
A_68_P28519206	chr12:71328237-71328281	NM_133198:412	Pygl	INSIDE	0.199	0.564	1439.20	811.22	0.112	1124.78	126.31
A_68_P29482227	chr14:27354230-27354274	NM_032008:-1026	Slmap	PROMOTER	0.199	0.534	3110.16	1661.18	0.106	2184.68	231.92
A_68_P27281036	chr10:79578010-79578054	NM_011492:-1248	Stk11	PROMOTER	0.199	0.605	1344.72	813.44	0.120	959.33	115.55
A_68_P30486394	chr15:100382394-100382438	NM_033476:-38	Tcfcp2	PROMOTER	0.199	0.611	2300.39	1405.40	0.122	1870.95	227.84
A_68_P28356088	chr12:36768830-36768874	NM_025359:213	Tspan13	INSIDE	0.199	0.604	3258.81	1968.73	0.120	2354.42	282.63
A_68_P20680089	chr1:145624837-145624881	NM_001159866:451	Uchl5	INSIDE	0.199	0.635	1275.72	810.46	0.126	960.30	121.29
A_68_P24541408	chr6:72330305-72330349	NM_001080742:136	Vamp5	INSIDE	0.199	0.553	3609.20	1994.65	0.110	2799.63	308.22
A_68_P27927819	chr11:75547027-75547071	NM_009536:660	Ywhae	INSIDE	0.199	0.574	4961.05	2848.34	0.114	3732.30	425.80
A_68_P21851437	chr2:169959061-169959105	NM_001033299:-2362	Zfp217	PROMOTER	0.199	0.543	1373.10	745.41	0.108	1100.18	118.92
A_68_P31625899	chr18:36953656-36953708	NM_025594:106	Zmat2	INSIDE	0.199	0.651	1267.50	825.40	0.129	927.30	120.06
A_68_P31412806	chr17:86200011-86200055	AK142122:810		INSIDE	0.199	0.490	1444.30	707.13	0.098	1196.30	116.75
A_68_P27383831	chr10:98378471-98378515	NM_026482:707	Atp2b1	INSIDE	0.198	0.586	1396.74	818.14	0.116	1044.50	121.02
A_68_P24172980	chr5:148117798-148117842	NM_007673:1005	Cdx2	INSIDE	0.198	0.439	1722.33	756.32	0.087	1366.22	118.65
A_68_P29270035	chr13:101545475-101545519	NM_021886:358	Cenph	INSIDE	0.198	0.517	3664.88	1893.96	0.103	2523.96	258.79
A_68_P20437269	chr1:92500284-92500337	NM_133805:311	Cops8	INSIDE	0.198	0.693	1048.40	726.11	0.137	890.24	121.83
A_68_P26015688	chr8:86132717-86132768	NM_018808:669	Dnajb1	INSIDE	0.198	0.503	1573.85	792.17	0.099	1170.32	116.43
A_68_P32183082	chr19:53604536-53604581	NM_001085390:751	Dusp5	INSIDE	0.198	0.691	1291.86	892.57	0.137	906.88	124.01
A_68_P27212434	chr10:66999516-66999563	NM_010118:-1077	Egr2	PROMOTER	0.198	2.177	3937.19	8572.79	0.431	2827.98	1219.76
A_68_P22128829	chr3:51080053-51080101	NM_023502:49833	Elf2	INSIDE	0.198	0.430	1871.37	804.06	0.085	1416.45	120.23
A_68_P29310182	chr13:109005275-109005324	NM_029001:702	Elovl7	INSIDE	0.198	0.580	1308.98	758.75	0.115	1013.94	116.38
A_68_P28529999	chr12:73171616-73171660	NM_181752:340	Gpr135	INSIDE	0.198	0.679	5572.04	3785.44	0.134	3970.28	533.12
A_68_P25174410	chr7:71084241-71084285	NM_021366:-461	Klf13	PROMOTER	0.198	0.491	1760.19	863.53	0.097	1213.78	117.72
A_68_P24129308	chr5:138635505-138635553	NM_177878:-13	Mblac1	PROMOTER	0.198	0.526	1362.28	716.73	0.104	1168.05	121.94
A_68_P27924626	chr11:74986914-74986958	NR_029794:47	Mir212	INSIDE	0.198	0.542	1497.93	811.22	0.107	1161.17	124.24
A_68_P24981699	chr7:17060079-17060123	NM_008718:2029	Npas1	INSIDE	0.198	0.694	1308.38	908.12	0.137	1075.54	147.48
A_68_P30368842	chr15:79664125-79664169	NM_001013360:617	Npcd	INSIDE	0.198	0.707	1360.74	961.81	0.140	834.02	116.60
A_68_P21418379	chr2:90519075-90519128	NM_021512:1730	Nup160	INSIDE	0.198	0.639	1306.12	834.87	0.127	920.60	116.71
A_68_P24438215	chr6:50406155-50406199	NM_001163645:-7	Osbpl3	PROMOTER	0.198	0.635	2993.58	1901.56	0.126	2327.92	293.40
A_68_P32240899	chrX:7499781-7499825	NM_013892:2855	Pcsk1n	INSIDE	0.198	1.476	3780.26	5580.09	0.292	1500.72	438.65
A_68_P30670427	chr16:35490517-35490561	NM_028295:421	Pdia5	INSIDE	0.198	0.487	1977.23	963.58	0.097	1496.50	144.72
A_68_P25988742	chr8:80959567-80959624	NM_138944:956	Pou4f2	INSIDE	0.198	0.557	1502.78	837.75	0.111	1094.76	121.00
A_68_P28057822	chr11:98544211-98544255	NM_009439:365	Psmd3	INSIDE	0.198	0.537	1431.08	768.90	0.106	1182.55	125.60
A_68_P22372025	chr3:100726540-100726584	NM_001165953:147	Trim45	INSIDE	0.198	1.549	5632.82	8726.45	0.307	3943.95	1209.26
A_68_P31210122	chr17:47147092-47147136	NM_001177374:367	Ubr2	INSIDE	0.198	0.375	2160.65	809.81	0.074	1648.66	122.20
A_68_P25958199	chr8:74194916-74194960	NM_001029873:718	Unc13a	INSIDE	0.198	0.511	3020.20	1544.04	0.101	2116.64	214.29
A_68_P24376836	chr6:38304039-38304083	NM_028421:543	Zc3hav1	INSIDE	0.198	0.594	1904.89	1132.26	0.118	1492.70	175.90
A_68_P25581872	chr7:147222785-147222830	NM_027201:518	Zfp511	INSIDE	0.198	0.307	2758.23	848.04	0.061	1939.46	118.02
A_68_P28350336	chr12:35591293-35591337	AK087563:335		INSIDE	0.198	0.547	3206.93	1754.78	0.108	2244.79	243.17
A_68_P30959870	chr16:90934584-90934628	NM_026502:488	1110004E09Rik	INSIDE	0.197	1.493	5615.36	8385.98	0.294	3441.60	1013.47
A_68_P28050587	chr11:97302015-97302059	NM_021493:-9437	Arhgap23	PROMOTER	0.197	0.691	2072.10	1432.11	0.136	1536.39	208.76
A_68_P28183223	chr11:120095537-120095581	NM_198423:1298	Bahcc1	INSIDE	0.197	0.628	3099.37	1945.17	0.123	2157.04	266.27
A_68_P24160791	chr5:145119346-145119390	NM_025833:-387	Baiap2l1	PROMOTER	0.197	0.511	2737.46	1399.69	0.101	1963.30	197.57
A_68_P32260568	chrX:11704944-11704992	NM_001168321:32513	Bcor	INSIDE	0.197	1.927	2757.03	5313.84	0.380	1025.70	389.31
A_68_P26486125	chr9:47338950-47338994	NM_001025600:538	Cadm1	INSIDE	0.197	0.484	2492.18	1207.29	0.096	2010.82	192.05
A_68_P25229722	chr7:80682604-80682648	NM_001081345:4006	Chd2	INSIDE	0.197	0.581	2332.22	1353.87	0.114	1730.07	197.85
A_68_P27540982	chr10:127805462-127805508	NM_001081040:1609	Coq10a	INSIDE	0.197	0.641	1315.01	843.25	0.126	963.91	121.86
A_68_P27991090	chr11:86620800-86620848	NM_026191:338	Dhx40	INSIDE	0.197	0.604	1360.71	821.31	0.119	990.68	118.08
A_68_P22318527	chr3:89120595-89120646	NM_010108:6181	Efna3	INSIDE	0.197	0.642	1459.59	937.30	0.127	990.46	125.31
A_68_P21940380	chr3:10012548-10012592	NM_010634:-35	Fabp5	PROMOTER	0.197	0.731	3055.98	2235.36	0.144	2143.35	308.92

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31948840	chr19:10257815-10257859	NM_146094:459	Fads1	INSIDE	0.197	0.627	2789.64	1750.15	0.124	2230.46	275.56
A_68_P25125430	chr7:59116936-59116980	NM_001115087:679	Fancf	INSIDE	0.197	0.438	2024.92	887.03	0.086	1566.38	135.31
A_68_P24793359	chr6:119431189-119431233	NM_133940:1525	Fbxl14	INSIDE	0.197	0.616	3279.68	2018.70	0.121	2399.85	291.28
A_68_P26406146	chr9:32348818-32348862	NM_008026:113	Fli1	INSIDE	0.197	0.696	4697.42	3267.47	0.137	3409.21	468.18
A_68_P31166994	chr17:37188152-37188196	NM_019439:5264	Gabbr1	INSIDE	0.197	0.705	1408.17	993.25	0.139	1047.40	145.25
A_68_P23968446	chr5:108154743-108154789	NM_010278:-1403	Gfi1	PROMOTER	0.197	0.423	1821.50	770.49	0.083	1481.81	123.26
A_68_P28067610	chr11:100216965-100217009	NM_010404:469	Hap1	INSIDE	0.197	0.415	1901.36	788.50	0.082	1501.29	122.56
A_68_P23252897	chr4:120404005-120404049	NM_001081142:15755	Kcnq4	INSIDE	0.197	0.550	1613.43	886.66	0.108	1095.09	118.31
A_68_P20864288	chr1:180458040-180458084	NM_001161665:-1193	Kif26b	PROMOTER	0.197	0.677	1096.79	742.44	0.133	880.68	117.44
A_68_P29696150	chr14:70009101-70009145	NM_033325:-160	Loxl2	PROMOTER	0.197	0.598	4983.34	2978.11	0.118	3416.03	401.66
A_68_P30655247	chr16:32914173-32914217	NM_001081255:9	Lrch3	INSIDE	0.197	0.574	1413.09	811.09	0.113	1289.46	146.07
A_68_P31130473	chr17:30026432-30026476	NM_001081160:-1627	Mdga1	PROMOTER	0.197	0.660	1154.37	761.80	0.130	942.24	122.67
A_68_P24610518	chr6:86475728-86475772	NM_011865:409	Pcbp1	INSIDE	0.197	0.480	2496.08	1198.88	0.094	1985.48	187.55
A_68_P23720374	chr5:58111556-58111604	NM_018764:2321	Pcdh7	INSIDE	0.197	0.565	1511.59	854.41	0.112	1098.63	122.57
A_68_P32535129	chrX:90877426-90877470	NM_008892:46	Pola1	INSIDE	0.197	1.708	1785.58	3049.75	0.337	646.78	218.00
A_68_P25015938	chr7:27964028-27964072	NM_029391:-148	Rab4b	PROMOTER	0.197	1.609	6446.80	10373.43	0.318	4121.72	1309.59
A_68_P26748149	chr9:96531046-96531090	NM_053268:854	Rasa2	INSIDE	0.197	0.591	1442.12	852.04	0.117	1172.93	136.65
A_68_P28535261	chr12:74146417-74146461	NM_009189:1261	Six1	INSIDE	0.197	0.492	1985.22	975.89	0.097	1337.98	129.75
A_68_P32564413	chrX:98728110-98728154	NM_001081008:59	Taf1	INSIDE	0.197	1.551	837.42	1298.49	0.306	376.49	115.13
A_68_P31644531	chr18:40378658-40378702	NM_023311:373	Yipf5	INSIDE	0.197	0.714	2126.77	1517.65	0.141	1486.92	209.42
A_68_P23302996	chr4:130417683-130417727	ENSMUST00000104193:-3909		PROMOTER	0.197	0.538	1534.97	825.39	0.106	1147.06	121.58
A_68_P22552059	chr3:135101503-135101547	NR_030689:105	4930539J05Rik	INSIDE	0.196	0.472	1831.15	863.82	0.092	1272.31	117.43
A_68_P28710689	chr12:106923839-106923883	NM_178613:299	4933433P14Rik	INSIDE	0.196	0.704	1230.52	866.51	0.138	979.94	135.01
A_68_P24114259	chr5:135484848-135484896	NM_001190437:-149	Abhd11	DIVERGENT_PROMOTER	0.196	0.630	1325.81	834.96	0.123	990.99	122.26
A_68_P30686065	chr16:38452492-38452536	NM_007414:255	Adprh	INSIDE	0.196	0.558	2277.40	1270.88	0.109	1709.95	187.03
A_68_P28059226	chr11:98769291-98769335	NM_011799:-152	Cdc6	PROMOTER	0.196	1.887	10924.37	20613.09	0.371	7249.68	2687.05
A_68_P30778452	chr16:55934493-55934544	NM_028815:443	Cep97	INSIDE	0.196	0.551	1765.37	973.22	0.108	1137.71	123.13
A_68_P29056202	chr13:55736711-55736755	NM_145975:345	Ddx46	INSIDE	0.196	0.649	4914.27	3191.70	0.127	3720.38	473.03
A_68_P20726997	chr1:155334160-155334214	NM_007842:604	Dhx9	INSIDE	0.196	0.534	1455.22	776.93	0.105	1158.21	121.50
A_68_P28732704	chr12:110691154-110691198	NM_001190703:-488	Dlk1	PROMOTER	0.196	0.561	1425.61	799.09	0.110	1181.70	129.80
A_68_P21114882	chr2:32208948-32208992	NM_010065:-146	Dnm1	DIVERGENT_PROMOTER	0.196	0.609	1283.73	781.66	0.119	1015.31	121.15
A_68_P20825998	chr1:172994760-172994804	NM_010188:-5248	Fcgr3	PROMOTER	0.196	0.557	6963.61	3879.52	0.109	5761.66	629.67
A_68_P27845445	chr11:60727478-60727528	NM_025294:-208	Gm16515	PROMOTER	0.196	0.655	1274.17	834.69	0.129	946.32	121.66
A_68_P24783944	chr6:117858262-117858321	NM_001166427:-9020	Hnrnpf	PROMOTER	0.196	0.619	1224.66	758.66	0.122	970.06	117.89
A_68_P30991547	chr16:96413886-96413930	NM_001001492:-44	Lca5l	DIVERGENT_PROMOTER	0.196	0.543	2338.07	1269.88	0.106	1744.40	185.29
A_68_P31829409	chr18:74224278-74224322	NM_172632:303	Mapk4	INSIDE	0.196	0.652	2563.25	1670.09	0.128	1920.54	245.38
A_68_P29446629	chr14:21212600-21212644	NM_025440:155	Mrps16	INSIDE	0.196	0.543	1403.41	761.67	0.106	1137.12	120.71
A_68_P30132589	chr15:35223344-35223388	NM_054049:-2500	Osr2	PROMOTER	0.196	0.499	1353.64	675.98	0.098	1179.00	115.20
A_68_P27708453	chr11:35582983-35583027	NM_145962:8	Pank3	INSIDE	0.196	0.442	1834.62	811.64	0.087	1387.60	120.16
A_68_P29618377	chr14:56159128-56159172	NM_028994:48	Pck2	INSIDE	0.196	0.562	1662.31	934.91	0.110	1178.46	129.72
A_68_P23313962	chr4:132324543-132324587	NM_011284:290	Rpa2	INSIDE	0.196	0.603	3888.61	2346.23	0.119	2862.84	339.39
A_68_P31755042	chr18:61173520-61173564	NM_201353:311	Slc6a7	INSIDE	0.196	0.528	1881.91	994.11	0.103	1465.17	151.44
A_68_P24114433	chr5:135517901-135517945	NM_016801:18481	Stx1a	INSIDE	0.196	1.446	2560.20	3703.22	0.283	1720.37	487.41
A_68_P20878652	chr1:182872565-182872613	NM_144794:-60	Tmem63a	PROMOTER	0.196	0.478	1818.60	870.04	0.094	1294.30	121.41
A_68_P31202520	chr17:45822206-45822252	NM_198167:939	Tmem63b	INSIDE	0.196	0.619	1416.25	876.64	0.121	994.70	120.65
A_68_P24019925	chr5:117769743-117769788	NM_001033311:491	Vsig10	INSIDE	0.196	0.476	1496.85	712.00	0.093	1262.77	117.99
A_68_P30665018	chr16:34574206-34574250	ENSMUST00000114961:-610		PROMOTER	0.196	0.390	1884.70	734.76	0.077	1509.78	115.55
A_68_P26443871	chr9:40338959-40339006	ENSMUST00000119373:-14		PROMOTER	0.196	0.447	1550.72	693.13	0.088	1313.04	115.08
A_68_P27106295	chr10:44249509-44249553	ENSMUST00000167340:-1223		PROMOTER	0.196	0.514	3407.68	1752.99	0.101	2569.56	259.32
A_68_P28068583	chr11:100389102-100389146	NM_001199296:190	Acly	INSIDE	0.195	0.399	1972.04	787.31	0.078	1513.68	118.02
A_68_P24355040	chr6:34267503-34267547	NM_009658:-35	Akr1b3	PROMOTER	0.195	0.528	1484.47	784.17	0.103	1179.64	121.74

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P30425163	chr15:89259930-89259974	NR_004843:406	BC090627	INSIDE	0.195	0.544	3456.39	1881.49	0.106	2649.67	281.50
A_68_P31134865	chr17:30712521-30712565	NM_027060:690	Btbd9	INSIDE	0.195	0.574	1343.54	770.52	0.112	1059.10	118.55
A_68_P22402367	chr3:106350620-106350664	NM_133869:37	Cept1	INSIDE	0.195	0.590	1253.08	739.59	0.115	1042.28	120.12
A_68_P23873911	chr5:89193834-89193878	NM_007832:-181	Dck	PROMOTER	0.195	0.548	1875.09	1027.72	0.107	1519.10	162.08
A_68_P22869096	chr4:42962948-42962992	NM_019874:-2995	Dnajb5	PROMOTER	0.195	0.729	3574.50	2607.49	0.142	2533.01	359.98
A_68_P23241426	chr4:118293372-118293419	NM_026932:-8	Ebna1bp2	DIVERGENT_PROMOTER	0.195	0.638	1235.31	788.08	0.124	927.85	115.34
A_68_P30423843	chr15:89027122-89027166	NM_027081:-239	Fam116b	PROMOTER	0.195	0.559	1347.01	752.51	0.109	1113.67	121.29
A_68_P26905371	chr10:4541584-4541628	NM_025995:531	Fbxo5	INSIDE	0.195	0.422	1778.22	750.04	0.082	1423.04	117.12
A_68_P26133209	chr8:107871674-107871718	NM_177699:174	Fhod1	INSIDE	0.195	0.514	1692.58	869.66	0.100	1245.76	125.01
A_68_P22405343	chr3:107082203-107082254	NM_026774:453	Hbxip	INSIDE	0.195	0.715	1392.62	996.07	0.139	971.40	135.42
A_68_P23417771	chr4:151664685-151664729	NM_008237:1065	Hes3	INSIDE	0.195	0.556	1313.42	729.88	0.108	1141.18	123.41
A_68_P28044105	chr11:96227597-96227641	NM_008266:547	Hoxb1	INSIDE	0.195	0.495	1785.36	884.48	0.097	1300.11	125.76
A_68_P23298318	chr4:129419063-129419107	NM_011317:442	Khdrbs1	INSIDE	0.195	0.411	1817.20	746.82	0.080	1428.52	114.25
A_68_P28693441	chr12:103981601-103981648	NM_001142937:246	Moap1	INSIDE	0.195	0.666	1141.53	760.21	0.130	952.75	123.70
A_68_P23637406	chr5:42153189-42153233	NM_007524:2249	Nkx3-2	INSIDE	0.195	0.442	1980.72	874.64	0.086	1472.33	127.09
A_68_P23617870	chr5:38550639-38550683	NM_010942:46	Nsg1	INSIDE	0.195	0.577	1256.40	725.24	0.112	1185.89	133.22
A_68_P32552414	chrX:96086168-96086212	NM_052976:134	Ophn1	INSIDE	0.195	1.373	1448.29	1988.71	0.268	619.69	166.07
A_68_P29479230	chr14:26513644-26513688	NM_134084:11	Ppif	INSIDE	0.195	0.482	1816.19	875.31	0.094	1342.43	126.31
A_68_P28071211	chr11:100830670-100830714	NM_008986:1239	Ptrf	INSIDE	0.195	1.562	7198.03	11241.73	0.305	4664.73	1420.47
A_68_P22342532	chr3:94964402-94964446	NM_011351:-3871	Sema6c	PROMOTER	0.195	0.548	1503.41	823.23	0.107	1130.11	120.72
A_68_P27804916	chr11:53280008-53280053	NM_027917:9324	Shroom1	INSIDE	0.195	0.707	2162.09	1527.52	0.138	1797.46	247.22
A_68_P30578493	chr16:18234733-18234777	NM_172151:475	Zdhhc8	INSIDE	0.195	0.653	1295.80	845.62	0.127	898.37	114.44
A_68_P25618382	chr8:4677520-4677564	ENSMUST00000058918:823		INSIDE	0.195	0.551	2691.49	1482.30	0.107	1952.07	209.27
A_68_P31465575	chr18:4921810-4921854	ENSMUST00000143254:109		INSIDE	0.195	0.391	3222.26	1259.73	0.076	2570.37	195.59
A_68_P32540012	chrX:92185879-92185923	ENSMUST00000168067:8011		DOWNSTREAM	0.195	3.384	2820.30	9543.72	0.658	1129.69	743.56
A_68_P29050105	chr13:54666706-54666750	NM_133797:15	4833439L19Rik	INSIDE	0.194	0.550	1363.30	749.81	0.107	1169.34	124.90
A_68_P28075090	chr11:101526871-101526915	NM_025404:38	Arl4d	INSIDE	0.194	0.626	2054.59	1287.08	0.121	1449.01	175.80
A_68_P23321454	chr4:133742757-133742801	NM_144527:222	Ccdc21	INSIDE	0.194	0.580	1512.87	877.58	0.112	1021.32	114.73
A_68_P21639432	chr2:132089391-132089435	NM_138651:420	Cds2	INSIDE	0.194	0.679	2146.73	1458.04	0.132	1708.67	225.09
A_68_P29310181	chr13:109005203-109005247	NM_029001:627	Elovl7	INSIDE	0.194	0.542	1712.22	928.73	0.105	1137.36	119.41
A_68_P31544264	chr18:21458028-21458072	NM_001033445:590	Fam59a	INSIDE	0.194	0.374	2023.66	756.91	0.073	1645.96	119.50
A_68_P24992575	chr7:19890451-19890495	NM_008036:4922	Fosb	INSIDE	0.194	0.507	2537.61	1286.21	0.099	1860.47	183.26
A_68_P32380508	chrX:49517357-49517405	NM_008150:720	Gpc4	INSIDE	0.194	1.566	934.20	1463.14	0.304	381.37	116.13
A_68_P28883199	chr13:23831258-23831302	NM_015786:605	Hist1h1c	INSIDE	0.194	0.450	1895.51	852.57	0.087	1428.11	124.46
A_68_P28556953	chr12:78063293-78063337	NM_001146176:-79	Max	PROMOTER	0.194	1.514	2927.83	4433.05	0.293	2024.08	593.04
A_68_P24117829	chr5:136254539-136254583	NM_008617:42	Mdh2	INSIDE	0.194	0.537	1534.04	823.93	0.104	1230.67	128.20
A_68_P23536409	chr5:22939362-22939412	NM_026984:-860	Mll5	PROMOTER	0.194	0.629	1221.10	768.58	0.122	1003.10	122.52
A_68_P26871809	chr9:119248880-119248924	NM_010851:256	Myd88	INSIDE	0.194	0.609	2528.26	1540.03	0.118	1924.18	227.84
A_68_P30512786	chr16:4939254-4939298	NM_025839:166	Nudt16l1	INSIDE	0.194	0.710	2106.79	1495.70	0.137	1362.72	187.33
A_68_P27903590	chr11:70783209-70783253	NM_001083331:234	Nup88	INSIDE	0.194	0.483	1721.41	831.37	0.093	1290.37	120.59
A_68_P29269011	chr13:101322401-101322445	NM_008756:31	Ocln	INSIDE	0.194	0.430	1613.59	694.20	0.084	1469.64	122.93
A_68_P32464979	chrX:71069627-71069676	NM_001029868:657	Pdzd4	INSIDE	0.194	1.750	1041.83	1823.36	0.339	435.07	147.53
A_68_P20641447	chr1:137662511-137662555	NM_013750:-129	Phlda3	PROMOTER	0.194	1.773	1946.44	3451.63	0.345	1457.90	502.66
A_68_P26918731	chr10:6980219-6980263	NM_133485:151	Ppp1r14c	INSIDE	0.194	0.696	1819.25	1266.44	0.135	1409.70	190.15
A_68_P22165088	chr3:57540040-57540084	NM_011883:75	Rnf13	INSIDE	0.194	0.571	1254.86	716.61	0.111	1041.16	115.48
A_68_P23593813	chr5:34679537-34679581	NM_011278:520	Rnf4	INSIDE	0.194	0.453	1658.92	750.71	0.088	1396.42	122.33
A_68_P31154741	chr17:34740094-34740143	NM_019403:388	Rnf5	INSIDE	0.194	1.967	1283.64	2525.31	0.381	901.01	343.39
A_68_P21078286	chr2:26236121-26236165	NM_172339:31	Snapc4	INSIDE	0.194	0.520	1546.42	803.53	0.101	1186.67	119.36
A_68_P26591018	chr9:65917336-65917381	NM_001025612:180	Snx22	INSIDE	0.194	0.615	1246.66	766.68	0.119	971.79	115.90
A_68_P27985513	chr11:85643144-85643194	NM_009324:-2948	Tbx2	PROMOTER	0.194	0.576	1622.49	933.82	0.112	1070.78	119.62
A_68_P26421200	chr9:35007442-35007486	NM_001177847:26	Tirap	INSIDE	0.194	0.332	2449.66	813.48	0.064	1934.19	124.68

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P23189069	chr4:106851457-106851501	NM_029565:244	Tmem59	INSIDE	0.194	0.601	2464.22	1481.85	0.117	1760.27	205.58
A_68_P30147677	chr15:38008870-38008917	NM_001081359:-285	Ubr5	PROMOTER	0.194	0.582	1400.60	815.45	0.113	1131.24	127.50
A_68_P28155482	chr11:115674860-115674904	NM_080643:24	Caskin2	INSIDE	0.193	0.515	1341.42	691.00	0.099	1189.23	118.05
A_68_P24444437	chr6:51420446-51420490	NM_007624:-146	Cbx3	DIVERGENT_PROMOTER	0.193	0.670	1005.84	674.35	0.129	914.19	118.11
A_68_P26519508	chr9:53056259-53056305	NM_029936:-65	Ddx10	PROMOTER	0.193	0.701	2583.81	1810.45	0.135	2035.72	275.47
A_68_P27187161	chr10:62114275-62114319	NM_053183:-350	Ddx50	PROMOTER	0.193	0.560	1385.79	776.04	0.108	1152.33	124.81
A_68_P20353308	chr1:75313628-75313672	NM_016878:-58	Dnpep	PROMOTER	0.193	0.586	2248.50	1318.67	0.113	1575.63	178.47
A_68_P22483658	chr3:122321383-122321434	NM_001114665:1177	Fnbp1l	INSIDE	0.193	0.592	1512.14	894.47	0.114	1050.53	120.14
A_68_P31982719	chr19:16949088-16949132	NM_008023:-790	Foxb2	PROMOTER	0.193	0.442	1831.95	810.28	0.085	1445.01	123.30
A_68_P24116812	chr5:136020886-136020930	NM_146001:84	Hip1	INSIDE	0.193	0.516	1705.07	879.76	0.100	1283.89	127.92
A_68_P23592028	chr5:34340360-34340404	NM_001001985:1750	Nat8l	INSIDE	0.193	0.513	2354.20	1207.24	0.099	1755.93	173.82
A_68_P31112751	chr17:26981297-26981344	NM_008700:-2810	Nkx2-5	PROMOTER	0.193	0.683	2648.97	1808.06	0.132	1957.72	257.63
A_68_P30368850	chr15:79664958-79665002	NM_001013360:-217	Npcd	PROMOTER	0.193	0.619	1309.22	811.01	0.119	975.64	116.47
A_68_P23292280	chr4:128331714-128331758	NM_001195130:-209	Phc2	PROMOTER	0.193	0.539	1414.75	762.41	0.104	1160.28	120.80
A_68_P23545735	chr5:24605832-24605876	NM_145401:606	Prkag2	INSIDE	0.193	0.495	1571.63	777.85	0.095	1228.51	117.24
A_68_P28556142	chr12:77923792-77923838	NM_134050:-303	Rab15	PROMOTER	0.193	0.495	1621.93	803.03	0.096	1254.91	120.04
A_68_P20723677	chr1:154749026-154749070	NM_001005507:728	Smg7	INSIDE	0.193	1.370	1351.08	1850.67	0.265	992.60	263.05
A_68_P29286846	chr13:104563824-104563877	NM_172592:-9188	Srek1	PROMOTER	0.193	0.570	1311.67	747.61	0.110	1110.43	122.08
A_68_P25068287	chr7:46799838-46799882	NM_001004139:26725	Zfp619	DOWNSTREAM	0.193	0.585	1305.08	763.29	0.113	1030.77	116.47
A_68_P22964916	chr4:62180749-62180793	NM_008525:327	Alad	INSIDE	0.192	0.537	1393.27	747.63	0.103	1143.27	117.60
A_68_P21219427	chr2:52279977-52280021	NM_182994:396	Arl5a	INSIDE	0.192	0.580	1441.71	836.71	0.111	1059.03	118.00
A_68_P24920859	chr6:145024368-145024419	NM_007532:284	Bcat1	INSIDE	0.192	0.566	1492.74	844.31	0.108	1078.33	116.81
A_68_P28596925	chr12:85533705-85533749	NM_001163502:1239	C130039O16Rik	INSIDE	0.192	0.530	1437.34	761.46	0.102	1168.46	118.93
A_68_P31125924	chr17:29231277-29231321	NM_007669:582	Cdkn1a	INSIDE	0.192	0.368	2451.01	903.09	0.071	1773.09	125.40
A_68_P21642100	chr2:132607157-132607201	NM_007694:165	Chgb	INSIDE	0.192	0.591	2294.98	1357.31	0.113	1674.37	189.70
A_68_P32145753	chr19:46835804-46835848	NM_001102471:-272	Cnnm2	PROMOTER	0.192	0.536	4318.38	2316.11	0.103	3203.51	330.69
A_68_P25272118	chr7:88600431-88600478	NM_007755:-892	Cpeb1	PROMOTER	0.192	0.531	2124.81	1128.16	0.102	1537.68	156.71
A_68_P25026463	chr7:30089112-30089158	NM_013874:111	Dpf1	INSIDE	0.192	0.657	1116.74	733.80	0.126	926.69	116.75
A_68_P24449832	chr6:52260556-52260605	NM_007966:-2911	Evx1	PROMOTER	0.192	0.640	1276.58	816.42	0.123	967.19	118.81
A_68_P22324049	chr3:90035487-90035531	NM_206924:-10	Jtb	PROMOTER	0.192	0.558	1541.99	860.32	0.107	1114.74	119.16
A_68_P26192689	chr8:118232168-118232225	NM_001025577:-1402	Maf	PROMOTER	0.192	0.462	1766.37	816.22	0.089	1352.51	119.73
A_68_P32383983	chrX:50097448-50097492	NR_029657:-1726	Mir106a	PROMOTER	0.192	1.502	1034.70	1553.93	0.288	414.97	119.42
A_68_P30883588	chr16:76293765-76293824	NM_173440:79500	Nrip1	INSIDE	0.192	1.687	1078.55	1819.69	0.324	767.18	248.48
A_68_P31926007	chr19:4942924-4942968	NM_172835:146	Peli3	INSIDE	0.192	1.330	6473.47	8606.76	0.255	4962.52	1267.16
A_68_P23585503	chr5:33127970-33128014	NM_177298:283	Pisd	INSIDE	0.192	0.467	1687.07	787.39	0.089	1325.96	118.62
A_68_P23435437	chr4:154357997-154358041	NM_001113360:27075	Plch2	INSIDE	0.192	1.597	480.09	766.75	0.306	444.58	136.23
A_68_P25367283	chr7:107520379-107520423	NM_028292:6	Ppme1	INSIDE	0.192	0.673	3551.19	2389.95	0.129	2503.89	323.89
A_68_P21110355	chr2:31492078-31492122	NM_001123362:-3456	Prdm12	PROMOTER	0.192	0.488	1523.58	743.79	0.094	1243.51	116.81
A_68_P21004674	chr2:11093675-11093725	NM_008859:-308	Prkcq	PROMOTER	0.192	0.533	1475.35	786.25	0.102	1162.51	118.87
A_68_P21750259	chr2:152452978-152453022	NM_009047:257	Rem1	INSIDE	0.192	0.588	1810.97	1065.00	0.113	1342.19	151.80
A_68_P25021324	chr7:29135677-29135721	NM_013647:-9	Rps16	PROMOTER	0.192	0.697	2240.25	1562.32	0.134	1498.69	200.78
A_68_P30296503	chr15:67007295-67007349	NM_009177:1122	St3gal1	INSIDE	0.192	0.628	1380.77	867.23	0.121	989.96	119.33
A_68_P27286220	chr10:80363685-80363729	NM_013895:8	Timm13	INSIDE	0.192	0.394	2090.39	823.04	0.075	1737.21	130.99
A_68_P21819632	chr2:164595210-164595259	NM_026785:-194	Ube2c	PROMOTER	0.192	0.507	1812.01	919.57	0.098	1389.77	135.69
A_68_P22485530	chr3:122687874-122687932	NM_133857:-537	Usp53	PROMOTER	0.192	0.674	1165.29	785.53	0.129	901.34	116.42
A_68_P24114550	chr5:135539661-135539705	NM_025375:298	Wbscr22	INSIDE	0.192	0.495	2603.69	1290.00	0.095	2108.83	200.85
A_68_P21819854	chr2:164630477-164630534	NM_178375:-108	Zswim3	DIVERGENT_PROMOTER	0.192	0.437	2240.88	978.95	0.084	1423.24	119.47
A_68_P22407293	chr3:107385718-107385777			Unknown	0.192	0.580	1389.64	806.57	0.112	1070.42	119.38
A_68_P25618388	chr8:4678211-4678255	ENSMUST00000058918:133		INSIDE	0.192	0.549	1420.56	779.95	0.106	1133.33	119.73
A_68_P23023125	chr4:74924188-74924236	NM_025849:-22	3110001D03Rik	PROMOTER	0.191	0.638	1264.85	806.60	0.122	1023.28	124.89
A_68_P20161231	chr1:38683942-38683986	NM_010678:37836	Aff3	INSIDE	0.191	0.433	1946.82	842.06	0.083	1422.82	117.60

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P23315178	chr4:132568014-132568058	NM_146155:616	Ahdc1	INSIDE	0.191	0.670	2242.42	1502.03	0.128	1618.48	207.13
A_68_P21617365	chr2:127951737-127951781	NM_009754:-15	Bcl2l11	PROMOTER	0.191	0.321	3559.69	1142.91	0.061	2582.36	157.98
A_68_P31323858	chr17:69767042-69767093	NR_026848:1281	C030034I22Rik	INSIDE	0.191	0.684	1127.06	770.71	0.131	921.76	120.68
A_68_P31323854	chr17:69766606-69766650	NR_026848:842	C030034I22Rik	INSIDE	0.191	0.471	1746.19	823.00	0.090	1292.38	116.56
A_68_P20880981	chr1:183282461-183282505	NM_001160211:-276	Cnih3	PROMOTER	0.191	0.578	1375.16	795.22	0.111	1102.05	121.91
A_68_P29987885	chr15:6336369-6336413	NM_001037905:-357	Dab2	PROMOTER	0.191	0.683	1021.79	698.10	0.131	899.71	117.67
A_68_P28914774	chr13:30075826-30075881	NM_010093:2079	E2f3	INSIDE	0.191	0.573	1418.79	813.17	0.109	1115.78	121.98
A_68_P32022550	chr19:24354685-24354736	NM_008044:366	Fxn	INSIDE	0.191	0.385	2407.72	926.92	0.074	1747.14	128.46
A_68_P25954808	chr8:73421306-73421350	NM_001111116:-17	Gm15427	PROMOTER	0.191	0.562	1680.38	945.20	0.107	1153.92	123.99
A_68_P27286895	chr10:80477880-80477928	NM_010319:-234	Gng7	PROMOTER	0.191	0.491	1568.92	770.85	0.094	1250.67	117.50
A_68_P23977819	chr5:110536642-110536688	NM_145147:552	Gtpbp6	INSIDE	0.191	1.714	11771.56	20172.69	0.327	7593.94	2486.50
A_68_P27543983	chr10:128370926-128370976	NM_008398:82	Itga7	INSIDE	0.191	0.597	1527.24	911.40	0.114	1089.23	123.86
A_68_P32539360	chrX:91786471-91786515	NM_019791:921	Maged1	INSIDE	0.191	1.882	1482.38	2789.20	0.359	567.37	203.64
A_68_P25266322	chr7:87515822-87515866	NM_172903:417	Man2a2	INSIDE	0.191	0.681	4472.38	3046.27	0.130	3535.23	458.91
A_68_P23931503	chr5:101227718-101227762	NM_026826:-37	Mrps18c	DIVERGENT_PROMOTER	0.191	0.626	2457.91	1538.68	0.120	1769.91	211.62
A_68_P23936297	chr5:102088485-102088535	NM_144955:5220	Nkx6-1	INSIDE	0.191	0.702	1248.69	876.50	0.134	929.87	124.68
A_68_P20221655	chr1:51535170-51535214	NM_028696:51	Obfc2a	INSIDE	0.191	0.468	1704.65	797.87	0.090	1345.45	120.43
A_68_P25009542	chr7:26082633-26082677	NM_008776:320	Pafah1b3	INSIDE	0.191	0.620	1313.21	813.87	0.118	1054.27	124.82
A_68_P20165368	chr1:39425278-39425322	NM_053257:605	Rpl31	INSIDE	0.191	1.493	6710.42	10020.69	0.286	4482.70	1281.82
A_68_P22412728	chr3:108247875-108247920	NM_001204979:280	Sars	INSIDE	0.191	0.559	1433.83	800.91	0.107	1107.48	118.39
A_68_P30424832	chr15:89204085-89204129	NM_001111288:143	Sco2	INSIDE	0.191	0.587	1327.50	779.70	0.112	1073.59	120.28
A_68_P32016820	chr19:23348207-23348251	NM_153808:139	Smc5	INSIDE	0.191	0.612	1393.84	852.92	0.117	1030.85	120.76
A_68_P31381753	chr17:80606810-80606854	NM_001195485:-187	Srsf7	DIVERGENT_PROMOTER	0.191	0.533	1673.20	891.30	0.102	1304.47	132.97
A_68_P24880085	chr6:137683395-137683454	NM_011499:-178	Strap	PROMOTER	0.191	0.550	1376.24	757.23	0.105	1134.99	119.24
A_68_P30207182	chr15:50721909-50721953	NM_032000:-343	Trps1	PROMOTER	0.191	0.533	2195.85	1171.01	0.102	1747.98	177.69
A_68_P22955052	chr4:59202854-59202909	NM_011673:460	Ugcg	INSIDE	0.191	0.493	2628.45	1296.85	0.094	1261.71	119.09
A_68_P24130229	chr5:138882742-138882786	NM_028130:61	Zfp157	INSIDE	0.191	0.575	1298.43	746.98	0.110	1082.33	119.03
A_68_P24922451	chr6:145289321-145289369			Unknown	0.191	0.587	1537.12	902.50	0.112	1104.48	123.71
A_68_P22509000	chr3:127201404-127201450	ENSMUST00000104965:493		DOWNSTREAM	0.191	0.685	1075.89	736.50	0.131	890.04	116.59
A_68_P21814245	chr2:163575768-163575812	NM_007398:123	Ada	INSIDE	0.190	0.575	2172.96	1250.34	0.109	1562.42	170.93
A_68_P26459683	chr9:42913398-42913453	NM_027144:376	Arhgef12	INSIDE	0.190	0.544	1537.57	835.73	0.103	1139.07	117.86
A_68_P24766251	chr6:114593227-114593277	NM_028835:110	Atg7	INSIDE	0.190	0.532	1515.19	805.42	0.101	1194.24	120.70
A_68_P26134610	chr8:108089960-108090004	NM_013477:-42	Atp6v0d1	PROMOTER	0.190	0.562	1340.84	752.90	0.107	1105.59	117.94
A_68_P23440850	chr4:155205944-155205991	NM_025338:213	Aurkaip1	INSIDE	0.190	0.514	1693.57	870.12	0.097	1242.51	121.00
A_68_P28836391	chr13:14046280-14046324	NM_178640:-638	B3galnt2	PROMOTER	0.190	0.545	1475.05	803.54	0.103	1131.74	116.94
A_68_P28103527	chr11:106650485-106650529	NM_001166685:-59	Ccdc45	DIVERGENT_PROMOTER	0.190	0.524	1551.87	813.42	0.099	1214.68	120.75
A_68_P24347496	chr6:33009915-33009959	NM_025336:216	Chchd3	INSIDE	0.190	0.685	3361.95	2302.32	0.130	2480.97	322.69
A_68_P25313631	chr7:97592513-97592557	NM_145151:1244	Crebzf	INSIDE	0.190	0.590	1691.83	998.28	0.112	1274.77	143.18
A_68_P31158511	chr17:35379261-35379306	NM_019693:593	Ddx39b	INSIDE	0.190	0.665	1603.70	1067.12	0.126	1117.59	141.27
A_68_P27895681	chr11:69359967-69360011	NM_001081330:2622	Dnahc2	INSIDE	0.190	0.551	1375.31	757.70	0.104	1123.98	117.42
A_68_P28923680	chr13:31651196-31651240	NM_008239:1180	Foxq1	INSIDE	0.190	0.435	1817.96	791.00	0.083	1430.00	118.14
A_68_P20351515	chr1:74998648-74998692	NM_010544:-445	Ihh	PROMOTER	0.190	0.582	1885.80	1097.69	0.111	1479.57	163.90
A_68_P25953303	chr8:73197017-73197061	NM_015816:-91	Lsm4	PROMOTER	0.190	0.633	3049.94	1931.25	0.120	2058.76	247.77
A_68_P29448046	chr14:21460257-21460301	NM_021508:15484	Myoz1	DOWNSTREAM	0.190	0.607	1437.59	872.07	0.115	1176.43	135.38
A_68_P32374347	chrX:48371964-48372008	NM_172413:-791	Rap2c	PROMOTER	0.190	1.458	1877.31	2737.70	0.277	894.54	247.55
A_68_P23233430	chr4:116961488-116961532	NM_025739:208010	Rnf220	INSIDE	0.190	0.674	1272.30	857.73	0.128	1015.19	129.73
A_68_P30577646	chr16:18127970-18128014	NM_022982:194	Rtn4r	INSIDE	0.190	0.524	1336.50	700.59	0.100	1200.85	119.71
A_68_P25362154	chr7:106631883-106631927	NR_002172:-462	Snord15a	PROMOTER	0.190	0.480	2397.94	1152.03	0.091	1735.84	158.48
A_68_P23590341	chr5:34000502-34000546	NM_026698:-43	Tmem129	DIVERGENT_PROMOTER	0.190	0.444	1953.75	866.77	0.084	1407.78	118.48
A_68_P31886140	chr18:84261455-84261501	NM_146090:3929	Zadh2	INSIDE	0.190	0.706	1682.30	1187.94	0.134	1350.96	181.01
A_68_P24951776	chr7:5003006-5003050	NM_026900:-105	Zfp580	PROMOTER	0.190	0.514	3152.43	1619.80	0.097	2211.55	215.50

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27563481	chr11:5345058-5345102	NM_001080924:-230	Znrf3	PROMOTER	0.190	0.554	3769.09	2087.22	0.105	2964.57	311.38
A_68_P21770587	chr2:156137562-156137616	NM_027585:-620	4921517L17Rik	PROMOTER	0.189	0.483	1762.59	851.11	0.091	1271.12	116.03
A_68_P26808313	chr9:107301962-107302006	NM_001174047:-226	Cacna2d2	PROMOTER	0.189	0.654	1831.03	1197.03	0.124	1408.19	174.06
A_68_P30792739	chr16:58670948-58670993	NM_007757:650	Cpox	INSIDE	0.189	0.680	1324.47	900.03	0.128	1009.72	129.66
A_68_P23145554	chr4:99323682-99323726	NM_010425:715	Foxd3	INSIDE	0.189	0.694	4633.99	3218.02	0.131	3146.09	412.53
A_68_P20294255	chr1:64783028-64783072	NM_001042659:1274	Fzd5	INSIDE	0.189	0.588	2056.42	1210.10	0.111	1543.33	172.02
A_68_P28082093	chr11:102754576-102754620	NM_010277:3916	Gfap	INSIDE	0.189	0.441	1791.23	789.73	0.084	1385.42	115.70
A_68_P22346156	chr3:95685923-95685967	NM_001033302:207	Gm129	INSIDE	0.189	0.555	2301.14	1276.79	0.105	1761.90	184.70
A_68_P32239707	chrX:7274604-7274648	NM_173747:367	Gpkow	INSIDE	0.189	2.356	1363.34	3212.02	0.446	587.75	262.05
A_68_P23778450	chr5:69947976-69948020	NM_172711:-182	Gufl	PROMOTER	0.189	0.647	2022.79	1308.46	0.122	1565.78	191.15
A_68_P22056223	chr3:35899395-35899439	NM_023644:184	Mccc1	INSIDE	0.189	0.613	4751.54	2913.71	0.116	3569.33	414.04
A_68_P25285301	chr7:91032798-91032845	NM_030705:30	Mesdc1	INSIDE	0.189	0.632	1311.23	829.13	0.120	982.24	117.63
A_68_P20354397	chr1:75483176-75483220	NM_178884:19829	Obsl1	INSIDE	0.189	0.684	1499.12	1026.11	0.129	938.26	121.49
A_68_P21913061	chr2:181572625-181572669	NM_153594:39	Pcmtd2	INSIDE	0.189	0.464	1747.52	810.57	0.088	1337.42	117.03
A_68_P28119821	chr11:109511777-109511821	NM_021880:-464	Prkar1a	PROMOTER	0.189	0.633	1457.86	922.16	0.120	974.94	116.81
A_68_P27280979	chr10:79565571-79565615	NM_183426:-145	Sbno2	PROMOTER	0.189	0.530	1545.81	818.67	0.100	1157.92	115.89
A_68_P28224330	chr12:8779493-8779537	NM_011519:1313	Sdc1	INSIDE	0.189	0.480	1837.77	882.41	0.091	1368.81	123.90
A_68_P21912034	chr2:181415230-181415274	NM_009326:238	Tcea2	INSIDE	0.189	0.419	2077.63	871.07	0.079	1646.34	130.75
A_68_P30385400	chr15:82742401-82742445	NM_001114140:142	Tcf20	INSIDE	0.189	1.406	5304.86	7456.46	0.266	3667.11	976.41
A_68_P24153543	chr5:143578378-143578435	NM_001122730:660	Tnrc18	INSIDE	0.189	0.700	1269.33	888.91	0.132	874.65	115.63
A_68_P29560572	chr14:41780482-41780526	NM_145928:-408	Tspan14	PROMOTER	0.189	0.561	1341.96	753.37	0.106	1101.77	117.12
A_68_P20421183	chr1:89905073-89905117	NM_001033291:32	Usp40	INSIDE	0.189	0.702	3735.32	2620.52	0.133	2823.27	374.41
A_68_P24955199	chr7:6335923-6335967	NM_175247:-83	Zfp28	PROMOTER	0.189	0.472	1659.57	783.58	0.089	1335.68	119.43
A_68_P24983045	A_68_P24983045			Unknown	0.189	2.173	3061.50	6653.77	0.411	2217.70	911.02
A_68_P31183534	chr17:42453113-42453157	NM_028474:239	3110082D06Rik	INSIDE	0.188	1.500	2124.97	3186.90	0.282	1389.09	391.23
A_68_P22407410	chr3:107399288-107399333	NM_007441:1362	Alx3	INSIDE	0.188	0.471	2328.02	1097.46	0.089	1540.32	136.72
A_68_P23440735	chr4:155186739-155186783	NM_207678:163	Ccnl2	INSIDE	0.188	0.500	4519.25	2258.53	0.094	3204.71	300.89
A_68_P23400905	chr4:148892711-148892755	NM_023465:383	Ctnnbip1	INSIDE	0.188	0.664	2722.42	1808.01	0.125	2067.79	257.58
A_68_P29056203	chr13:55736834-55736882	NM_145975:471	Ddx46	INSIDE	0.188	0.572	1555.52	889.72	0.107	1118.25	120.08
A_68_P25009064	chr7:26004847-26004897	NM_207677:6	Dedd2	INSIDE	0.188	0.446	2132.53	951.36	0.084	1541.43	129.58
A_68_P26132766	chr8:107813805-107813857	NM_177788:6168	Exoc3l	INSIDE	0.188	0.666	1471.32	979.44	0.125	948.32	118.81
A_68_P27835269	chr11:58990423-58990467	NM_175452:5884	Gjc2	INSIDE	0.188	0.538	1437.85	773.29	0.101	1179.38	119.00
A_68_P28080240	chr11:102417615-102417659	NM_001159492:-164	Gpatch8	PROMOTER	0.188	0.733	2111.17	1546.99	0.138	1590.26	219.47
A_68_P25095367	chr7:53085924-53085970	NM_153419:213	Grwd1	INSIDE	0.188	0.503	2503.33	1260.16	0.095	1743.64	165.37
A_68_P28269098	chr12:17183229-17183273	NM_201531:444	Kcnf1	INSIDE	0.188	0.579	2611.73	1511.42	0.109	1961.17	213.40
A_68_P24117834	chr5:136255023-136255074	NM_008617:530	Mdh2	INSIDE	0.188	0.531	1482.95	787.91	0.100	1213.50	121.36
A_68_P23188357	chr4:106739700-106739748	NM_025500:-253	Mrpl37	DIVERGENT_PROMOTER	0.188	0.589	1769.24	1042.63	0.111	1397.62	154.83
A_68_P23134122	chr4:97412574-97412618	NM_001122952:163963	Nfia	INSIDE	0.188	0.361	2286.25	825.06	0.068	1694.82	114.91
A_68_P31201773	chr17:45692924-45692968	NM_008690:282	Nfkbie	INSIDE	0.188	0.472	1942.55	917.53	0.089	1348.68	119.77
A_68_P26460523	chr9:43047879-43047923	NM_178644:-1	Oaf	PROMOTER	0.188	0.422	2116.38	893.93	0.079	1577.08	125.36
A_68_P20927660	chr1:191552263-191552307	NM_008976:138	Ptpn14	INSIDE	0.188	0.720	1453.97	1046.44	0.135	1248.33	168.54
A_68_P21142143	chr2:37298714-37298758	NM_146121:-68	Rabgap1	DIVERGENT_PROMOTER	0.188	0.570	1347.67	767.67	0.107	1132.51	121.25
A_68_P32575425	chrX:101176563-101176615	NM_011276:35	Rlim	INSIDE	0.188	1.645	907.54	1493.05	0.310	399.65	123.90
A_68_P30013954	chr15:10965913-10965957	NM_178717:1789	Rxfp3	INSIDE	0.188	0.711	1397.06	992.87	0.133	1076.55	143.56
A_68_P29904270	chr14:112074911-112074955	NM_198865:596	Slitrk5	INSIDE	0.188	0.529	1531.50	810.51	0.100	1155.28	115.06
A_68_P20218132	chr1:50984895-50984939	NM_019790:550	Tmeff2	INSIDE	0.188	0.533	1535.11	818.16	0.100	1207.67	121.27
A_68_P22129252	chr3:51163003-51163047			Unknown	0.188	0.492	1591.22	782.83	0.092	1280.43	118.14
A_68_P31759410	chr18:61886034-61886078	NR_029432:13	1500015A07Rik	INSIDE	0.187	0.441	1836.90	809.51	0.083	1401.31	115.76
A_68_P32710884	chrX:139400658-139400702	NM_019496:591	Ammecr1	INSIDE	0.187	2.202	1850.91	4076.51	0.412	808.53	333.31
A_68_P25123372	chr7:58766676-58766720	NM_177694:300	Ano5	INSIDE	0.187	0.542	1536.46	832.27	0.101	1188.28	120.37
A_68_P31102615	chr17:25392896-25392940	NM_001163270:391	Baiap3	INSIDE	0.187	0.710	1736.49	1232.94	0.133	1359.67	180.28

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P21564939	chr2:118424101-118424145	NM_009773:176	Bub1b	INSIDE	0.187	2.521	1635.60	4123.18	0.471	1037.77	488.62
A_68_P32385503	chrX:50410575-50410619	NR_038184:-229	C430049B03Rik	PROMOTER	0.187	2.036	3303.44	6726.82	0.380	1329.00	505.02
A_68_P23240385	chr4:118109464-118109508	NM_023223:462	Cdc20	INSIDE	0.187	0.679	1416.43	961.24	0.127	921.42	117.20
A_68_P20149809	chr1:36748265-36748309	NM_009942:-45	Cox5b	DIVERGENT_PROMOTER	0.187	0.599	1609.22	963.51	0.112	1236.80	138.80
A_68_P31838819	chr18:75856123-75856171	NM_201354:1204	Ctif	INSIDE	0.187	0.587	1597.47	937.31	0.110	1322.73	145.18
A_68_P28176851	chr11:119129170-119129216	NM_001159324:-88	Gaa	PROMOTER	0.187	0.682	1293.27	881.53	0.128	962.50	122.97
A_68_P32090696	chr19:36628500-36628544	NM_001163471:-606	Hectd2	PROMOTER	0.187	0.620	3761.43	2332.90	0.116	2595.28	301.48
A_68_P29604764	chr14:52723955-52723999	NM_001170981:-273	Hnrnpc	DIVERGENT_PROMOTER	0.187	0.538	1609.29	865.54	0.100	1215.71	122.11
A_68_P23019857	chr4:73898113-73898157	NM_144787:352	Kdm4c	INSIDE	0.187	0.580	1672.21	970.40	0.109	1586.42	172.49
A_68_P32147204	chr19:47090203-47090247	NM_001164363:-545	Nt5c2	PROMOTER	0.187	0.710	1808.50	1284.59	0.133	1471.62	195.03
A_68_P30424871	chr15:89208941-89208985	NM_001013022:723	Odf3b	INSIDE	0.187	1.450	2442.21	3540.10	0.271	1608.19	435.68
A_68_P21853418	chr2:170322093-170322137	NM_001013369:187	Pfdn4	INSIDE	0.187	0.465	1684.48	783.27	0.087	1350.47	117.58
A_68_P25093689	chr7:52793682-52793726	NM_148927:12005	Plekha4	INSIDE	0.187	0.630	1765.63	1112.17	0.118	1337.90	157.64
A_68_P26825470	chr9:110629961-110630005	NM_001083936:15132	Pth1r	INSIDE	0.187	1.773	1441.41	2556.16	0.332	951.18	316.00
A_68_P24464121	chr6:54516133-54516177	NM_027268:222	Scrn1	INSIDE	0.187	0.562	1461.21	820.71	0.105	1132.37	119.20
A_68_P21986756	chr3:21974577-21974636	NM_030732:-967	Tbl1xr1	PROMOTER	0.187	0.445	1879.65	836.66	0.083	1462.30	122.04
A_68_P26347560	chr9:21314771-21314829	NM_010744:-170	Tmed1	PROMOTER	0.187	0.661	1363.31	901.58	0.124	965.41	119.26
A_68_P27357055	chr10:93498582-93498626	NM_172538:-111	Vezt	DIVERGENT_PROMOTER	0.187	0.591	3740.14	2209.91	0.111	2827.06	313.16
A_68_P21568805	chr2:119114248-119114292	NM_172269:-207	Vps18	PROMOTER	0.187	0.463	1877.48	869.97	0.086	1371.56	118.54
A_68_P21424293	chr2:91570286-91570331	NM_001080754:14	Ambra1	INSIDE	0.186	0.427	1821.53	777.97	0.079	1444.12	114.72
A_68_P31834412	chr18:75165713-75165757	NM_001001181:181	BC031181	INSIDE	0.186	0.627	2602.69	1632.91	0.117	1798.45	210.31
A_68_P28743715	chr12:112615120-112615164	NM_183016:787	Cdc42bpb	INSIDE	0.186	0.463	2455.96	1138.12	0.086	1861.06	160.55
A_68_P25045001	chr7:35460951-35460995	NM_175140:136758	Chst8	INSIDE	0.186	0.663	1687.40	1119.33	0.123	1184.68	145.82
A_68_P25351869	chr7:104845090-104845134	NM_023671:-88	Clns1a	PROMOTER	0.186	0.648	1149.10	745.08	0.120	978.81	117.90
A_68_P21489013	chr2:104249944-104249988	NM_001033347:525	D430041D05Rik	INSIDE	0.186	0.631	2467.55	1556.27	0.117	1679.45	196.91
A_68_P22903297	chr4:49072600-49072644	NM_178756:289	E130309F12Rik	INSIDE	0.186	0.542	1581.49	857.66	0.101	1224.29	123.30
A_68_P30580078	chr16:18498994-18499038	NM_023120:53	Gnb1l	INSIDE	0.186	0.349	2572.54	898.62	0.065	2048.72	133.31
A_68_P21077788	chr2:26171431-26171475	NM_001199147:-3837	Gpsm1	PROMOTER	0.186	0.695	2432.36	1691.13	0.130	1639.41	212.31
A_68_P32777675	chrX:156426686-156426730	NM_001163085:344	Map3k15	INSIDE	0.186	1.497	772.35	1155.89	0.278	431.33	119.92
A_68_P23154636	chr4:101028607-101028651	NR_029537:-8996	Mir101a	PROMOTER	0.186	0.564	3032.52	1710.82	0.105	2193.25	230.68
A_68_P20227604	chr1:52556860-52556904	NM_008667:410	Nab1	INSIDE	0.186	0.483	2120.26	1025.04	0.090	1499.80	135.05
A_68_P24595553	chr6:83745392-83745436	NM_001164187:263	Nagk	INSIDE	0.186	0.681	1256.74	855.76	0.127	922.81	116.90
A_68_P23419143	chr4:151852331-151852375	NM_153424:102	Nphp4	INSIDE	0.186	0.687	2407.37	1653.22	0.128	1760.58	225.08
A_68_P29057342	chr13:55937765-55937809	NM_011097:-5000	Pitx1	PROMOTER	0.186	0.583	1825.86	1064.61	0.109	1410.67	153.31
A_68_P27756338	chr11:44332144-44332188	NM_028862:-299	Rnf145	PROMOTER	0.186	0.637	1078.96	687.45	0.119	1001.17	118.78
A_68_P31411737	chr17:86017485-86017529	NR_038085:230	Six3os1	INSIDE	0.186	0.508	1666.57	847.22	0.094	1286.03	121.31
A_68_P28161648	chr11:116714471-116714515	NM_011358:-84	Srsf2	DIVERGENT_PROMOTER	0.186	0.551	1366.73	753.46	0.102	1158.23	118.49
A_68_P20530741	chr1:114313355-114313399			Unknown	0.186	0.498	1817.63	905.91	0.093	1488.32	138.23
A_68_P20061791	chr1:18048589-18048633			Unknown	0.186	0.695	1281.68	891.34	0.130	1155.99	149.70
A_68_P23589614	chr5:33882953-33883010			Unknown	0.186	1.359	1757.31	2387.80	0.253	1195.04	302.03
A_68_P31412803	chr17:86199549-86199593	AK142122:348		INSIDE	0.186	0.640	4105.14	2627.86	0.119	3210.72	382.80
A_68_P21626549	chr2:129627707-129627751	NR_029452:-533	4932416H05Rik	PROMOTER	0.185	0.590	3038.78	1794.00	0.109	2191.57	239.36
A_68_P31152204	chr17:34255264-34255308	NR_037970:1559	Brd2	INSIDE	0.185	1.665	5401.10	8995.19	0.308	3536.85	1090.15
A_68_P25011514	chr7:26503814-26503858	NM_028771:236	Ccdc97	INSIDE	0.185	0.624	1508.25	941.49	0.116	1041.96	120.40
A_68_P26406181	chr9:32353158-32353202	NM_008026:-4227	Fli1	PROMOTER	0.185	0.460	1778.13	818.45	0.085	1447.37	123.32
A_68_P24992574	chr7:19890287-19890331	NM_008036:5086	Fosb	INSIDE	0.185	0.518	2361.03	1223.60	0.096	1677.33	160.66
A_68_P30513459	chr16:5049380-5049424	NM_001079814:601	Glyr1	INSIDE	0.185	0.385	2033.48	782.98	0.071	1603.69	114.32
A_68_P25727980	chr8:26707531-26707578	NM_173012:405	Letm2	INSIDE	0.185	0.690	1228.19	846.90	0.128	992.94	127.01
A_68_P29696151	chr14:70009216-70009260	NM_033325:-44	Loxl2	PROMOTER	0.185	0.694	2406.26	1671.06	0.128	1801.19	231.32
A_68_P23192855	chr4:107476214-107476258	NM_001080926:1373	Lrp8	INSIDE	0.185	0.344	2441.43	840.11	0.064	1828.68	116.58
A_68_P20440041	chr1:92949532-92949576	NM_001111311:-466	Lrrfip1	PROMOTER	0.185	0.693	1236.30	856.88	0.128	963.01	123.18

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P24993425	chr7:20043646-20043690	NM_172279:175	Mark4	INSIDE	0.185	2.249	10218.67	22985.36	0.415	6641.72	2756.53
A_68_P30557334	chr16:13448585-13448633	NR_030549:-1007	Mir193b	PROMOTER	0.185	0.700	1281.65	897.45	0.129	931.67	120.61
A_68_P22310708	chr3:87723736-87723780	NM_026591:293	Mrpl24	INSIDE	0.185	0.613	1347.00	826.36	0.113	1023.99	116.13
A_68_P24819300	chr6:125141938-125141982	NM_025595:-257	Mrpl51	DIVERGENT_PROMOTER	0.185	0.667	1176.60	784.24	0.124	953.32	117.85
A_68_P25144264	chr7:63217409-63217453	NM_023647:390	Nipa2	INSIDE	0.185	0.625	1332.57	832.52	0.115	1047.59	120.90
A_68_P22880641	chr4:45031688-45031732	NM_022811:214	Polr1e	INSIDE	0.185	0.492	1716.64	844.91	0.091	1324.33	120.69
A_68_P29612846	chr14:55136095-55136139	NM_013768:191	Prmt5	INSIDE	0.185	0.554	1520.75	842.86	0.102	1203.87	123.19
A_68_P28071923	chr11:100956472-100956516	NM_008949:221	Psmc3ip	INSIDE	0.185	0.690	1160.43	800.63	0.127	903.95	115.20
A_68_P30436281	chr15:91402869-91402913	NM_001033633:802	Slc2a13	INSIDE	0.185	0.441	1931.15	851.47	0.081	1457.54	118.77
A_68_P26579680	chr9:63870057-63870101	NM_008542:-212	Smad6	PROMOTER	0.185	0.547	2258.91	1236.31	0.101	1610.69	162.89
A_68_P25725927	chr8:26311587-26311631	NM_177089:313	Tacc1	INSIDE	0.185	0.387	2292.71	887.34	0.072	1693.11	121.27
A_68_P27971715	chr11:83286236-83286295	NM_027427:-344	Taf15	DIVERGENT_PROMOTER	0.185	0.604	1459.98	881.99	0.112	1097.66	122.81
A_68_P31096074	chr17:24345798-24345842	NM_001163847:-3313	Tbc1d24	PROMOTER	0.185	0.625	1172.76	733.37	0.115	1013.58	116.95
A_68_P28988731	chr13:43267019-43267063	NM_025935:-312	Tbc1d7	PROMOTER	0.185	0.602	1345.41	809.27	0.112	1080.68	120.50
A_68_P26564385	chr9:61220827-61220871	NM_001083927:676	Tle3	INSIDE	0.185	0.471	1635.56	770.05	0.087	1315.33	114.78
A_68_P24459340	chr6:53769060-53769104	NM_025817:1737	Tril	INSIDE	0.185	0.613	4396.63	2697.18	0.114	2944.14	334.33
A_68_P21767075	chr2:155517577-155517621	NM_001163452:522	Trpc4ap	INSIDE	0.185	0.745	5254.94	3915.07	0.137	3538.16	486.40
A_68_P30423271	chr15:88953473-88953517	NM_001163319:86	Tubgcp6	INSIDE	0.185	2.593	4119.29	10679.64	0.481	2792.71	1342.48
A_68_P26494148	chr9:48643704-48643758	NM_001033324:320	Zbtb16	INSIDE	0.185	0.589	1411.78	832.08	0.109	1080.11	117.65
A_68_P25618384	chr8:4677768-4677812	ENSMUST00000058918:575		INSIDE	0.185	0.445	2334.04	1038.68	0.082	1835.44	151.18
A_68_P25261708	chr7:86681223-86681267	ENSMUST00000141822:36242		DOWNSTREAM	0.185	0.680	1427.15	970.40	0.126	1230.80	155.20
A_68_P25961390	chr8:74967839-74967883	NM_028170:82	1700030K09Rik	INSIDE	0.184	1.398	2528.19	3534.89	0.257	1772.52	456.11
A_68_P21112312	chr2:31805862-31805906	NM_145144:62	Aif1l	INSIDE	0.184	0.505	1702.28	859.54	0.093	1254.23	116.52
A_68_P28739136	chr12:111829407-111829460	NR_033340:-150	B930059L03Rik	PROMOTER	0.184	0.461	1918.56	884.50	0.085	1387.78	117.67
A_68_P24920736	chr6:144996969-144997013	NM_001024468:342	Bcat1	INSIDE	0.184	0.610	3431.78	2091.70	0.112	2598.47	292.15
A_68_P23366007	chr4:141349370-141349414	NM_015733:-134	Casp9	DIVERGENT_PROMOTER	0.184	1.354	4764.33	6450.46	0.249	3352.77	836.26
A_68_P28175801	chr11:118952251-118952295	NM_007625:-4721	Cbx4	PROMOTER	0.184	0.488	2060.99	1006.73	0.090	1576.34	141.99
A_68_P30381575	chr15:81958547-81958591	NM_172428:217	Ccdc134	INSIDE	0.184	0.688	2056.79	1414.21	0.126	1528.30	193.02
A_68_P20148456	chr1:36528653-36528697	NM_033570:233	Cnnm4	INSIDE	0.184	0.572	1630.07	932.58	0.105	1172.89	123.35
A_68_P28099221	chr11:105898542-105898586	NM_027946:379	Dcaf7	INSIDE	0.184	0.534	1674.37	894.36	0.098	1210.96	119.27
A_68_P26221252	chr8:123113160-123113204	NM_178856:-207	Gins2	PROMOTER	0.184	0.648	3138.23	2033.78	0.119	2273.75	271.27
A_68_P30404764	chr15:85888808-85888852	NM_001205353:-326	Gramd4	PROMOTER	0.184	0.509	1718.53	875.47	0.094	1288.34	121.02
A_68_P24449462	chr6:52203025-52203069	NR_015348:7805	Hoxa11as	DOWNSTREAM	0.184	0.480	2973.37	1425.96	0.088	2472.11	218.04
A_68_P22403737	chr3:106839605-106839649	NM_008418:547	Kcna3	INSIDE	0.184	0.548	3062.15	1679.45	0.101	2124.46	214.84
A_68_P32095251	chr19:37450692-37450736	NM_010615:-178	Kif11	PROMOTER	0.184	0.513	3322.40	1705.44	0.095	2397.48	226.61
A_68_P24038671	chr5:120881905-120881949	NM_008499:32	Lhx5	INSIDE	0.184	0.728	1770.78	1289.00	0.134	1363.93	182.33
A_68_P28377241	chr12:40949707-40949751	NR_035459:-330	Mir1938	PROMOTER	0.184	0.548	1762.34	966.09	0.101	1301.25	131.05
A_68_P22082999	chr3:40886268-40886325	NM_027558:672	Pgrmc2	INSIDE	0.184	0.576	1627.36	937.55	0.106	1189.47	126.33
A_68_P22488128	chr3:123149644-123149696	NM_008939:-160	Prss12	PROMOTER	0.184	0.674	1356.81	913.87	0.124	975.11	120.81
A_68_P25842224	chr8:48619355-48619399	NM_203507:378	Rwdd4a	INSIDE	0.184	0.430	2782.07	1197.41	0.079	2011.19	159.67
A_68_P21081136	chr2:26772191-26772235	NM_013677:-162	Surf1	PROMOTER	0.184	0.553	2078.85	1149.54	0.102	1443.85	147.07
A_68_P27944034	chr11:78364333-78364383	NM_133706:-121	Tmem97	PROMOTER	0.184	0.628	1454.68	913.75	0.115	1053.69	121.58
A_68_P21652099	chr2:134469945-134469989	NM_029148:-109	Tmx4	PROMOTER	0.184	0.575	1436.16	825.16	0.106	1144.01	121.00
A_68_P25500779	chr7:133631050-133631094	NM_001163713:204	Tufm	INSIDE	0.184	0.520	1427.60	741.82	0.095	1224.95	116.81
A_68_P22398702	chr3:105508064-105508108	NM_001163356:-289	6530418L21Rik	PROMOTER	0.183	0.382	1991.05	759.84	0.070	1677.78	117.45
A_68_P27179599	chr10:60735806-60735850	NM_001081127:358	Adamts14	INSIDE	0.183	0.700	2886.75	2021.85	0.128	2179.58	278.88
A_68_P26569979	chr9:62192471-62192515	NM_009672:3343	Anp32a	INSIDE	0.183	0.455	1803.17	820.29	0.083	1410.16	117.37
A_68_P24864239	chr6:134871088-134871141	NM_009875:696	Cdkn1b	INSIDE	0.183	0.513	2205.53	1131.37	0.094	1269.46	119.28
A_68_P21569217	chr2:119176751-119176795	NM_026929:-205	Chac1	PROMOTER	0.183	0.519	1593.16	826.99	0.095	1215.22	115.31
A_68_P22319260	chr3:89222015-89222059	NM_016904:177	Cks1b	INSIDE	0.183	1.871	3134.04	5864.79	0.343	2010.64	689.92
A_68_P21740704	chr2:150574793-150574837	NM_172117:-2	Entpd6	PROMOTER	0.183	0.432	1946.95	841.04	0.079	1573.74	124.63

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28242247	chr12:12269223-12269267	NM_001146119:300	Fam49a	INSIDE	0.183	0.696	1504.27	1046.98	0.128	1023.11	130.56
A_68_P29055029	chr13:55547182-55547226	NM_011938:510	Grk6	INSIDE	0.183	0.473	1651.20	780.85	0.087	1384.51	119.97
A_68_P30130468	chr15:34767120-34767164	NM_181317:7	Kcns2	INSIDE	0.183	0.442	1909.65	844.39	0.081	1400.70	113.65
A_68_P21137825	chr2:35959267-35959311	NM_001083126:292	Lhx6	INSIDE	0.183	0.726	2268.44	1646.77	0.133	1756.97	233.27
A_68_P31130153	chr17:29979350-29979394	NM_001081160:45455	Mdga1	INSIDE	0.183	0.619	1900.79	1177.29	0.113	1366.30	154.62
A_68_P26611007	chr9:69301684-69301728	NR_037296:-3044	Mir3109	PROMOTER	0.183	0.550	1407.39	774.53	0.101	1161.21	116.77
A_68_P27536461	chr10:126972343-126972387	NM_183297:-749	Nxph4	PROMOTER	0.183	0.538	2326.13	1251.91	0.098	1517.35	149.09
A_68_P21495905	chr2:105509058-105509107	NR_002867:1405	Pax6os1	INSIDE	0.183	0.725	1950.25	1414.48	0.133	1395.68	185.05
A_68_P24873768	chr6:136610320-136610368	NM_025806:70	Plbd1	INSIDE	0.183	0.594	1276.49	757.71	0.109	1089.98	118.30
A_68_P21913222	chr2:181599335-181599379	NM_025901:292	Polr3k	INSIDE	0.183	0.588	1352.22	794.67	0.108	1083.96	116.61
A_68_P21077271	chr2:26092393-26092439	NM_153559:524	Qsox2	INSIDE	0.183	0.644	1176.75	758.17	0.118	989.76	116.45
A_68_P31925256	chr19:4811668-4811714	NM_019869:-56	Rbm14	PROMOTER	0.183	0.522	1427.01	744.50	0.096	1211.67	115.81
A_68_P29011796	chr13:47217864-47217923	NM_146042:-195	Rnf144b	PROMOTER	0.183	0.549	1568.74	861.46	0.101	1200.27	120.67
A_68_P28578485	chr12:82046655-82046699	NM_001079694:186	Srsf5	INSIDE	0.183	0.392	2396.97	939.51	0.072	1897.39	136.07
A_68_P22492342	chr3:124024204-124024248	NM_146140:272	Tram1l1	INSIDE	0.183	0.634	1498.47	949.44	0.116	1189.22	138.15
A_68_P26345606	chr9:20935934-20935978	NM_001205312:-237	Tyk2	PROMOTER	0.183	0.523	2169.75	1135.59	0.096	1687.23	161.85
A_68_P25717772	chr8:24780109-24780156	NM_177086:0	Zmat4	INSIDE	0.183	0.708	1720.10	1217.42	0.130	1233.41	160.02
A_68_P20551799	chr1:120356444-120356488	NR_027901:-624	2900060B14Rik	PROMOTER	0.182	0.680	2315.07	1575.21	0.124	1653.86	204.26
A_68_P23588492	chr5:33721019-33721068	NM_001081101:-301	4933407H18Rik	PROMOTER	0.182	0.576	1422.67	818.82	0.105	1132.97	118.89
A_68_P21766024	chr2:155343697-155343741	NM_019811:-60	Acss2	DIVERGENT_PROMOTER	0.182	0.528	1762.34	931.09	0.096	1473.68	141.61
A_68_P23599454	chr5:35621406-35621450	NM_007418:214	Adra2c	INSIDE	0.182	0.553	1598.51	883.50	0.100	1161.96	116.66
A_68_P29575951	chr14:47006999-47007043	NM_007554:3254	Bmp4	INSIDE	0.182	0.556	2634.16	1465.46	0.101	2039.64	206.07
A_68_P25458764	chr7:125676519-125676570	NM_009940:283	Coq7	INSIDE	0.182	0.621	1310.99	813.62	0.113	1035.79	116.70
A_68_P24600308	chr6:84539342-84539397	NM_175475:4435	Cyp26b1	INSIDE	0.182	0.694	1167.85	811.02	0.126	958.11	120.98
A_68_P27795128	chr11:51463862-51463906	NR_027958:-571	D930048N14Rik	PROMOTER	0.182	0.468	1738.94	813.16	0.085	1365.94	116.28
A_68_P21114877	chr2:32208336-32208380	NM_010065:466	Dnm1	INSIDE	0.182	0.439	2139.13	939.13	0.080	1545.52	123.35
A_68_P25310576	chr7:97128694-97128740	NM_021876:770	Eed	INSIDE	0.182	0.593	1592.32	944.22	0.108	1107.26	119.66
A_68_P32684275	chrX:133652900-133652944	NM_007957:1943	Esx1	INSIDE	0.182	1.491	2353.02	3509.45	0.272	820.08	223.06
A_68_P23968454	chr5:108155866-108155910	NM_010278:-2525	Gfi1	PROMOTER	0.182	0.589	2544.34	1497.52	0.107	1957.54	210.20
A_68_P20864292	chr1:180458491-180458535	NM_001161665:-743	Kif26b	PROMOTER	0.182	0.614	1523.68	935.46	0.112	1084.76	121.40
A_68_P31104860	chr17:25716044-25716088	NM_029624:-52	Lmf1	DIVERGENT_PROMOTER	0.182	0.493	1763.91	870.04	0.090	1406.46	126.53
A_68_P21338177	chr2:74416496-74416545	NM_001110209:485	Lnp	INSIDE	0.182	0.694	1429.85	991.99	0.126	1201.84	151.70
A_68_P28010563	chr11:90111119-90111163	NM_026178:351	Mmd	INSIDE	0.182	0.537	1392.39	747.76	0.098	1216.44	119.17
A_68_P32181752	chr19:53389016-53389065	NM_001008542:4045	Mxi1	INSIDE	0.182	0.603	1309.82	789.28	0.109	1068.00	116.93
A_68_P21070363	chr2:25037051-25037095	NM_025980:795	Nrarp	INSIDE	0.182	0.638	1694.75	1080.83	0.116	1259.37	145.94
A_68_P28950724	chr13:36818604-36818663	NM_153529:7690	Nrn1	INSIDE	0.182	0.540	1648.09	890.21	0.098	1233.86	121.18
A_68_P29237603	chr13:95654247-95654300	NM_011021:8692	Otp	DOWNSTREAM	0.182	0.589	1535.76	904.01	0.107	1129.08	121.13
A_68_P31154665	chr17:34729645-34729690	NM_017463:252	Pbx2	INSIDE	0.182	0.709	1466.36	1039.81	0.129	925.73	119.51
A_68_P26056692	chr8:93594415-93594471	NM_011250:450	Rbl2	INSIDE	0.182	0.594	1386.35	823.65	0.108	1123.90	121.48
A_68_P31383391	chr17:80878801-80878845	NM_009231:971	Sos1	INSIDE	0.182	0.509	1623.90	826.37	0.093	1268.82	117.54
A_68_P24521963	chr6:67485504-67485548	NM_020047:290	Tacstd2	INSIDE	0.182	0.625	1355.82	847.36	0.114	1084.56	123.42
A_68_P21740453	chr2:150514165-150514209	NM_054068:687	Vsx1	INSIDE	0.182	0.599	1922.73	1151.76	0.109	1459.65	158.99
A_68_P27291141	chr10:81167742-81167786	BC064812:195		INSIDE	0.182	0.318	2539.46	807.21	0.058	2045.19	118.50
A_68_P30645469	chr16:31080852-31080896	NM_198626:644	AI480653	INSIDE	0.181	0.322	2651.92	854.51	0.058	2070.11	120.64
A_68_P20026601	chr1:10222483-10222527	NM_001102430:247	Arfgef1	INSIDE	0.181	0.586	1307.97	766.37	0.106	1126.76	119.19
A_68_P27275484	chr10:78215712-78215756	NM_027630:78	Ccdc105	INSIDE	0.181	0.558	2358.13	1314.68	0.101	1792.99	181.33
A_68_P26170767	chr8:114414110-114414154	NM_019950:19967	Chst5	INSIDE	0.181	0.495	1585.65	784.79	0.090	1403.18	125.96
A_68_P25025637	chr7:29940517-29940567	NM_001146023:687	Fam98c	INSIDE	0.181	0.556	1451.94	807.71	0.101	1163.45	117.14
A_68_P31631189	chr18:38129379-38129423	NM_175684:-15	Fchsd1	PROMOTER	0.181	0.669	2092.14	1398.67	0.121	1673.93	202.19
A_68_P20842590	chr1:176432550-176432594	NM_019445:617	Fmn2	INSIDE	0.181	0.638	1574.02	1004.34	0.115	1155.67	133.46
A_68_P26073621	chr8:96335410-96335454	NM_001113384:695	Gnao1	INSIDE	0.181	0.552	2769.36	1529.05	0.100	2015.45	200.99

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25502648	chr7:134005213-134005270	NM_172746:-244	Hirip3	DIVERGENT_PROMOTER	0.181	0.659	1454.84	959.35	0.120	1046.73	125.14
A_68_P24038737	chr5:120890387-120890431	NM_008499:8514	Lhx5	INSIDE	0.181	0.572	1899.66	1086.15	0.104	1449.40	150.04
A_68_P20148353	chr1:36501896-36501940	NM_001013374:166	Lman2l	INSIDE	0.181	0.726	2408.16	1749.22	0.132	1650.16	217.32
A_68_P21122318	chr2:33436169-33436213	NM_010725:59841	Lmx1b	INSIDE	0.181	0.541	1521.56	822.65	0.098	1185.10	115.98
A_68_P29619152	chr14:56279216-56279260	NM_023397:107	Mdp1	INSIDE	0.181	0.725	2116.29	1534.67	0.132	1468.61	193.27
A_68_P26610633	chr9:69245586-69245639	NM_145618:-192	Narg2	PROMOTER	0.181	0.673	1114.09	750.22	0.122	952.46	115.92
A_68_P30165307	chr15:41278629-41278673	NM_001130166:-377	Oxr1	PROMOTER	0.181	0.506	1656.22	838.61	0.092	1344.99	123.31
A_68_P24995083	chr7:20334983-20335030	NM_008990:-84	Pvrl2	PROMOTER	0.181	1.931	6073.00	11724.05	0.350	3805.69	1332.55
A_68_P31000876	chr16:97985140-97985184	NM_023663:200	Ripk4	INSIDE	0.181	0.434	2082.83	904.70	0.079	1521.97	119.59
A_68_P21081135	chr2:26772103-26772147	NM_013677:-74	Surf1	PROMOTER	0.181	0.625	4877.48	3050.33	0.113	3438.21	389.04
A_68_P20908721	chr1:188528261-188528311	NM_009367:1585	Tgfb2	INSIDE	0.181	0.709	1323.93	938.52	0.128	953.64	122.07
A_68_P24946869	chr7:3645931-3645975	NM_024168:-157	Tsen34	PROMOTER	0.181	0.722	2688.92	1942.53	0.131	1972.03	258.20
A_68_P28072085	chr11:100981492-100981536	NM_134024:70	Tubg1	INSIDE	0.181	0.493	2031.08	1001.35	0.089	1424.27	126.75
A_68_P27357053	chr10:93498402-93498447	NM_172538:69	Vezt	INSIDE	0.181	0.651	1418.07	923.77	0.118	1056.89	124.90
A_68_P24152596	chr5:143105941-143105985	NM_178398:425	Wipi2	INSIDE	0.181	0.475	1697.21	806.27	0.086	1383.16	119.16
A_68_P27804180	chr11:53138329-53138380	NM_026479:164	Zcchc10	INSIDE	0.181	0.432	2399.18	1036.96	0.078	1702.79	133.06
A_68_P24994119	chr7:20162872-20162916	NM_022409:259	Zfp296	INSIDE	0.181	0.392	2668.91	1045.35	0.071	1836.11	129.85
A_68_P29051401	A_68_P29051401			Unknown	0.181	1.742	4051.15	7058.16	0.316	2755.71	870.08
A_68_P23763025	chr5:67011439-67011483	NM_001201413:-1404	Apbb2	PROMOTER	0.180	0.645	5037.93	3247.43	0.116	4030.61	468.32
A_68_P25352107	chr7:104886338-104886382	NM_175105:397	Aqp11	INSIDE	0.180	0.737	2131.95	1571.00	0.133	1621.23	215.26
A_68_P28088312	chr11:103827831-103827875	NM_007477:-332	Arf2	PROMOTER	0.180	0.522	1991.90	1038.99	0.094	1486.10	139.51
A_68_P20831243	chr1:174078348-174078392	NM_153555:225	Dcaf8	INSIDE	0.180	0.543	1808.79	982.31	0.098	1229.52	120.15
A_68_P28890407	chr13:25147770-25147817	NM_001195617:-79	Dcdc2a	PROMOTER	0.180	0.432	1824.85	789.13	0.078	1513.07	117.75
A_68_P21767852	chr2:155652392-155652439	NM_010579:246	Eif6	INSIDE	0.180	0.578	2736.92	1581.08	0.104	1938.08	201.22
A_68_P27077942	chr10:39090283-39090342	NM_001122892:708	Fyn	INSIDE	0.180	3.150	6416.29	20214.34	0.566	3781.55	2139.74
A_68_P27784886	chr11:49608055-49608100	NM_013529:421	Gfpt2	INSIDE	0.180	0.638	2029.21	1294.67	0.115	1681.83	192.78
A_68_P23364007	chr4:140981800-140981844	NM_013868:5129	Hspb7	DOWNSTREAM	0.180	0.706	2165.62	1527.90	0.127	1598.95	202.64
A_68_P24538445	chr6:71781870-71781919	NM_029673:570	Immt	INSIDE	0.180	0.503	1708.21	858.99	0.090	1305.46	118.05
A_68_P31791018	chr18:67449050-67449094	NM_053261:196	Impa2	INSIDE	0.180	0.744	4171.49	3104.40	0.134	3098.51	414.33
A_68_P26065131	chr8:94880961-94881005	NM_018826:-712	Irx5	DIVERGENT_PROMOTER	0.180	0.569	2009.01	1142.78	0.103	1364.64	139.90
A_68_P20290945	chr1:64168690-64168734	NM_033563:-749	Klf7	PROMOTER	0.180	0.586	1484.49	870.28	0.105	1106.58	116.54
A_68_P24119632	chr5:136611907-136611951	NM_027891:16	Lrwd1	INSIDE	0.180	0.435	2165.95	942.65	0.078	1614.95	126.51
A_68_P25266321	chr7:87515732-87515779	NM_172903:506	Man2a2	INSIDE	0.180	0.695	2106.99	1463.86	0.125	1410.98	176.06
A_68_P27788132	chr11:50172976-50173028	NR_030529:-1621	Mir804	PROMOTER	0.180	0.654	1286.76	841.29	0.118	1003.26	118.06
A_68_P24362056	chr6:35489772-35489816	NM_008098:94	Mtpn	INSIDE	0.180	0.428	1963.24	840.72	0.077	1668.73	128.37
A_68_P26242531	chr8:126472768-126472821	NM_172288:371	Nup133	INSIDE	0.180	0.589	2114.34	1245.39	0.106	1447.79	153.73
A_68_P22356950	chr3:97692610-97692655	NM_001039376:-2	Pde4dip	PROMOTER	0.180	0.581	1515.51	880.91	0.105	1143.04	119.58
A_68_P30346974	chr15:76062654-76062698	NM_001163542:-868	Plec	PROMOTER	0.180	0.463	1944.49	901.27	0.083	1415.25	117.86
A_68_P26533942	chr9:55889666-55889710	NM_011992:37	Rcn2	INSIDE	0.180	0.433	1976.80	855.38	0.078	1529.11	118.78
A_68_P24946917	chr7:3655779-3655833	NM_029767:164	Rps9	INSIDE	0.180	0.571	1422.66	812.06	0.103	1166.18	120.11
A_68_P23327084	chr4:134731141-134731185	NM_019732:54603	Runx3	INSIDE	0.180	0.672	1193.06	801.36	0.121	988.42	119.79
A_68_P31412148	chr17:86091318-86091363	NM_011380:-3746	Six2	PROMOTER	0.180	0.475	1908.55	906.61	0.085	1365.48	116.60
A_68_P21395065	chr2:84706336-84706380	NM_001083809:25576	Slc43a1	DOWNSTREAM	0.180	0.526	3371.98	1774.51	0.095	2424.73	229.96
A_68_P22049384	chr3:34548485-34548529	NM_011443:-420	Sox2	PROMOTER	0.180	0.689	2288.19	1577.17	0.124	1629.69	202.39
A_68_P31096072	chr17:24345615-24345659	NM_001163847:-3129	Tbc1d24	PROMOTER	0.180	0.609	1317.18	802.77	0.110	1082.52	118.90
A_68_P21796145	chr2:160471648-160471692	NM_009408:38	Top1	INSIDE	0.180	0.712	1596.72	1136.89	0.128	1198.05	153.55
A_68_P21642319	chr2:132641532-132641578	NM_175113:236	Trmt6	INSIDE	0.180	0.537	1786.05	958.61	0.097	1240.30	119.83
A_68_P31771006	chr18:63851716-63851760	NM_016792:275	Txnl1	INSIDE	0.180	0.338	2655.78	897.07	0.061	2002.14	121.86
A_68_P21567194	chr2:118798746-118798790	AK184532:45300		INSIDE	0.180	0.625	1227.86	767.91	0.113	1024.87	115.36
A_68_P22130347	chr3:51364112-51364156	NR_033624:456	5031434O11Rik	INSIDE	0.179	0.478	1863.67	890.38	0.085	1364.20	116.63
A_68_P21483985	chr2:103406320-103406364	NM_178890:-124	Abtb2	PROMOTER	0.179	1.477	3797.96	5609.94	0.264	2414.63	638.31

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31762245	chr18:62340024-62340068	NM_007420:-433	Adrb2	PROMOTER	0.179	1.460	5578.55	8143.74	0.262	3947.58	1032.70
A_68_P25657171	chr8:11727694-11727738	NM_001113517:-388	Arhgef7	PROMOTER	0.179	0.584	1503.22	877.26	0.104	1135.66	118.52
A_68_P20147469	chr1:36364742-36364786	NM_001172205:187	Arid5a	INSIDE	0.179	0.533	1711.95	913.27	0.095	1292.59	123.34
A_68_P31545964	chr18:21811364-21811410	NM_001081403:-517	Klhl14	PROMOTER	0.179	0.623	1563.99	974.57	0.112	1184.81	132.50
A_68_P21583616	chr2:121781508-121781552	NM_008545:298	Mageb3	INSIDE	0.179	0.561	2686.96	1508.04	0.100	1953.02	196.18
A_68_P32252888	chrX:10294568-10294612	NM_001166635:100	Mid1ip1	INSIDE	0.179	2.996	2297.32	6882.51	0.536	930.03	498.07
A_68_P25394533	chr7:112959197-112959241	NM_025301:383	Mrpl17	INSIDE	0.179	0.522	1705.03	890.18	0.093	1259.14	117.49
A_68_P22129524	chr3:51220706-51220750	NM_053089:791	Naa15	INSIDE	0.179	0.681	1206.14	821.71	0.122	1011.94	123.47
A_68_P26343619	chr9:20531260-20531304	NM_173777:1376	Olfm2	INSIDE	0.179	0.522	1783.14	930.71	0.094	1271.45	118.88
A_68_P23575370	chr5:31209922-31209966	NM_001134692:151	Ost4	INSIDE	0.179	0.473	4382.49	2073.94	0.085	2858.10	241.87
A_68_P25366405	chr7:107375733-107375777	NM_027629:-362	Pgm2l1	PROMOTER	0.179	0.686	1188.00	814.92	0.123	969.53	119.37
A_68_P21913219	chr2:181599054-181599098	NM_025901:12	Polr3k	INSIDE	0.179	0.607	1461.74	887.60	0.109	1166.18	126.95
A_68_P23393509	chr4:147661752-147661796	NM_001083342:300	Ptchd2	INSIDE	0.179	0.704	3244.74	2285.80	0.126	2490.23	314.76
A_68_P29696767	chr14:70107122-70107166	NM_001146012:243	R3hcc1	INSIDE	0.179	0.480	2629.67	1261.18	0.086	2007.08	172.62
A_68_P20598626	chr1:129999945-129999989	NM_181750:84	R3hdm1	INSIDE	0.179	0.680	1163.91	791.07	0.121	967.60	117.56
A_68_P28535623	chr12:74213467-74213511	NM_011382:744	Six4	INSIDE	0.179	0.632	1480.46	935.19	0.113	1084.65	122.46
A_68_P27554681	chr11:3813626-3813670	NM_153142:1019	Slc35e4	INSIDE	0.179	0.665	1359.73	904.61	0.119	1012.87	120.44
A_68_P27779983	chr11:48614301-48614357	NR_028563:-1206	Snord96a	PROMOTER	0.179	0.631	1358.53	857.39	0.113	1073.11	121.33
A_68_P31255140	chr17:56443504-56443548	NM_001111078:-209	Uhrf1	PROMOTER	0.179	0.492	2188.59	1076.76	0.088	1546.69	136.25
A_68_P25030741	chr7:31065286-31065332	NM_146186:132	Wdr62	INSIDE	0.179	0.561	1506.21	844.99	0.101	1176.12	118.34
A_68_P29630483	chr14:58509439-58509485	NM_029492:-363	Zdhhc20	PROMOTER	0.179	1.573	650.04	1022.74	0.282	553.45	156.16
A_68_P21092717	chr2:28555343-28555389	NM_027283:-195	1700026L06Rik	DIVERGENT_PROMOTER	0.178	0.655	1843.17	1207.22	0.116	1391.48	162.00
A_68_P20147470	chr1:36364812-36364860	NM_001172205:259	Arid5a	INSIDE	0.178	0.711	1746.68	1241.52	0.127	1260.98	159.54
A_68_P21424191	chr2:91550574-91550618	NM_145528:137	Atg13	INSIDE	0.178	0.473	1858.80	878.54	0.084	1387.62	116.93
A_68_P24763305	chr6:113991563-113991607	NM_009723:490	Atp2b2	INSIDE	0.178	2.059	2370.00	4879.63	0.366	1373.47	502.65
A_68_P21632199	chr2:130732765-130732810	NM_009730:556	Atrn	INSIDE	0.178	0.698	1194.82	834.42	0.125	938.74	116.92
A_68_P21630551	chr2:130406332-130406390	NM_009732:1917	Avp	DOWNSTREAM	0.178	1.730	1320.96	2285.70	0.308	911.32	280.29
A_68_P27899586	chr11:70042779-70042828	NM_007528:497	Bcl6b	INSIDE	0.178	0.707	1860.62	1315.18	0.126	1418.07	178.73
A_68_P28175446	chr11:118902080-118902124	NM_013926:125	Cbx8	INSIDE	0.178	0.588	3311.35	1947.04	0.105	2201.83	230.95
A_68_P28602894	chr12:86560864-86560908	NM_145445:424	Eif2b2	INSIDE	0.178	0.661	1526.31	1008.15	0.118	1129.99	132.96
A_68_P31948068	chr19:10116519-10116563	NM_021890:503	Fads3	INSIDE	0.178	0.600	1581.44	948.93	0.107	1133.36	120.95
A_68_P26224676	chr8:123649716-123649760	NM_008024:-1846	Foxl1	PROMOTER	0.178	0.486	1908.77	927.75	0.086	1476.05	127.61
A_68_P28221328	chr12:8308980-8309024	NM_013527:-242	Gdf7	PROMOTER	0.178	0.566	1528.93	864.66	0.101	1200.00	120.75
A_68_P28155560	chr11:115685911-115685955	NM_145438:561	Llgl2	INSIDE	0.178	0.519	2565.41	1330.25	0.092	1869.48	172.17
A_68_P21122757	chr2:33496008-33496052	NM_010725:1	Lmx1b	INSIDE	0.178	0.495	1718.67	851.39	0.088	1333.11	117.87
A_68_P27848679	chr11:61307617-61307661	NM_011841:67	Mapk7	INSIDE	0.178	0.647	1338.78	866.40	0.115	1014.69	116.64
A_68_P22312509	chr3:88019343-88019387	NR_029817:-155	Mir9-1	PROMOTER	0.178	0.704	1355.53	953.77	0.125	941.17	118.08
A_68_P24114757	chr5:135583228-135583272	NM_021455:468	Mlxipl	INSIDE	0.178	0.696	1265.56	880.64	0.124	935.18	115.78
A_68_P31055436	chr17:13109119-13109167	NM_026310:-185	Mrpl18	DIVERGENT_PROMOTER	0.178	0.692	1534.51	1061.22	0.123	1131.07	139.01
A_68_P31112797	chr17:26987123-26987182	NM_008700:-8642	Nkx2-5	PROMOTER	0.178	1.689	594.11	1003.18	0.301	401.73	120.88
A_68_P31066339	chr17:15701385-15701429	NM_144809:-1119	Prdm9	PROMOTER	0.178	0.554	1517.87	840.84	0.099	1188.33	117.49
A_68_P32957124	chr17:8533875-8533919	NM_178774:293	Prr18	INSIDE	0.178	0.444	1898.57	842.57	0.079	1453.11	114.99
A_68_P28726320	chr12:109416772-109416817	NM_028262:700	Setd3	INSIDE	0.178	0.516	1860.07	959.94	0.092	1310.87	120.28
A_68_P30485733	chr15:100253963-100254009	NM_008732:-500	Slc11a2	PROMOTER	0.178	0.606	2749.82	1665.72	0.108	2146.70	231.20
A_68_P28550371	chr12:76920085-76920143	NM_001005510:810	Syne2	INSIDE	0.178	0.419	2072.35	868.40	0.075	1623.89	121.31
A_68_P26247735	chr8:127318077-127318121	NM_198632:1180	Trim67	INSIDE	0.178	0.382	2268.52	865.46	0.068	1732.63	117.89
A_68_P31257918	chr17:56856812-56856859	NM_178926:-491	Vmac	PROMOTER	0.178	0.711	1313.12	933.32	0.126	919.68	116.17
A_68_P22400150	chr3:105761819-105761870	NM_027432:-571	Wdr77	PROMOTER	0.178	0.456	1956.63	891.26	0.081	1557.28	126.30
A_68_P23299525	chr4:129662999-129663043	NM_001199696:699	Bai2	INSIDE	0.177	1.930	5092.59	9827.63	0.342	2909.27	994.51
A_68_P24605098	chr6:85401665-85401709	NM_007638:188	Cct7	INSIDE	0.177	0.492	1677.19	825.62	0.087	1338.67	116.59
A_68_P23103758	chr4:91041293-91041337	NM_010486:-2568	Elavl2	PROMOTER	0.177	0.728	2369.28	1724.79	0.129	1762.39	227.00

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P26779727	chr9:102256967-102257011	NM_001168296:35	Ephb1	INSIDE	0.177	0.607	4893.64	2968.88	0.107	3316.01	355.60
A_68_P23613114	chr5:37728265-37728310	NM_021292:-167	Evc	DIVERGENT_PROMOTER	0.177	0.579	1583.03	916.19	0.102	1174.62	120.25
A_68_P22392958	chr3:104561530-104561574	NM_183224:18913	Fam19a3	DOWNSTREAM	0.177	0.617	1349.72	833.05	0.109	1104.18	120.34
A_68_P27980049	chr11:84683380-84683424	NM_153144:838	Ggnbp2	INSIDE	0.177	0.632	1488.84	941.06	0.112	1155.09	129.12
A_68_P24168905	chr5:147396571-147396615	NM_008151:-612	Gpr12	PROMOTER	0.177	0.445	1817.97	809.44	0.079	1519.45	119.57
A_68_P23571064	chr5:30481871-30481915	NM_145558:31	Hadhb	INSIDE	0.177	0.509	3436.32	1749.92	0.090	2549.02	229.29
A_68_P23416916	chr4:151534184-151534228	NM_008236:1231	Hes2	INSIDE	0.177	0.454	2238.35	1016.34	0.080	1494.86	120.07
A_68_P21338894	chr2:74536266-74536310	NM_013555:469	Hoxd9	INSIDE	0.177	0.544	1477.23	803.63	0.096	1236.00	119.12
A_68_P21129648	chr2:34627186-34627230	NM_001163434:-401	Hspa5	PROMOTER	0.177	0.707	1444.82	1022.11	0.125	1126.15	140.86
A_68_P28293528	chr12:25783564-25783608	NM_010496:-2629	Id2	PROMOTER	0.177	0.597	1489.70	889.03	0.105	1139.54	120.04
A_68_P26317489	chr9:14304655-14304699	NM_173433:250	Kdm4d	INSIDE	0.177	0.575	2013.19	1156.58	0.101	1392.24	141.29
A_68_P27279737	chr10:79384185-79384238	NM_053244:4496	Kiss1r	INSIDE	0.177	1.533	1071.29	1642.47	0.272	799.13	217.16
A_68_P27947420	chr11:78960035-78960079	NM_013571:-200	Ksr1	PROMOTER	0.177	0.373	2319.40	865.07	0.066	1805.20	119.02
A_68_P31104861	chr17:25716207-25716251	NM_029624:110	Lmf1	INSIDE	0.177	0.492	2633.19	1294.44	0.087	1919.27	167.02
A_68_P24563513	chr6:77193982-77194026	NM_028880:1294	Lrrtm1	INSIDE	0.177	0.457	1945.42	888.59	0.081	1482.37	119.94
A_68_P30295276	chr15:66801140-66801184	NM_008681:41	Ndrg1	INSIDE	0.177	0.434	3852.04	1672.29	0.077	3098.07	238.36
A_68_P31099229	chr17:24861250-24861296	NM_026684:61	Ndufb10	INSIDE	0.177	0.711	2065.37	1468.64	0.126	1496.96	188.66
A_68_P32201474	chr19:56623518-56623562	NM_025811:790	Nhlrc2	INSIDE	0.177	0.666	1445.69	963.43	0.118	1061.21	125.12
A_68_P30397616	chr15:84753564-84753608	NM_016714:-271	Nup50	PROMOTER	0.177	0.446	2041.68	911.47	0.079	1585.46	125.19
A_68_P24595789	chr6:83781804-83781857	NM_146169:-95	Paip2b	PROMOTER	0.177	0.494	1921.04	948.76	0.087	1366.72	119.32
A_68_P22518759	chr3:128919062-128919106	NM_001042502:2230	Pitx2	INSIDE	0.177	0.544	2054.18	1116.66	0.096	1399.82	134.47
A_68_P26079048	chr8:97219780-97219824	NM_026385:340	Pllp	INSIDE	0.177	0.477	2353.33	1123.46	0.085	1746.55	147.88
A_68_P21952656	chr3:13473217-13473261	NM_001163328:1584	Ralyl	INSIDE	0.177	0.658	1229.02	809.30	0.117	1061.28	123.71
A_68_P28513220	chr12:70284706-70284750	NM_025589:326	Rpl36al	INSIDE	0.177	0.702	1282.42	900.25	0.124	998.76	123.94
A_68_P32016818	chr19:23347992-23348036	NM_153808:353	Smc5	INSIDE	0.177	0.502	1825.29	915.41	0.089	1399.17	124.51
A_68_P28186321	chr11:120574903-120574948	NM_016665:156	Stra13	INSIDE	0.177	0.546	3576.16	1952.29	0.096	2694.71	259.95
A_68_P28974244	chr13:40833219-40833263	NM_011547:-4048	Tcfap2a	PROMOTER	0.177	0.669	1395.70	934.25	0.119	1036.11	122.84
A_68_P31213967	chr17:47875064-47875108	NM_001161723:207	Tcfeb	INSIDE	0.177	0.697	1858.49	1295.83	0.123	1342.55	165.59
A_68_P22900943	chr4:48598769-48598813	NM_021436:726	Tmeff1	INSIDE	0.177	2.012	3128.67	6294.60	0.357	2112.15	753.81
A_68_P25098515	chr7:53604139-53604183	AK015435:229		INSIDE	0.177	2.403	6299.31	15136.00	0.426	4274.96	1820.84
A_68_P23692823	chr5:52505949-52505993	AK076709:-2581		PROMOTER	0.177	0.716	1385.53	992.50	0.127	947.67	120.39
A_68_P23588820	chr5:33772994-33773048	ENSMUST00000030994:824		DOWNSTREAM	0.177	0.610	1500.98	915.70	0.108	1134.98	122.42
A_68_P27846102	chr11:60835765-60835809	ENSMUST00000089184:-279		PROMOTER	0.177	0.432	4545.09	1961.59	0.076	3364.12	257.23
A_68_P28956454	chr13:37870668-37870712	ENSMUST00000122842:422		INSIDE	0.177	0.501	2105.50	1055.28	0.089	1466.79	130.24
A_68_P27282446	chr10:79783036-79783080	NM_025521:235	2310011J03Rik	INSIDE	0.176	0.489	1952.13	955.33	0.086	1409.78	121.28
A_68_P25459894	chr7:125884088-125884134	NM_027815:326	9030624J02Rik	INSIDE	0.176	0.618	3105.32	1918.00	0.109	2116.17	230.08
A_68_P27789380	chr11:50416439-50416486	NM_175643:876	Adamts2	INSIDE	0.176	0.474	1930.20	915.07	0.083	1400.30	116.75
A_68_P26430108	chr9:37155823-37155867	NM_001081429:133	Ccdc15	INSIDE	0.176	0.675	1495.98	1009.74	0.119	1046.17	124.28
A_68_P26571035	chr9:62384198-62384249	NM_175484:628	Coro2b	INSIDE	0.176	0.647	1360.55	880.36	0.114	1039.51	118.12
A_68_P30573855	chr16:17452673-17452717	NM_007764:615	Crkl	INSIDE	0.176	0.673	1312.79	882.97	0.118	978.99	115.74
A_68_P25776075	chr8:35869882-35869926	NM_176933:-759	Dusp4	PROMOTER	0.176	0.435	2041.21	888.65	0.077	1589.93	121.80
A_68_P28067416	chr11:100180895-100180948	NM_011508:-388	Eif1	PROMOTER	0.176	0.619	1706.07	1056.87	0.109	1144.17	125.07
A_68_P26546333	chr9:58046118-58046162	NM_001161535:3382	Islr2	INSIDE	0.176	0.407	3297.07	1343.18	0.072	2350.88	169.01
A_68_P30345377	chr15:75828316-75828360	NM_177922:4140	Mapk15	INSIDE	0.176	0.653	1469.85	960.03	0.115	1061.69	122.25
A_68_P24819299	chr6:125141841-125141885	NM_146171:-258	Ncapd2	DIVERGENT_PROMOTER	0.176	0.434	2165.18	938.70	0.076	1579.73	120.74
A_68_P25995582	chr8:82163121-82163165	NM_001081164:-432	Otud4	PROMOTER	0.176	0.474	2162.96	1025.66	0.084	1395.84	116.61
A_68_P29620551	chr14:56518869-56518914	NM_001082975:178	Sdr39u1	INSIDE	0.176	0.632	1687.88	1066.23	0.111	1049.63	116.66
A_68_P24447792	chr6:51962699-51962743	NM_018773:-172	Skap2	PROMOTER	0.176	0.552	1572.06	867.38	0.097	1213.14	118.04
A_68_P31943157	chr19:8788272-8788316	NM_008577:93	Slc3a2	INSIDE	0.176	0.613	1539.03	943.38	0.108	1082.47	116.78
A_68_P23616980	chr5:38430589-38430633	NM_026959:137	Stx18	INSIDE	0.176	0.537	1651.76	887.73	0.095	1235.71	117.17
A_68_P21265457	chr2:61494997-61495041	NM_001164071:63865	Tank	DOWNSTREAM	0.176	0.610	1551.97	946.09	0.107	1221.48	130.74

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25510946	chr7:135603923-135603972	NM_009383:1080	Tial1	INSIDE	0.176	0.540	1590.33	858.61	0.095	1259.21	119.69
A_68_P25082977	chr7:50817749-50817793	NM_001008549:31	Zfp658	INSIDE	0.176	0.563	1600.81	900.83	0.099	1206.00	119.75
A_68_P27054330	chr10:33670738-33670782	NM_028287:258	Zufsp	INSIDE	0.176	0.608	1478.15	899.10	0.107	1126.53	120.72
A_68_P27829965	chr11:58052895-58052939			Unknown	0.176	1.953	15681.64	30630.80	0.345	10003.40	3446.49
A_68_P32389693	chrX:51278099-51278143	ENSMUST00000120892:-154		PROMOTER	0.176	1.415	967.60	1368.97	0.249	470.27	116.94
A_68_P24330581	chr6:30123488-30123532	NR_038124:-3112	BB283400	DIVERGENT_PROMOTER	0.175	0.640	3801.39	2431.18	0.112	2702.26	302.72
A_68_P29618486	chr14:56179164-56179210	NM_001199009:-573	Dcaf11	PROMOTER	0.175	0.715	2883.56	2062.36	0.125	2143.86	267.81
A_68_P23917031	chr5:98683201-98683245	NM_010203:20	Fgf5	INSIDE	0.175	0.699	1750.58	1224.45	0.122	1265.06	154.45
A_68_P23250455	chr4:119959495-119959539	NM_194060:350	Foxo6	INSIDE	0.175	0.463	1916.34	888.09	0.081	1501.80	121.52
A_68_P28083427	chr11:102977675-102977719	NM_138753:58	Hexim1	INSIDE	0.175	0.511	1849.53	945.58	0.090	1352.84	121.25
A_68_P21339175	chr2:74570928-74570982	NM_010468:20905	Hoxd3	INSIDE	0.175	0.672	1839.81	1237.11	0.118	1054.44	124.16
A_68_P23598368	chr5:35448526-35448576	NM_013587:-204	Lrpap1	PROMOTER	0.175	0.675	1419.04	957.73	0.118	968.39	114.65
A_68_P32240002	chrX:7327694-7327738	NR_030454:-2498	Mir684-1	DIVERGENT_PROMOTER	0.175	1.361	1699.90	2314.19	0.239	593.09	141.49
A_68_P20765301	chr1:162125216-162125275	NM_025474:-145	Mrps14	PROMOTER	0.175	0.647	2204.54	1426.05	0.113	1582.08	178.69
A_68_P20852906	chr1:178205311-178205355	NM_176916:111	Pld5	INSIDE	0.175	0.620	3447.14	2137.91	0.109	2578.68	280.07
A_68_P20349521	chr1:74647661-74647705	NM_021313:289	Rnf25	INSIDE	0.175	0.607	5399.84	3280.06	0.106	4086.00	433.52
A_68_P29454672	chr14:22570199-22570243	NM_026283:468	Samd8	INSIDE	0.175	0.658	1611.64	1059.89	0.115	1149.32	132.07
A_68_P24092947	chr5:130731194-130731238	NM_023248:116	Sbds	INSIDE	0.175	0.649	1450.87	941.34	0.113	1059.46	119.97
A_68_P29034450	chr13:51888603-51888647	NM_013660:389	Sema4d	INSIDE	0.175	0.539	1663.93	896.28	0.094	1284.85	121.24
A_68_P27131168	chr10:50620782-50620826	NM_011376:5348	Sim1	INSIDE	0.175	0.712	1361.61	969.35	0.124	978.40	121.59
A_68_P22031732	chr3:30992663-30992708	NM_001039090:-1297	Skil	PROMOTER	0.175	0.538	1678.20	903.20	0.094	1223.13	114.95
A_68_P25840860	chr8:48373600-48373648	NM_001114311:1132	Stox2	INSIDE	0.175	0.512	1732.66	887.09	0.090	1330.12	119.39
A_68_P26921714	chr10:7676666-7676718	NM_138667:-771	Tab2	PROMOTER	0.175	0.629	1484.26	933.95	0.110	1229.81	135.45
A_68_P27693353	chr11:33102552-33102596	NM_019916:1014	Tlx3	INSIDE	0.175	0.564	1488.77	839.17	0.098	1262.33	124.20
A_68_P28931388	chr13:32895025-32895071	NM_030215:1150	Wrnip1	INSIDE	0.175	0.571	1916.49	1094.34	0.100	1294.07	129.40
A_68_P26018919	chr8:86760604-86760650	NM_172503:315	Zswim4	INSIDE	0.175	2.010	653.32	1313.04	0.351	491.37	172.66
A_68_P24624509	chr6:88792201-88792245	NM_030251:-293	Abtb1	PROMOTER	0.174	1.570	5082.42	7978.09	0.273	3210.12	876.93
A_68_P30092464	chr15:27396409-27396457	NM_020332:1	Ank	INSIDE	0.174	1.764	1351.34	2383.72	0.308	918.98	282.77
A_68_P26317494	chr9:14305171-14305215	NM_023153:130	Cwc15	INSIDE	0.174	0.589	2438.09	1436.86	0.102	2042.22	208.86
A_68_P21317591	chr2:70956240-70956284	NM_028593:152	Cybrd1	INSIDE	0.174	0.585	1607.24	939.63	0.102	1194.98	121.41
A_68_P28100239	chr11:106078730-106078775	NM_028074:513	Ddx42	INSIDE	0.174	1.479	1082.85	1601.05	0.258	781.99	201.65
A_68_P28732705	chr12:110691224-110691271	NM_001190703:-417	Dlk1	PROMOTER	0.174	0.564	1693.86	954.75	0.098	1255.25	123.15
A_68_P31106383	chr17:25945693-25945737	NM_001164225:-315	Fbxl16	PROMOTER	0.174	0.569	1926.85	1096.78	0.099	1409.88	139.80
A_68_P23231912	chr4:116668443-116668487	NM_175244:512	Hectd3	INSIDE	0.174	0.669	2504.04	1675.53	0.116	1937.40	225.04
A_68_P27581115	chr11:8910943-8910987	NM_008316:176	Hus1	INSIDE	0.174	0.398	2247.94	893.58	0.069	1759.14	121.96
A_68_P26920442	chr10:7446059-7446115	NM_011835:289	Katna1	INSIDE	0.174	0.630	1481.08	932.78	0.109	1104.77	120.80
A_68_P20025036	chr1:9957153-9957197	NM_145692:42027	Lrrc67	DOWNSTREAM	0.174	0.703	1286.63	905.00	0.123	993.52	121.82
A_68_P29718025	chr14:73924796-73924840	NM_172527:23231	Nudt15	INSIDE	0.174	0.663	5473.03	3631.03	0.115	3869.57	445.76
A_68_P20768470	chr1:162722306-162722353	NM_013862:740	Rabgap1l	INSIDE	0.174	1.430	1370.04	1959.76	0.249	1051.90	261.79
A_68_P25950469	chr8:72736531-72736577	NM_001007570:-374	Slc25a42	PROMOTER	0.174	0.598	1531.97	915.90	0.104	1155.40	119.93
A_68_P21608669	chr2:126379290-126379337	NM_011978:554	Slc27a2	INSIDE	0.174	0.554	1744.95	967.04	0.096	1200.39	115.56
A_68_P28101955	chr11:106362323-106362370	NR_030703:42	Snord104	INSIDE	0.174	0.626	3342.72	2092.04	0.109	2440.65	265.07
A_68_P25840857	chr8:48373280-48373324	NM_001114311:1454	Stox2	INSIDE	0.174	0.625	1857.49	1160.78	0.108	1276.11	138.37
A_68_P26022397	chr8:87396203-87396247	NM_001168244:68	Syce2	INSIDE	0.174	1.579	8319.12	13136.59	0.275	5430.36	1492.67
A_68_P30479872	chr15:99223536-99223580	NM_001171035:-91	Tmbim6	PROMOTER	0.174	0.487	2046.14	997.19	0.085	1450.77	123.22
A_68_P27846982	chr11:60988669-60988713	NM_001004143:-129	Usp22	PROMOTER	0.174	0.704	1374.08	967.17	0.123	978.49	119.89
A_68_P27469300	chr10:114821835-114821879	NM_001033261:-158	Zfc3h1	DIVERGENT_PROMOTER	0.174	0.588	1675.89	985.64	0.102	1184.83	121.21
A_68_P29102609	chr13:65380152-65380198	NM_178364:13	Zfp369	INSIDE	0.174	0.544	1622.39	882.81	0.095	1278.17	121.07
A_68_P26430752	chr9:37267961-37268005			Unknown	0.174	0.704	2259.43	1591.71	0.122	1912.72	234.10
A_68_P25890692	chr8:59820063-59820107	ENSMUST00000132988:9170		DOWNSTREAM	0.174	0.646	1300.26	839.68	0.113	1055.04	118.80
A_68_P24039806	chr5:121062707-121062753	NM_029096:-132	1110008J03Rik	DIVERGENT_PROMOTER	0.173	0.605	1671.34	1011.87	0.104	1153.56	120.49

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P23299526	chr4:129663110-129663154	NM_001199696:811	Bai2	INSIDE	0.173	1.847	10078.00	18611.84	0.319	6203.11	1981.77
A_68_P27980570	chr11:84771638-84771682	NM_007607:405	Car4	INSIDE	0.173	0.465	2011.08	935.28	0.081	1491.58	120.23
A_68_P28059227	chr11:98769369-98769413	NM_011799:-74	Cdc6	PROMOTER	0.173	2.564	6792.48	17416.08	0.444	4223.49	1874.92
A_68_P31620305	chr18:35990289-35990333	NM_133687:839	Cxxc5	INSIDE	0.173	0.572	4581.05	2620.95	0.099	3103.76	307.44
A_68_P31286851	chr17:63231331-63231377	NM_010109:-688	Efna5	PROMOTER	0.173	0.682	1466.36	1000.36	0.118	1025.23	121.29
A_68_P20351050	chr1:74932235-74932279	NM_153111:-274	Fev	PROMOTER	0.173	2.211	6752.79	14933.72	0.383	4043.83	1549.35
A_68_P23356006	chr4:139665293-139665352	NM_198610:137404	Igsf21	INSIDE	0.173	0.509	1799.44	915.72	0.088	1372.39	120.92
A_68_P23138265	chr4:98062281-98062325	NM_001005784:-214	Inadl	PROMOTER	0.173	0.541	1634.56	885.02	0.094	1289.39	120.79
A_68_P20804906	chr1:169324243-169324289	NM_025569:-338	Mgst3	PROMOTER	0.173	0.684	1301.21	889.97	0.118	1005.60	119.00
A_68_P25261467	chr7:86650381-86650425	NR_029818:253	Mir9-3	DOWNSTREAM	0.173	0.587	1804.05	1058.83	0.101	1356.12	137.31
A_68_P25993841	chr8:81819136-81819180	NM_133823:-303	Mmaa	PROMOTER	0.173	0.565	1655.96	936.07	0.098	1177.56	115.08
A_68_P25954854	chr8:73430001-73430045	NM_173013:150	Mtap1s	INSIDE	0.173	0.716	9666.59	6923.16	0.124	6411.88	792.74
A_68_P26815491	chr9:108470017-108470061	NM_023247:-365	Ndufaf3	DIVERGENT_PROMOTER	0.173	0.533	1780.83	948.68	0.092	1342.15	123.59
A_68_P27285558	chr10:80261134-80261187	NM_023900:211	Plekhj1	INSIDE	0.173	0.625	1549.63	967.88	0.108	1119.19	120.71
A_68_P27282698	chr10:79819083-79819127	NM_183152:-99	Plk5	DIVERGENT_PROMOTER	0.173	0.580	1689.64	980.34	0.101	1210.77	121.87
A_68_P30379305	chr15:81560318-81560371	NM_001146174:5	Rangap1	INSIDE	0.173	0.717	1472.99	1056.85	0.124	946.00	117.49
A_68_P24533018	chr6:70741721-70741765	NM_009075:427	Rpia	INSIDE	0.173	0.510	2330.13	1188.80	0.088	1759.33	155.01
A_68_P26660234	chr9:78435451-78435495	NM_172773:362	Slc17a5	INSIDE	0.173	0.605	1398.56	846.38	0.105	1128.57	118.50
A_68_P20353638	chr1:75379009-75379053	NM_001085370:-3154	Speg	PROMOTER	0.173	0.692	7252.21	5019.83	0.120	4874.62	583.64
A_68_P32242102	chrX:7752757-7752806	NM_001166437:526	Tbc1d25	INSIDE	0.173	1.792	950.57	1703.61	0.311	377.75	117.32
A_68_P20261290	chr1:59030112-59030156	NM_172406:192	Trak2	INSIDE	0.173	0.576	1347.13	775.38	0.099	1223.76	121.66
A_68_P20135165	chr1:33871553-33871598	NM_133817:-303	Zfp451	PROMOTER	0.173	0.688	1734.76	1194.10	0.119	1370.44	163.41
A_68_P20565672	chr1:123074540-123074584	AK045543:90512		INSIDE	0.173	0.495	1582.24	782.61	0.086	1399.12	119.96
A_68_P23315176	chr4:132567687-132567731	NM_146155:288	Ahdc1	INSIDE	0.172	1.466	1685.86	2471.02	0.251	1289.17	324.19
A_68_P27646188	chr11:23397444-23397495	NM_172391:477	Ahsa2	INSIDE	0.172	0.686	1131.32	775.95	0.118	1041.98	122.75
A_68_P28553309	chr12:77426063-77426107	NM_001101471:207	Akap5	INSIDE	0.172	0.552	2337.65	1289.53	0.095	1749.51	165.95
A_68_P27847520	chr11:61081060-61081115	NM_007437:-458	Aldh3a2	PROMOTER	0.172	0.455	2115.04	961.48	0.078	1541.58	120.82
A_68_P26595471	chr9:66682687-66682731	NM_026674:-195	Aph1c	PROMOTER	0.172	0.609	1452.99	884.84	0.105	1197.01	125.27
A_68_P26158730	chr8:112261101-112261147	NM_001080930:515	Atxn1l	INSIDE	0.172	1.711	788.99	1349.74	0.295	543.84	160.18
A_68_P20794610	chr1:167391699-167391743	NM_027430:382	Brp44	INSIDE	0.172	0.544	1884.09	1025.75	0.093	1323.72	123.61
A_68_P20408511	chr1:87691108-87691154	NM_133781:1109	Cab39	INSIDE	0.172	0.546	1562.43	852.44	0.094	1248.16	117.17
A_68_P23196911	chr4:108292854-108292898	NM_177045:316	Cc2d1b	INSIDE	0.172	0.657	1710.43	1124.28	0.113	1164.67	131.62
A_68_P26814988	chr9:108363033-108363077	NM_133744:206	Ccdc71	INSIDE	0.172	0.549	1732.60	951.35	0.094	1255.02	118.20
A_68_P31792968	chr18:67800428-67800477	NM_001081073:538	Cep76	INSIDE	0.172	0.670	1353.59	906.32	0.115	1046.08	120.56
A_68_P27551032	chr11:3166258-3166302	NM_007879:109	Drg1	INSIDE	0.172	0.690	3620.02	2497.50	0.118	2488.61	294.72
A_68_P30497082	chr15:102126996-102127044	NM_001014976:297	Espl1	INSIDE	0.172	0.619	1374.00	850.32	0.106	1125.71	119.88
A_68_P28493249	chr12:66067546-66067594	NM_177805:842	Fam179b	INSIDE	0.172	0.632	1670.05	1055.36	0.109	1100.07	119.66
A_68_P23607762	chr5:36807361-36807405	NM_024478:-451	Grpel1	PROMOTER	0.172	0.684	1366.16	935.00	0.118	985.94	115.89
A_68_P21628930	chr2:130109870-130109914	NM_130884:295	Idh3b	INSIDE	0.172	0.606	6715.17	4072.51	0.104	4499.49	469.42
A_68_P25656213	chr8:11556085-11556129	NM_011919:41	Ing1	INSIDE	0.172	0.477	1844.84	879.72	0.082	1463.77	120.37
A_68_P24381996	chr6:39156448-39156492	NM_001033430:302	Jhdm1d	INSIDE	0.172	0.497	4031.18	2004.31	0.085	2675.98	228.51
A_68_P27828607	chr11:57822062-57822109	NM_028451:-480	Larp1	PROMOTER	0.172	0.630	1418.58	893.35	0.108	1154.91	124.84
A_68_P25285304	chr7:91033159-91033207	NM_030705:-331	Mesdc1	DIVERGENT_PROMOTER	0.172	0.583	1623.03	945.70	0.100	1225.91	122.59
A_68_P32252894	chrX:10295292-10295336	NM_001166635:824	Mid1ip1	INSIDE	0.172	1.365	2864.83	3910.65	0.235	1086.57	255.37
A_68_P27555852	chr11:4035495-4035539	NR_037220:-3850	Mir3060	PROMOTER	0.172	0.532	1746.82	929.11	0.092	1272.87	116.62
A_68_P29689072	chr14:68701679-68701726	NM_010910:-238	Nefl	PROMOTER	0.172	1.428	1057.46	1510.57	0.245	821.26	201.25
A_68_P20937428	chr1:193141556-193141600	NM_025424:419	Nenf	INSIDE	0.172	0.636	1542.92	981.71	0.109	1296.83	141.61
A_68_P32134165	chr19:44825072-44825116	NM_011037:-6789	Pax2	PROMOTER	0.172	1.527	2932.08	4477.73	0.263	1876.06	492.54
A_68_P25666151	chr8:13104540-13104584	NM_178708:781	Pcid2	INSIDE	0.172	0.596	1830.38	1090.26	0.103	1440.76	147.81
A_68_P23393507	chr4:147661524-147661570	NM_001083342:528	Ptchd2	INSIDE	0.172	0.693	1340.86	929.17	0.119	1016.98	121.46
A_68_P24537774	chr6:71658275-71658319	NM_178608:622	Reep1	INSIDE	0.172	0.446	1735.98	773.43	0.077	1525.65	116.74

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P22871359	chr4:43395245-43395289	NM_001037709:413	Rusc2	INSIDE	0.172	0.676	1726.81	1166.66	0.116	1393.29	162.11
A_68_P27827566	chr11:57614919-57614965	NM_001081168:-196	Sap30l	PROMOTER	0.172	1.782	1897.59	3381.73	0.306	1183.28	361.79
A_68_P24092946	chr5:130731035-130731079	NM_023248:276	Sbds	INSIDE	0.172	0.644	5110.85	3292.95	0.111	3901.95	432.30
A_68_P31142314	chr17:31993086-31993130	NM_010831:-371	Sik1	PROMOTER	0.172	0.504	1973.59	994.89	0.087	1737.94	150.89
A_68_P31108361	chr17:26250094-26250138	NM_021793:-144	Tmem8	PROMOTER	0.172	0.673	1159.93	780.64	0.115	1061.02	122.53
A_68_P32320542	chrX:34414678-34414722	NM_019668:340	Ube2a	INSIDE	0.172	1.843	976.13	1798.99	0.317	387.01	122.84
A_68_P31257916	chr17:56856619-56856667	NM_178926:-298	Vmac	PROMOTER	0.172	3.875	7531.15	29185.39	0.666	4225.32	2812.82
A_68_P22394204	chr3:104765246-104765290	NM_009520:-641	Wnt2b	PROMOTER	0.172	0.649	1303.97	846.77	0.112	1058.28	118.00
A_68_P27541963	chr10:127984584-127984628	NM_134003:194	Zc3h10	INSIDE	0.172	1.435	2103.89	3018.19	0.247	1405.73	346.62
A_68_P24155790	chr5:144031255-144031299	NM_017467:425	Zfp316	INSIDE	0.172	0.612	1471.81	900.28	0.105	1108.29	116.69
A_68_P21426270	chr2:91895456-91895502	ENSMUST00000123840:4048		INSIDE	0.172	0.548	1484.59	813.23	0.094	1248.95	117.46
A_68_P24463220	chr6:54379822-54379866	NR_033635:371	9130019P16Rik	INSIDE	0.171	0.493	1713.98	844.41	0.084	1433.43	120.68
A_68_P26397642	chr9:30729620-30729675	NM_001024139:390	Adamts15	INSIDE	0.171	0.599	1573.92	943.39	0.102	1205.69	123.52
A_68_P27282647	chr10:79811365-79811409	NM_001113548:-195	Adamtsl5	DIVERGENT_PROMOTER	0.171	0.568	1666.32	946.24	0.097	1236.10	119.81
A_68_P27892735	chr11:68859244-68859288	NM_011496:122	Aurkb	INSIDE	0.171	0.425	3872.89	1647.01	0.073	2824.15	205.58
A_68_P32364064	chrX:45698666-45698710	NM_178782:4154	Bcorl1	INSIDE	0.171	2.431	1583.53	3850.12	0.415	827.91	343.61
A_68_P30388922	chr15:83357128-83357179	NM_007546:-138	Bik	PROMOTER	0.171	0.618	1537.68	950.90	0.106	1104.36	116.61
A_68_P29413818	chr14:13655644-13655688	NM_001042617:-73	Cadps	PROMOTER	0.171	0.411	2506.75	1031.03	0.070	2001.49	140.55
A_68_P32287127	chrX:19638262-19638306	NM_021715:1589	Chst7	INSIDE	0.171	1.581	875.30	1383.85	0.271	432.07	117.11
A_68_P32567796	chrX:99445717-99445761	NM_007709:1370	Cited1	INSIDE	0.171	1.639	980.81	1607.14	0.281	426.80	119.91
A_68_P24600270	chr6:84534486-84534530	NM_175475:9296	Cyp26b1	INSIDE	0.171	0.698	1418.90	989.91	0.119	1227.07	146.30
A_68_P20825279	chr1:172838779-172838823	NM_001029984:4272	Fcrlb	INSIDE	0.171	0.650	1961.31	1274.92	0.111	1504.44	167.14
A_68_P28083436	chr11:102978646-102978690	NM_138753:1030	Hexim1	INSIDE	0.171	0.598	1671.62	1000.41	0.102	1348.68	137.80
A_68_P23333247	chr4:135867486-135867530	NM_028871:618	Hnrnpr	INSIDE	0.171	0.698	3342.59	2331.65	0.119	2477.62	295.06
A_68_P23332244	chr4:135691181-135691230	NM_008321:-8531	Id3	PROMOTER	0.171	1.592	548.78	873.47	0.272	421.95	114.84
A_68_P25310385	chr7:97089281-97089328	NM_026304:391	l7Rn6	INSIDE	0.171	0.728	3396.19	2474.01	0.124	2516.93	312.98
A_68_P24993784	chr7:20109810-20109854	NM_027116:5753	Nkpd1	INSIDE	0.171	0.455	1981.77	901.20	0.078	1583.94	123.46
A_68_P25096457	chr7:53289487-53289535	NM_153057:445	Nomo1	INSIDE	0.171	0.658	1670.73	1098.71	0.112	1259.93	141.59
A_68_P20413377	chr1:88566126-88566173	NM_010933:999	Nppc	INSIDE	0.171	0.656	1373.05	901.25	0.112	1121.32	125.56
A_68_P21820250	chr2:164704772-164704816	NM_146129:-73	Pcif1	PROMOTER	0.171	0.620	1393.16	864.05	0.106	1130.88	120.09
A_68_P32464981	chrX:71069831-71069875	NM_001029868:456	Pdzd4	INSIDE	0.171	1.688	1122.43	1894.74	0.288	528.09	152.05
A_68_P24757362	chr6:113027834-113027882	NM_028385:226	Setd5	INSIDE	0.171	0.685	1325.64	907.99	0.117	1037.87	121.43
A_68_P29512055	chr14:32248911-32248955	NM_011894:287	Sh3bp5	INSIDE	0.171	0.372	2699.92	1005.53	0.064	1824.95	116.34
A_68_P28151694	chr11:115024434-115024480	NM_012030:-198	Slc9a3r1	PROMOTER	0.171	0.626	1464.21	916.70	0.107	1140.40	121.85
A_68_P31381748	chr17:80606129-80606175	NM_001195485:493	Srsf7	INSIDE	0.171	1.517	4212.40	6389.69	0.260	2651.26	689.30
A_68_P24817210	chr6:124779618-124779662	NM_013700:-175	Usp5	DIVERGENT_PROMOTER	0.171	0.594	2734.83	1623.20	0.102	1951.57	198.61
A_68_P32290858	chrX:20539135-20539180	NM_013840:-53	Uxt	DIVERGENT_PROMOTER	0.171	2.121	1155.39	2450.36	0.362	473.19	171.34
A_68_P30476456	chr15:98619939-98619989	NM_021279:-323	Wnt1	PROMOTER	0.171	1.510	678.62	1024.83	0.259	452.29	117.00
A_68_P30506408	chr16:3744081-3744125	NM_148924:4	Zfp263	INSIDE	0.171	0.548	2998.60	1643.21	0.094	2308.15	215.88
A_68_P24165134	chr5:146041748-146041800	NM_001081431:-2437	Zfp498	PROMOTER	0.171	0.552	1481.40	817.50	0.094	1286.94	121.57
A_68_P28818474	chr13:9763095-9763139	NM_001199141:1444	Zmynd11	INSIDE	0.171	0.476	2344.92	1117.22	0.081	1766.11	143.52
A_68_P25459708	chr7:125856496-125856541	NM_182995:394	6330503K22Rik	INSIDE	0.170	0.584	2112.61	1234.70	0.099	1517.05	150.82
A_68_P21630552	chr2:130406411-130406455	NM_009732:1845	Avp	INSIDE	0.170	0.685	1598.44	1095.20	0.116	1039.70	120.99
A_68_P30588544	chr16:20622405-20622449	NM_028420:-1075	Camk2n2	DIVERGENT_PROMOTER	0.170	0.624	1347.74	840.42	0.106	1107.61	117.49
A_68_P23455496	chr5:5380045-5380094	NM_011074:182	Cdk14	INSIDE	0.170	0.572	1663.32	951.24	0.097	1270.44	123.40
A_68_P23252016	chr4:120243027-120243071	NM_016748:-167	Ctps	PROMOTER	0.170	0.552	2445.91	1351.29	0.094	1616.25	151.68
A_68_P20863709	chr1:180336540-180336584	NM_026626:551	Efcab2	INSIDE	0.170	0.458	3807.40	1743.50	0.078	2925.00	227.43
A_68_P25766298	chr8:33994085-33994129	NM_001177589:66392	Gm3985	DOWNSTREAM	0.170	0.496	1919.57	952.71	0.084	1459.04	123.19
A_68_P23778715	chr5:69983278-69983322	NM_001038015:224	Gnpda2	INSIDE	0.170	0.698	2200.94	1535.44	0.118	1745.74	206.77
A_68_P20453277	chr1:94998219-94998263	NM_001110315:202	Kif1a	INSIDE	0.170	0.622	1535.58	955.02	0.106	1147.99	121.25
A_68_P25780627	chr8:36650640-36650684	NM_001081279:-189	Mfhas1	PROMOTER	0.170	0.626	1764.56	1105.26	0.106	1344.87	142.89

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P30476734	chr15:98661277-98661332	NM_016781:635	Prkag1	INSIDE	0.170	0.617	1471.75	907.61	0.105	1094.16	114.87
A_68_P23294616	chr4:128725929-128725973	NM_029219:-9564	Rnf19b	PROMOTER	0.170	0.668	1735.83	1159.41	0.114	1393.20	158.41
A_68_P23417944	chr4:151687118-151687162	NM_001033489:5594	Rnf207	INSIDE	0.170	0.716	3158.26	2259.78	0.122	2062.98	251.32
A_68_P27675741	chr11:29593764-29593808	NM_194051:13	Rtn4	INSIDE	0.170	0.606	3599.56	2180.48	0.103	2723.51	280.55
A_68_P28535262	chr12:74146492-74146537	NM_009189:1185	Six1	INSIDE	0.170	0.666	2732.43	1820.79	0.113	1938.38	219.78
A_68_P30955583	chr16:90220671-90220715	NM_011434:-294	Sod1	PROMOTER	0.170	0.566	1703.51	963.76	0.096	1208.35	116.14
A_68_P25094675	chr7:52970796-52970843	NM_020011:-242	Sphk2	PROMOTER	0.170	0.709	1390.39	986.07	0.120	974.67	117.26
A_68_P31123423	chr17:28758242-28758293	NM_016795:1132	Srpk1	INSIDE	0.170	0.582	1647.29	959.35	0.099	1251.97	123.87
A_68_P25388365	chr7:111650415-111650462	NM_001167828:5925	Trim30d	INSIDE	0.170	0.630	1362.31	857.84	0.107	1107.63	118.37
A_68_P21957615	chr3:14611165-14611209	NM_001099674:70	1810022K09Rik	INSIDE	0.169	1.627	10250.23	16677.58	0.275	6020.26	1657.59
A_68_P27752256	chr11:43589831-43589875	NM_007416:59982	Adra1b	INSIDE	0.169	0.528	1676.76	885.01	0.089	1353.69	120.75
A_68_P26035014	chr8:89994814-89994859	NM_019626:1655	Cbln1	INSIDE	0.169	0.540	1620.93	875.25	0.091	1331.72	121.85
A_68_P22861618	chr4:41261982-41262026	NM_026893:-70	Dcaf12	PROMOTER	0.169	0.636	1582.37	1006.29	0.108	1066.36	114.66
A_68_P31930375	chr19:5716486-5716534	NM_001114595:9807	Ehbp1l1	INSIDE	0.169	0.504	1845.37	929.82	0.085	1357.42	115.87
A_68_P30356904	chr15:77800920-77800964	NM_018749:312	Eif3d	INSIDE	0.169	0.429	2066.94	886.70	0.073	1592.48	115.63
A_68_P31948839	chr19:10257741-10257785	NM_146094:385	Fads1	INSIDE	0.169	0.606	2386.06	1446.42	0.103	1881.63	192.95
A_68_P20351043	chr1:74931488-74931534	NM_153111:472	Fev	INSIDE	0.169	0.476	2040.17	971.48	0.080	1514.48	121.80
A_68_P26065130	chr8:94880881-94880925	NM_018826:-792	Irx5	DIVERGENT_PROMOTER	0.169	0.542	4847.98	2627.21	0.092	3183.37	292.31
A_68_P22530170	chr3:130814530-130814579	NM_010703:1166	Lef1	INSIDE	0.169	0.713	1306.94	931.43	0.121	1001.02	120.63
A_68_P32470782	chrX:72376286-72376330	NM_008621:-20	Mpp1	PROMOTER	0.169	1.549	3268.88	5064.48	0.262	1340.62	350.77
A_68_P23545730	chr5:24605328-24605372	NM_145401:1110	Prkag2	INSIDE	0.169	1.411	1249.85	1763.50	0.238	925.14	220.40
A_68_P25842225	chr8:48619443-48619487	NM_203507:466	Rwdd4a	INSIDE	0.169	0.677	1489.95	1009.30	0.114	1051.65	120.14
A_68_P24061230	chr5:124874812-124874856	NM_001081203:1089	Sbno1	INSIDE	0.169	0.571	3945.66	2252.86	0.096	2651.15	255.52
A_68_P32127976	chr19:43748957-43749001	NM_145156:393	Slc25a28	INSIDE	0.169	0.510	1858.26	947.25	0.086	1352.81	116.60
A_68_P31712046	chr18:53405025-53405069	NM_029394:-269	Snx24	PROMOTER	0.169	0.490	1942.13	951.15	0.083	1472.37	122.03
A_68_P22199717	chr3:65196220-65196264	NM_026155:233	Ssr3	INSIDE	0.169	0.720	6823.25	4911.23	0.122	5046.74	613.64
A_68_P23278807	chr4:125879742-125879788	NM_146153:190	Thrap3	INSIDE	0.169	0.589	2022.15	1191.30	0.100	1432.91	142.76
A_68_P30160401	chr15:40487098-40487142	NM_011766:533	Zfpm2	INSIDE	0.169	0.680	1427.21	970.91	0.115	1061.15	121.88
A_68_P21099287	chr2:29606956-29607000	ENSMUST00000113812:-3415		PROMOTER	0.169	0.571	2010.71	1149.11	0.097	1494.34	144.52
A_68_P21810973	chr2:163029390-163029446	ENSMUST00000128999:-870		PROMOTER	0.169	0.742	2589.00	1921.38	0.125	1850.47	232.05
A_68_P26422477	chr9:35228776-35228820	ENSMUST00000137200:-340		PROMOTER	0.169	0.482	1846.88	890.69	0.081	1481.20	120.43
A_68_P27675036	chr11:29447352-29447406	NM_001163521:-571	1700034F02Rik	PROMOTER	0.168	0.691	1265.71	874.46	0.116	1063.16	123.63
A_68_P27332753	chr10:89194937-89194988	NM_025914:78	Actr6	INSIDE	0.168	0.521	1795.15	935.48	0.087	1382.16	120.83
A_68_P32186057	chr19:54120878-54120926	NM_007417:1231	Adra2a	INSIDE	0.168	0.536	1918.46	1027.47	0.090	1372.09	123.73
A_68_P28025143	chr11:92961409-92961453	NM_028296:827	Car10	INSIDE	0.168	1.628	4195.42	6831.32	0.273	2752.95	752.64
A_68_P21583233	chr2:121692537-121692581	NM_001205369:-147	Casc4	PROMOTER	0.168	0.650	1582.77	1029.49	0.109	1109.67	121.50
A_68_P24078736	chr5:128113050-128113094	NM_177005:441	Glt1d1	INSIDE	0.168	0.527	2456.25	1293.46	0.089	1862.68	164.85
A_68_P24156212	chr5:144125779-144125823	NM_133355:214	Grid2ip	INSIDE	0.168	0.457	2012.18	919.98	0.077	1609.33	123.26
A_68_P24186282	chr5:150438837-150438890	NM_013559:27	Hsph1	INSIDE	0.168	0.493	2255.05	1112.39	0.083	1597.19	132.49
A_68_P21137835	chr2:35960385-35960443	NM_001083126:-834	Lhx6	PROMOTER	0.168	0.634	1477.68	937.11	0.106	1118.38	119.09
A_68_P21137750	chr2:35949963-35950016	NM_001083126:9591	Lhx6	INSIDE	0.168	0.657	1695.06	1113.25	0.110	1196.99	132.17
A_68_P32318077	chrX:33870275-33870326	NM_028894:1897	Lonrf3	INSIDE	0.168	1.844	973.19	1794.96	0.309	378.95	117.19
A_68_P31130465	chr17:30025201-30025252	NM_001081160:-399	Mdga1	PROMOTER	0.168	0.458	2153.69	986.16	0.077	1512.45	116.44
A_68_P31151559	chr17:34162253-34162297	NR_029800:-237	Mir219-1	PROMOTER	0.168	0.640	2005.53	1284.41	0.108	1479.66	159.47
A_68_P30977847	chr16:93832195-93832251	NM_001045529:-143	Morc3	PROMOTER	0.168	0.605	1539.24	931.50	0.101	1154.19	117.05
A_68_P32696398	chrX:136406178-136406222	NM_001193309:-7	Morc4	PROMOTER	0.168	1.980	2753.63	5451.06	0.332	1044.26	346.92
A_68_P27969034	chr11:82721872-82721916	NM_145431:3	Nle1	INSIDE	0.168	0.593	1655.59	981.13	0.100	1210.24	120.73
A_68_P30728923	chr16:45844322-45844366	NM_153412:147	Phldb2	INSIDE	0.168	0.559	4648.33	2598.67	0.094	3381.44	318.14
A_68_P22518740	chr3:128916656-128916700	NM_001042502:-176	Pitx2	PROMOTER	0.168	0.372	2754.32	1024.02	0.062	2008.37	125.52
A_68_P27568393	chr11:6315493-6315540	NM_008907:-356	Ppia	PROMOTER	0.168	0.679	1431.78	972.87	0.114	1044.41	119.53
A_68_P27840803	chr11:59919168-59919212	NM_009021:676	Rai1	INSIDE	0.168	0.674	5339.83	3600.58	0.113	4163.27	470.39

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P24777650	chr6:116623776-116623820	NM_178045:56	Rassf4	INSIDE	0.168	0.732	1966.25	1439.87	0.123	1437.39	176.71
A_68_P27096531	chr10:42481959-42482003	NM_153055:679	Sec63	INSIDE	0.168	2.489	2830.36	7045.36	0.418	1743.99	728.62
A_68_P20559395	chr1:121809675-121809721	NM_175106:47	Tmem177	INSIDE	0.168	0.682	1364.17	931.04	0.115	1013.87	116.17
A_68_P31257917	chr17:56856713-56856757	NM_178926:-390	Vmac	PROMOTER	0.168	2.180	6992.44	15243.02	0.367	4178.40	1532.51
A_68_P30476477	chr15:98622390-98622434	NM_021279:2125	Wnt1	INSIDE	0.168	0.584	3621.06	2114.93	0.098	2609.51	256.64
A_68_P24164946	chr5:145992407-145992453	NM_001083958:-153	Zfp655	PROMOTER	0.168	0.497	1853.86	920.47	0.083	1411.20	117.60
A_68_P31129448	chr17:29854041-29854085	NM_001163741:-100	1110021J02Rik	PROMOTER	0.167	1.646	4708.75	7749.57	0.275	3153.45	868.55
A_68_P22350134	chr3:96402650-96402694	NM_001024851:2114	Ankrd34a	INSIDE	0.167	0.582	1875.84	1091.15	0.097	1435.18	139.49
A_68_P27892738	chr11:68859556-68859600	NM_011496:434	Aurkb	INSIDE	0.167	0.703	1338.53	941.36	0.117	999.22	117.24
A_68_P21087495	chr2:27742216-27742260	NM_015734:294	Col5a1	INSIDE	0.167	0.528	2987.33	1576.89	0.088	2176.71	191.99
A_68_P28186436	chr11:120588411-120588455	NM_026428:163	Dcxr	INSIDE	0.167	0.732	3076.87	2253.17	0.122	2260.95	276.71
A_68_P27212431	chr10:66999287-66999333	NM_010118:-1306	Egr2	PROMOTER	0.167	0.567	1741.96	987.37	0.095	1249.12	118.39
A_68_P28054685	chr11:98010627-98010671	NM_028149:282	Fbxl20	INSIDE	0.167	0.494	2679.41	1323.04	0.082	2056.77	169.66
A_68_P21107212	chr2:30996536-30996580	NM_001038700:970	Fnbp1	INSIDE	0.167	0.663	1847.81	1224.67	0.111	1328.38	146.85
A_68_P23892218	chr5:92512396-92512440	NM_001080797:-475	G3bp2	PROMOTER	0.167	0.609	1476.13	898.72	0.102	1127.90	114.73
A_68_P21059052	chr2:22479080-22479124	NM_008078:1256	Gad2	INSIDE	0.167	0.475	1994.87	948.28	0.079	1525.06	120.88
A_68_P32383359	chrX:49965740-49965784	NM_016697:1389	Gpc3	INSIDE	0.167	1.414	1187.23	1678.79	0.237	505.04	119.52
A_68_P24864941	chr6:135015515-135015567	NM_181444:-139	Gprc5a	PROMOTER	0.167	0.528	1948.37	1028.07	0.088	1360.19	119.65
A_68_P24589801	chr6:82723921-82723966	NM_013820:505	Hk2	INSIDE	0.167	0.689	1467.27	1011.14	0.115	1037.19	119.63
A_68_P21550148	chr2:115887946-115888001	NM_001159569:2384	Meis2	INSIDE	0.167	0.631	1793.58	1132.21	0.105	1249.50	131.44
A_68_P25285350	chr7:91040523-91040567	NM_023403:35	Mesdc2	INSIDE	0.167	0.650	4459.46	2898.61	0.108	3202.79	347.19
A_68_P30532724	chr16:8471150-8471194	NM_146247:267	Mettl22	INSIDE	0.167	0.473	2176.31	1028.99	0.079	1670.76	131.59
A_68_P25993842	chr8:81819240-81819295	NM_133823:-412	Mmaa	PROMOTER	0.167	0.521	1868.13	972.73	0.087	1329.92	115.54
A_68_P22567224	chr3:137806385-137806429	NM_001163457:-54	Mttp	DIVERGENT_PROMOTER	0.167	0.709	1704.46	1209.28	0.118	1202.05	142.29
A_68_P21350023	chr2:76245283-76245327	NM_145525:710	Osbpl6	INSIDE	0.167	0.389	2506.16	976.01	0.065	2061.98	133.94
A_68_P26554816	chr9:59528311-59528358	NM_011099:23920	Pkm2	DOWNSTREAM	0.167	0.386	2290.30	885.07	0.065	1808.73	116.99
A_68_P22778523	chr4:22417085-22417134	NM_008899:-1831	Pou3f2	PROMOTER	0.167	0.506	1795.29	908.22	0.084	1394.05	117.56
A_68_P21110357	chr2:31492430-31492474	NM_001123362:-3104	Prdm12	PROMOTER	0.167	0.396	2719.63	1075.85	0.066	1892.23	125.35
A_68_P26463567	chr9:43552486-43552530	NM_021424:-150	Pvrl1	PROMOTER	0.167	0.447	2032.39	908.61	0.075	1611.49	120.60
A_68_P20878433	chr1:182834482-182834526	NM_133705:100	Pycr2	INSIDE	0.167	0.622	1580.89	983.05	0.104	1154.60	120.26
A_68_P24773074	chr6:115758230-115758281	NR_028546:-134	Snora7a	PROMOTER	0.167	0.586	1450.14	849.60	0.098	1209.77	118.50
A_68_P25959791	chr8:74658901-74658954	NM_001001491:-263	Tpm4	PROMOTER	0.167	1.576	620.44	977.71	0.263	457.97	120.45
A_68_P32540977	chrX:92391918-92391962	ENSMUST00000113884:220		INSIDE	0.167	1.672	2390.20	3995.39	0.280	931.13	260.53
A_68_P31341458	chr17:72953415-72953461	NM_007439:209	Alk	INSIDE	0.166	0.460	2298.82	1057.21	0.076	1553.46	118.26
A_68_P26074973	chr8:96535729-96535781	NM_011787:786	Amfr	INSIDE	0.166	0.400	3487.11	1395.55	0.067	2481.13	165.01
A_68_P30010833	chr15:10415572-10415616	NM_026396:98	Brix1	INSIDE	0.166	0.685	1910.79	1308.77	0.113	1330.06	150.94
A_68_P30836892	chr16:67620668-67620712	NM_001145977:463	Cadm2	INSIDE	0.166	1.518	991.00	1504.13	0.251	720.76	181.25
A_68_P29618485	chr14:56179012-56179056	NM_001199009:-725	Dcaf11	PROMOTER	0.166	0.603	1791.88	1081.12	0.100	1229.70	123.35
A_68_P24218884	chr6:6831933-6831977	NM_010056:114	Dlx5	INSIDE	0.166	0.630	1786.61	1125.89	0.105	1214.20	127.35
A_68_P24992779	chr7:19930361-19930405	NM_001127324:-37	Ercc1	PROMOTER	0.166	0.644	1912.46	1231.67	0.107	1333.04	142.09
A_68_P21575069	chr2:120229642-120229686	NM_172672:33	Ganc	INSIDE	0.166	0.594	2214.61	1315.25	0.098	1757.52	172.83
A_68_P20941839	chr1:193961046-193961090	NR_033536:289	Gm10516	INSIDE	0.166	0.538	4764.51	2565.43	0.090	3621.27	324.58
A_68_P24038673	chr5:120882123-120882167	NM_008499:250	Lhx5	INSIDE	0.166	0.539	1776.36	957.52	0.089	1337.60	119.65
A_68_P20723959	chr1:154802284-154802330	NM_175460:76	Nmnat2	INSIDE	0.166	0.705	1302.24	918.59	0.117	1007.86	117.88
A_68_P28397152	chr12:45370530-45370574	NM_026164:412	Pnpla8	INSIDE	0.166	0.655	1701.23	1113.60	0.109	1094.96	119.04
A_68_P25435182	chr7:121419370-121419414	NM_011965:238	Psma1	INSIDE	0.166	0.501	1843.87	923.12	0.083	1452.26	120.89
A_68_P24829778	chr6:126889168-126889219	NM_009013:380	Rad51ap1	INSIDE	0.166	0.500	2037.07	1018.09	0.083	1424.51	118.04
A_68_P25587465	chr7:148401434-148401478	NM_025886:-302	Rassf7	DIVERGENT_PROMOTER	0.166	0.605	1453.65	879.77	0.100	1148.80	115.26
A_68_P21833062	chr2:166821989-166822037	NM_001109905:-234	Stau1	PROMOTER	0.166	0.659	1422.26	937.41	0.110	1113.63	122.03
A_68_P26036157	chr8:90184552-90184597	NM_033327:298920	Zfp423	DOWNSTREAM	0.166	0.616	1439.35	886.32	0.102	1138.78	116.10
A_68_P31148787	chr17:33495685-33495729	NM_207541:117	Zfp81	INSIDE	0.166	0.496	1792.46	889.21	0.082	1430.98	117.67

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P32134054	chr19:44809087-44809144			Unknown	0.166	0.665	2890.85	1921.37	0.110	2049.66	225.64
A_68_P24034672	chr5:120246641-120246685	AK006202:11216		DOWNSTREAM	0.166	0.522	1786.04	931.97	0.087	1345.32	116.79
A_68_P26018705	chr8:86721688-86721732	AK089363:-3057		PROMOTER	0.166	0.650	1492.48	970.20	0.108	1118.05	120.90
A_68_P23167115	chr4:103292261-103292306	ENSMUST00000106827:14		INSIDE	0.166	1.460	3950.81	5767.65	0.242	2734.12	661.65
A_68_P23259661	chr4:122563178-122563222	NM_007598:-76	Cap1	PROMOTER	0.165	0.622	1470.39	914.75	0.102	1174.15	120.25
A_68_P22319259	chr3:89221857-89221906	NM_016904:332	Cks1b	INSIDE	0.165	1.891	3058.36	5784.20	0.312	2099.25	654.19
A_68_P25430847	chr7:120657214-120657258	NM_026143:-139	Far1	PROMOTER	0.165	1.424	2227.29	3170.93	0.235	1609.66	377.51
A_68_P28158447	chr11:116144333-116144377	NM_010254:2102	Galr2	INSIDE	0.165	0.541	1652.92	894.54	0.089	1276.44	113.98
A_68_P21903066	chr2:180068973-180069017	NM_008093:390	Gata5	INSIDE	0.165	0.604	1416.62	855.66	0.099	1186.31	117.92
A_68_P26035034	chr8:89997077-89997121	NR_033430:388	Gm2694	INSIDE	0.165	0.630	3175.04	2001.39	0.104	2212.28	229.59
A_68_P27280642	chr10:79516583-79516627	NM_001037741:-177	Gpx4	PROMOTER	0.165	0.306	3440.50	1053.80	0.051	2600.79	131.41
A_68_P27452135	chr10:111410230-111410274	NM_178610:502	Krr1	INSIDE	0.165	1.345	2836.31	3815.35	0.222	1978.99	439.64
A_68_P24152505	chr5:143084497-143084543	NM_175217:186	Mmd2	INSIDE	0.165	0.645	1646.80	1062.90	0.107	1105.43	117.73
A_68_P25581952	chr7:147234431-147234477	NM_010836:533	Msx3	INSIDE	0.165	0.681	2794.24	1902.77	0.112	1971.31	221.10
A_68_P21826986	chr2:165818945-165818989	NM_008679:830	Ncoa3	INSIDE	0.165	1.974	6308.14	12453.14	0.327	4331.62	1414.75
A_68_P32134210	chr19:44830843-44830902	NM_011037:-1011	Pax2	PROMOTER	0.165	0.489	1882.38	920.56	0.081	1460.59	118.05
A_68_P21114132	chr2:32091883-32091928	NM_145145:-297	Pomt1	PROMOTER	0.165	0.584	1824.95	1065.34	0.096	1301.02	125.19
A_68_P28223702	chr12:8680649-8680696	NM_001160221:-267	Pum2	PROMOTER	0.165	0.697	1143.84	796.86	0.115	1045.99	120.19
A_68_P26345409	chr9:20896597-20896641	NR_038081:-166	Raver1-fdx1l	PROMOTER	0.165	0.695	1766.46	1226.87	0.114	1290.26	147.57
A_68_P20616246	chr1:133423879-133423923	NM_001081011:38	Srgap2	INSIDE	0.165	0.750	5910.20	4432.85	0.123	4115.64	507.99
A_68_P23395328	chr4:147965305-147965349	NM_009272:-295	Srm	PROMOTER	0.165	0.681	2347.57	1598.71	0.112	1660.23	186.30
A_68_P25952984	chr8:73133754-73133798	NM_133772:-1563	Ssbp4	DIVERGENT_PROMOTER	0.165	0.728	1875.54	1364.47	0.120	1483.08	178.43
A_68_P21017267	chr2:13496235-13496279	NM_011701:319	Vim	INSIDE	0.165	0.620	1830.73	1134.17	0.102	1388.10	142.16
A_68_P30019878	chr15:12047227-12047275	NM_011767:-355	Zfr	PROMOTER	0.165	1.476	2159.40	3187.97	0.243	1475.39	359.07
A_68_P31465574	chr18:4921738-4921782	ENSMUST00000143254:37		INSIDE	0.165	0.594	2751.14	1634.80	0.098	2137.33	209.64
A_68_P31467178	chr18:5163541-5163591	ENSMUST00000150337:2163		INSIDE	0.165	0.569	2075.83	1180.43	0.094	1567.70	147.19
A_68_P30284259	chr15:64753330-64753385	NM_009623:501	Adcy8	INSIDE	0.164	0.614	1507.56	925.75	0.101	1182.61	119.05
A_68_P28041223	chr11:95720113-95720157	NM_008081:56051	B4galnt2	DOWNSTREAM	0.164	0.706	3433.64	2424.23	0.116	2318.82	268.57
A_68_P32050469	chr19:29065228-29065272	NM_025950:267	Cdc37l1	INSIDE	0.164	0.678	2356.73	1598.79	0.111	1781.24	197.88
A_68_P22318235	chr3:89070608-89070657	NM_026767:159	Dpm3	INSIDE	0.164	0.715	1680.15	1200.62	0.117	1150.04	134.93
A_68_P24607723	chr6:85978919-85978963	NM_012013:11756	Figla	DOWNSTREAM	0.164	0.503	1886.70	948.48	0.082	1424.37	117.35
A_68_P23331442	chr4:135519710-135519754	NM_178389:-1347	Gale	PROMOTER	0.164	0.634	4490.02	2844.55	0.104	2903.65	301.49
A_68_P20864287	chr1:180457911-180457955	NM_001161665:-1323	Kif26b	PROMOTER	0.164	0.495	2357.97	1166.98	0.081	1885.46	153.30
A_68_P25101649	chr7:54101500-54101544	NM_001136069:-929	Ldha	PROMOTER	0.164	0.529	1557.57	823.47	0.087	1395.24	120.98
A_68_P27998472	chr11:88017697-88017741	NM_024174:-201	Mrps23	PROMOTER	0.164	0.710	2072.68	1470.72	0.116	1545.59	179.32
A_68_P28875775	chr13:22098833-22098877	NM_019429:2756	Prss16	INSIDE	0.164	0.624	1531.19	955.62	0.102	1187.08	121.26
A_68_P30979595	chr16:94346850-94346894	NM_011377:261368	Sim2	INSIDE	0.164	0.696	2233.47	1553.92	0.114	1799.55	205.68
A_68_P20354640	chr1:75518210-75518265	NM_027886:134	Stk11ip	INSIDE	0.164	0.460	2161.70	993.42	0.076	1600.44	120.99
A_68_P29141047	chr13:73764398-73764442	NM_009354:-28	Tert	PROMOTER	0.164	1.730	2630.18	4549.43	0.284	1706.64	484.87
A_68_P31161200	chr17:35975270-35975315	NM_011655:-46	Tubb5	DIVERGENT_PROMOTER	0.164	0.643	1931.59	1241.20	0.105	1407.87	147.99
A_68_P25670550	chr8:13785336-13785380	NM_025924:-256	Upf3a	PROMOTER	0.164	0.418	2270.42	949.67	0.069	1798.70	123.76
A_68_P30471848	chr15:97738946-97738998	NM_009504:-245	Vdr	PROMOTER	0.164	0.620	1669.97	1035.46	0.102	1209.23	123.13
A_68_P29672988	chr14:65977163-65977207	NM_199029:-328	Zfp395	PROMOTER	0.164	0.706	1716.30	1210.95	0.116	1424.76	164.68
A_68_P31620729	chr18:36049726-36049770			Unknown	0.164	0.493	2169.01	1068.59	0.081	1509.50	121.87
A_68_P21567192	chr2:118798592-118798636	AK184532:45454		INSIDE	0.164	0.644	1479.09	952.29	0.106	1159.91	122.42
A_68_P31992375	chr19:18745959-18746006	NM_026120:713	2410127L17Rik	INSIDE	0.163	0.490	1897.14	929.53	0.080	1429.31	113.89
A_68_P26569958	chr9:62189997-62190041	NM_009672:869	Anp32a	INSIDE	0.163	0.550	2442.60	1342.26	0.090	1711.46	153.46
A_68_P26035016	chr8:89994962-89995006	NM_019626:1507	Cbln1	INSIDE	0.163	0.547	1863.52	1019.39	0.089	1317.44	117.26
A_68_P30349757	chr15:76490222-76490266	NM_019396:247	Cyhr1	INSIDE	0.163	0.651	2882.75	1876.43	0.106	1975.22	208.99
A_68_P29699033	chr14:70479382-70479426	NM_018781:2153	Egr3	INSIDE	0.163	0.460	2042.28	938.77	0.075	1575.72	118.15
A_68_P28602893	chr12:86560681-86560733	NM_145445:244	Eif2b2	INSIDE	0.163	0.438	2476.38	1084.81	0.071	1621.67	115.92

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27937914	chr11:77306484-77306528	NM_001004144:-407	Git1	DIVERGENT_PROMOTER	0.163	0.318	3524.28	1120.61	0.052	2433.98	126.21
A_68_P23352769	chr4:139130258-139130302	NM_001205173:-354	Iffo2	PROMOTER	0.163	0.602	1547.58	931.48	0.098	1193.31	117.01
A_68_P24817384	chr6:124806960-124807011	NM_013534:720	Leprel2	INSIDE	0.163	0.560	1692.23	947.48	0.091	1288.16	117.63
A_68_P23185679	chr4:106323706-106323750	NM_001083887:55	Pars2	INSIDE	0.163	0.566	2228.52	1261.77	0.092	1438.05	132.66
A_68_P29047306	chr13:54167631-54167675	NM_027324:439	Sfxn1	INSIDE	0.163	0.584	1716.87	1002.57	0.095	1252.42	119.43
A_68_P21395956	chr2:84877845-84877892	NM_001136081:261	Ssrp1	INSIDE	0.163	1.640	519.38	851.92	0.268	445.15	119.23
A_68_P23189068	chr4:106851270-106851320	NM_029565:60	Tmem59	INSIDE	0.163	0.533	2035.46	1084.33	0.087	1406.85	122.20
A_68_P31644532	chr18:40378757-40378801	NM_023311:275	Yipf5	INSIDE	0.163	1.778	6506.46	11569.67	0.289	4385.35	1267.87
A_68_P31323669	chr17:69733337-69733381	NM_009547:41	Zfp161	INSIDE	0.163	0.592	1683.35	996.60	0.096	1209.57	116.53
A_68_P32115178	chr19:41558052-41558105	ENSMUST00000067795:952		INSIDE	0.163	1.742	1442.57	2513.25	0.285	942.70	268.33
A_68_P26505579	chr9:50583333-50583384	NM_133981:-76	Alg9	PROMOTER	0.162	0.588	1731.65	1018.31	0.095	1203.41	114.79
A_68_P25833744	chr8:47085514-47085558	NM_001039562:-332	Ankrd37	PROMOTER	0.162	0.659	6235.37	4107.47	0.107	4090.02	436.65
A_68_P21075527	chr2:25838017-25838061	NM_001115076:764	Camsap1	INSIDE	0.162	0.734	3121.54	2289.68	0.119	2110.39	250.73
A_68_P30589277	chr16:20733808-20733856	NM_009893:633	Chrd	INSIDE	0.162	0.569	1908.64	1086.20	0.092	1314.14	121.00
A_68_P29033460	chr13:51741130-51741185	NM_025415:557	Cks2	INSIDE	0.162	0.568	1872.70	1063.29	0.092	1323.90	121.98
A_68_P20794596	chr1:167389914-167389958	NM_028759:658	Dcaf6	INSIDE	0.162	0.535	1923.31	1029.17	0.087	1345.78	116.58
A_68_P32135378	chr19:45005914-45005958	NM_001081225:328	Fam178a	INSIDE	0.162	1.620	2180.75	3532.95	0.262	1585.12	415.47
A_68_P31357838	chr17:75951190-75951234	NM_133747:74	Fam98a	INSIDE	0.162	0.671	1504.50	1009.87	0.109	1106.13	120.44
A_68_P29448411	chr14:21514995-21515039	NM_028428:827	Fut11	INSIDE	0.162	0.621	2215.40	1375.21	0.100	1696.01	170.16
A_68_P23438376	chr4:154771887-154771931	NM_008072:270	Gabrd	INSIDE	0.162	0.539	1732.08	933.40	0.087	1431.60	124.88
A_68_P30849202	chr16:70314865-70314917	NM_028803:559	Gbe1	INSIDE	0.162	0.642	1707.73	1097.06	0.104	1161.22	120.54
A_68_P31373925	chr17:79234724-79234768	NM_001081179:-25	Heatr5b	DIVERGENT_PROMOTER	0.162	0.613	1688.00	1035.56	0.100	1290.76	128.53
A_68_P31150129	chr17:33822024-33822068	NM_001109913:357	Hnrnpm	INSIDE	0.162	0.528	1867.53	986.84	0.086	1526.06	130.80
A_68_P26026699	chr8:88364441-88364485	NM_028007:386	Itfg1	INSIDE	0.162	0.527	1729.81	911.22	0.085	1423.62	121.35
A_68_P30290897	chr15:66117445-66117492	NM_152923:318	Kcnq3	INSIDE	0.162	0.628	1729.08	1085.51	0.102	1184.62	120.64
A_68_P26805730	chr9:106793972-106794020	NM_029103:273	Manf	INSIDE	0.162	0.726	1691.90	1229.03	0.117	1236.20	145.19
A_68_P26463578	chr9:43553721-43553771	NM_021424:1088	Pvrl1	INSIDE	0.162	0.686	1618.63	1111.18	0.111	1081.26	120.43
A_68_P22315263	chr3:88520957-88521001	NM_001163310:203	Rit1	INSIDE	0.162	0.399	4190.98	1670.30	0.065	3125.81	202.04
A_68_P23201330	chr4:109148797-109148841	NM_013876:292	Rnf11	INSIDE	0.162	0.553	1864.00	1030.94	0.090	1367.47	122.82
A_68_P26442128	chr9:40076808-40076852	NM_001083917:30	Scn3b	INSIDE	0.162	0.495	2012.11	996.61	0.080	1520.69	121.77
A_68_P24992393	chr7:19856667-19856716	NM_009499:512	Vasp	INSIDE	0.162	1.495	1320.58	1974.31	0.242	944.98	228.85
A_68_P30641651	chr16:30388272-30388316	NM_001128094:322	Atp13a3	INSIDE	0.161	0.634	1567.10	994.05	0.102	1204.28	122.65
A_68_P22322690	chr3:89767430-89767474	NM_001081182:-22	Atp8b2	PROMOTER	0.161	0.673	2283.87	1538.14	0.109	1457.85	158.39
A_68_P20827008	chr1:173200751-173200795	NM_020579:314	B4galt3	INSIDE	0.161	0.461	2298.72	1059.57	0.074	1584.77	117.29
A_68_P31157817	chr17:35272686-35272730	NM_057171:522	Bag6	INSIDE	0.161	0.451	2178.45	982.58	0.073	1588.13	115.64
A_68_P30381572	chr15:81958155-81958201	NM_172428:-173	Ccdc134	PROMOTER	0.161	0.544	2619.49	1425.71	0.088	1801.50	157.69
A_68_P23195896	chr4:108079185-108079229	NM_024198:112	Gpx7	INSIDE	0.161	0.629	1653.33	1039.44	0.101	1128.72	113.93
A_68_P28834522	chr13:13682471-13682515	NM_010748:-183	Lyst	PROMOTER	0.161	0.482	2052.21	988.96	0.078	1560.66	121.27
A_68_P31055437	chr17:13109036-13109080	NM_026310:-101	Mrpl18	DIVERGENT_PROMOTER	0.161	0.518	1969.15	1019.98	0.083	1380.44	115.13
A_68_P20188964	chr1:43503293-43503346	NM_010879:724	Nck2	INSIDE	0.161	0.474	2440.58	1157.83	0.077	1623.29	124.31
A_68_P30397300	chr15:84685696-84685740	NM_001081166:841	Phf21b	INSIDE	0.161	1.372	1438.57	1974.32	0.221	931.51	205.95
A_68_P25728675	chr8:26830785-26830829	NM_028000:287	Ppapdc1b	INSIDE	0.161	0.576	1848.70	1064.49	0.093	1341.83	124.14
A_68_P32374349	chrX:48372156-48372200	NM_172413:-983	Rap2c	PROMOTER	0.161	1.550	916.33	1420.77	0.249	484.48	120.83
A_68_P27165510	chr10:58276430-58276477	NM_172788:347	Sh3rf3	INSIDE	0.161	0.566	2763.45	1563.59	0.091	1999.48	182.00
A_68_P23543621	chr5:24236647-24236691	NM_001081441:-170	Wdr86	PROMOTER	0.161	0.650	1490.59	968.61	0.105	1131.20	118.30
A_68_P25082978	chr7:50817824-50817869	NM_001008549:107	Zfp658	INSIDE	0.161	0.595	1693.69	1008.10	0.096	1244.50	119.40
A_68_P30337603	chr15:74348034-74348078	NM_174991:1431	Bai1	INSIDE	0.160	0.511	2107.94	1077.42	0.082	1478.80	120.66
A_68_P21905703	chr2:180445288-180445335	NM_177852:-607	Dido1	DIVERGENT_PROMOTER	0.160	0.625	1566.59	979.57	0.100	1159.82	116.26
A_68_P28036771	chr11:94981735-94981779	NM_010055:326	Dlx3	INSIDE	0.160	0.694	1430.45	992.60	0.111	1064.15	118.07
A_68_P22318336	chr3:89084785-89084834	NM_010107:-1242	Efna1	PROMOTER	0.160	0.626	1735.52	1086.78	0.100	1236.35	123.95
A_68_P21573668	chr2:119980528-119980572	NM_133838:-239	Ehd4	PROMOTER	0.160	0.456	2041.22	930.87	0.073	1609.40	117.49

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P28865537	chr13:20182539-20182583	NM_080288:185	Elmo1	INSIDE	0.160	0.428	3567.37	1526.30	0.068	2815.55	192.78
A_68_P26132614	chr8:107793016-107793064	NM_015821:4493	Fbxl8	INSIDE	0.160	0.555	2094.84	1162.85	0.089	1370.76	121.96
A_68_P21071264	chr2:25160798-25160842	NM_001177656:13863	Grin1	INSIDE	0.160	0.513	3294.87	1691.13	0.082	2379.11	195.48
A_68_P29668829	chr14:65271192-65271238	NM_001081177:-153	Kif13b	PROMOTER	0.160	0.493	1794.03	885.17	0.079	1495.33	118.26
A_68_P23439844	chr4:155027433-155027477	NM_011985:39	Mmp23	INSIDE	0.160	0.664	1677.61	1114.23	0.106	1142.94	121.64
A_68_P23894274	chr5:92863985-92864029	NM_183392:219	Nup54	INSIDE	0.160	0.580	1668.34	968.02	0.093	1240.45	115.41
A_68_P30558433	chr16:13668026-13668070	NM_028761:215	Parn	INSIDE	0.160	0.541	1759.66	952.82	0.087	1443.54	124.88
A_68_P20642550	chr1:137815675-137815719	NM_019645:-95	Pkp1	PROMOTER	0.160	0.550	3846.71	2116.20	0.088	2820.11	247.88
A_68_P21490975	chr2:104656460-104656504	NM_001123327:371	Qser1	INSIDE	0.160	0.714	1495.29	1068.21	0.114	1076.84	122.90
A_68_P31024850	chr17:7374080-7374124	NM_011299:-361	Rps6ka2	PROMOTER	0.160	0.483	2850.15	1375.90	0.077	2241.33	173.47
A_68_P22215796	chr3:68298884-68298928	NR_036665:792	Schip1	INSIDE	0.160	0.506	5750.71	2909.70	0.081	4159.49	336.40
A_68_P21133064	chr2:35192370-35192414	NM_013515:137	Stom	INSIDE	0.160	0.652	1567.37	1021.47	0.104	1175.73	122.53
A_68_P29455893	chr14:22807230-22807274	NM_145459:1571	Zfp503	INSIDE	0.160	0.467	2433.51	1135.41	0.075	1945.26	145.44
A_68_P22360097	chr3:98232384-98232428	NM_172863:46003	Zfp697	INSIDE	0.160	0.498	1747.31	870.94	0.080	1458.40	116.57
A_68_P23195050	chr4:107890175-107890219	NM_001167936:331	Zyg11a	INSIDE	0.160	0.678	2288.46	1552.64	0.109	2011.46	218.44
A_68_P23589615	chr5:33883046-33883098			Unknown	0.160	1.472	2731.97	4022.19	0.236	1954.10	461.01
A_68_P31013267	chr17:4908022-4908066	AK186662:127801		INSIDE	0.160	0.512	1840.97	943.47	0.082	1439.02	117.66
A_68_P26467844	chr9:44291603-44291647	ENSMUST00000136322:4764		DOWNSTREAM	0.160	0.735	2618.75	1924.97	0.118	1740.72	204.83
A_68_P28050588	chr11:97302102-97302146	NM_021493:-9349	Arhgap23	PROMOTER	0.159	0.685	1509.05	1033.98	0.109	1098.69	119.55
A_68_P22859653	chr4:40895771-40895815	NM_029814:207	Chmp5	INSIDE	0.159	0.656	2943.86	1930.79	0.104	2197.19	228.71
A_68_P30588476	chr16:20611624-20611668	NM_025462:-27	Ece2	DIVERGENT_PROMOTER	0.159	0.612	1636.15	1001.51	0.098	1193.98	116.53
A_68_P24533906	chr6:70906262-70906307	NM_001101464:-315	Foxi3	PROMOTER	0.159	0.633	3695.05	2340.27	0.101	2582.63	260.88
A_68_P31213681	chr17:47831661-47831705	NM_144939:-473	Frs3	DIVERGENT_PROMOTER	0.159	0.476	6187.53	2944.19	0.076	3978.62	301.12
A_68_P31260063	chr17:57245094-57245138	NR_033508:249	Gm11110	INSIDE	0.159	0.691	1609.13	1112.43	0.110	1085.37	119.30
A_68_P22187974	chr3:62407714-62407758	NM_177346:1326	Gpr149	INSIDE	0.159	0.555	1639.45	910.62	0.088	1377.95	121.42
A_68_P32090697	chr19:36628656-36628700	NM_001163471:-450	Hectd2	PROMOTER	0.159	0.673	1365.57	918.67	0.107	1113.34	118.88
A_68_P26655646	chr9:77502889-77502936	NM_172925:18374	Klhl31	INSIDE	0.159	0.706	1266.67	893.82	0.112	1058.36	118.95
A_68_P32451587	chrX:68303129-68303173	NM_001081354:-280	Mamld1	PROMOTER	0.159	2.534	1396.22	3538.14	0.403	613.24	247.39
A_68_P22028767	chr3:30407126-30407173	NM_021442:1260	Mecom	INSIDE	0.159	0.715	1488.17	1063.97	0.113	1059.84	120.29
A_68_P25089970	chr7:52147618-52147662	NM_029365:96	Med25	INSIDE	0.159	0.434	2815.10	1223.08	0.069	2156.39	148.87
A_68_P25088092	chr7:51803991-51804035	NM_011131:173	Pold1	INSIDE	0.159	0.697	2838.95	1977.55	0.111	1874.27	207.66
A_68_P31929909	chr19:5654397-5654451	NM_001164480:9283	Sipa1	INSIDE	0.159	0.540	1876.73	1013.72	0.086	1353.16	116.39
A_68_P28744648	chr12:112776290-112776334	NR_033168:-2844	Snora28	PROMOTER	0.159	0.535	4270.42	2286.59	0.085	3019.34	257.39
A_68_P26706408	chr9:87625899-87625944	NM_023814:174	Tbx18	INSIDE	0.159	0.689	1381.98	952.27	0.110	1081.58	118.54
A_68_P25500989	chr7:133679675-133679719			Unknown	0.159	0.686	1521.47	1043.45	0.109	1080.71	117.57
A_68_P26568892	chr9:61969537-61969589	mmu-mir-5133:839		DOWNSTREAM	0.159	0.659	1356.94	894.68	0.105	1145.17	120.43
A_68_P24358386	chr6:34827862-34827906	NM_001135611:181	3110062M04Rik	INSIDE	0.158	0.465	2119.36	984.89	0.073	1593.11	116.88
A_68_P31351858	chr17:74928310-74928354	NM_007566:698	Birc6	INSIDE	0.158	0.503	2795.33	1404.81	0.080	2107.81	167.89
A_68_P21114932	chr2:32218910-32218958	NM_028412:181	Ciz1	INSIDE	0.158	2.241	636.64	1426.73	0.354	398.04	141.03
A_68_P31150909	chr17:34045790-34045846	NM_007829:-571	Daxx	PROMOTER	0.158	0.468	2184.09	1023.15	0.074	1585.86	117.42
A_68_P29654698	chr14:62911858-62911904	NM_173419:-64	Dleu7	PROMOTER	0.158	0.599	1463.37	877.18	0.095	1288.13	122.38
A_68_P23155401	chr4:101181535-101181581	NM_001164584:978	Dnajc6	INSIDE	0.158	0.467	2248.25	1049.28	0.074	1648.03	121.68
A_68_P29713895	chr14:73110156-73110200	NM_207636:-368	Fndc3a	PROMOTER	0.158	0.678	1409.74	956.30	0.107	1165.62	125.23
A_68_P28604402	chr12:86827971-86828024	NM_010234:13147	Fos	DOWNSTREAM	0.158	0.618	3691.79	2280.92	0.097	2586.93	252.13
A_68_P23571065	chr5:30481976-30482020	NM_145558:137	Hadhb	INSIDE	0.158	0.608	1512.98	919.33	0.096	1222.17	117.62
A_68_P24448822	chr6:52127106-52127159	NM_010452:35934	Hoxa3	INSIDE	0.158	0.636	1596.56	1015.95	0.100	1238.86	124.26
A_68_P20778371	chr1:164478469-164478518	NM_144877:-17	Mettl13	PROMOTER	0.158	0.603	1649.91	995.20	0.095	1268.58	120.94
A_68_P29689306	chr14:68743165-68743210	NM_008691:-126	Nefm	PROMOTER	0.158	0.541	1964.20	1062.64	0.086	1348.78	115.38
A_68_P23057173	chr4:82150827-82150874	NM_001113209:362	Nfib	INSIDE	0.158	0.512	1950.75	997.92	0.081	1438.31	115.99
A_68_P21096074	chr2:29107607-29107664	NM_133500:-4075	Ntng2	PROMOTER	0.158	1.553	2861.42	4444.43	0.245	1933.41	473.66
A_68_P26476664	chr9:45714791-45714835	NM_178709:148	Rnf214	INSIDE	0.158	0.448	2329.57	1044.43	0.071	1776.66	125.70

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P21631237	chr2:130522606-130522650	NM_001081162:627	Slc4a11	INSIDE	0.158	0.616	2096.96	1291.76	0.098	1671.59	163.02
A_68_P31207578	chr17:46692314-46692358	NM_020493:775	Srf	INSIDE	0.158	0.667	1514.02	1009.94	0.106	1123.57	118.57
A_68_P28158411	chr11:116135230-116135274	NM_146032:279	Srp68	INSIDE	0.158	1.446	2201.26	3183.70	0.229	1480.33	338.74
A_68_P27234342	chr10:70700324-70700368	NM_009360:446	Tfam	INSIDE	0.158	0.561	3070.69	1723.97	0.089	2439.78	216.40
A_68_P21433077	chr2:93028116-93028160	NM_001025246:398	Trp53i11	INSIDE	0.158	0.454	2258.93	1026.01	0.072	1723.33	123.44
A_68_P24817207	chr6:124779297-124779341	NM_013700:147	Usp5	INSIDE	0.158	0.485	2622.24	1273.09	0.077	1796.26	137.57
A_68_P21179663	chr2:44782139-44782193	ENSMUST00000133442:503		INSIDE	0.158	0.452	2371.65	1071.06	0.071	1673.69	119.52
A_68_P30403120	chr15:85641984-85642028	NM_001164625:121	2210021J22Rik	INSIDE	0.157	0.639	2838.89	1814.25	0.101	2116.42	212.73
A_68_P24135765	chr5:139936243-139936287	NM_028469:224	3110082I17Rik	INSIDE	0.157	1.365	4117.54	5621.09	0.214	2785.72	596.43
A_68_P20161228	chr1:38683615-38683660	NM_010678:38163	Aff3	INSIDE	0.157	0.686	3374.56	2315.49	0.108	2187.27	235.93
A_68_P32673102	chrX:131220969-131221013	NM_001202500:-6872	Armcx4	PROMOTER	0.157	1.696	2755.68	4674.73	0.267	1102.55	294.43
A_68_P32364052	chrX:45697351-45697395	NM_178782:2838	Bcorl1	INSIDE	0.157	2.064	901.87	1861.49	0.324	365.05	118.27
A_68_P20413587	chr1:88600174-88600218	NM_001172157:-182	Dis3l2	PROMOTER	0.157	0.542	1819.73	986.39	0.085	1376.97	117.52
A_68_P26630496	chr9:72806623-72806667	NM_001163725:53	Dyx1c1	INSIDE	0.157	0.536	2529.38	1354.55	0.084	1858.00	156.40
A_68_P31615128	chr18:35020826-35020870	NM_007913:-12	Egr1	PROMOTER	0.157	0.471	2150.96	1012.61	0.074	1559.68	115.61
A_68_P21122320	chr2:33436378-33436430	NM_010725:59627	Lmx1b	INSIDE	0.157	0.511	2344.33	1197.65	0.080	1504.80	120.45
A_68_P22210127	chr3:67267701-67267745	NM_016753:107	Lxn	INSIDE	0.157	1.760	6664.05	11727.54	0.276	4566.69	1259.04
A_68_P32691811	chrX:135448869-135448913	NM_013724:-78	Nrk	PROMOTER	0.157	2.243	12204.76	27377.88	0.353	4834.37	1705.29
A_68_P23277936	chr4:125736057-125736104	NM_172701:272	Oscp1	INSIDE	0.157	2.357	6203.43	14621.64	0.370	4070.21	1506.50
A_68_P28397153	chr12:45370604-45370657	NM_026164:490	Pnpla8	INSIDE	0.157	0.609	1835.36	1116.95	0.095	1290.54	123.05
A_68_P22778505	chr4:22414595-22414639	NM_008899:662	Pou3f2	INSIDE	0.157	1.647	4813.48	7929.94	0.259	3343.69	864.41
A_68_P23656663	chr5:45841705-45841749	NM_024236:-258	Qdpr	DIVERGENT_PROMOTER	0.157	0.492	1967.61	968.18	0.077	1556.45	120.01
A_68_P25377911	chr7:109398265-109398309	NM_019566:346	Rhog	INSIDE	0.157	0.505	1887.92	952.76	0.079	1453.13	115.33
A_68_P30013961	chr15:10966774-10966818	NM_178717:927	Rxfp3	INSIDE	0.157	0.697	4372.73	3046.88	0.109	3396.17	371.03
A_68_P26574110	chr9:62993652-62993696	NM_172446:1113	Skor1	INSIDE	0.157	0.575	1920.92	1104.72	0.090	1307.67	117.97
A_68_P21221439	chr2:52601733-52601777	NM_019667:-571	Stam2	PROMOTER	0.157	0.671	1572.17	1054.98	0.105	1138.67	119.99
A_68_P24591245	chr6:83019654-83019698	NM_009392:543	Tlx2	INSIDE	0.157	0.470	2183.16	1026.90	0.074	1742.88	128.83
A_68_P28853132	chr13:17786964-17787008	NM_025479:-260	2810021B07Rik	DIVERGENT_PROMOTER	0.156	0.737	2772.38	2041.88	0.115	1955.65	224.62
A_68_P24045430	chr5:122043561-122043605	NM_009656:251	Aldh2	INSIDE	0.156	0.476	3110.23	1481.66	0.074	2240.34	165.99
A_68_P24172962	chr5:148115952-148116010	NM_007673:2845	Cdx2	INSIDE	0.156	0.580	1919.73	1113.43	0.091	1311.99	118.90
A_68_P30476587	chr15:98636550-98636594	NM_001013741:1784	Ddn	INSIDE	0.156	0.636	1771.26	1126.18	0.099	1304.68	129.63
A_68_P28672817	chr12:100138890-100138934	NM_001081191:782	Eml5	INSIDE	0.156	0.608	2431.43	1478.25	0.095	1894.60	179.73
A_68_P23582142	chr5:32435789-32435833	NM_008037:-3034	Fosl2	PROMOTER	0.156	0.658	1698.17	1117.73	0.103	1267.59	130.06
A_68_P31213682	chr17:47831829-47831878	NM_144939:-302	Frs3	DIVERGENT_PROMOTER	0.156	0.518	2006.03	1039.56	0.081	1492.51	121.04
A_68_P32213514	chr19:58529502-58529546	NM_010279:-568	Gfra1	PROMOTER	0.156	0.544	2506.69	1362.64	0.085	1910.18	161.47
A_68_P25727978	chr8:26707398-26707452	NM_173012:535	Letm2	INSIDE	0.156	0.694	1541.18	1069.57	0.108	1101.85	119.26
A_68_P22601419	chr3:143865258-143865302	NM_001161770:16	Lmo4	INSIDE	0.156	0.603	2736.89	1650.83	0.094	1758.72	165.69
A_68_P21642726	chr2:132704942-132704986	NM_177303:1634	Lrrn4	INSIDE	0.156	0.508	1990.75	1011.60	0.079	1456.84	115.15
A_68_P31208333	chr17:46818209-46818253	NM_010787:145	Mea1	INSIDE	0.156	0.716	1656.82	1185.83	0.111	1208.63	134.59
A_68_P28047118	chr11:96711362-96711406	NR_029562:-322	Mir152	PROMOTER	0.156	0.708	1874.02	1327.33	0.110	1395.07	154.09
A_68_P32465509	chrX:71167300-71167346	NM_001177965:-39	Naa10	PROMOTER	0.156	1.382	1542.19	2131.35	0.215	558.92	120.40
A_68_P29773648	chr14:84846227-84846278	NM_001013753:2883	Pcdh17	INSIDE	0.156	0.714	1627.35	1162.52	0.111	1097.28	122.18
A_68_P23271505	chr4:124667492-124667536	NM_138683:3841	Rspo1	INSIDE	0.156	0.622	1647.29	1024.08	0.097	1286.56	124.97
A_68_P30595530	chr16:22009516-22009560	NM_029457:-18	Senp2	PROMOTER	0.156	0.564	1753.46	989.64	0.088	1411.18	124.37
A_68_P25989169	chr8:81033142-81033186	NM_029736:-69	Slc10a7	DIVERGENT_PROMOTER	0.156	0.647	2714.74	1756.46	0.101	2096.02	211.97
A_68_P23322943	chr4:134024577-134024621	NM_019641:364	Stmn1	INSIDE	0.156	0.645	2161.19	1392.93	0.100	1533.24	153.95
A_68_P23325609	chr4:134487161-134487205	NM_026780:288	Syf2	INSIDE	0.156	0.486	2314.27	1123.92	0.076	1624.03	122.75
A_68_P22338876	chr3:94217322-94217366	NM_028307:105	Tdrkh	INSIDE	0.156	1.368	9561.43	13081.72	0.214	6500.13	1391.10
A_68_P32136793	chr19:45227850-45227894	NM_021901:2668	Tlx1	INSIDE	0.156	0.650	5489.08	3566.55	0.101	3798.26	384.68
A_68_P28225579	chr12:8980872-8980920	NM_001159527:90	Wdr35	INSIDE	0.156	0.649	1687.23	1094.60	0.101	1151.98	116.56
A_68_P29671858	chr14:65768534-65768580	BC096449:686333		DOWNSTREAM	0.156	2.613	4200.27	10975.38	0.406	2559.50	1040.06

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P25737282	chr8:28338659-28338703	NM_013462:1380	Adrb3	INSIDE	0.155	0.659	2667.12	1756.75	0.102	1824.16	186.68
A_68_P24160789	chr5:145119094-145119138	NM_025833:-135	Baiap2l1	PROMOTER	0.155	0.461	2338.47	1077.40	0.071	1862.46	132.88
A_68_P28184672	chr11:120319589-120319633	NM_152807:168	Ccdc137	INSIDE	0.155	0.666	1592.81	1060.55	0.103	1147.62	118.38
A_68_P24831041	chr6:127100503-127100547	NM_009829:542	Ccnd2	INSIDE	0.155	0.605	1758.37	1063.19	0.094	1315.53	123.56
A_68_P22663511	chr3:154259686-154259731	NM_009968:-267	Cryz	PROMOTER	0.155	0.472	2252.36	1062.45	0.073	1605.74	117.14
A_68_P32224193	chr19:60302406-60302450	NM_029648:172	D19Ertd737e	INSIDE	0.155	0.696	1366.16	951.17	0.108	1088.68	117.33
A_68_P25950970	chr8:72826351-72826395	NM_001024922:-21	Ddx49	DIVERGENT_PROMOTER	0.155	0.543	2324.12	1261.95	0.084	1634.63	137.64
A_68_P20353314	chr1:75314278-75314322	NM_001110831:-88	Dnpep	PROMOTER	0.155	0.484	2326.43	1126.36	0.075	1794.33	134.37
A_68_P32364768	chrX:45807315-45807359	NM_019680:8973	Elf4	INSIDE	0.155	1.674	3291.28	5510.12	0.260	1215.78	315.94
A_68_P21107213	chr2:30996649-30996693	NM_001038700:858	Fnbp1	INSIDE	0.155	0.658	1885.44	1241.40	0.102	1219.02	124.70
A_68_P28604312	chr12:86814373-86814417	NM_010234:-456	Fos	PROMOTER	0.155	0.490	1847.43	904.56	0.076	1536.61	116.89
A_68_P27278157	chr10:79132042-79132087	NM_148934:-90	Gm16517	PROMOTER	0.155	0.511	1817.73	928.53	0.079	1486.61	117.85
A_68_P24501236	chr6:63206960-63207004	NM_008167:132	Grid2	INSIDE	0.155	0.458	2045.42	937.19	0.071	1639.64	116.76
A_68_P29055020	chr13:55545946-55545990	NM_011938:-726	Grk6	PROMOTER	0.155	1.478	810.86	1198.23	0.229	513.73	117.72
A_68_P28883386	chr13:23855470-23855521	NM_030609:-41	Hist1h1a	DIVERGENT_PROMOTER	0.155	0.727	4442.08	3230.36	0.113	3046.22	342.78
A_68_P21147687	chr2:38212141-38212185	NM_010710:5335	Lhx2	INSIDE	0.155	0.638	2348.15	1498.43	0.099	1624.60	161.05
A_68_P26815492	chr9:108470126-108470170	NM_023247:-475	Ndufaf3	DIVERGENT_PROMOTER	0.155	1.401	2272.14	3182.58	0.217	1525.04	331.05
A_68_P32127987	chr19:43750198-43750243	NM_145156:-849	Slc25a28	PROMOTER	0.155	0.696	1895.01	1319.27	0.108	1366.48	147.51
A_68_P27365026	chr10:94878069-94878116	NM_001168657:-175	Socs2	PROMOTER	0.155	1.339	2319.06	3105.68	0.207	1617.09	335.02
A_68_P30570619	chr16:16829103-16829147	NM_015773:332	Spag6	INSIDE	0.155	0.527	4089.76	2155.27	0.082	3015.83	245.92
A_68_P25232260	chr7:81157728-81157772	NM_009181:818	St8sia2	INSIDE	0.155	0.486	2003.93	974.16	0.075	1564.10	117.54
A_68_P28087056	chr11:103635473-103635522	NM_009521:9	Wnt3	INSIDE	0.155	0.606	1689.48	1023.53	0.094	1284.16	120.59
A_68_P27781837	chr11:49016791-49016837	NM_001024846:-187	Zfp62	PROMOTER	0.155	1.535	747.40	1147.24	0.238	520.00	123.51
A_68_P29671859	chr14:65768667-65768711	BC096449:686465		DOWNSTREAM	0.155	1.363	10339.02	14096.99	0.211	6234.80	1316.59
A_68_P24482545	chr6:58590224-58590281	NM_011920:43587	Abcg2	INSIDE	0.154	0.712	1539.68	1095.49	0.109	1144.30	125.11
A_68_P21061287	chr2:22924684-22924728	NM_001102437:115	Acbd5	INSIDE	0.154	1.430	5212.07	7455.00	0.220	3718.61	816.61
A_68_P28118515	chr11:109287477-109287521	NM_025275:239	Amz2	INSIDE	0.154	0.616	1711.81	1054.24	0.095	1242.60	117.91
A_68_P26595468	chr9:66682422-66682466	NM_026674:69	Aph1c	INSIDE	0.154	0.471	3924.39	1849.39	0.073	2883.89	209.19
A_68_P27308093	chr10:84850152-84850196	NM_028709:616	Btbd11	INSIDE	0.154	0.453	3317.82	1504.20	0.070	2310.99	160.95
A_68_P24057000	chr5:124133425-124133474	NM_019765:851	Clip1	INSIDE	0.154	0.570	1792.18	1020.80	0.088	1374.02	120.69
A_68_P32128432	chr19:43827652-43827696	NM_001113562:162	Cutc	INSIDE	0.154	0.546	5862.75	3201.70	0.084	4363.22	367.43
A_68_P26473573	chr9:45239483-45239530	NM_001081270:1131	Dscaml1	INSIDE	0.154	0.525	1944.60	1019.95	0.081	1516.86	122.16
A_68_P32227250	chr19:60866724-60866768	NM_010123:-150	Eif3a	PROMOTER	0.154	0.701	1395.48	977.90	0.108	1126.20	121.40
A_68_P24078735	chr5:128112945-128112989	NM_177005:335	Glt1d1	INSIDE	0.154	0.586	1799.84	1054.40	0.090	1351.22	122.23
A_68_P23591969	chr5:34326576-34326620	NM_001033458:476	Gm1673	INSIDE	0.154	0.456	2418.12	1102.67	0.070	1711.46	119.90
A_68_P22391857	chr3:104315282-104315333	NM_001025067:472	Lrig2	INSIDE	0.154	0.657	1835.53	1206.21	0.101	1503.48	152.02
A_68_P29643653	chr14:60884373-60884418	NM_144843:331	Mtmr6	INSIDE	0.154	0.610	1562.70	953.37	0.094	1241.19	116.93
A_68_P30382864	chr15:82169262-82169306	NM_008669:-28	Naga	DIVERGENT_PROMOTER	0.154	0.637	1530.88	975.38	0.098	1260.29	123.30
A_68_P26242539	chr8:126473498-126473548	NM_172288:-357	Nup133	PROMOTER	0.154	0.579	1680.69	973.87	0.089	1301.58	116.11
A_68_P32134818	chr19:44911149-44911193	NM_011037:79287	Pax2	INSIDE	0.154	0.626	6495.60	4068.15	0.096	4693.29	452.72
A_68_P23228358	chr4:115894280-115894324	NM_181585:-216	Pik3r3	PROMOTER	0.154	0.481	1913.43	920.52	0.074	1611.99	119.44
A_68_P20348978	chr1:74551985-74552034	NM_021383:-624	Rqcd1	PROMOTER	0.154	0.670	1504.09	1007.87	0.103	1193.56	123.26
A_68_P26814193	chr9:108208141-108208185	NM_133986:120	Tcta	INSIDE	0.154	0.478	2565.09	1226.13	0.073	1787.83	131.22
A_68_P28744113	chr12:112680513-112680557	NM_009396:-337	Tnfaip2	PROMOTER	0.154	0.680	2124.48	1444.75	0.105	1578.48	165.41
A_68_P25018371	chr7:28438749-28438793	NM_028417:-172	Ttc9b	PROMOTER	0.154	0.678	3610.47	2446.11	0.104	2537.41	264.46
A_68_P26710502	chr9:88418231-88418277	ENSMUST00000034997:-533		PROMOTER	0.154	0.564	1951.89	1101.11	0.087	1382.69	120.21
A_68_P23746644	chr5:64040795-64040839	NM_177006:475	3110047P20Rik	INSIDE	0.153	0.509	1926.17	981.37	0.078	1544.37	120.72
A_68_P25327115	chr7:100023177-100023221	NM_001080995:-456	4632434I11Rik	DIVERGENT_PROMOTER	0.153	1.432	4311.10	6174.69	0.219	2980.57	653.60
A_68_P25509653	chr7:135381206-135381250	NM_177001:317	9130023H24Rik	INSIDE	0.153	0.636	2384.71	1516.26	0.097	1502.10	145.82
A_68_P31922243	chr19:4282842-4282886	NM_026720:273	Ankrd13d	INSIDE	0.153	0.627	3628.31	2276.09	0.096	2599.10	249.14
A_68_P22128530	chr3:51028680-51028724	NM_009834:334	Ccrn4l	INSIDE	0.153	0.490	2018.20	989.37	0.075	1568.82	117.60

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P23005993	chr4:70071160-70071204	NM_145990:219	Cdk5rap2	INSIDE	0.153	0.647	5103.18	3300.01	0.099	3635.49	359.90
A_68_P27504659	chr10:121079155-121079199	NM_177335:420	D930020B18Rik	INSIDE	0.153	0.702	2104.99	1478.60	0.108	1535.01	165.34
A_68_P26224698	chr8:123652159-123652203	NM_008024:596	Foxl1	INSIDE	0.153	0.610	1808.61	1102.87	0.094	1324.91	123.89
A_68_P28882027	chr13:23627101-23627153	NM_145073:-160	Hist1h3g	PROMOTER	0.153	0.617	1652.11	1018.62	0.094	1282.28	120.61
A_68_P31615691	chr18:35113624-35113674	NM_010481:357	Hspa9	INSIDE	0.153	0.436	2560.61	1117.66	0.067	1810.03	120.69
A_68_P31109175	chr17:26390511-26390556	NM_025881:679	Luc7l	INSIDE	0.153	0.671	1465.52	983.62	0.103	1192.28	122.58
A_68_P23308627	chr4:131399668-131399712	NM_025297:305	Mecr	INSIDE	0.153	0.516	1774.46	915.24	0.079	1464.90	115.24
A_68_P23536410	chr5:22939501-22939545	NM_026984:-724	Mll5	PROMOTER	0.153	0.549	2304.38	1265.79	0.084	1735.97	145.75
A_68_P27293631	chr10:82226680-82226728	NM_010914:182	Nfyb	INSIDE	0.153	0.717	1409.74	1010.22	0.110	1117.02	122.44
A_68_P28004879	chr11:89160026-89160082	NM_008711:3819	Nog	DOWNSTREAM	0.153	0.688	1607.67	1106.36	0.105	1171.61	123.17
A_68_P26268784	chr8:130883235-130883284	NM_008737:287	Nrp1	INSIDE	0.153	0.498	2154.51	1073.27	0.076	1558.54	118.92
A_68_P30139524	chr15:36538383-36538427	NM_008774:324	Pabpc1	INSIDE	0.153	0.710	8352.49	5929.71	0.109	5975.04	650.28
A_68_P28458300	chr12:57797914-57797958	NM_011041:1311	Pax9	INSIDE	0.153	0.445	2475.66	1102.51	0.068	1790.79	122.04
A_68_P22518658	chr3:128907203-128907247	NM_001042502:-9630	Pitx2	PROMOTER	0.153	0.574	1612.92	925.36	0.088	1370.17	120.64
A_68_P29619512	chr14:56340802-56340846	NM_019519:189	Rabggta	INSIDE	0.153	1.548	4599.91	7122.05	0.237	2634.55	624.59
A_68_P21783953	chr2:158439712-158439756	NM_009508:3241	Slc32a1	INSIDE	0.153	0.524	4106.70	2153.66	0.080	2916.93	233.58
A_68_P32147457	chr19:47142031-47142081	NM_177342:-181	Taf5	PROMOTER	0.153	0.465	2668.17	1239.73	0.071	1920.01	136.51
A_68_P28974205	chr13:40828820-40828871	NM_001122948:-3033	Tcfap2a	PROMOTER	0.153	0.716	1524.23	1091.89	0.110	1085.20	119.10
A_68_P25465171	chr7:126863923-126863967	NM_145585:335	Thumpd1	INSIDE	0.153	0.457	2540.49	1162.22	0.070	1716.53	120.47
A_68_P27780214	chr11:48651115-48651159	NM_053166:11497	Trim7	INSIDE	0.153	0.541	2002.24	1083.94	0.083	1477.48	122.07
A_68_P22934130	chr4:55493545-55493589			Unknown	0.153	0.675	1467.98	991.37	0.103	1173.35	120.91
A_68_P25714451	chr8:24168891-24168935	NM_031158:166	Ank1	INSIDE	0.152	0.525	2178.04	1142.55	0.080	1552.58	124.11
A_68_P29122630	chr13:70776238-70776282	NM_144837:252	BC018507	INSIDE	0.152	0.658	4530.78	2981.85	0.100	3223.00	323.04
A_68_P32289634	chrX:20265458-20265502	NM_011049:-138	Cdk16	PROMOTER	0.152	1.369	1922.20	2631.62	0.208	800.76	166.60
A_68_P30589168	chr16:20716549-20716593	NM_009900:139	Clcn2	INSIDE	0.152	0.551	1863.85	1027.07	0.084	1407.81	118.24
A_68_P24359961	chr6:35084163-35084220	NM_001164412:-454	Cnot4	PROMOTER	0.152	0.699	1378.85	964.29	0.106	1083.88	115.12
A_68_P27171642	chr10:59414981-59415025	NM_029083:-484	Ddit4	PROMOTER	0.152	0.481	2143.31	1031.59	0.073	1604.35	117.23
A_68_P27386030	chr10:98725559-98725613	NM_026268:-278	Dusp6	PROMOTER	0.152	0.577	1825.14	1052.84	0.087	1325.87	115.94
A_68_P29683700	chr14:67854699-67854743	NM_010095:2592	Ebf2	INSIDE	0.152	0.685	3435.06	2351.80	0.104	2541.11	264.34
A_68_P30328931	chr15:73015939-73015989	NM_153178:-587	Eif2c2	PROMOTER	0.152	0.665	1581.51	1051.35	0.101	1152.23	116.70
A_68_P31610611	chr18:34166774-34166818	NM_013512:64	Epb4.1l4a	INSIDE	0.152	0.690	1760.82	1215.32	0.105	1416.16	148.78
A_68_P28056288	chr11:98273791-98273835	NM_001003817:15	Erbb2	INSIDE	0.152	0.634	4465.48	2830.37	0.096	3259.86	313.39
A_68_P20259678	chr1:58643163-58643207	NM_172513:-7	Fam126b	DIVERGENT_PROMOTER	0.152	0.600	1947.22	1167.79	0.091	1468.06	133.54
A_68_P32467038	chrX:71491563-71491607	NM_010227:289	Flna	INSIDE	0.152	1.538	2086.99	3209.16	0.234	721.94	168.92
A_68_P28924078	chr13:31718670-31718714	NM_010225:1008	Foxf2	INSIDE	0.152	0.455	2481.07	1129.51	0.069	1703.53	118.07
A_68_P28684633	chr12:102137516-102137560	NM_001177674:196	Gpr68	INSIDE	0.152	0.514	2130.13	1094.36	0.078	1553.16	121.28
A_68_P26580968	chr9:64100873-64100917	NM_008927:518	Map2k1	INSIDE	0.152	0.433	2290.58	991.80	0.066	1770.03	116.82
A_68_P31130472	chr17:30026258-30026302	NM_001081160:-1453	Mdga1	PROMOTER	0.152	0.662	2377.77	1573.85	0.101	1842.43	185.49
A_68_P26345184	chr9:20841202-20841246	NR_035438:-4452	Mir1900	PROMOTER	0.152	0.572	1863.06	1065.66	0.087	1419.14	123.28
A_68_P28058586	chr11:98656221-98656265	NM_028722:-840	Msl1	PROMOTER	0.152	0.653	5236.24	3417.67	0.099	3424.99	339.57
A_68_P20010817	chr1:5907429-5907473	NM_010342:29	Npbwr1	INSIDE	0.152	0.543	1572.48	854.32	0.082	1421.97	117.09
A_68_P29237543	chr13:95647408-95647452	NM_011021:1849	Otp	INSIDE	0.152	0.566	1800.61	1019.69	0.086	1393.42	120.19
A_68_P32775563	chrX:156064795-156064839	NM_001135727:-523	Sh3kbp1	PROMOTER	0.152	1.691	1378.43	2330.66	0.257	510.94	131.07
A_68_P32427540	chrX:61528858-61528902	NM_178740:1291	Slitrk4	INSIDE	0.152	1.779	2360.34	4199.69	0.270	913.40	247.07
A_68_P25102502	chr7:54263847-54263895	NM_175318:-86	Spty2d1	PROMOTER	0.152	0.552	1815.47	1001.40	0.084	1421.04	119.51
A_68_P31131059	chr17:30141179-30141223	NM_148926:-831	Zfand3	PROMOTER	0.152	0.563	1954.31	1101.06	0.086	1466.94	125.93
A_68_P29102456	chr13:65344000-65344046			Unknown	0.152	2.405	1526.80	3671.76	0.367	1065.66	390.79
A_68_P33013891	chrUn_random:3233790-3233834			Unknown	0.152	0.655	1583.16	1037.06	0.100	1183.12	117.84
A_68_P32601442	chrX:109008049-109008100			Unknown	0.152	2.064	884.33	1825.25	0.314	374.36	117.47
A_68_P21705753	chr2:143991362-143991406	ENSMUST00000099292:23642		DOWNSTREAM	0.152	0.355	2890.18	1026.68	0.054	2188.81	118.30
A_68_P24810291	chr6:122714891-122714935	ENSMUST00000171541:15063		INSIDE	0.152	0.609	1809.84	1102.81	0.093	1327.61	123.12

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31599400	chr18:31919398-31919452	NM_153515:-109	Ammecr1l	PROMOTER	0.151	0.448	2364.51	1060.24	0.068	1841.00	124.67
A_68_P25677405	chr8:14911386-14911430	NM_001037736:-308	Arhgef10	PROMOTER	0.151	0.581	2206.29	1282.91	0.088	1550.03	136.06
A_68_P28976951	chr13:41345598-41345642	NM_001135577:408	BC024659	INSIDE	0.151	0.571	2558.07	1461.88	0.086	1951.13	168.75
A_68_P27281431	chr10:79630462-79630506	NM_007705:-101	Cirbp	PROMOTER	0.151	0.509	2366.89	1205.70	0.077	1611.98	123.75
A_68_P23970972	chr5:108697917-108697961	NM_026106:23	Dr1	INSIDE	0.151	0.408	3760.10	1533.47	0.062	2765.36	170.10
A_68_P22803175	chr4:28740439-28740495	NM_001122889:172	Epha7	INSIDE	0.151	0.657	2030.47	1333.44	0.099	1663.44	164.59
A_68_P32135376	chr19:45005642-45005686	NM_001081225:56	Fam178a	INSIDE	0.151	0.690	1515.64	1046.26	0.104	1121.45	116.78
A_68_P24131922	chr5:139297257-139297301	NM_001195128:1245	Gm5294	INSIDE	0.151	0.538	2285.55	1229.21	0.081	1741.04	141.62
A_68_P22531297	chr3:130974718-130974765	NM_008212:214	Hadh	INSIDE	0.151	0.468	2361.74	1105.35	0.071	1734.32	122.67
A_68_P30991210	chr16:96349056-96349100	NM_008251:254	Hmgn1	INSIDE	0.151	0.564	2242.06	1264.82	0.085	1657.50	141.29
A_68_P23120706	chr4:94717919-94717966	NM_010591:971	Jun	INSIDE	0.151	0.574	2266.77	1300.54	0.087	1636.71	142.02
A_68_P30423408	chr15:88971259-88971303	NM_013871:-147	Mapk12	PROMOTER	0.151	0.661	1607.55	1062.25	0.100	1190.75	118.98
A_68_P25955965	chr8:73796966-73797010	NM_001142322:376	Myo9b	INSIDE	0.151	0.700	2562.07	1792.89	0.106	1903.58	201.38
A_68_P21107807	chr2:31101894-31101938	NM_019681:474	Ncs1	INSIDE	0.151	0.584	1890.14	1103.28	0.088	1415.86	125.00
A_68_P23415890	chr4:151370343-151370387	NM_172705:-76	Phf13	PROMOTER	0.151	0.431	2263.75	974.70	0.065	1857.21	121.13
A_68_P32464004	chrX:70904998-70905042	NM_001199351:173	Pnck	INSIDE	0.151	2.664	9345.08	24897.50	0.401	3853.71	1545.52
A_68_P24536429	chr6:71391138-71391182	NM_024288:-529	Rmnd5a	PROMOTER	0.151	0.542	1918.14	1039.65	0.082	1435.06	117.56
A_68_P23576461	chr5:31397375-31397419	NM_011773:-1496	Slc30a3	PROMOTER	0.151	0.674	1658.04	1117.04	0.102	1144.17	116.34
A_68_P30496206	chr15:101966579-101966623	NM_001033277:46	Spryd3	INSIDE	0.151	0.345	2743.26	945.31	0.052	2330.38	121.35
A_68_P28567141	chr12:80108301-80108345	NM_178745:-58	Tmem229b	PROMOTER	0.151	0.376	2864.45	1077.51	0.057	2224.36	126.66
A_68_P21106327	chr2:30837787-30837831	NM_028846:10	Usp20	INSIDE	0.151	0.628	1694.49	1063.48	0.095	1276.90	120.83
A_68_P26805303	chr9:106724052-106724097	NM_001015507:-232	Vprbp	PROMOTER	0.151	0.630	1992.32	1254.31	0.095	1611.18	153.39
A_68_P27899782	chr11:70068529-70068574	NM_007440:292	Alox12	INSIDE	0.150	0.677	1773.54	1200.29	0.101	1165.93	118.12
A_68_P20509928	chr1:108610270-108610327	NM_009741:569	Bcl2	INSIDE	0.150	0.622	1578.73	981.39	0.093	1230.71	115.06
A_68_P21617375	chr2:127952895-127952939	NM_009754:1143	Bcl2l11	INSIDE	0.150	0.717	2033.76	1458.34	0.107	1685.58	181.05
A_68_P25948520	chr8:72411249-72411293	NM_026818:21	Cilp2	INSIDE	0.150	0.690	2370.82	1636.94	0.104	1680.64	174.26
A_68_P31157713	chr17:35257880-35257924	NM_009975:490	Csnk2b	INSIDE	0.150	0.559	2161.91	1208.66	0.084	1703.06	142.82
A_68_P29480508	chr14:26746521-26746565	NM_025311:194	D14Ertd449e	INSIDE	0.150	0.537	5034.47	2705.84	0.080	4056.60	326.20
A_68_P21317255	chr2:70893877-70893924	NM_001165982:100	Dcaf17	INSIDE	0.150	0.661	1606.01	1062.03	0.099	1230.69	121.85
A_68_P23379974	chr4:144482718-144482768	NM_011303:-297	Dhrs3	PROMOTER	0.150	1.494	2470.32	3689.51	0.224	1584.09	355.10
A_68_P31615540	chr18:35091234-35091284	NM_144866:399	Etf1	INSIDE	0.150	0.657	1663.12	1092.97	0.098	1185.57	116.58
A_68_P31615546	chr18:35092064-35092109	NM_144866:-429	Etf1	PROMOTER	0.150	0.482	2393.05	1153.68	0.072	1700.61	122.64
A_68_P28888196	chr13:24730767-24730811	NM_001080381:272	Fam65b	INSIDE	0.150	0.540	1737.10	937.18	0.081	1443.13	117.13
A_68_P29631506	chr14:58695032-58695076	NM_013518:3532	Fgf9	INSIDE	0.150	0.698	2848.64	1988.57	0.105	2150.26	225.35
A_68_P29386052	chr14:8651174-8651222	NM_134080:728	Flnb	INSIDE	0.150	0.545	2078.34	1133.72	0.082	1452.92	118.54
A_68_P32454737	chrX:68917956-68918000	NM_010340:1037	Gpr50	INSIDE	0.150	1.914	3135.75	6003.36	0.288	1138.91	328.04
A_68_P24816729	chr6:124690602-124690649	NM_013535:472	Grcc10	INSIDE	0.150	0.716	1744.89	1249.61	0.107	1212.94	130.21
A_68_P28044102	chr11:96227285-96227329	NM_008266:235	Hoxb1	INSIDE	0.150	0.716	3630.03	2599.93	0.108	2369.35	255.08
A_68_P28225275	chr12:8928468-8928512	NM_008640:378	Laptm4a	INSIDE	0.150	0.633	2476.22	1568.69	0.095	1910.40	182.00
A_68_P26805729	chr9:106793805-106793862	NM_029103:436	Manf	INSIDE	0.150	0.695	1621.48	1126.14	0.104	1165.93	121.60
A_68_P30558909	chr16:13780665-13780710	NM_001039521:-104	Rrn3	PROMOTER	0.150	0.610	1611.25	982.63	0.092	1332.71	122.28
A_68_P26344892	chr9:20780634-20780678	NM_010333:581	S1pr2	INSIDE	0.150	0.721	2810.39	2025.90	0.108	2201.03	237.29
A_68_P23594807	chr5:34868707-34868751	NM_011893:296	Sh3bp2	INSIDE	0.150	2.222	4823.82	10720.52	0.333	3204.04	1067.04
A_68_P21836027	chr2:167363971-167364015	NM_011427:266	Snai1	INSIDE	0.150	0.528	2122.27	1120.19	0.079	1607.15	127.17
A_68_P23590346	chr5:34000962-34001006	NM_001040435:189	Tacc3	INSIDE	0.150	0.562	2048.93	1151.90	0.085	1386.66	117.30
A_68_P31152610	chr17:34324622-34324668	NM_001161730:144	Tap1	INSIDE	0.150	0.577	2120.30	1223.20	0.086	1547.66	133.51
A_68_P24541278	chr6:72305613-72305657	NM_144916:158	Tmem150a	INSIDE	0.150	0.711	4004.53	2846.26	0.107	2735.04	292.03
A_68_P25034259	chr7:31742709-31742753	NM_011680:-908	Usf2	PROMOTER	0.150	0.626	1646.18	1029.94	0.094	1299.90	121.88
A_68_P27644761	chr11:23155625-23155669	NM_001035226:-394	Xpo1	PROMOTER	0.150	0.428	2430.62	1040.22	0.064	1822.87	116.67
A_68_P30787361	chr16:57606603-57606647	NM_025599:356	2610528E23Rik	INSIDE	0.149	0.558	1787.63	997.60	0.083	1398.14	116.59
A_68_P22921610	chr4:53173018-53173062	NM_013454:-273	Abca1	PROMOTER	0.149	0.597	1907.07	1138.50	0.089	1345.39	119.70

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P21334155	chr2:73729976-73730020	NM_001025093:687	Atf2	INSIDE	0.149	1.442	3688.30	5319.20	0.216	2553.75	550.51
A_68_P27371449	chr10:96079420-96079468	NM_007569:-190	Btg1	PROMOTER	0.149	1.915	3073.84	5887.06	0.286	2093.55	598.18
A_68_P22058853	chr3:36470390-36470434	NM_009828:506	Ccna2	INSIDE	0.149	0.518	3345.40	1733.49	0.077	2152.20	166.69
A_68_P24593884	chr6:83447860-83447916	NM_001162521:9075	Dguok	INSIDE	0.149	1.778	555.57	987.75	0.264	445.81	117.71
A_68_P31561531	chr18:24868543-24868587	NM_175276:619	Fhod3	INSIDE	0.149	0.620	1660.31	1029.07	0.092	1352.22	125.06
A_68_P20332288	chr1:71699744-71699788	NM_010233:-21	Fn1	PROMOTER	0.149	0.581	1889.71	1097.16	0.086	1357.67	117.40
A_68_P23281392	chr4:126354680-126354732	NM_011970:-180	Psmb2	PROMOTER	0.149	0.548	1907.60	1045.23	0.081	1430.29	116.46
A_68_P21762356	chr2:154616308-154616364	NM_001139511:-509	Raly	PROMOTER	0.149	0.574	2066.36	1187.01	0.086	1455.79	124.90
A_68_P21817622	chr2:164226486-164226530	NM_009036:-2185	Rbpjl	PROMOTER	0.149	0.562	2891.71	1624.92	0.084	2178.00	182.49
A_68_P24946916	chr7:3655703-3655755	NM_029767:86	Rps9	INSIDE	0.149	0.670	1740.31	1165.76	0.100	1222.34	121.70
A_68_P31106580	chr17:25969693-25969737	NM_019719:592	Stub1	INSIDE	0.149	0.531	2140.17	1135.90	0.079	1526.64	120.86
A_68_P32290626	chrX:20497844-20497888	NM_001110780:178	Syn1	INSIDE	0.149	1.424	1314.25	1871.98	0.213	567.33	120.62
A_68_P20634931	chr1:136605584-136605628	NM_009307:62349	Syt2	INSIDE	0.149	0.569	1850.55	1053.27	0.085	1400.73	118.94
A_68_P22894259	chr4:47365606-47365650	NM_009370:-548	Tgfbr1	PROMOTER	0.149	1.682	4487.99	7547.65	0.251	2946.64	740.06
A_68_P32698230	chrX:136813127-136813171	ENSMUST00000130153:-747		PROMOTER	0.149	2.343	2789.44	6536.57	0.350	1056.91	370.03
A_68_P31022859	chr17:7032261-7032308	ENSMUST00000165850:55		INSIDE	0.149	0.623	1744.26	1087.44	0.093	1230.42	114.61
A_68_P27977999	chr11:84339401-84339452	NR_038057:265	1500016L03Rik	INSIDE	0.148	0.520	2271.78	1180.29	0.077	1698.36	130.30
A_68_P20997499	chr2:9804639-9804695	NR_024257:1794	4930412O13Rik	INSIDE	0.148	0.705	1524.16	1075.11	0.104	1142.43	119.23
A_68_P23262156	chr4:123019628-123019672	NM_007558:396	Bmp8a	INSIDE	0.148	0.694	2120.32	1471.63	0.103	1521.93	156.18
A_68_P20561488	chr1:122239104-122239151	NM_207233:1969	C1ql2	INSIDE	0.148	0.537	2023.78	1086.08	0.080	1559.66	124.08
A_68_P32337351	chrX:38754697-38754743	NM_016886:240	Gria3	INSIDE	0.148	1.590	1415.23	2249.72	0.236	503.64	118.83
A_68_P28042988	chr11:96064572-96064616	NM_008267:8920	Hoxb13	DOWNSTREAM	0.148	0.673	2519.76	1696.56	0.100	1915.09	190.66
A_68_P23658787	chr5:46247794-46247838	NM_172153:-25	Lcorl	PROMOTER	0.148	0.525	4074.36	2140.18	0.078	2739.42	213.26
A_68_P26344986	chr9:20807641-20807685	NM_023167:482	Mrpl4	INSIDE	0.148	0.579	2912.47	1686.79	0.086	2153.49	184.72
A_68_P26460524	chr9:43048046-43048090	NM_178644:-169	Oaf	PROMOTER	0.148	0.597	2265.97	1352.33	0.088	1894.99	167.05
A_68_P23360936	chr4:140462092-140462151	NM_008812:-153	Padi2	PROMOTER	0.148	1.833	508.54	932.20	0.270	430.89	116.52
A_68_P31154934	chr17:34767881-34767925	NM_030890:1272	Prrt1	INSIDE	0.148	0.432	5022.36	2168.37	0.064	3732.73	239.24
A_68_P30128578	chr15:34373065-34373109	NM_001163485:-55	Rpl30	DIVERGENT_PROMOTER	0.148	0.543	1890.07	1027.02	0.081	1500.12	121.03
A_68_P28291149	chr12:25393568-25393620	NM_009104:476	Rrm2	INSIDE	0.148	0.719	1770.14	1272.33	0.106	1182.39	125.76
A_68_P24657050	chr6:94450275-94450319	NM_026255:-11	Slc25a26	PROMOTER	0.148	0.659	1733.51	1141.55	0.098	1259.85	123.03
A_68_P28100612	chr11:106134531-106134575	NM_001130187:-266	Smarcd2	DIVERGENT_PROMOTER	0.148	0.717	2817.48	2019.75	0.106	1950.45	206.37
A_68_P23591879	chr5:34279139-34279183	NM_011914:-253	Whsc2	PROMOTER	0.148	0.534	2089.38	1115.94	0.079	1486.76	117.47
A_68_P22262791	chr3:79090407-79090451	AK032506:-885		PROMOTER	0.148	0.621	3721.53	2309.28	0.092	2446.44	224.50
A_68_P26568903	chr9:61970644-61970688	mmu-mir-5133:-265		PROMOTER	0.148	0.511	1924.06	982.76	0.076	1698.19	128.32
A_68_P26237598	chr8:125565114-125565166	NM_001081379:1044	Ankrd11	INSIDE	0.147	1.414	991.73	1401.99	0.208	769.56	160.26
A_68_P25007188	chr7:25689481-25689525	NM_001130152:138	Arhgef1	INSIDE	0.147	0.653	1911.53	1247.54	0.096	1358.90	130.04
A_68_P25657170	chr8:11727542-11727589	NM_001113517:-539	Arhgef7	PROMOTER	0.147	0.519	2257.04	1170.55	0.076	1612.50	123.06
A_68_P24511775	chr6:65331286-65331330	NM_175524:21	C130060K24Rik	INSIDE	0.147	0.530	2081.02	1102.85	0.078	1554.64	120.73
A_68_P27533816	chr10:126500794-126500838	NM_009870:158	Cdk4	INSIDE	0.147	0.642	1855.86	1191.82	0.095	1239.12	117.31
A_68_P31791362	chr18:67503417-67503461	NM_007702:221	Cidea	INSIDE	0.147	0.750	6607.30	4956.51	0.111	4295.64	475.23
A_68_P22411201	chr3:108003559-108003603	NM_001081320:172	Cyb561d1	INSIDE	0.147	0.723	2406.39	1739.12	0.106	1685.36	179.31
A_68_P30347865	chr15:76200037-76200087	NM_021555:735	Fam203a	INSIDE	0.147	1.388	1576.99	2189.31	0.203	1228.77	250.05
A_68_P24589809	chr6:82724860-82724912	NM_013820:-438	Hk2	PROMOTER	0.147	0.594	1934.19	1149.04	0.087	1311.08	114.30
A_68_P25114497	chr7:57014275-57014319	NM_001146049:-179	Htatip2	PROMOTER	0.147	0.632	1827.68	1155.55	0.093	1317.74	122.80
A_68_P20296826	chr1:65225580-65225625	NM_010497:114	Idh1	INSIDE	0.147	0.530	2027.47	1073.80	0.078	1536.58	119.71
A_68_P27805842	chr11:53449954-53449998	NM_008355:-1772	Il13	PROMOTER	0.147	0.532	2695.44	1433.25	0.078	1983.97	155.09
A_68_P29134809	chr13:72766875-72766919	NM_010574:471	Irx2	INSIDE	0.147	0.486	2334.06	1134.35	0.071	1873.96	133.64
A_68_P30482198	chr15:99602344-99602388	NM_028015:580	Lass5	INSIDE	0.147	0.660	1573.99	1039.52	0.097	1216.34	118.16
A_68_P20025044	chr1:9958133-9958177	NM_145692:41047	Lrrc67	DOWNSTREAM	0.147	0.458	2357.32	1079.34	0.067	1700.36	114.20
A_68_P24137624	chr5:140267260-140267304	NM_010757:-207	Mafk	PROMOTER	0.147	0.617	1768.63	1091.14	0.091	1360.91	123.35
A_68_P24424405	chr6:47763384-47763429	NR_030485:-9755	Mir704	PROMOTER	0.147	0.427	2688.43	1148.66	0.063	1981.75	124.42

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P29773654	chr14:84846918-84846962	NM_001013753:3571	Pcdh17	INSIDE	0.147	0.570	3206.13	1827.43	0.084	2164.94	180.99
A_68_P26629702	chr9:72654701-72654745	NM_175485:-358	Prtg	PROMOTER	0.147	0.718	4221.62	3030.89	0.106	3133.78	330.92
A_68_P28534661	chr12:74040784-74040828	NM_011384:-125	Six6	PROMOTER	0.147	0.603	2438.40	1471.16	0.089	1838.01	163.19
A_68_P32036086	chr19:26681225-26681269	NM_011416:1597	Smarca2	INSIDE	0.147	0.496	2365.78	1174.36	0.073	1580.24	115.13
A_68_P31924554	chr19:4712508-4712552	NM_021287:1308	Spnb3	INSIDE	0.147	0.633	2518.67	1593.51	0.093	1762.68	164.01
A_68_P22538544	chr3:132347238-132347282	NM_173032:153	Tbck	INSIDE	0.147	0.539	1856.66	1000.80	0.079	1473.03	116.98
A_68_P26785090	chr9:103207295-103207339	NM_176979:-340	Topbp1	PROMOTER	0.147	0.388	2743.91	1064.70	0.057	2150.14	122.56
A_68_P24648067	chr6:92893117-92893161	NR_015530:2563	9530026P05Rik	INSIDE	0.146	0.552	2239.11	1235.64	0.081	1714.78	138.49
A_68_P32582138	chrX:103124420-103124464	NM_009530:269	Atrx	INSIDE	0.146	1.403	1563.93	2193.88	0.204	737.55	150.59
A_68_P31746205	chr18:59335935-59335979	NM_001081328:963	Chsy3	INSIDE	0.146	0.590	2367.87	1397.88	0.086	1681.82	144.95
A_68_P32094201	chr19:37249291-37249335	NM_198300:32471	Cpeb3	INSIDE	0.146	0.533	4915.16	2618.02	0.078	4221.46	328.25
A_68_P21489860	chr2:104430467-104430511	NM_001037326:-152	Cstf3	PROMOTER	0.146	0.705	2994.71	2109.85	0.103	2084.39	214.56
A_68_P30156153	chr15:39688931-39688978	NM_022722:62	Dpys	INSIDE	0.146	0.705	1631.29	1149.86	0.103	1188.32	122.11
A_68_P28614433	chr12:88488594-88488639	NM_010363:-51	Gstz1	PROMOTER	0.146	0.613	1975.54	1211.73	0.089	1383.70	123.75
A_68_P28961838	chr13:38726587-38726631	NM_139063:370	Muted	INSIDE	0.146	0.650	1652.99	1074.70	0.095	1293.75	122.85
A_68_P24176163	chr5:148672587-148672634	NM_025624:407	Pomp	INSIDE	0.146	0.529	2026.06	1071.92	0.077	1571.59	121.26
A_68_P25435184	chr7:121419570-121419614	NM_011965:38	Psma1	INSIDE	0.146	0.703	1512.13	1063.11	0.103	1137.00	116.81
A_68_P28540842	chr12:75065446-75065490	NM_178392:-48	Snapc1	PROMOTER	0.146	0.520	2184.93	1136.69	0.076	1599.66	121.17
A_68_P32239402	chrX:7215889-7215933	NM_009305:205	Syp	INSIDE	0.146	2.741	2039.56	5590.66	0.400	797.29	319.04
A_68_P24018824	chr5:117569883-117569927	NM_001199685:-233	Taok3	DIVERGENT_PROMOTER	0.146	0.565	1899.34	1073.81	0.083	1433.26	118.63
A_68_P20555798	chr1:121086183-121086227			Unknown	0.146	0.713	1997.86	1424.83	0.104	1621.69	168.71
A_68_P23962030	chr5:106990411-106990455	ENSMUST00000131029:13302		INSIDE	0.146	0.467	2489.24	1162.31	0.068	1922.58	130.64
A_68_P24138293	chr5:140389088-140389132	NM_175522:5214	Elfn1	INSIDE	0.145	0.524	2335.48	1223.21	0.076	1655.78	126.15
A_68_P25835354	chr8:47380103-47380147	NM_173789:-99	Helt	PROMOTER	0.145	0.659	1657.80	1092.20	0.095	1306.90	124.55
A_68_P22325452	chr3:90280402-90280446	NM_026374:302	Ilf2	INSIDE	0.145	0.691	1734.83	1198.46	0.100	1432.82	143.04
A_68_P24921912	chr6:145197978-145198027	NM_021284:749	Kras	INSIDE	0.145	0.721	2164.39	1561.55	0.105	1620.53	169.47
A_68_P22872798	chr4:43644462-43644506	NM_173788:-322	Npr2	PROMOTER	0.145	0.685	3693.85	2530.88	0.099	2601.01	258.44
A_68_P27279289	chr10:79317369-79317415	NM_001077363:43	Ptbp1	INSIDE	0.145	0.643	3440.87	2213.88	0.093	2369.15	221.00
A_68_P22450166	chr3:116298284-116298328	NM_028349:381	Sass6	INSIDE	0.145	0.590	1968.04	1161.25	0.085	1393.24	119.11
A_68_P26587801	chr9:65309057-65309101	NM_138584:335	Spg21	INSIDE	0.145	0.610	3316.04	2023.07	0.089	2586.25	229.16
A_68_P31096038	chr17:24342160-24342204	NM_001163847:325	Tbc1d24	INSIDE	0.145	1.358	5357.45	7277.47	0.197	3351.03	659.28
A_68_P24838521	chr6:128305667-128305711	NM_011657:181	Tulp3	INSIDE	0.145	0.746	6524.39	4868.60	0.108	4634.17	501.95
A_68_P31962498	chr19:12870780-12870828	NR_024093:-191	U05342	DIVERGENT_PROMOTER	0.145	0.672	1627.79	1093.84	0.098	1213.82	118.51
A_68_P32975184	chr9:108393603-108393647	NM_027804:618	Usp19	INSIDE	0.145	0.448	2553.08	1142.68	0.065	1982.21	128.47
A_68_P27241483	chr10:72117792-72117836	NM_025635:172	Zwint	INSIDE	0.145	0.593	1715.60	1017.51	0.086	1370.75	117.82
A_68_P25841612	chr8:48498559-48498603	ENSMUST00000074466:98		INSIDE	0.145	0.642	1654.14	1062.14	0.093	1437.72	133.73
A_68_P24819099	chr6:125114766-125114820	NM_008084:809	Gapdh	INSIDE	0.144	0.713	1595.12	1137.65	0.103	1135.74	116.87
A_68_P31603481	chr18:32719632-32719687	NM_001048207:29	Gypc	INSIDE	0.144	0.652	1678.83	1095.19	0.094	1275.87	119.70
A_68_P25954141	chr8:73321121-73321165	NM_199308:-4810	Mast3	PROMOTER	0.144	2.216	3856.19	8546.18	0.320	2589.98	828.89
A_68_P27281294	chr10:79612495-79612539	NM_021565:1482	Midn	INSIDE	0.144	0.575	3449.71	1982.84	0.083	2534.98	209.94
A_68_P26011762	chr8:85387432-85387476	NM_177378:200	Rnf150	INSIDE	0.144	0.373	2953.75	1100.78	0.054	2359.11	126.34
A_68_P30546793	chr16:11203333-11203377	NM_025546:31	Rsl1d1	INSIDE	0.144	0.673	1570.09	1056.73	0.097	1216.18	118.06
A_68_P22412729	chr3:108247976-108248020	NM_001204979:179	Sars	INSIDE	0.144	0.620	1784.22	1106.24	0.089	1331.89	119.05
A_68_P28535265	chr12:74146791-74146835	NM_009189:887	Six1	INSIDE	0.144	0.419	2479.21	1037.84	0.060	2086.28	125.71
A_68_P21783955	chr2:158439931-158439975	NM_009508:3459	Slc32a1	INSIDE	0.144	0.708	1510.80	1068.98	0.102	1160.61	118.27
A_68_P28581895	chr12:82732734-82732780	NM_001033149:401	Ttc9	INSIDE	0.144	0.544	2004.45	1091.41	0.078	1490.13	116.75
A_68_P30422257	chr15:88785384-88785428	NM_172818:-558	Ttll8	PROMOTER	0.144	0.634	1698.15	1077.19	0.091	1346.29	122.97
A_68_P24973049	chr7:13388821-13388865	NM_026046:15367	Zfp329	DOWNSTREAM	0.144	0.674	1664.69	1121.87	0.097	1183.86	114.95
A_68_P29455892	chr14:22807139-22807185	NM_145459:1661	Zfp503	INSIDE	0.144	0.636	1611.16	1024.55	0.092	1288.71	118.05
A_68_P26710355	A_68_P26710355			Unknown	0.144	0.715	5807.06	4152.40	0.103	4214.33	433.26
A_68_P20026598	chr1:10222127-10222186	NM_001102430:595	Arfgef1	INSIDE	0.143	1.528	1118.22	1708.68	0.218	795.12	173.60

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P30371086	chr15:80085860-80085904	NM_009716:269	Atf4	INSIDE	0.143	0.739	6418.96	4741.92	0.106	4567.50	482.91
A_68_P31458881	chr18:3508571-3508630	NM_026505:646	Bambi	INSIDE	0.143	0.715	1410.05	1008.83	0.102	1201.39	122.95
A_68_P25093841	chr7:52825908-52825952	NM_009737:198	Bcat2	INSIDE	0.143	0.524	2014.69	1054.89	0.075	1611.22	120.81
A_68_P23362368	chr4:140695411-140695455	NM_001025608:279	D4Ertd22e	INSIDE	0.143	0.680	1498.73	1019.43	0.097	1202.61	117.16
A_68_P32553698	chrX:96331493-96331537	NM_010110:46	Efnb1	INSIDE	0.143	1.438	1503.49	2161.96	0.206	785.68	161.92
A_68_P21771130	chr2:156247152-156247196	NM_001003815:387	Epb4.1l1	INSIDE	0.143	1.853	2136.61	3959.67	0.264	1540.17	407.01
A_68_P23301441	chr4:129985717-129985761	NM_010174:-283	Fabp3	PROMOTER	0.143	2.006	3897.41	7818.90	0.286	2360.07	675.17
A_68_P28419951	chr12:50484189-50484235	NM_008241:219	Foxg1	INSIDE	0.143	0.663	1701.63	1128.29	0.095	1264.70	119.59
A_68_P22311351	chr3:87826838-87826882	NM_022031:4573	Hapln2	INSIDE	0.143	0.622	5199.28	3233.76	0.089	3528.41	314.89
A_68_P20826869	chr1:173177373-173177425	NM_153064:-155	Ndufs2	DIVERGENT_PROMOTER	0.143	0.695	1648.83	1145.93	0.099	1175.65	116.93
A_68_P25514699	chr7:136400655-136400699	NM_001080963:69	Ppapdc1a	INSIDE	0.143	0.548	1757.12	963.73	0.079	1485.47	116.63
A_68_P32066438	chr19:31838454-31838498	NM_001013833:1047	Prkg1	INSIDE	0.143	0.715	1475.93	1054.89	0.102	1131.58	115.42
A_68_P32289248	chrX:20195553-20195607	NM_001167776:696	Rbm10	INSIDE	0.143	2.026	1692.56	3428.57	0.291	715.96	208.02
A_68_P24061481	chr5:124927981-124928025	NM_030259:242	Rilpl2	INSIDE	0.143	0.696	3170.36	2206.78	0.100	2288.85	227.81
A_68_P20617850	chr1:133724396-133724440	NM_173865:-170	Slc41a1	PROMOTER	0.143	0.648	3597.66	2331.67	0.093	2661.22	247.15
A_68_P25724847	chr8:26127928-26127972	NM_027194:268	Tm2d2	INSIDE	0.143	0.479	2579.85	1236.96	0.069	1716.41	117.76
A_68_P24136178	chr5:140022739-140022790	NM_013702:2913	Uncx	INSIDE	0.143	0.547	1889.50	1033.10	0.078	1509.11	118.01
A_68_P22394202	chr3:104764921-104764965	NM_009520:-315	Wnt2b	PROMOTER	0.143	0.703	1711.20	1202.13	0.101	1180.85	118.91
A_68_P21664159	chr2:136504670-136504714			Unknown	0.143	0.660	1850.04	1220.98	0.095	1452.73	137.28
A_68_P26235837	chr8:125299586-125299630	NM_144932:204	Acsf3	INSIDE	0.142	0.632	1690.76	1068.31	0.090	1295.99	116.19
A_68_P32717148	chrX:140752921-140752965	NM_026247:434	Alg13	INSIDE	0.142	2.935	7059.89	20719.84	0.417	2859.28	1192.69
A_68_P22069523	chr3:38383943-38383987	NM_001167883:-226	Ankrd50	PROMOTER	0.142	1.541	10968.42	16902.02	0.218	7499.82	1638.58
A_68_P22058854	chr3:36470470-36470514	NM_009828:426	Ccna2	INSIDE	0.142	0.588	5226.28	3071.76	0.083	3578.10	297.82
A_68_P22874798	chr4:44026078-44026122	NM_001080384:586	Clta	INSIDE	0.142	0.594	3563.10	2116.44	0.084	2508.59	211.54
A_68_P22128837	chr3:51081149-51081193	NM_023502:48739	Elf2	INSIDE	0.142	0.545	2634.44	1434.62	0.078	2014.56	156.16
A_68_P25947454	chr8:71919340-71919384	NR_038043:81	Gm10033	INSIDE	0.142	0.631	1761.42	1111.03	0.090	1309.54	117.36
A_68_P28882218	chr13:23654270-23654316	NM_178205:-58	Hist1h3e	PROMOTER	0.142	0.579	3050.22	1765.67	0.082	2142.61	175.81
A_68_P26061534	chr8:94325346-94325390	NM_008393:-95	Irx3	PROMOTER	0.142	0.667	3841.50	2562.64	0.095	2815.88	266.28
A_68_P32227001	chr19:60832863-60832907	NM_178421:995	Nanos1	INSIDE	0.142	0.467	2123.47	992.04	0.066	1757.05	116.56
A_68_P28767700	chr12:117643877-117643921	NM_133762:24	Ncapg2	INSIDE	0.142	2.324	8194.30	19044.50	0.330	5306.27	1749.19
A_68_P26951409	chr10:13193710-13193754	NM_001195065:470	Phactr2	INSIDE	0.142	0.516	3272.04	1686.83	0.073	2460.01	179.63
A_68_P32567638	chrX:99384443-99384487	NM_009094:-754	Rps4x	PROMOTER	0.142	1.502	1346.64	2022.92	0.214	561.33	120.06
A_68_P29699882	chr14:70591597-70591641	NM_011366:15826	Sorbs3	INSIDE	0.142	0.740	4672.18	3458.45	0.105	3122.61	329.25
A_68_P28154079	chr11:115397941-115397990	NM_133354:-421	Sumo2	PROMOTER	0.142	0.550	1981.25	1090.26	0.078	1531.33	119.91
A_68_P28078652	chr11:102146344-102146398	NM_028076:96	Tmub2	INSIDE	0.142	2.534	2094.28	5307.20	0.360	1324.01	476.80
A_68_P28280597	chr12:21423661-21423705	NM_011739:-385	Ywhaq	PROMOTER	0.142	0.515	2174.82	1120.31	0.073	1666.47	121.62
A_68_P28601430	chr12:86311556-86311600	NM_178065:258	1110018G07Rik	INSIDE	0.141	0.694	2777.69	1926.56	0.098	2013.51	197.55
A_68_P32365089	chrX:45866544-45866588	NM_012019:37	Aifm1	INSIDE	0.141	1.937	2558.66	4956.93	0.273	1047.74	285.92
A_68_P32121139	chr19:42505784-42505828	NM_145123:467	Crtac1	INSIDE	0.141	1.354	4979.47	6743.92	0.191	3461.59	662.13
A_68_P22882386	chr4:45355486-45355530	NM_153167:536	Dcaf10	INSIDE	0.141	0.673	1928.95	1298.60	0.095	1355.43	128.66
A_68_P26167379	chr8:113782539-113782583	NM_009149:542	Glg1	INSIDE	0.141	0.394	2867.48	1130.21	0.056	2154.21	119.57
A_68_P31143793	chr17:32250971-32251015	NM_008716:52805	Notch3	DOWNSTREAM	0.141	0.589	1923.80	1133.46	0.083	1442.95	120.04
A_68_P28107248	chr11:107330701-107330745	NM_145823:1312	Pitpnc1	INSIDE	0.141	0.532	2114.44	1124.23	0.075	1579.74	118.72
A_68_P31937055	chr19:7048934-7048978	NM_008889:-581	Ppp1r14b	DIVERGENT_PROMOTER	0.141	0.712	1970.00	1401.84	0.100	1417.99	142.16
A_68_P31713378	chr18:53623569-53623613	NM_001033281:-609	Prdm6	PROMOTER	0.141	0.720	1801.75	1296.47	0.101	1308.97	132.57
A_68_P23308591	chr4:131393677-131393729	NM_001083119:491	Ptpru	INSIDE	0.141	1.655	2144.36	3549.76	0.233	1535.45	357.65
A_68_P30572550	chr16:17209655-17209699	NM_001033338:1449	Rimbp3	INSIDE	0.141	0.747	4156.80	3106.86	0.106	2778.69	293.50
A_68_P26710070	chr9:88334164-88334211	NM_172926:-398	Snx14	PROMOTER	0.141	0.522	2405.68	1255.27	0.074	1962.30	144.84
A_68_P26215000	chr8:122128943-122128988	NM_021441:175	Taf1c	INSIDE	0.141	0.699	1865.55	1304.40	0.099	1397.70	137.69
A_68_P30380064	chr15:81688492-81688536	NM_020507:242	Tob2	INSIDE	0.141	0.691	1994.19	1377.13	0.097	1532.96	149.05
A_68_P23317940	chr4:133054507-133054551	NM_001081156:-63	Trnp1	PROMOTER	0.141	0.584	2921.82	1705.71	0.083	2092.08	172.62

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31669249	chr18:44988742-44988786	NM_001163013:446	Ythdc2	INSIDE	0.141	0.709	1587.57	1126.27	0.100	1245.48	124.69
A_68_P31620881	chr18:36078954-36078998	AK021191:6191		DOWNSTREAM	0.141	0.513	2471.28	1268.09	0.072	1813.50	131.43
A_68_P21957614	chr3:14611075-14611119	NM_001099674:160	1810022K09Rik	INSIDE	0.140	1.474	1437.04	2118.18	0.207	1109.71	229.17
A_68_P20504214	chr1:107561226-107561270	NM_029349:811	2310035C23Rik	INSIDE	0.140	0.684	2519.03	1723.27	0.096	1977.98	189.90
A_68_P25045002	chr7:35461038-35461082	NM_175140:136670	Chst8	INSIDE	0.140	0.684	1690.55	1156.88	0.096	1216.16	116.90
A_68_P32467455	chrX:71558602-71558649	NM_138607:254	Fam50a	INSIDE	0.140	1.791	1017.43	1822.19	0.251	474.27	118.97
A_68_P24620291	chr6:88140777-88140827	NM_008090:-7855	Gata2	PROMOTER	0.140	2.317	2466.70	5716.21	0.325	1622.65	527.89
A_68_P28836952	chr13:14155652-14155696	NM_010282:-6	Ggps1	DIVERGENT_PROMOTER	0.140	0.658	2971.62	1956.18	0.092	2215.76	203.63
A_68_P21129657	chr2:34628148-34628192	NM_001163434:561	Hspa5	INSIDE	0.140	0.581	2196.73	1276.73	0.082	1521.06	124.03
A_68_P25092716	chr7:52625642-52625686	NM_011698:270	Lin7b	INSIDE	0.140	0.512	2044.28	1047.66	0.072	1622.61	116.58
A_68_P25587299	chr7:148380231-148380275	NM_153777:-789	Lrrc56	PROMOTER	0.140	0.608	1949.57	1184.88	0.085	1391.28	118.56
A_68_P32071012	chr19:32670221-32670265	NM_001201470:38	Papss2	INSIDE	0.140	0.694	1559.72	1082.10	0.097	1288.82	125.51
A_68_P27901889	chr11:70467270-70467315	NM_011072:860	Pfn1	INSIDE	0.140	0.714	2299.71	1641.87	0.100	1771.30	177.23
A_68_P22340913	chr3:94641242-94641288	NM_001165948:-224	Pogz	PROMOTER	0.140	0.694	2141.72	1485.92	0.097	1462.10	141.58
A_68_P20557414	chr1:121401510-121401554	NM_022327:-173	Ralb	PROMOTER	0.140	0.616	1876.08	1155.68	0.086	1397.04	120.39
A_68_P31496430	chr18:11816616-11816661	NM_001081223:288	Rbbp8	INSIDE	0.140	0.659	1681.30	1108.46	0.092	1244.74	114.89
A_68_P29288686	chr13:104899839-104899883	NM_144838:-9	Sgtb	DIVERGENT_PROMOTER	0.140	0.641	2931.60	1878.98	0.090	2053.70	183.87
A_68_P26574086	chr9:62990509-62990553	NM_172446:4257	Skor1	INSIDE	0.140	1.471	2598.37	3822.72	0.205	1699.93	349.32
A_68_P26787848	chr9:103663928-103663974	NM_178638:217	Tmem108	INSIDE	0.140	0.520	2130.84	1107.00	0.073	1676.23	121.91
A_68_P32564022	chrX:98614921-98614970	NM_001177985:308	Zmym3	INSIDE	0.140	1.403	1636.79	2296.51	0.197	767.63	150.92
A_68_P22864043	chr4:41678560-41678610	NM_001017362:-410	Arid3c	PROMOTER	0.139	2.159	3516.81	7591.05	0.300	2035.89	611.32
A_68_P25810705	chr8:42459691-42459735	NM_019734:339	Asah1	INSIDE	0.139	0.561	2521.91	1414.34	0.078	2001.07	155.57
A_68_P26665706	chr9:79566930-79566982	NM_007730:-471	Col12a1	PROMOTER	0.139	0.578	1800.42	1040.62	0.080	1449.70	116.37
A_68_P25301855	chr7:95426643-95426687	NM_009982:62	Ctsc	INSIDE	0.139	0.586	2010.20	1178.91	0.081	1438.24	117.22
A_68_P29698995	chr14:70474363-70474407	NM_018781:-2867	Egr3	PROMOTER	0.139	0.548	1932.06	1058.90	0.076	1522.60	115.60
A_68_P32461576	chrX:70474445-70474489	NM_007978:822	F8a	INSIDE	0.139	2.026	1120.02	2269.46	0.282	438.88	123.64
A_68_P32750743	chrX:149216712-149216756	NM_010951:271	Gpr143	INSIDE	0.139	1.605	1725.72	2770.55	0.223	657.78	146.37
A_68_P25093127	chr7:52690084-52690132	NM_030678:-100	Gys1	DIVERGENT_PROMOTER	0.139	0.698	1559.87	1088.21	0.097	1260.83	122.64
A_68_P32727713	chrX:143397691-143397735	NM_008312:657	Htr2c	INSIDE	0.139	2.080	4322.19	8992.22	0.289	1750.79	505.29
A_68_P21906910	chr2:180629073-180629117	NR_029538:350	Mir124a-3	DOWNSTREAM	0.139	0.570	1948.81	1110.72	0.079	1525.94	120.67
A_68_P27950593	chr11:79524583-79524627	NR_029579:-866	Mir193	PROMOTER	0.139	0.587	2752.97	1614.84	0.081	1959.04	159.29
A_68_P20352132	chr1:75121636-75121680	NM_029342:142	Nhej1	INSIDE	0.139	0.526	2274.82	1195.65	0.073	1641.83	120.23
A_68_P27056941	chr10:34138297-34138341	NM_176968:16	Nt5dc1	INSIDE	0.139	1.588	5026.10	7980.69	0.220	3697.00	813.78
A_68_P27889095	chr11:68200015-68200060	NM_008744:291	Ntn1	INSIDE	0.139	0.675	1757.64	1186.31	0.094	1243.46	116.80
A_68_P32134234	chr19:44833782-44833828	NM_011037:1921	Pax2	INSIDE	0.139	1.435	851.73	1221.82	0.200	596.65	119.30
A_68_P23916649	chr5:98615733-98615777	NM_029947:5867	Prdm8	INSIDE	0.139	1.483	5168.37	7663.67	0.206	3478.63	718.01
A_68_P30475881	chr15:98507653-98507697	NM_172612:218	Rnd1	INSIDE	0.139	0.618	2848.29	1759.93	0.086	2208.97	189.56
A_68_P32182252	chr19:53465097-53465141	NM_172429:-55	Smndc1	PROMOTER	0.139	0.640	1952.58	1249.18	0.089	1351.06	119.87
A_68_P28523840	chr12:72116565-72116609	NM_001081195:-367	Arid4a	PROMOTER	0.138	0.721	2671.37	1926.18	0.100	2074.18	206.87
A_68_P24995570	chr7:20437597-20437641	NM_001033419:9030	Ceacam16	INSIDE	0.138	0.716	1584.42	1134.90	0.099	1230.46	121.30
A_68_P24138260	chr5:140385057-140385101	NM_175522:1182	Elfn1	INSIDE	0.138	0.567	1989.09	1128.13	0.078	1511.23	117.91
A_68_P27289056	chr10:80813448-80813492	NM_001163166:-268	Hmg20b	DIVERGENT_PROMOTER	0.138	0.557	2214.07	1232.20	0.077	1578.63	120.94
A_68_P28077065	chr11:101887780-101887824	NM_007863:467	Mpp3	INSIDE	0.138	0.486	2188.74	1063.17	0.067	1777.48	118.97
A_68_P27184377	chr10:61596546-61596590	NM_009719:731	Neurog3	INSIDE	0.138	0.702	4953.55	3479.40	0.097	3214.96	312.33
A_68_P30000046	chr15:8394229-8394273	NM_027707:213	Nipbl	INSIDE	0.138	0.424	2560.38	1085.56	0.059	2056.75	120.77
A_68_P27541262	chr10:127846864-127846908	NM_027257:-34	Obfc2b	DIVERGENT_PROMOTER	0.138	0.649	3690.52	2394.30	0.090	2625.23	235.69
A_68_P24832846	chr6:127403694-127403738	NM_181402:-24	Parp11	PROMOTER	0.138	0.672	1613.64	1084.01	0.093	1365.72	126.94
A_68_P29753328	chr14:80168173-80168220	NM_001042726:2923	Pcdh8	INSIDE	0.138	0.588	2210.42	1300.81	0.081	1591.26	129.65
A_68_P24172759	chr5:148081959-148082003	NM_008814:274	Pdx1	INSIDE	0.138	0.733	3678.81	2696.06	0.101	2571.85	259.42
A_68_P26605676	chr9:68502227-68502277	NM_013646:644	Rora	INSIDE	0.138	0.712	1565.16	1113.89	0.098	1176.29	115.52
A_68_P26579681	chr9:63870209-63870254	NM_008542:-365	Smad6	PROMOTER	0.138	0.631	2199.25	1387.07	0.087	1305.69	113.99

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P22386738	chr3:103379153-103379197	NM_018800:-29	Syt6	PROMOTER	0.138	0.547	3752.83	2051.75	0.075	2824.36	212.93
A_68_P23590347	chr5:34001167-34001211	NM_001040435:393	Tacc3	INSIDE	0.138	0.532	2087.73	1110.09	0.074	1585.54	116.58
A_68_P20638621	chr1:137210401-137210445	NM_011590:-108	Timm17a	PROMOTER	0.138	0.737	4696.09	3461.85	0.102	3208.97	325.98
A_68_P25021123	chr7:29097166-29097212	NM_025616:-123	Timm50	PROMOTER	0.138	0.611	3272.01	1999.33	0.084	2232.88	188.39
A_68_P32114042	chr19:41337768-41337812	NM_133352:704	Tm9sf3	INSIDE	0.138	0.645	1884.33	1215.40	0.089	1308.07	116.34
A_68_P25947577	chr8:72149392-72149438	NM_001045553:-340	Zfp868	PROMOTER	0.138	0.704	1744.78	1227.91	0.097	1254.48	121.53
A_68_P27835439	chr11:59015720-59015764	NR_037964:191	2610507I01Rik	INSIDE	0.137	0.588	2042.86	1201.16	0.080	1539.89	123.82
A_68_P26373431	chr9:26806964-26807008	NM_025862:148	Acad8	INSIDE	0.137	0.474	2559.24	1211.87	0.065	1811.77	117.56
A_68_P30337592	chr15:74346503-74346547	NM_174991:-101	Bai1	PROMOTER	0.137	0.677	1685.50	1141.21	0.093	1259.89	116.84
A_68_P26042567	chr8:91220855-91220899	NM_001128170:-50	Cyld	PROMOTER	0.137	0.680	3877.03	2636.67	0.093	2731.99	254.67
A_68_P28914791	chr13:30077924-30077972	NM_010093:-16	E2f3	PROMOTER	0.137	0.436	2865.18	1250.54	0.060	1910.86	114.42
A_68_P27542071	chr10:128002533-128002577	NM_011119:436	Pa2g4	INSIDE	0.137	0.727	5194.48	3777.12	0.100	3678.94	366.69
A_68_P23185681	chr4:106323879-106323923	NM_001083887:227	Pars2	INSIDE	0.137	0.584	2148.44	1254.58	0.080	1505.26	120.70
A_68_P32575423	chrX:101176377-101176421	NM_011276:225	Rlim	INSIDE	0.137	1.409	1738.02	2448.18	0.193	705.74	136.32
A_68_P22049509	chr3:34562671-34562720	NR_015580:103393	Sox2ot	INSIDE	0.137	0.636	1901.02	1208.17	0.087	1400.57	122.27
A_68_P24327617	chr6:29559260-29559304	NM_177296:325	Tnpo3	INSIDE	0.137	0.735	6423.12	4720.37	0.101	4616.03	464.23
A_68_P22314484	chr3:88358116-88358160	NM_033526:501	Ubqln4	INSIDE	0.137	0.544	2132.16	1160.56	0.074	1560.54	115.96
A_68_P21418962	chr2:90623430-90623474	NM_178755:552	Agbl2	INSIDE	0.136	1.458	737.57	1075.64	0.199	591.98	117.60
A_68_P22941964	chr4:56877971-56878015	NM_018761:91	Ctnnal1	INSIDE	0.136	0.566	4259.49	2410.06	0.077	3282.49	251.89
A_68_P21905698	chr2:180444588-180444638	NM_175551:-7807	Dido1	PROMOTER	0.136	0.472	2594.30	1225.42	0.064	1819.21	117.19
A_68_P29386051	chr14:8651064-8651108	NM_134080:616	Flnb	INSIDE	0.136	0.522	2409.82	1257.60	0.071	1705.76	121.46
A_68_P30540360	chr16:9994787-9994831	NM_008170:-2182	Grin2a	PROMOTER	0.136	0.567	1991.22	1129.72	0.077	1490.93	115.17
A_68_P32507213	chrX:83022104-83022148	NM_008194:32	Gyk	INSIDE	0.136	3.630	4744.25	17219.68	0.495	1881.94	930.63
A_68_P31625592	chr18:36904491-36904538	NM_011879:205	Ik	INSIDE	0.136	0.678	1751.88	1188.45	0.092	1303.10	120.10
A_68_P28079749	chr11:102328621-102328668	NM_010575:2553	Itga2b	INSIDE	0.136	0.669	2204.81	1475.73	0.091	1409.57	127.98
A_68_P28178579	chr11:119408457-119408501	NM_008730:656	Nptx1	INSIDE	0.136	0.696	1871.48	1302.93	0.095	1301.95	123.21
A_68_P24133760	chr5:139605384-139605428	NM_008923:300	Prkar1b	INSIDE	0.136	0.574	2248.19	1289.39	0.078	1659.87	129.63
A_68_P32481889	chrX:75828853-75828902	NM_001164275:244	Prrg1	INSIDE	0.136	1.555	1385.57	2154.44	0.212	576.68	122.29
A_68_P21115161	chr2:32252153-32252197	NM_133783:765	Ptges2	INSIDE	0.136	0.594	2144.51	1273.43	0.081	1420.51	114.72
A_68_P27910560	chr11:72080885-72080933	NM_001004148:-802	Slc13a5	PROMOTER	0.136	0.700	1720.46	1203.84	0.095	1331.47	126.50
A_68_P32401095	chrX:54646102-54646148	NR_002903:-1438	Snord61	PROMOTER	0.136	1.529	1540.62	2355.91	0.209	624.49	130.23
A_68_P21396039	chr2:84888658-84888702	NM_001081260:-1936	Tnks1bp1	PROMOTER	0.136	0.598	3705.39	2214.45	0.082	2725.49	222.19
A_68_P27804727	chr11:53244769-53244814	NM_025352:-458	Uqcrq	DIVERGENT_PROMOTER	0.136	0.472	2385.36	1124.72	0.064	1820.09	117.07
A_68_P23296400	chr4:129054411-129054455	NM_028603:840	Zbtb8a	INSIDE	0.136	0.622	4062.61	2525.45	0.085	3035.03	257.52
A_68_P25657168	chr8:11727352-11727396	NM_001113517:-730	Arhgef7	PROMOTER	0.135	1.363	1967.00	2681.30	0.184	1363.99	250.51
A_68_P23961348	chr5:106886251-106886295	NM_001005477:913	Barhl2	INSIDE	0.135	0.591	2335.12	1379.35	0.080	1669.97	133.27
A_68_P32040830	chr19:27504703-27504752	NR_027987:201	C030016D13Rik	INSIDE	0.135	0.698	1691.61	1180.67	0.094	1241.33	116.78
A_68_P26132332	chr8:107748862-107748908	NM_145604:-203	D230025D16Rik	PROMOTER	0.135	0.694	1698.26	1178.06	0.094	1288.11	120.64
A_68_P29160014	chr13:77847868-77847912	NM_001163419:-60	Fam172a	PROMOTER	0.135	0.727	2969.61	2157.54	0.098	2344.87	230.17
A_68_P21477082	chr2:102290453-102290497	NM_010218:1475	Fjx1	INSIDE	0.135	1.859	930.80	1730.25	0.250	714.43	178.68
A_68_P28043606	chr11:96165053-96165098	NM_008268:250	Hoxb5	INSIDE	0.135	0.595	2809.13	1671.01	0.080	1699.38	136.07
A_68_P32375459	chrX:48558594-48558638	NM_134163:393	Mbnl3	INSIDE	0.135	1.594	2211.23	3523.80	0.215	885.86	190.30
A_68_P24796451	chr6:119987387-119987431	NR_030487:-3079	Mir706	PROMOTER	0.135	0.530	2312.86	1226.42	0.071	1732.05	123.66
A_68_P23608588	chr5:36925165-36925210	NM_133910:-141	Tbc1d14	PROMOTER	0.135	0.507	2254.95	1143.40	0.068	1693.06	115.56
A_68_P24153542	chr5:143578302-143578350	NM_001122730:740	Tnrc18	INSIDE	0.135	0.577	2329.17	1344.42	0.078	1499.81	116.77
A_68_P28166392	chr11:117517198-117517249	NM_198022:1621	Tnrc6c	INSIDE	0.135	0.677	1899.77	1286.31	0.091	1297.93	118.68
A_68_P32700055	chrX:137132673-137132722	NM_001077364:2364	Tsc22d3	INSIDE	0.135	1.560	1367.22	2133.18	0.211	569.62	119.94
A_68_P27942765	chr11:78157408-78157455	NM_011676:408	Unc119	INSIDE	0.135	0.599	1847.99	1106.68	0.081	1445.23	116.78
A_68_P28694453	chr12:104187317-104187361	NM_001081017:270	Unc79	INSIDE	0.135	0.658	1775.46	1169.04	0.089	1317.48	116.97
A_68_P21425362	chr2:91761645-91761689	NM_007699:-679	Chrm4	PROMOTER	0.134	0.659	2073.81	1367.59	0.088	1417.75	124.99
A_68_P26659811	chr9:78328698-78328742	NM_010106:811	Eef1a1	INSIDE	0.134	0.497	2332.21	1159.60	0.067	1815.37	121.26

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31493048	chr18:11053045-11053099	NM_010258:565	Gata6	INSIDE	0.134	0.629	2098.04	1318.64	0.084	1449.86	122.10
A_68_P30501066	chr15:102798113-102798164	NM_010462:912	Hoxc10	INSIDE	0.134	1.464	822.14	1203.90	0.196	593.66	116.37
A_68_P23356913	chr4:139800280-139800324	NM_198610:2424	Igsf21	INSIDE	0.134	0.551	2225.57	1226.01	0.074	1662.21	122.44
A_68_P26884587	chr9:121550968-121551014	NM_026915:-306	Lyzl4	DIVERGENT_PROMOTER	0.134	0.413	3297.10	1363.09	0.055	2095.23	115.81
A_68_P32252895	chrX:10295371-10295422	NM_001166635:906	Mid1ip1	INSIDE	0.134	1.498	1469.74	2202.29	0.201	584.01	117.45
A_68_P24993777	chr7:20108952-20108996	NM_027116:4895	Nkpd1	INSIDE	0.134	0.706	1525.27	1076.21	0.094	1239.64	117.04
A_68_P25326015	chr7:99817991-99818041	NM_029078:406	Pcf11	INSIDE	0.134	0.614	2628.65	1613.87	0.082	1783.14	147.02
A_68_P31542489	chr18:21160241-21160286	NM_019706:422	Rnf138	INSIDE	0.134	0.490	2635.47	1291.67	0.066	1794.92	117.62
A_68_P31936365	chr19:6914837-6914881	NM_019924:233	Rps6ka4	INSIDE	0.134	0.578	2018.64	1167.04	0.078	1500.59	116.39
A_68_P24066623	chr5:125869716-125869760	NM_019639:649	Ubc	INSIDE	0.134	0.634	6152.72	3902.70	0.085	4499.47	382.72
A_68_P23440546	chr4:155148502-155148549	NM_147776:145	Vwa1	INSIDE	0.134	0.746	3334.18	2486.17	0.100	2021.41	201.88
A_68_P26337051	chr9:18277941-18277985	NM_028935:41	Zfp558	INSIDE	0.134	1.754	5047.42	8850.97	0.235	3329.71	780.91
A_68_P23278552	chr4:125840552-125840597	NM_025856:-665	1700029G01Rik	PROMOTER	0.133	0.599	1894.74	1134.87	0.080	1477.44	117.46
A_68_P31834411	chr18:75165635-75165679	NM_001001181:103	BC031181	INSIDE	0.133	0.492	2926.85	1439.99	0.065	2239.99	146.57
A_68_P22733181	chr4:12016440-12016484	NM_198957:-54	C430048L16Rik	DIVERGENT_PROMOTER	0.133	0.608	3136.35	1906.29	0.081	2171.18	176.00
A_68_P25392273	chr7:112574745-112574790	NM_007627:434	Cckbr	INSIDE	0.133	1.597	1130.99	1806.52	0.213	807.15	172.02
A_68_P31715729	chr18:54021378-54021423	NM_152809:-366	Csnk1g3	PROMOTER	0.133	0.698	1796.19	1253.59	0.093	1298.58	120.61
A_68_P20864294	chr1:180458639-180458683	NM_001161665:-595	Kif26b	PROMOTER	0.133	0.590	1901.92	1121.91	0.079	1535.15	120.81
A_68_P24990787	chr7:19577120-19577164	NM_145579:549	Mypop	INSIDE	0.133	0.688	2030.37	1397.06	0.092	1293.77	118.59
A_68_P32564062	chrX:98625083-98625127	NM_023144:115	Nono	INSIDE	0.133	2.727	2528.62	6895.70	0.363	1121.06	406.96
A_68_P26318242	chr9:14419308-14419352	NM_001081395:114	Amotl1	INSIDE	0.132	0.390	2953.45	1152.58	0.052	2339.58	120.67
A_68_P31786168	chr18:66451122-66451166	NM_178793:348	Ccbe1	INSIDE	0.132	0.583	2758.49	1607.95	0.077	2137.94	164.38
A_68_P24218883	chr6:6831846-6831891	NM_010056:200	Dlx5	INSIDE	0.132	0.639	1804.65	1152.74	0.084	1392.22	117.51
A_68_P24992782	chr7:19930618-19930662	NM_001127324:221	Ercc1	INSIDE	0.132	0.641	2054.47	1316.54	0.085	1416.51	119.88
A_68_P30630405	chr16:28445397-28445447	NM_183064:-109	Fgf12	PROMOTER	0.132	0.604	1991.04	1201.71	0.080	1536.08	122.51
A_68_P27784885	chr11:49607988-49608032	NM_013529:354	Gfpt2	INSIDE	0.132	0.724	2312.34	1674.19	0.095	1774.82	169.11
A_68_P23637423	chr5:42155238-42155282	NM_007524:199	Nkx3-2	INSIDE	0.132	0.503	2263.37	1138.25	0.066	1817.30	120.68
A_68_P23398660	chr4:148473749-148473793	NM_019781:151	Pex14	INSIDE	0.132	0.512	2249.34	1152.53	0.068	1731.93	116.97
A_68_P26022893	chr8:87493563-87493607	NM_011563:38	Prdx2	INSIDE	0.132	0.692	1815.95	1256.13	0.091	1297.37	118.31
A_68_P32699218	chrX:136991656-136991701	NM_021463:537	Prps1	INSIDE	0.132	1.782	2722.01	4849.49	0.235	1221.70	286.79
A_68_P21838402	chr2:167757994-167758038	NM_011201:190	Ptpn1	INSIDE	0.132	0.707	3742.12	2644.22	0.093	2602.61	242.23
A_68_P32182254	chr19:53465262-53465306	NM_172429:-221	Smndc1	PROMOTER	0.132	1.442	4708.15	6791.25	0.190	2951.27	561.30
A_68_P26426686	chr9:36575536-36575582	NM_008408:-395	Stt3a	PROMOTER	0.132	0.475	2701.04	1283.39	0.063	1951.49	122.58
A_68_P28712203	chr12:107201190-107201235	BC156654:163352		INSIDE	0.132	0.599	2051.59	1228.35	0.079	1487.66	117.74
A_68_P26640503	chr9:74696233-74696287	ENSMUST00000160950:-9		PROMOTER	0.132	0.725	1651.57	1197.11	0.096	1253.99	120.22
A_68_P26569953	chr9:62189357-62189414	NM_009672:236	Anp32a	INSIDE	0.131	1.346	3294.51	4435.43	0.176	2266.30	399.76
A_68_P22376200	chr3:101408960-101409004	NM_144900:-402	Atp1a1	PROMOTER	0.131	0.564	2175.68	1226.08	0.074	1686.48	124.14
A_68_P27892739	chr11:68859626-68859680	NM_011496:508	Aurkb	INSIDE	0.131	0.673	1749.18	1176.88	0.088	1324.96	116.93
A_68_P29020701	chr13:48761510-48761554	NM_007526:3128	Barx1	INSIDE	0.131	0.583	2230.01	1299.99	0.077	1576.23	120.77
A_68_P21617363	chr2:127951507-127951551	NM_009754:-245	Bcl2l11	PROMOTER	0.131	0.540	3192.45	1724.28	0.071	2353.84	166.18
A_68_P32260619	chrX:11710953-11710997	NM_001168321:26507	Bcor	INSIDE	0.131	1.496	1663.66	2489.66	0.196	587.51	115.14
A_68_P29682517	chr14:67627899-67627944	NM_009761:-207	Bnip3l	PROMOTER	0.131	0.540	2816.41	1521.44	0.071	2123.86	150.15
A_68_P30940064	chr16:87495686-87495730	NM_009840:406	Cct8	INSIDE	0.131	0.663	1643.15	1089.66	0.087	1360.88	118.03
A_68_P31145618	chr17:32589827-32589872	NM_177307:182	Cyp4f39	INSIDE	0.131	1.497	3862.24	5780.25	0.197	2548.25	501.03
A_68_P27618338	chr11:17853460-17853504	NM_026576:396	Etaa1	INSIDE	0.131	0.309	3631.53	1123.96	0.041	3010.45	122.49
A_68_P25949749	chr8:72610964-72611013	NM_177900:3561	Hapln4	INSIDE	0.131	0.627	1941.82	1218.02	0.082	1464.96	120.13
A_68_P26674970	chr9:81525437-81525481	NM_010482:701	Htr1b	INSIDE	0.131	1.657	1442.29	2389.37	0.216	1120.28	242.37
A_68_P25577540	chr7:146574599-146574643	NM_001127363:-387	Inpp5a	PROMOTER	0.131	0.719	1925.47	1384.90	0.094	1298.73	122.41
A_68_P22210126	chr3:67267629-67267673	NM_016753:179	Lxn	INSIDE	0.131	1.604	3191.32	5120.21	0.210	2275.08	476.80
A_68_P30295267	chr15:66800261-66800306	NM_008681:920	Ndrg1	INSIDE	0.131	0.714	5724.36	4086.71	0.094	3879.17	363.39
A_68_P26640636	chr9:74711696-74711740	NM_008262:1991	Onecut1	INSIDE	0.131	0.727	1690.21	1229.19	0.095	1204.16	114.72

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31128243	chr17:29629131-29629176	NM_008842:1164	Pim1	INSIDE	0.131	0.642	1937.35	1244.54	0.084	1438.02	120.82
A_68_P20085263	chr1:22812453-22812497	NM_001012623:89	Rims1	INSIDE	0.131	2.441	2858.24	6977.07	0.320	1868.49	597.44
A_68_P22215801	chr3:68299336-68299380	NR_036665:1244	Schip1	INSIDE	0.131	0.728	1665.00	1211.78	0.095	1256.49	119.50
A_68_P32240689	chrX:7461201-7461245	NM_001083937:-147	Slc35a2	PROMOTER	0.131	2.395	2067.91	4953.34	0.314	730.87	229.37
A_68_P21626533	chr2:129625984-129626034	NM_001038635:-244	Stk35	PROMOTER	0.131	0.624	2138.25	1333.29	0.082	1454.08	118.73
A_68_P29493860	chr14:29319799-29319843	NM_009524:1162	Wnt5a	INSIDE	0.131	0.700	5111.08	3578.10	0.092	3653.85	336.16
A_68_P31468070	chr18:5334710-5334760	NM_178722:-297	Zfp438	PROMOTER	0.131	2.465	1927.74	4752.17	0.324	1133.78	366.87
A_68_P29509868	chr14:31941877-31941922	NR_024069:217	2010107H07Rik	INSIDE	0.130	0.704	2899.08	2041.86	0.091	1914.49	174.97
A_68_P27534317	chr10:126602065-126602109	NM_008080:-194	B4galnt1	PROMOTER	0.130	0.678	2554.98	1733.41	0.088	1791.88	158.48
A_68_P32448984	chrX:67730148-67730192	NM_001033328:48	BC023829	INSIDE	0.130	1.472	1503.18	2212.90	0.191	603.15	115.41
A_68_P22715818	chr4:8619237-8619281	NM_001081417:1191	Chd7	INSIDE	0.130	0.666	1707.28	1136.37	0.086	1404.23	121.23
A_68_P21612302	chr2:127073420-127073472	NM_025296:106	Ciao1	INSIDE	0.130	0.530	2767.80	1465.57	0.069	1905.78	130.69
A_68_P21767847	chr2:155651782-155651827	NM_010579:857	Eif6	INSIDE	0.130	1.558	884.45	1377.62	0.202	573.61	115.78
A_68_P32752564	chrX:149672338-149672390	NM_173780:-223	Klf8	PROMOTER	0.130	2.195	1003.62	2203.31	0.286	416.60	119.04
A_68_P30961704	chr16:91227772-91227816	NM_016967:2000	Olig2	INSIDE	0.130	0.577	2070.35	1193.89	0.075	1565.33	117.67
A_68_P26429014	chr9:36953463-36953512	NM_001029838:1364	Pknox2	INSIDE	0.130	0.716	1838.18	1316.95	0.093	1397.56	130.05
A_68_P25368679	chr7:107755747-107755795	NM_001163663:-329	Rab6	PROMOTER	0.130	0.489	2520.81	1231.91	0.064	1815.48	115.33
A_68_P31151053	chr17:34067535-34067579	NM_009059:718	Rgl2	INSIDE	0.130	2.716	4198.16	11404.20	0.352	2488.69	877.13
A_68_P31383392	chr17:80878882-80878927	NM_009231:889	Sos1	INSIDE	0.130	0.617	1928.79	1189.92	0.080	1500.61	120.37
A_68_P23330845	chr4:135412711-135412755	NM_001080387:726	Srsf10	INSIDE	0.130	0.704	2020.04	1421.74	0.091	1484.32	135.30
A_68_P26247723	chr8:127316765-127316809	NM_198632:-132	Trim67	PROMOTER	0.130	0.582	2110.45	1229.32	0.076	1611.02	122.21
A_68_P27837323	chr11:59320124-59320168	NM_001130529:-4	Zkscan17	PROMOTER	0.130	0.660	1810.35	1194.00	0.085	1387.29	118.52
A_68_P26892248	chr9:122860010-122860061	NM_025419:83	1110059G10Rik	INSIDE	0.129	0.610	2098.94	1280.17	0.078	1497.80	117.56
A_68_P22398705	chr3:105508370-105508414	NM_001163356:17	6530418L21Rik	INSIDE	0.129	1.684	7314.69	12316.09	0.218	5002.22	1090.55
A_68_P32321494	chrX:34588841-34588885	NM_173779:23	Ankrd58	INSIDE	0.129	2.083	923.08	1923.07	0.268	435.96	116.80
A_68_P25484114	chr7:130514088-130514135	NM_001122640:-682	Arhgap17	DIVERGENT_PROMOTER	0.129	0.670	1932.37	1294.52	0.086	1376.75	118.92
A_68_P25588374	chr7:148547481-148547530	NR_033532:3504	B230206H07Rik	INSIDE	0.129	1.759	3300.83	5805.26	0.227	2256.96	512.73
A_68_P28041231	chr11:95721147-95721199	NM_008081:55013	B4galnt2	DOWNSTREAM	0.129	0.632	1736.33	1097.68	0.082	1457.13	119.06
A_68_P32448986	chrX:67730422-67730470	NM_001033328:-228	BC023829	PROMOTER	0.129	2.099	1192.19	2502.00	0.271	455.59	123.30
A_68_P23094685	chr4:88922650-88922694	NM_001040654:5424	Cdkn2a	INSIDE	0.129	0.449	2482.98	1113.76	0.058	2022.74	117.38
A_68_P25082380	chr7:50699539-50699583	NM_026695:48	Etfb	INSIDE	0.129	0.584	2169.19	1267.53	0.075	1600.96	120.22
A_68_P27897167	chr11:69614867-69614911	NM_010198:239	Fgf11	INSIDE	0.129	0.646	2032.92	1312.96	0.083	1410.84	117.31
A_68_P24874512	chr6:136757288-136757338	NM_177688:544	H2afj	INSIDE	0.129	1.345	3864.97	5199.27	0.173	2528.08	438.36
A_68_P30500964	chr15:102785193-102785237	NM_001024842:258	Hoxc11	INSIDE	0.129	0.585	2165.22	1266.42	0.076	1605.07	121.34
A_68_P22056224	chr3:35899487-35899534	NM_023644:90	Mccc1	INSIDE	0.129	0.627	2218.23	1390.88	0.081	1506.04	121.77
A_68_P32563202	chrX:98469396-98469440	NM_021521:-11	Med12	DIVERGENT_PROMOTER	0.129	1.795	3286.56	5899.12	0.231	1244.23	287.86
A_68_P27794923	chr11:51433377-51433421	NM_026631:124	Nhp2	INSIDE	0.129	0.688	5485.20	3774.02	0.089	3748.07	333.08
A_68_P21723787	chr2:147191374-147191418	NM_008780:667	Pax1	INSIDE	0.129	0.702	1777.16	1247.03	0.091	1304.96	118.15
A_68_P25607698	chr7:151739256-151739302	NM_001033319:356	Ppfia1	INSIDE	0.129	0.554	2015.67	1117.52	0.071	1612.47	115.05
A_68_P22210464	chr3:67319384-67319428	NM_001164763:39	Rarres1	INSIDE	0.129	0.715	5444.87	3895.74	0.092	4132.73	380.10
A_68_P21395950	chr2:84877269-84877313	NM_182990:-67	Ssrp1	DIVERGENT_PROMOTER	0.129	0.655	4429.49	2899.56	0.084	3164.63	267.09
A_68_P30296504	chr15:67007424-67007469	NM_009177:998	St3gal1	INSIDE	0.129	0.738	3133.21	2312.57	0.095	2072.70	197.79
A_68_P21831888	chr2:166612033-166612077	NM_023815:-7212	Trp53rk	PROMOTER	0.129	3.650	3562.89	13005.70	0.471	2209.23	1041.49
A_68_P31977523	chr19:16058932-16058979	NM_198019:524	Cep78	INSIDE	0.128	0.673	1732.51	1166.79	0.086	1360.79	117.39
A_68_P32145754	chr19:46835869-46835913	NM_001102471:-208	Cnnm2	PROMOTER	0.128	0.596	2133.60	1271.49	0.076	1611.46	123.22
A_68_P29651214	chr14:62267812-62267856	NR_028264:33376	Dleu2	INSIDE	0.128	1.640	4837.12	7933.72	0.210	3150.69	661.54
A_68_P24839024	chr6:128388816-128388862	NR_028592:64	Gm10069	INSIDE	0.128	0.586	1903.76	1115.11	0.075	1663.82	124.44
A_68_P28565713	chr12:79849962-79850008	NM_019579:51	Mpp5	INSIDE	0.128	1.530	971.41	1486.55	0.196	804.23	157.64
A_68_P30732552	chr16:46496367-46496411	NM_021496:692	Pvrl3	INSIDE	0.128	0.394	3493.19	1377.76	0.050	2607.68	131.51
A_68_P23922675	chr5:99681822-99681866	NM_145839:102	Rasgef1b	INSIDE	0.128	0.513	2574.10	1321.64	0.066	1827.96	119.74
A_68_P32401097	chrX:54646265-54646313	NR_029425:-75	Rbmx	PROMOTER	0.128	1.422	1637.78	2328.45	0.182	653.37	118.78

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27687370	chr11:32105281-32105325	NM_030093:-112	Snrnp25	DIVERGENT_PROMOTER	0.128	0.712	5116.91	3643.70	0.091	3504.23	318.35
A_68_P31632490	chr18:38345712-38345769	ENSMUST00000160721:25967		INSIDE	0.128	2.704	1699.48	4594.65	0.345	1227.59	423.70
A_68_P30472461	chr15:97832553-97832597	NM_001113515:2581	Col2a1	INSIDE	0.127	0.664	2322.67	1542.97	0.084	1548.26	130.13
A_68_P28610001	chr12:87763573-87763617	NM_011934:1001	Esrrb	INSIDE	0.127	0.636	3568.00	2268.71	0.081	2543.10	205.08
A_68_P26129635	chr8:107165709-107165753	NM_026753:-102	Fam96b	PROMOTER	0.127	0.686	1791.31	1228.27	0.087	1378.49	119.71
A_68_P21129807	chr2:34655295-34655339	NM_145522:-5	Rabepk	PROMOTER	0.127	0.607	2249.73	1365.76	0.077	1530.40	117.81
A_68_P24591630	chr6:83085934-83085978	NM_009106:-1121	Rtkn	PROMOTER	0.127	0.606	2364.55	1432.02	0.077	1647.87	127.14
A_68_P21835387	chr2:167247383-167247427	NM_148929:184	Slc9a8	INSIDE	0.127	0.351	3404.37	1196.55	0.045	2679.10	119.63
A_68_P26023339	chr8:87561977-87562021	NM_001122843:932	Tnpo2	INSIDE	0.127	0.513	2537.94	1303.00	0.065	1860.45	121.30
A_68_P20632252	chr1:136132290-136132334	NM_001039510:-304	Adora1	PROMOTER	0.126	0.486	2639.68	1282.81	0.061	1928.81	118.51
A_68_P31102614	chr17:25392741-25392785	NM_001163270:547	Baiap3	INSIDE	0.126	0.569	2446.22	1392.56	0.072	1652.46	118.29
A_68_P24008814	chr5:115729967-115730011	NM_026504:278	Coq5	INSIDE	0.126	0.506	2392.61	1209.75	0.064	1832.64	116.88
A_68_P21134955	chr2:35517597-35517641	NM_001114124:40118	Dab2ip	INSIDE	0.126	0.466	3157.98	1473.09	0.059	2508.24	147.00
A_68_P32467037	chrX:71491458-71491502	NM_010227:393	Flna	INSIDE	0.126	1.843	3760.51	6930.66	0.232	1298.04	301.57
A_68_P25582013	chr7:147243953-147243997	NM_010836:-8987	Msx3	PROMOTER	0.126	0.660	2504.54	1653.55	0.083	1781.17	148.44
A_68_P23399010	chr4:148540735-148540779	NM_001081274:60	Pgd	INSIDE	0.126	0.529	2356.26	1247.01	0.067	1780.51	118.91
A_68_P24950807	chr7:4796189-4796233	NM_172737:88	Shisa7	INSIDE	0.126	1.434	3560.55	5105.55	0.180	2393.68	432.05
A_68_P27688940	chr11:32354802-32354846	NM_173784:-547	Ubtd2	PROMOTER	0.126	0.492	2761.76	1358.95	0.062	1967.27	122.45
A_68_P32239781	chrX:7291710-7291754	NM_172372:-7642	Wdr45	PROMOTER	0.126	1.812	1260.22	2284.02	0.228	529.90	120.67
A_68_P25026074	chr7:30023055-30023109	NM_001110201:-259	Yif1b	DIVERGENT_PROMOTER	0.126	0.731	1790.00	1308.71	0.092	1284.30	118.20
A_68_P32388635	chrX:51019534-51019578	NM_029142:-8451	4930502E18Rik	PROMOTER	0.125	1.397	1691.96	2363.75	0.174	691.77	120.70
A_68_P23456813	chr5:5664349-5664400	NM_172447:-142	A330021E22Rik	PROMOTER	0.125	0.695	1930.87	1342.01	0.087	1419.02	123.07
A_68_P25776089	chr8:35871359-35871403	NM_176933:717	Dusp4	INSIDE	0.125	0.701	2310.37	1619.92	0.088	1707.32	150.16
A_68_P28530099	chr12:73186645-73186689	NM_001205067:-159	Jkamp	DIVERGENT_PROMOTER	0.125	0.505	2580.37	1301.83	0.063	2039.39	128.45
A_68_P25960687	chr8:74843237-74843281	NM_008452:298	Klf2	INSIDE	0.125	1.386	4459.19	6180.08	0.173	2925.50	507.23
A_68_P23668851	chr5:48375153-48375197	NM_178804:781	Slit2	INSIDE	0.125	0.662	2755.17	1823.56	0.083	1884.78	155.78
A_68_P31929158	chr19:5510644-5510688	NM_001024560:-177	Snx32	PROMOTER	0.125	0.551	2326.60	1281.65	0.069	1788.48	123.46
A_68_P20936014	chr1:192886534-192886578	NM_001163421:255	Tatdn3	INSIDE	0.125	0.724	2061.60	1492.45	0.090	1561.98	140.93
A_68_P22413376	chr3:108365347-108365394	NM_026198:14	Tmem167b	INSIDE	0.125	0.560	2408.04	1347.79	0.070	1649.43	114.99
A_68_P24994886	chr7:20300585-20300629	NM_001109748:172	Tomm40	INSIDE	0.125	0.549	2347.38	1289.31	0.069	1698.43	116.58
A_68_P22589080	chr3:141831851-141831895	ENSMUST00000098568:305		INSIDE	0.125	0.495	3749.75	1857.87	0.062	2791.64	172.60
A_68_P22727925	chr4:11003436-11003481	NM_001085493:-107	2310030N02Rik	PROMOTER	0.124	0.484	3046.12	1474.87	0.060	2014.35	120.50
A_68_P26569954	chr9:62189473-62189517	NM_009672:345	Anp32a	INSIDE	0.124	2.725	6282.22	17120.84	0.338	4433.06	1500.03
A_68_P22058284	chr3:36374544-36374588	NM_009673:243	Anxa5	INSIDE	0.124	0.607	2100.48	1274.01	0.075	1531.04	115.44
A_68_P27308102	chr10:84851199-84851243	NM_028709:1662	Btbd11	INSIDE	0.124	0.604	2262.41	1366.82	0.075	1635.23	122.97
A_68_P29928901	chr14:117325143-117325187	NM_001079844:628	Gpc6	INSIDE	0.124	0.488	3170.00	1545.95	0.061	2569.44	155.61
A_68_P30425256	chr15:89284256-89284300	NM_021921:-63	Mapk8ip2	PROMOTER	0.124	1.457	2526.93	3681.12	0.180	1644.22	296.73
A_68_P25448400	chr7:123648290-123648334	NM_016773:425	Nucb2	INSIDE	0.124	1.395	4436.86	6188.51	0.173	2668.75	460.58
A_68_P27567707	chr11:6191869-6191913	NM_010956:291	Ogdh	INSIDE	0.124	0.481	6923.48	3326.88	0.060	5190.09	309.95
A_68_P28152867	chr11:115195826-115195870	NM_027132:-199	Otop3	PROMOTER	0.124	0.539	2165.40	1167.89	0.067	1730.15	115.63
A_68_P32672687	chrX:131120488-131120543	NM_019865:323	Rpl36a	INSIDE	0.124	2.125	1292.59	2746.20	0.264	453.43	119.72
A_68_P31142315	chr17:31993161-31993205	NM_010831:-445	Sik1	PROMOTER	0.124	0.520	2504.48	1302.91	0.065	1876.04	121.20
A_68_P30546420	chr16:11134105-11134152	NM_029582:497	Txndc11	INSIDE	0.124	0.494	2990.76	1478.87	0.062	2120.31	130.46
A_68_P27912781	chr11:72503632-72503676	NM_009671:151	Ankfy1	INSIDE	0.123	0.621	2038.00	1264.73	0.077	1511.33	115.69
A_68_P26511318	chr9:51574321-51574365	NM_175535:886	Arhgap20	INSIDE	0.123	0.651	2394.91	1559.34	0.080	1801.54	143.76
A_68_P31458877	chr18:3508057-3508101	NM_026505:124	Bambi	INSIDE	0.123	0.667	1882.72	1255.86	0.082	1447.38	119.13
A_68_P32572441	chrX:100551713-100551757	NM_009767:-80	Chic1	PROMOTER	0.123	1.887	3718.74	7015.74	0.232	1422.98	329.87
A_68_P27541866	chr10:127962475-127962519	NM_011843:419	Esyt1	INSIDE	0.123	1.410	999.92	1409.50	0.174	685.70	119.16
A_68_P20842589	chr1:176432473-176432517	NM_019445:539	Fmn2	INSIDE	0.123	0.446	3203.00	1427.30	0.055	2178.44	119.27
A_68_P24992660	chr7:19905290-19905334	NM_008036:-9918	Fosb	PROMOTER	0.123	0.710	2042.26	1450.16	0.087	1557.15	135.59
A_68_P20997432	chr2:9796607-9796655	NM_008091:3597	Gata3	INSIDE	0.123	1.582	3687.92	5833.72	0.195	2669.74	519.95

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P32378022	chrX:49033742-49033786	NM_015819:-110	Hs6st2	PROMOTER	0.123	2.217	3471.88	7696.60	0.274	1469.37	401.91
A_68_P23352770	chr4:139130352-139130396	NM_001205173:-260	Iffo2	PROMOTER	0.123	0.618	4871.11	3009.05	0.076	3422.52	259.95
A_68_P20138851	chr1:34496844-34496888	NM_178601:193	Imp4	INSIDE	0.123	0.647	1745.92	1129.72	0.079	1505.66	119.43
A_68_P23956788	chr5:106129546-106129590	NM_178701:-260	Lrrc8d	PROMOTER	0.123	0.655	1992.46	1305.40	0.080	1507.63	121.00
A_68_P24819297	chr6:125141590-125141635	NM_146171:-8	Ncapd2	DIVERGENT_PROMOTER	0.123	0.585	2401.71	1405.14	0.072	1778.15	127.85
A_68_P32082682	chr19:34953665-34953709	NM_023792:-1279	Pank1	PROMOTER	0.123	0.687	1815.11	1246.87	0.084	1436.69	120.99
A_68_P26818269	chr9:108998498-108998542	NM_172775:571	Plxnb1	INSIDE	0.123	0.660	2060.00	1360.27	0.081	1481.71	120.42
A_68_P20472799	chr1:99666240-99666284	NM_173760:407	Ppip5k2	INSIDE	0.123	0.628	2042.56	1281.87	0.077	1514.72	117.17
A_68_P32699219	chrX:136991758-136991802	NM_021463:639	Prps1	INSIDE	0.123	1.590	2272.75	3614.55	0.195	864.05	168.70
A_68_P23152973	chr4:100742175-100742219	NM_183024:554	Raver2	INSIDE	0.123	2.177	3486.44	7590.62	0.268	2492.45	667.52
A_68_P21420492	chr2:90910618-90910662	NM_026721:-262	Slc39a13	PROMOTER	0.123	0.611	2065.79	1262.26	0.075	1559.32	117.02
A_68_P23236660	chr4:117508118-117508162	NM_008135:278	Slc6a9	INSIDE	0.123	1.455	3112.36	4528.70	0.179	2055.57	367.46
A_68_P22869408	chr4:43013304-43013349	NM_009503:53	Vcp	INSIDE	0.123	0.560	2539.12	1421.82	0.069	1820.77	125.42
A_68_P32403901	chrX:55283389-55283441	NM_009575:-390	Zic3	PROMOTER	0.123	2.087	1230.12	2567.23	0.256	471.82	120.76
A_68_P20046439	chr1:14496966-14497010			Unknown	0.123	0.534	2416.60	1289.36	0.066	1770.32	116.31
A_68_P22202960	chr3:65778708-65778752	AK133062:4895		DOWNSTREAM	0.123	0.513	3982.07	2042.19	0.063	3057.39	192.12
A_68_P27288850	chr10:80783292-80783342	NM_027381:-531	2510012J08Rik	PROMOTER	0.122	1.612	9780.00	15761.68	0.196	5849.40	1146.91
A_68_P28615065	chr12:88607920-88607964	NM_146036:265	Ahsa1	INSIDE	0.122	0.638	2048.00	1306.59	0.078	1546.60	120.84
A_68_P27170204	chr10:59165501-59165545	NM_144822:140	Cbara1	INSIDE	0.122	0.649	2515.02	1632.99	0.079	1963.89	155.06
A_68_P25952216	chr8:73018033-73018077	NM_018827:1000	Crlf1	INSIDE	0.122	0.669	1916.75	1282.14	0.081	1472.21	119.92
A_68_P30673613	chr16:36071461-36071505	NM_027342:119	Fam162a	INSIDE	0.122	0.572	3357.25	1921.90	0.070	2572.09	179.47
A_68_P31559063	chr18:24365030-24365074	NM_001160404:558	Galnt1	INSIDE	0.122	0.448	2673.05	1196.27	0.055	2135.21	116.59
A_68_P31672403	chr18:45719784-45719828	NM_080465:-1	Kcnn2	PROMOTER	0.122	0.682	3612.23	2463.14	0.083	2621.15	217.18
A_68_P27796185	chr11:51670574-51670621	NM_199299:386	Phf15	INSIDE	0.122	0.697	1875.77	1307.39	0.085	1377.92	116.85
A_68_P26469282	chr9:44542109-44542153	NM_153537:1147	Phldb1	INSIDE	0.122	0.617	2150.08	1326.41	0.075	1559.08	117.66
A_68_P23308584	chr4:131392713-131392757	NM_001083119:1459	Ptpru	INSIDE	0.122	4.185	11964.07	50074.15	0.512	7209.21	3692.26
A_68_P23152972	chr4:100742061-100742105	NM_183024:440	Raver2	INSIDE	0.122	2.092	3660.61	7659.09	0.255	2427.75	618.92
A_68_P30381703	chr15:81977883-81977927	NM_033218:206	Srebf2	INSIDE	0.122	0.735	7136.20	5242.94	0.090	4976.80	445.44
A_68_P23400515	chr4:148800617-148800661	NM_022022:102	Ube4b	INSIDE	0.122	0.452	3107.56	1405.64	0.055	2084.13	114.58
A_68_P28598366	chr12:85791678-85791722	NM_134042:200	Aldh6a1	INSIDE	0.121	1.332	7482.58	9964.34	0.161	4747.57	765.86
A_68_P20936670	chr1:193007730-193007774	NM_007498:-540	Atf3	PROMOTER	0.121	0.524	2412.38	1263.17	0.064	1813.19	115.16
A_68_P24586431	chr6:81991939-81991986	NM_145570:341	Fam176a	INSIDE	0.121	0.510	2562.49	1307.44	0.062	1949.39	120.16
A_68_P27898357	chr11:69805074-69805118	NM_019749:225	Gabarap	INSIDE	0.121	0.715	6255.46	4472.78	0.087	4212.30	364.58
A_68_P31936885	chr19:7026235-7026279	NM_001177361:-9316	Gpr137	PROMOTER	0.121	0.695	1914.49	1330.29	0.084	1427.45	119.85
A_68_P21092001	chr2:28438373-28438417	NM_148928:405	Gtf3c5	INSIDE	0.121	0.596	2181.26	1299.59	0.072	1686.92	121.48
A_68_P25044856	chr7:35438432-35438491	NM_146188:-601	Kctd15	PROMOTER	0.121	0.663	1966.91	1303.13	0.080	1459.30	116.61
A_68_P30559668	chr16:13941247-13941291	NM_033564:481	Mpv17l	INSIDE	0.121	0.701	2164.81	1518.24	0.085	1616.77	137.42
A_68_P29269006	chr13:101321942-101321987	NM_008756:489	Ocln	INSIDE	0.121	1.621	1050.20	1701.96	0.196	752.48	147.50
A_68_P20745868	chr1:158870188-158870239	NM_001159965:-456	Ralgps2	PROMOTER	0.121	0.713	1773.03	1264.17	0.086	1351.45	116.36
A_68_P24950806	chr7:4796112-4796158	NM_172737:164	Shisa7	INSIDE	0.121	1.807	1285.74	2323.97	0.219	728.10	159.74
A_68_P22488497	chr3:123211440-123211484	NR_028574:-208	Snhg8	PROMOTER	0.121	0.544	2563.94	1393.82	0.066	1843.59	121.55
A_68_P20870808	chr1:181476368-181476413	NM_008249:8	Tfb2m	INSIDE	0.121	0.557	3069.15	1710.86	0.068	2181.28	147.28
A_68_P26504539	chr9:50412320-50412364	NM_013897:337	Timm8b	INSIDE	0.121	0.619	2527.45	1565.30	0.075	1687.83	126.48
A_68_P21797520	chr2:160698110-160698154	NM_177263:594	Zhx3	INSIDE	0.121	0.556	4546.46	2527.45	0.067	3220.19	217.36
A_68_P25429183	chr7:120351014-120351062	NM_007489:60	Arntl	INSIDE	0.120	0.613	2021.53	1239.23	0.073	1635.69	120.17
A_68_P23237356	chr4:117599653-117599697	NM_009711:2694	Artn	INSIDE	0.120	0.681	2787.19	1896.90	0.082	2092.35	171.28
A_68_P32260575	chrX:11705762-11705806	NM_001168321:31697	Bcor	INSIDE	0.120	2.661	5788.90	15404.08	0.320	2050.19	656.24
A_68_P28054684	chr11:98010545-98010589	NM_028149:364	Fbxl20	INSIDE	0.120	0.546	3521.42	1921.09	0.066	2742.18	180.13
A_68_P28054692	chr11:98011319-98011364	NM_028149:-411	Fbxl20	PROMOTER	0.120	0.423	3374.31	1427.53	0.051	2373.73	120.90
A_68_P20618261	chr1:133806870-133806914	NM_001145804:-142	Nucks1	PROMOTER	0.120	0.645	2518.02	1623.65	0.077	1776.11	136.92
A_68_P21141628	chr2:37214555-37214599	NM_026176:276	Pdcl	INSIDE	0.120	0.666	6876.50	4579.52	0.080	4719.56	378.34

						Sham group			TiO$_2$-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P33012166	chr9_random:55669-55721	NM_011154:-662	Ppp2r3d	PROMOTER	0.120	1.474	3323.84	4900.44	0.177	2200.93	388.78
A_68_P21796146	chr2:160471717-160471761	NM_009408:106	Top1	INSIDE	0.120	0.735	2672.00	1965.25	0.088	1902.34	167.62
A_68_P32289746	chrX:20281381-20281426	NM_145628:369	Usp11	INSIDE	0.120	4.915	2187.48	10750.72	0.587	841.62	494.36
A_68_P28164939	chr11:117255727-117255786	AK020888:9870		DOWNSTREAM	0.120	1.776	737.41	1309.46	0.212	569.00	120.85
A_68_P28833743	chr13:12794811-12794860	ENSMUST00000104944:207		INSIDE	0.120	0.644	2159.85	1390.41	0.077	1624.23	125.01
A_68_P28175454	chr11:118902921-118902967	NM_013926:-717	Cbx8	PROMOTER	0.119	0.624	2397.33	1496.36	0.075	1616.81	120.46
A_68_P24141722	chr5:140981721-140981765	NM_021528:180	Chst12	INSIDE	0.119	0.703	2447.89	1721.20	0.083	1826.94	152.43
A_68_P31473763	chr18:6516415-6516459	NM_007935:-351	Epc1	PROMOTER	0.119	0.396	3517.30	1394.07	0.047	2585.96	122.12
A_68_P28493248	chr12:66067408-66067452	NM_177805:702	Fam179b	INSIDE	0.119	0.562	2658.49	1493.43	0.067	1807.59	120.61
A_68_P25260792	chr7:86537034-86537078	NM_145946:-167	Fanci	DIVERGENT_PROMOTER	0.119	0.577	3528.27	2035.24	0.069	2574.59	177.44
A_68_P28696316	chr12:104480086-104480133	NM_133364:247	Prima1	INSIDE	0.119	1.830	4927.57	9019.29	0.217	3356.33	729.43
A_68_P29568495	chr14:45608828-45608874	NM_008964:1065	Ptger2	INSIDE	0.119	0.650	2329.74	1514.40	0.077	1565.49	120.82
A_68_P20412616	chr1:88425208-88425252	NM_008972:1920	Ptma	INSIDE	0.119	0.612	2756.72	1688.08	0.073	1995.33	145.61
A_68_P20348986	chr1:74552917-74552961	NM_021383:305	Rqcd1	INSIDE	0.119	0.604	3884.63	2347.81	0.072	2909.90	209.55
A_68_P25372612	chr7:108470032-108470076	NM_019990:222	Stard10	INSIDE	0.119	0.634	1962.15	1244.37	0.075	1567.90	118.15
A_68_P23429333	chr4:153515623-153515667	NM_021499:-836	Wdr8	DIVERGENT_PROMOTER	0.119	0.723	2820.28	2039.80	0.086	1905.93	164.32
A_68_P24325497	chr6:29222598-29222642	NM_023516:-5	2310016C08Rik	PROMOTER	0.118	0.676	2101.49	1420.29	0.080	1546.45	123.23
A_68_P26237607	chr8:125566355-125566399	NM_001081379:-192	Ankrd11	PROMOTER	0.118	0.542	2633.19	1426.02	0.064	1914.55	122.42
A_68_P20166296	chr1:39592351-39592396	NM_028043:-273	D1Bwg0212e	PROMOTER	0.118	0.686	1771.19	1215.27	0.081	1484.78	120.16
A_68_P26591484	chr9:66005801-66005855	NM_010019:-204	Dapk2	PROMOTER	0.118	1.566	4337.79	6795.09	0.185	2827.90	524.49
A_68_P31925905	chr19:4928339-4928383	NM_133803:-73	Dpp3	PROMOTER	0.118	0.740	2862.19	2119.12	0.087	2088.62	182.69
A_68_P30356906	chr15:77801158-77801202	NM_018749:74	Eif3d	INSIDE	0.118	0.574	2446.97	1403.66	0.068	1774.70	120.56
A_68_P32560535	chrX:97821487-97821531	NM_008446:105	Kif4	INSIDE	0.118	2.407	3312.54	7972.91	0.283	1261.11	356.94
A_68_P23057187	chr4:82152716-82152762	NM_001113209:-1526	Nfib	PROMOTER	0.118	1.803	1003.91	1810.13	0.213	665.53	141.99
A_68_P23415879	chr4:151368860-151368904	NM_172705:1406	Phf13	INSIDE	0.118	0.591	2449.97	1449.12	0.070	1678.49	116.66
A_68_P30146825	chr15:37890467-37890516	NM_199476:319	Rrm2b	INSIDE	0.118	0.694	2097.80	1456.49	0.082	1460.65	119.90
A_68_P29937467	chr14:118633748-118633793	NM_177753:2482	Sox21	INSIDE	0.118	0.747	3815.18	2850.82	0.089	2628.25	232.63
A_68_P24603257	chr6:85087734-85087778	NM_011467:2	Spr	INSIDE	0.118	0.636	1909.44	1213.74	0.075	1589.35	119.51
A_68_P26023334	chr8:87561401-87561445	NM_001122843:356	Tnpo2	INSIDE	0.118	2.630	15621.84	41083.68	0.311	10145.26	3155.63
A_68_P23560760	chr5:28444814-28444860			Unknown	0.118	1.546	1307.99	2022.48	0.183	915.59	167.35
A_68_P27798578	chr11:52127606-52127657	L12152:204721		INSIDE	0.118	1.679	755.65	1268.77	0.199	598.53	118.96
A_68_P24362054	chr6:35489548-35489592	NM_008098:318	Mtpn	INSIDE	0.117	0.500	2604.67	1301.98	0.058	2118.06	123.82
A_68_P30497294	chr15:102162316-102162360	NM_021713:199	Myg1	INSIDE	0.117	0.483	3419.15	1651.18	0.057	2543.67	144.28
A_68_P32564063	chrX:98625189-98625233	NM_023144:221	Nono	INSIDE	0.117	1.638	1939.09	3175.27	0.191	774.86	148.30
A_68_P27693121	chr11:33063184-33063228	NM_008722:-150	Npm1	PROMOTER	0.117	0.440	3131.95	1379.56	0.052	2250.00	116.41
A_68_P26640621	chr9:74709991-74710035	NM_008262:285	Onecut1	INSIDE	0.117	0.739	6982.63	5156.91	0.086	4531.49	390.53
A_68_P23277932	chr4:125735548-125735592	NM_172701:-238	Oscp1	PROMOTER	0.117	0.700	2061.16	1443.65	0.082	1485.22	122.08
A_68_P24066362	chr5:125821382-125821426	NM_001205082:60	Scarb1	INSIDE	0.117	0.693	3135.41	2172.49	0.081	2016.71	164.03
A_68_P26540093	chr9:56924054-56924108	NM_001110350:-102	Sin3a	PROMOTER	0.117	0.635	2431.69	1544.02	0.075	1730.32	129.05
A_68_P32341131	chrX:39503134-39503178	NM_021465:-721	Stag2	PROMOTER	0.117	1.760	3510.26	6179.39	0.206	1499.73	308.32
A_68_P25598465	chr7:150255389-150255433	NM_001115085:138	Tssc4	INSIDE	0.117	0.590	3081.52	1817.23	0.069	2287.58	158.45
A_68_P30350784	chr15:76648087-76648131	NM_001168288:492	Arhgap39	INSIDE	0.116	5.436	21824.95	118649.00	0.632	14501.69	9161.22
A_68_P22503486	chr3:126300384-126300428	NM_001025438:516	Camk2d	INSIDE	0.116	0.600	2437.09	1463.02	0.070	1683.84	117.34
A_68_P31565720	chr18:25645973-25646017	NM_001146292:266490	Celf4	INSIDE	0.116	0.644	2386.56	1537.11	0.075	1600.31	119.46
A_68_P21425363	chr2:91761712-91761756	NM_007699:-611	Chrm4	PROMOTER	0.116	0.654	2283.50	1493.54	0.076	1559.52	118.08
A_68_P31121207	chr17:28360556-28360600	NM_027185:15856	Def6	INSIDE	0.116	0.624	2452.55	1530.13	0.072	1955.89	141.70
A_68_P21601162	chr2:125073336-125073380	NM_023595:108	Dut	INSIDE	0.116	0.746	3746.94	2796.44	0.087	2518.72	217.98
A_68_P30377509	chr15:81191134-81191178	NM_011399:39	Slc25a17	INSIDE	0.116	0.650	2295.39	1492.02	0.076	1681.37	127.13
A_68_P32747584	chrX:148450937-148450989	NM_019710:-8	Smc1a	DIVERGENT_PROMOTER	0.116	1.495	1800.44	2691.20	0.174	692.72	120.34
A_68_P23238475	chr4:117807044-117807088	NM_009176:429	St3gal3	INSIDE	0.116	0.714	2675.68	1910.93	0.083	2011.02	166.26
A_68_P30642144	chr16:30510918-30510962	NM_172614:39724	Tmem44	DOWNSTREAM	0.116	0.534	2371.78	1267.35	0.062	1918.45	119.23

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P30651594	chr16:32247382-32247433	NM_026898:69	Wdr53	INSIDE	0.116	0.636	2138.23	1359.01	0.074	1626.32	119.77
A_68_P26234304	chr8:125100653-125100697	NM_009698:133	Aprt	INSIDE	0.115	0.744	4203.02	3125.02	0.086	3182.83	273.05
A_68_P29523611	chr14:34164707-34164753	NM_153800:134722	Arhgap22	INSIDE	0.115	1.439	1301.16	1872.93	0.166	902.64	149.45
A_68_P28737547	chr12:111517314-111517358	NM_172119:-103	Dio3	DIVERGENT_PROMOTER	0.115	0.660	1901.27	1254.57	0.076	1540.42	116.86
A_68_P31515593	chr18:15223323-15223369	NM_001142731:-1255	Kctd1	PROMOTER	0.115	0.542	2658.26	1440.09	0.062	1974.93	123.08
A_68_P26815490	chr9:108469907-108469951	NM_023247:-255	Ndufaf3	DIVERGENT_PROMOTER	0.115	0.441	3490.45	1538.00	0.051	2500.22	126.94
A_68_P21421554	chr2:91097131-91097175	NM_028733:-333	Pacsin3	PROMOTER	0.115	0.629	2507.47	1577.11	0.072	1691.59	122.47
A_68_P28072366	chr11:101032330-101032374	NM_146030:264	Plekhh3	INSIDE	0.115	0.623	4359.82	2716.47	0.072	3095.40	221.70
A_68_P23916648	chr5:98615578-98615622	NM_029947:5713	Prdm8	INSIDE	0.115	1.436	3010.13	4323.03	0.165	2076.03	343.14
A_68_P28451628	chr12:56499606-56499653	NM_011968:-182	Psma6	PROMOTER	0.115	0.677	2272.71	1538.34	0.078	1774.29	138.57
A_68_P32071916	chr19:32830947-32830991	NM_008960:-1098	Pten	PROMOTER	0.115	0.687	5738.49	3942.91	0.079	3993.79	314.99
A_68_P28168284	chr11:117829892-117829936	NM_007707:766	Socs3	INSIDE	0.115	0.673	1956.73	1317.12	0.077	1544.55	119.17
A_68_P26002691	chr8:83538819-83538865	NM_027554:-37	Usp38	PROMOTER	0.115	0.544	2694.02	1466.30	0.063	2055.40	129.13
A_68_P28753097	chr12:114116011-114116055	AK018992:-2007		PROMOTER	0.115	0.637	2557.43	1630.15	0.073	1908.64	139.37
A_68_P32321493	chrX:34588727-34588771	NM_173779:-91	Ankrd58	PROMOTER	0.114	1.501	4199.39	6302.27	0.171	1810.12	309.98
A_68_P25542189	chr7:140901181-140901225	NM_025392:187	Bccip	INSIDE	0.114	0.543	2814.16	1527.67	0.062	1986.22	123.34
A_68_P23401328	chr4:148961215-148961259	NM_023051:490	Clstn1	INSIDE	0.114	1.709	9352.64	15982.37	0.195	6029.65	1178.52
A_68_P32651797	chrX:126284617-126284662	NM_172493:362	Diap2	INSIDE	0.114	1.830	1684.44	3083.15	0.209	677.82	141.66
A_68_P26893207	chr9:123022692-123022739	NM_001081188:367	Exosc7	INSIDE	0.114	2.117	1044.95	2211.92	0.242	763.78	184.76
A_68_P32779374	chrX:156828817-156828861	NM_001079847:217	Gpr64	INSIDE	0.114	1.648	1878.78	3095.79	0.189	749.51	141.29
A_68_P22907353	chr4:49858612-49858656	NM_001033351:-681	Grin3a	PROMOTER	0.114	0.735	3348.02	2460.06	0.084	2248.59	188.77
A_68_P31259555	chr17:57150392-57150436	NM_133801:297	Gtf2f1	INSIDE	0.114	0.510	2824.94	1442.11	0.058	2016.32	117.47
A_68_P24449402	chr6:52196249-52196297	NM_010450:-506	Hoxa11	PROMOTER	0.114	0.715	2020.02	1443.81	0.081	1473.78	119.83
A_68_P26375207	chr9:27107032-27107084	NM_001033323:246	Igsf9b	INSIDE	0.114	0.563	2596.28	1460.71	0.064	1879.35	120.86
A_68_P24152254	chr5:143026387-143026435	NM_178702:621	Radil	INSIDE	0.114	1.559	2185.39	3406.71	0.178	1407.95	250.40
A_68_P27096532	chr10:42482055-42482099	NM_153055:775	Sec63	INSIDE	0.114	1.824	10066.38	18363.01	0.207	6271.40	1298.66
A_68_P26316370	chr9:14080581-14080626	NM_030261:-141	Sesn3	PROMOTER	0.114	0.604	2863.27	1729.16	0.069	1960.62	135.26
A_68_P21395068	chr2:84706724-84706775	NM_001083809:25967	Slc43a1	DOWNSTREAM	0.114	0.673	2322.84	1563.25	0.077	1539.46	117.95
A_68_P24118744	chr5:136438405-136438449	NM_001160366:11920	Srcrb4d	INSIDE	0.114	0.543	3947.13	2142.47	0.062	2645.93	163.34
A_68_P31932349	chr19:6047162-6047206	NM_001164709:40	Syvn1	INSIDE	0.114	0.633	1976.36	1251.08	0.072	1616.46	116.79
A_68_P22336394	chr3:93247847-93247891	NM_001163098:1617	Tchh	INSIDE	0.114	0.530	2607.52	1382.63	0.060	1967.41	118.88
A_68_P30374035	chr15:80541596-80541640	NM_144812:-124	Tnrc6b	PROMOTER	0.114	0.595	2247.59	1336.71	0.068	1723.90	117.03
A_68_P22982497	chr4:65265989-65266033	NM_001161782:-9	Trim32	PROMOTER	0.114	0.610	2629.47	1605.00	0.070	1876.15	130.92
A_68_P25747454	chr8:30329630-30329674	NM_153135:456	Unc5d	INSIDE	0.114	0.658	2688.28	1768.87	0.075	1939.09	145.04
A_68_P32567807	chrX:99447270-99447325	NM_007709:-189	Cited1	PROMOTER	0.113	1.565	1595.09	2496.11	0.177	687.09	121.34
A_68_P20352842	chr1:75233266-75233310	NM_001159885:12	Dnajb2	INSIDE	0.113	0.677	2053.90	1391.18	0.077	1505.54	115.35
A_68_P22317214	chr3:88905621-88905667	NM_134469:223	Fdps	INSIDE	0.113	0.705	2236.03	1576.61	0.080	1667.48	133.43
A_68_P24225086	chr6:8209405-8209449	NR_033518:139	Gm16039	INSIDE	0.113	0.622	5268.18	3276.99	0.070	3832.71	268.46
A_68_P32241078	chrX:7525375-7525419	NM_001130416:-381	Hdac6	PROMOTER	0.113	1.621	1528.19	2476.52	0.183	636.95	116.45
A_68_P22920589	chr4:53024957-53025001	NM_025623:183	Nipsnap3b	INSIDE	0.113	1.672	4718.76	7888.37	0.190	3202.14	607.07
A_68_P22920590	chr4:53025131-53025175	NM_025623:357	Nipsnap3b	INSIDE	0.113	1.461	10345.19	15116.54	0.166	6698.52	1109.63
A_68_P32672689	chrX:131120700-131120748	NM_019865:532	Rpl36a	INSIDE	0.113	1.830	1594.58	2918.44	0.206	565.96	116.71
A_68_P22970869	chr4:63155665-63155709	NM_001008791:1299	Whrn	INSIDE	0.113	0.742	3050.37	2264.25	0.084	2223.68	186.60
A_68_P32578102	chrX:101865933-101865986	NM_175358:444	Zdhhc15	INSIDE	0.113	1.649	1438.59	2372.71	0.187	669.18	125.04
A_68_P21112313	chr2:31806031-31806075	NM_145144:230	Aif1l	INSIDE	0.112	0.736	2051.78	1509.51	0.082	1448.79	119.03
A_68_P28727042	chr12:109514039-109514083	NM_001159910:-433	Ccdc85c	PROMOTER	0.112	0.683	2271.74	1550.90	0.077	1539.47	118.17
A_68_P32351253	chrX:42143286-42143330	NM_001190718:30	Dcaf12l1	INSIDE	0.112	1.381	1695.79	2341.11	0.155	744.88	115.23
A_68_P32241075	chrX:7525044-7525088	NM_001130416:-51	Hdac6	PROMOTER	0.112	2.703	4241.32	11465.94	0.303	1528.29	462.44
A_68_P28058585	chr11:98656131-98656175	NM_028722:-930	Msl1	PROMOTER	0.112	0.556	2952.96	1640.98	0.062	2016.57	125.79
A_68_P21834485	chr2:167066151-167066195	NM_008968:-135	Ptgis	PROMOTER	0.112	1.544	7613.76	11758.96	0.174	5179.26	899.08
A_68_P24991727	chr7:19735291-19735345	NM_026943:132	Snrpd2	INSIDE	0.112	0.687	1994.22	1370.38	0.077	1564.65	120.20

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P29218722	chr13:91600765-91600809	NM_024186:85	Ssbp2	INSIDE	0.112	0.614	3203.40	1967.63	0.069	2229.34	153.62
A_68_P28031420	chr11:94072519-94072563	NM_009427:-227	Tob1	PROMOTER	0.112	0.690	1945.63	1342.85	0.077	1587.01	122.52
A_68_P26024222	chr8:87823113-87823157	NM_022997:262	Vps35	INSIDE	0.112	0.527	3767.11	1984.30	0.059	2728.73	161.17
A_68_P24735177	chr6:108618758-108618808	NM_011498:8160	Bhlhe40	DOWNSTREAM	0.111	1.624	1047.87	1701.79	0.180	808.09	145.76
A_68_P22407674	chr3:107434065-107434109	NM_153563:542	Fam40a	INSIDE	0.111	1.436	1752.13	2516.68	0.159	1311.00	208.60
A_68_P31150130	chr17:33822156-33822206	NM_001109913:223	Hnrnpm	INSIDE	0.111	0.476	3140.60	1495.74	0.053	2380.94	125.45
A_68_P32767188	chrX:154035988-154036043	NM_172307:632	Mbtps2	INSIDE	0.111	1.744	1575.08	2746.45	0.194	594.09	115.24
A_68_P32242263	chrX:7783783-7783827	NM_016913:-153	Porcn	PROMOTER	0.111	1.546	2695.29	4165.80	0.172	1037.07	178.63
A_68_P23196701	chr4:108251917-108251961	NM_172697:3	Prpf38a	INSIDE	0.111	0.589	2768.15	1630.15	0.065	2036.75	133.26
A_68_P30330337	chr15:73253106-73253150	NM_007982:493	Ptk2	INSIDE	0.111	0.566	5635.53	3191.39	0.063	4147.93	259.69
A_68_P32709179	chrX:139116571-139116615	NM_001199360:324	Tmem164	INSIDE	0.111	3.814	3928.28	14980.50	0.421	1741.08	733.83
A_68_P20405967	chr1:84835781-84835825	NM_133975:77	Trip12	INSIDE	0.111	0.583	2472.51	1442.66	0.065	1833.90	118.44
A_68_P25082976	chr7:50817634-50817683	NM_001008549:-81	Zfp658	PROMOTER	0.111	0.621	2416.77	1500.29	0.069	1777.42	122.54
A_68_P25376019	chr7:109054202-109054254	NM_025605:-122	2400001E08Rik	PROMOTER	0.110	0.718	2195.53	1577.26	0.079	1625.39	128.69
A_68_P31111775	chr17:26813633-26813677	NM_025272:314	Atp6v0e	INSIDE	0.110	0.490	2647.43	1298.45	0.054	2132.37	114.84
A_68_P25047606	chr7:35903706-35903750	NM_007678:-583	Cebpa	PROMOTER	0.110	0.681	2602.76	1772.23	0.075	1633.83	122.82
A_68_P24607363	chr6:85911171-85911215	NM_028099:469	Dusp11	INSIDE	0.110	0.562	2551.77	1433.52	0.062	1891.29	116.92
A_68_P28043946	chr11:96205491-96205535	NM_010458:430	Hoxb3	INSIDE	0.110	0.493	2866.05	1411.73	0.054	2193.26	118.74
A_68_P32539359	chrX:91786297-91786345	NM_019791:1093	Maged1	INSIDE	0.110	2.611	1501.58	3920.54	0.287	566.67	162.83
A_68_P30497296	chr15:102162515-102162559	NM_021713:397	Myg1	INSIDE	0.110	0.703	2397.05	1684.13	0.078	1472.60	114.29
A_68_P30421714	chr15:88692421-88692465	NM_145478:-181	Pim3	PROMOTER	0.110	0.545	3841.18	2094.99	0.060	2759.09	165.65
A_68_P32071912	chr19:32830438-32830489	NM_008960:-1603	Pten	PROMOTER	0.110	0.509	2568.07	1306.01	0.056	2138.97	120.13
A_68_P24537772	chr6:71657975-71658019	NM_178608:322	Reep1	INSIDE	0.110	0.506	2540.77	1285.70	0.056	2130.18	119.01
A_68_P21835857	chr2:167329794-167329838	NM_030743:11672	Rnf114	INSIDE	0.110	0.551	2461.40	1355.01	0.061	1908.26	115.58
A_68_P29676509	chr14:66572807-66572857	NM_172604:-251	Scara3	PROMOTER	0.110	1.425	1005.72	1433.29	0.156	762.96	119.34
A_68_P27468586	chr10:114688584-114688628	NM_025706:-57	Tbc1d15	PROMOTER	0.110	1.338	3399.19	4547.68	0.147	2431.45	357.55
A_68_P24993673	chr7:20094233-20094277	NM_025960:177	Trappc6a	INSIDE	0.110	0.688	2221.60	1528.73	0.076	1595.84	121.13
A_68_P25411546	chr7:117205275-117205334	NM_009281:89	Zfp143	INSIDE	0.110	2.701	481.41	1300.06	0.298	390.63	116.42
A_68_P24336405	chr6:31166095-31166146	ENSMUST00000115107:2313		INSIDE	0.110	1.661	774.84	1286.79	0.183	627.01	114.90
A_68_P25693341	chr8:17534942-17534988	NM_053171:421	Csmd1	INSIDE	0.109	0.534	3144.37	1680.06	0.058	2141.23	124.73
A_68_P32746468	chrX:148238435-148238479	NM_021523:632	Huwe1	INSIDE	0.109	2.829	3242.16	9171.33	0.309	1114.26	343.91
A_68_P27327919	chr10:88349039-88349083	NM_145423:324	Slc5a8	INSIDE	0.109	0.716	4081.81	2921.07	0.078	3003.97	234.05
A_68_P29855894	chr14:102008105-102008149	NM_001081278:282	Tbc1d4	INSIDE	0.109	0.544	2654.64	1444.88	0.059	2059.87	121.67
A_68_P32340126	chrX:39264963-39265012	NM_001033422:91	Thoc2	INSIDE	0.109	3.117	2622.57	8173.43	0.341	866.85	295.27
A_68_P26584999	chr9:64808747-64808792	NM_175153:26	2010321M09Rik	INSIDE	0.108	1.509	6771.50	10220.88	0.163	4637.15	755.05
A_68_P23961361	chr5:106887861-106887906	NM_001005477:-698	Barhl2	PROMOTER	0.108	0.687	2747.15	1888.55	0.074	2022.23	149.99
A_68_P24397655	chr6:42274146-42274190	NM_001113327:471	Fam131b	INSIDE	0.108	0.546	3761.64	2052.52	0.059	2354.77	138.42
A_68_P32683850	chrX:133583924-133583968	NM_146261:-186	Fam199x	PROMOTER	0.108	1.697	1612.97	2736.65	0.183	817.88	149.56
A_68_P20332289	chr1:71699909-71699953	NM_010233:-185	Fn1	PROMOTER	0.108	0.569	2794.25	1591.26	0.061	1927.05	118.48
A_68_P24656010	chr6:94234328-94234372	NM_001029850:-452	Magi1	PROMOTER	0.108	0.583	2365.89	1378.76	0.063	1820.99	114.56
A_68_P25503658	chr7:134170789-134170833	NM_010772:-817	Maz	PROMOTER	0.108	2.170	20497.19	44486.13	0.235	12606.55	2958.09
A_68_P27941848	chr11:78002243-78002287	NM_033475:15	Rab34	INSIDE	0.108	0.606	2856.48	1729.90	0.065	2086.50	136.39
A_68_P31598893	chr18:31794423-31794469	NM_172965:410	Sap130	INSIDE	0.108	0.710	2044.22	1450.72	0.076	1568.02	119.73
A_68_P32259721	chrX:11576312-11576356			Unknown	0.108	0.655	4226.51	2767.07	0.071	1637.93	115.49
A_68_P26897419	A_68_P26897419			Unknown	0.108	0.731	2083.64	1523.00	0.079	1455.43	115.21
A_68_P32710881	chrX:139400366-139400410	NM_019496:883	Ammecr1	INSIDE	0.107	2.310	1482.67	3425.50	0.246	578.71	142.39
A_68_P29234318	chr13:95128761-95128805	NM_009680:-132	Ap3b1	PROMOTER	0.107	0.733	2427.48	1778.62	0.078	1583.23	124.13
A_68_P23797908	chr5:73882402-73882446	NM_001190733:160	Dcun1d4	INSIDE	0.107	0.495	3141.07	1554.79	0.053	2306.55	121.67
A_68_P24126716	chr5:138070623-138070667	NM_001168652:294	Lrch4	INSIDE	0.107	0.690	2647.20	1825.83	0.074	1832.18	135.32
A_68_P28480019	chr12:62623999-62624043	NM_178714:-1598	Lrfn5	PROMOTER	0.107	0.697	2153.58	1500.76	0.075	1554.05	116.10
A_68_P30267534	chr15:61819131-61819181	NM_001177352:2261	Myc	INSIDE	0.107	0.618	2362.38	1461.03	0.066	1787.71	117.95

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P20454941	chr1:95239500-95239544	NM_080850:-157	Pask	DIVERGENT_PROMOTER	0.107	0.473	3446.19	1631.35	0.050	2631.85	132.78
A_68_P22878640	chr4:44716235-44716287	NM_008782:7052	Pax5	INSIDE	0.107	0.735	2237.57	1644.59	0.079	1541.99	121.19
A_68_P28009091	chr11:89864227-89864271	NM_008796:-40	Pctp	PROMOTER	0.107	1.961	1527.77	2996.19	0.210	1137.92	239.47
A_68_P22957025	chr4:59561479-59561533	NM_144904:730	Rod1	INSIDE	0.107	0.559	2486.69	1389.22	0.060	1947.88	116.26
A_68_P29937481	chr14:118635351-118635395	NM_177753:880	Sox21	INSIDE	0.107	1.819	962.28	1750.05	0.194	699.66	135.63
A_68_P28167195	chr11:117644840-117644884	NM_001195088:891	Tmc8	INSIDE	0.107	1.657	2818.32	4670.59	0.178	1961.96	348.37
A_68_P31202521	chr17:45822303-45822347	NM_198167:843	Tmem63b	INSIDE	0.107	0.597	3648.58	2178.39	0.064	2543.60	161.86
A_68_P28599059	chr12:85910912-85910956	NM_007701:133	Vsx2	INSIDE	0.107	0.642	4496.75	2888.33	0.069	3263.32	223.78
A_68_P28833741	chr13:12794586-12794630	ENSMUST00000104944:-20		PROMOTER	0.107	0.744	3122.49	2322.11	0.080	2339.54	186.13
A_68_P22609954	chr3:145312413-145312457	NM_010516:515	Cyr61	INSIDE	0.106	0.509	3045.06	1549.09	0.054	2202.75	119.22
A_68_P26467020	chr9:44135161-44135205	NM_007875:255	Dpagt1	INSIDE	0.106	0.571	2939.59	1679.83	0.061	1893.04	114.95
A_68_P21909705	chr2:181022801-181022845	NM_198169:-151	Gmeb2	PROMOTER	0.106	0.667	2462.12	1641.71	0.070	1723.44	121.47
A_68_P27279736	chr10:79384102-79384146	NM_053244:4409	Kiss1r	INSIDE	0.106	0.654	2489.30	1627.83	0.069	1728.67	119.93
A_68_P31757530	chr18:61558577-61558621	NM_133249:1487	Ppargc1b	INSIDE	0.106	0.699	3221.43	2251.85	0.074	2165.58	160.16
A_68_P21783954	chr2:158439815-158439861	NM_009508:3345	Slc32a1	INSIDE	0.106	0.599	2771.22	1658.63	0.063	1913.30	121.06
A_68_P24605102	chr6:85402096-85402141	NR_028081:-154	1700040I03Rik	PROMOTER	0.105	0.516	2808.24	1449.38	0.054	2203.86	119.42
A_68_P24127313	chr5:138182525-138182569	NM_175521:-1320	6430598A04Rik	DIVERGENT_PROMOTER	0.105	1.887	6790.45	12814.33	0.198	4405.83	874.09
A_68_P31217295	chr17:48549255-48549304	NM_207219:-125	AI314976	DIVERGENT_PROMOTER	0.105	0.542	4840.56	2622.58	0.057	3366.25	191.33
A_68_P30213285	chr15:51696567-51696616	NM_080635:416	Eif3h	INSIDE	0.105	1.622	1322.73	2145.54	0.170	941.63	160.24
A_68_P21114435	chr2:32143977-32144021	NM_001080968:226	Golga2	INSIDE	0.105	0.725	2305.50	1670.42	0.076	1647.98	125.77
A_68_P26550024	chr9:58670000-58670044	NM_001081192:-1296	Hcn4	PROMOTER	0.105	0.624	2513.84	1568.23	0.066	1872.85	123.09
A_68_P31515592	chr18:15223215-15223266	NM_001142731:-1149	Kctd1	PROMOTER	0.105	0.588	2969.77	1746.58	0.061	1962.40	120.61
A_68_P26821068	chr9:109835124-109835175	NM_001205331:872	Mtap4	INSIDE	0.105	0.690	2234.59	1541.09	0.072	1615.81	116.74
A_68_P27970616	chr11:83112191-83112235	NM_134025:267	Pex12	INSIDE	0.105	0.507	2952.27	1498.13	0.053	2221.79	118.43
A_68_P28078648	chr11:102145969-102146013	NM_028076:-284	Tmub2	PROMOTER	0.105	0.621	5025.74	3119.72	0.065	3714.55	241.90
A_68_P26538536	chr9:56644194-56644238	AK155716:4852		DOWNSTREAM	0.105	0.702	5323.81	3736.92	0.073	3877.86	284.82
A_68_P23296722	chr4:129138895-129138941	NM_133889:-4	Bsdc1	PROMOTER	0.104	2.164	3236.95	7003.60	0.224	2243.55	503.07
A_68_P24772854	chr6:115724644-115724688	NM_025958:92	Cand2	INSIDE	0.104	1.742	3122.07	5438.23	0.182	2126.47	386.65
A_68_P26591487	chr9:66006201-66006245	NM_010019:190	Dapk2	INSIDE	0.104	0.727	2279.42	1657.08	0.076	1592.45	120.73
A_68_P23363213	chr4:140857120-140857165	NM_010139:-12	Epha2	PROMOTER	0.104	1.529	967.41	1478.91	0.159	724.37	115.36
A_68_P21727905	chr2:147870580-147870624	NM_010446:2103	Foxa2	INSIDE	0.104	0.662	8649.96	5730.24	0.069	6086.19	419.37
A_68_P31545967	chr18:21811707-21811752	NM_001081403:-860	Klhl14	PROMOTER	0.104	1.613	3155.93	5091.46	0.168	2050.86	344.17
A_68_P24591351	chr6:83036388-83036432	NM_010692:52	Lbx2	INSIDE	0.104	0.672	2691.68	1809.04	0.070	1704.80	119.69
A_68_P30368844	chr15:79664362-79664415	NM_001013360:375	Npcd	INSIDE	0.104	1.771	891.14	1578.34	0.184	635.42	116.64
A_68_P25771679	chr8:35040712-35040756	NM_001042674:-421	Rbpms	PROMOTER	0.104	0.673	2574.00	1732.31	0.070	1861.78	130.03
A_68_P32078821	chr19:34266845-34266890	NM_029682:108	Stambpl1	INSIDE	0.104	2.001	2573.12	5149.74	0.208	1651.50	343.86
A_68_P24818152	chr6:124958758-124958812	NM_175557:-1038	Zfp384	PROMOTER	0.104	0.621	2468.36	1533.90	0.065	1888.64	122.54
A_68_P26085411	chr8:98330678-98330722	NR_015574:-29	4930513N10Rik	PROMOTER	0.103	0.695	7015.31	4878.62	0.071	4904.43	350.38
A_68_P26065129	chr8:94880803-94880847	NR_033641:-805	4933436C20Rik	DIVERGENT_PROMOTER	0.103	0.628	2822.65	1772.14	0.065	1886.33	122.16
A_68_P20350884	chr1:74902743-74902787	NM_009872:1162	Cdk5r2	INSIDE	0.103	0.618	2538.87	1568.75	0.064	1872.97	119.36
A_68_P25737431	chr8:28371155-28371199	NM_007918:378	Eif4ebp1	INSIDE	0.103	0.601	2545.81	1529.03	0.062	1846.76	114.75
A_68_P32467039	chrX:71491630-71491682	NM_010227:217	Flna	INSIDE	0.103	1.642	2153.63	3535.33	0.168	716.93	120.63
A_68_P29055022	chr13:55546184-55546228	NM_011938:-488	Grk6	PROMOTER	0.103	0.639	2723.94	1741.07	0.066	1913.17	125.93
A_68_P25005383	chr7:25316968-25317015	NM_153134:1325	Irgq	INSIDE	0.103	0.685	2313.36	1585.67	0.070	1710.32	120.50
A_68_P29624050	chr14:57287581-57287630	NM_023773:521	Mphosph8	INSIDE	0.103	1.468	1563.36	2294.48	0.151	1049.13	158.53
A_68_P26642806	chr9:75079725-75079769	NM_001081322:-74	Myo5c	PROMOTER	0.103	0.649	2333.40	1513.45	0.067	1800.68	120.28
A_68_P21006480	chr2:11423558-11423602	NM_001177752:137	Pfkfb3	INSIDE	0.103	0.622	2601.96	1619.63	0.064	1816.90	116.65
A_68_P26554815	chr9:59528234-59528278	NM_011099:23842	Pkm2	DOWNSTREAM	0.103	0.582	2631.43	1531.54	0.060	1948.29	117.21
A_68_P23592737	chr5:34512192-34512236	NM_181857:-117	Poln	PROMOTER	0.103	0.682	7047.68	4804.10	0.070	4710.00	330.17
A_68_P21217119	chr2:51928961-51929008	NM_175238:628	Rif1	INSIDE	0.103	3.352	1710.96	5735.83	0.345	897.51	309.75
A_68_P27675734	chr11:29592809-29592856	NM_194052:-65	Rtn4	PROMOTER	0.103	1.871	969.72	1814.44	0.194	622.03	120.41

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P30160402	chr15:40487224-40487274	NM_011766:661	Zfpm2	INSIDE	0.103	0.733	2682.53	1967.08	0.075	1773.98	133.72
A_68_P30959868	chr16:90934441-90934485	NM_026502:632	1110004E09Rik	INSIDE	0.102	1.625	2187.27	3554.32	0.166	1532.00	254.74
A_68_P24127047	chr5:138126002-138126046	NM_145566:-103	Agfg2	PROMOTER	0.102	0.612	2730.81	1672.50	0.063	1991.80	124.89
A_68_P25708993	chr8:23171282-23171328	NM_183142:113	Alg11	INSIDE	0.102	0.617	2628.99	1622.12	0.063	1888.49	118.64
A_68_P21007908	chr2:11699545-11699589	NM_177268:187	Ankrd16	INSIDE	0.102	0.663	2470.87	1638.24	0.067	1759.34	118.59
A_68_P29575959	chr14:47007992-47008036	NM_007554:2260	Bmp4	INSIDE	0.102	0.743	2711.94	2014.71	0.076	1957.06	148.65
A_68_P25693339	chr8:17534712-17534756	NM_053171:651	Csmd1	INSIDE	0.102	0.565	4990.32	2818.22	0.057	3377.19	194.11
A_68_P21732684	chr2:148701174-148701218	NM_009976:8	Cst3	INSIDE	0.102	0.467	3411.58	1592.02	0.047	2577.17	122.17
A_68_P23226804	chr4:115612306-115612352	NM_001025567:203	Dmbx1	INSIDE	0.102	1.420	1220.94	1733.19	0.145	802.38	116.35
A_68_P28198624	chr12:4082843-4082887	NM_153082:291	Dnajc27	INSIDE	0.102	0.597	6184.51	3691.19	0.061	4158.08	253.91
A_68_P27677356	chr11:29924368-29924417	NM_146016:1641	Eml6	INSIDE	0.102	2.039	835.83	1704.43	0.208	598.55	124.56
A_68_P25260795	chr7:86537392-86537436	NM_145946:191	Fanci	INSIDE	0.102	0.594	2596.27	1541.64	0.060	1943.83	117.34
A_68_P22010771	chr3:27271350-27271394	NM_177330:1100	Ghsr	INSIDE	0.102	0.673	3318.83	2235.15	0.069	2148.80	147.41
A_68_P30500862	chr15:102773465-102773509	NM_010463:6203	Hoxc12	DOWNSTREAM	0.102	0.686	2710.75	1859.78	0.070	1726.95	120.68
A_68_P28600140	chr12:86114302-86114346	NM_028863:105	Isca2	INSIDE	0.102	1.409	3398.71	4789.39	0.144	2317.64	333.26
A_68_P32798241	chrX:160857957-160858011	NM_011081:266	Piga	INSIDE	0.102	1.457	2146.44	3126.36	0.149	807.01	120.17
A_68_P24225084	chr6:8209188-8209232	NM_026632:-69	Rpa3	DIVERGENT_PROMOTER	0.102	1.348	4137.62	5578.65	0.138	2556.86	352.94
A_68_P25089653	chr7:52103806-52103850	NM_001042655:621	Tbc1d17	INSIDE	0.102	0.696	2513.65	1748.40	0.071	1809.48	128.72
A_68_P26552550	chr9:59139013-59139070	NM_028121:-337	Adpgk	PROMOTER	0.101	1.660	908.07	1507.08	0.168	688.46	115.73
A_68_P21486780	chr2:103868083-103868131	NM_020593:151	Fbxo3	INSIDE	0.101	2.395	699.92	1676.08	0.243	495.55	120.36
A_68_P32696394	chrX:136405677-136405721	NM_001193309:495	Morc4	INSIDE	0.101	1.642	2535.81	4164.73	0.166	1103.02	182.57
A_68_P27534166	chr10:126558114-126558159	NM_001171026:80	Os9	INSIDE	0.101	1.364	3748.51	5114.02	0.138	2553.80	353.06
A_68_P32456129	chrX:69208413-69208457	NM_001081135:75	Prrg3	INSIDE	0.101	2.052	2479.58	5089.18	0.208	973.52	202.13
A_68_P32465510	chrX:71167458-71167506	NM_001164704:8707	Renbp	INSIDE	0.101	2.040	1651.28	3369.26	0.205	574.49	118.03
A_68_P31809752	chr18:70632290-70632335	NM_029019:114	Stard6	INSIDE	0.101	1.505	1184.65	1783.13	0.151	786.22	119.10
A_68_P27680036	chr11:30549094-30549138	NM_029344:280	Acyp2	INSIDE	0.100	0.378	4018.16	1517.92	0.038	3253.51	122.83
A_68_P24004706	chr5:115021554-115021604	NM_001004180:3319	BC057022	INSIDE	0.100	1.572	2898.66	4556.83	0.157	1713.57	269.70
A_68_P24799556	chr6:120616027-120616071	NM_001128151:-390	Cecr2	PROMOTER	0.100	0.687	3552.49	2441.58	0.069	2449.23	167.96
A_68_P27901910	chr11:70469767-70469811	NM_001136062:-926	Eno3	DIVERGENT_PROMOTER	0.100	0.582	3006.37	1749.57	0.058	2087.66	121.08
A_68_P29259682	chr13:99585022-99585066	NM_172591:360	Fcho2	INSIDE	0.100	0.530	3021.18	1600.17	0.053	2475.84	131.59
A_68_P25150562	chr7:64642665-64642709	NR_033504:45	Gm9962	INSIDE	0.100	0.526	3078.98	1620.38	0.053	2241.26	118.13
A_68_P28082319	chr11:102786133-102786177	NM_197959:284	Kif18b	INSIDE	0.100	0.605	4265.79	2579.55	0.061	2768.17	168.18
A_68_P21151628	chr2:38860218-38860262	NM_025592:411	Rpl35	INSIDE	0.100	0.656	3001.82	1968.35	0.066	2335.39	153.75
A_68_P31257289	chr17:56753149-56753198	NM_018730:356	Rpl36	INSIDE	0.100	0.657	2368.40	1555.93	0.066	1774.54	116.93
A_68_P27274091	chr10:77875465-77875509	NM_010925:302	Rrp1	INSIDE	0.100	0.543	3127.89	1699.28	0.055	2218.82	121.00
A_68_P28751515	chr12:113883521-113883565	NM_001161737:504	Siva1	INSIDE	0.100	0.686	2619.46	1797.55	0.068	1845.59	126.25
A_68_P31145138	chr17:32487412-32487456	NM_017476:88	Akap8l	INSIDE	0.099	0.749	4511.75	3377.65	0.074	2899.74	214.89
A_68_P32260250	chrX:11654399-11654443	NM_029510:3259	Bcor	INSIDE	0.099	1.476	6046.26	8925.59	0.146	1946.65	284.92
A_68_P29018477	chr13:48357119-48357169	NM_031166:349	Id4	INSIDE	0.099	0.601	2733.85	1642.16	0.059	1996.37	118.19
A_68_P27947415	chr11:78959320-78959364	NM_013571:514	Ksr1	INSIDE	0.099	0.690	2768.75	1909.62	0.068	1801.10	122.82
A_68_P20587181	chr1:127808737-127808781	NM_145100:33	Lypd1	INSIDE	0.099	1.824	2114.75	3858.07	0.181	1318.43	239.07
A_68_P25664799	chr8:12915651-12915695	NM_178076:-220	Mcf2l	PROMOTER	0.099	0.713	2965.67	2115.78	0.071	1847.24	130.46
A_68_P32466326	chrX:71330622-71330666	NM_010788:288	Mecp2	INSIDE	0.099	1.935	2987.87	5781.00	0.192	1034.32	198.18
A_68_P25988740	chr8:80959381-80959425	NM_138944:1149	Pou4f2	INSIDE	0.099	2.163	15337.40	33180.84	0.215	9247.74	1985.87
A_68_P20352745	chr1:75216487-75216531	NM_009447:-680	Tuba4a	PROMOTER	0.099	0.597	2801.56	1673.20	0.059	2084.90	123.34
A_68_P28078915	chr11:102181318-102181368	NM_011551:-932	Ubtf	PROMOTER	0.099	1.396	1276.09	1781.33	0.139	869.46	120.73
A_68_P32795512	chrX:160346535-160346579	NM_026887:-535	Ap1s2	PROMOTER	0.098	1.570	2884.52	4528.49	0.155	1094.51	169.22
A_68_P24104837	chr5:133017392-133017444	NM_177047:795	Auts2	INSIDE	0.098	1.484	1154.17	1712.27	0.145	835.43	121.01
A_68_P20778062	chr1:164407645-164407689	NM_001038619:495	Dnm3	INSIDE	0.098	0.553	4111.38	2271.78	0.054	3052.44	166.13
A_68_P21933403	chr3:8664956-8665000	NM_010423:2060	Hey1	INSIDE	0.098	0.613	2701.20	1656.23	0.060	1964.09	118.45
A_68_P30572652	chr16:17233443-17233487	NM_178922:-215	Hic2	PROMOTER	0.098	0.571	2791.23	1595.13	0.056	2187.85	122.38

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P31866356	chr18:80910683-80910727	NM_001164110:-894	Nfatc1	PROMOTER	0.098	0.682	2648.16	1806.05	0.067	1876.69	125.67
A_68_P22518745	chr3:128917350-128917394	NM_001042502:518	Pitx2	INSIDE	0.098	0.713	2440.81	1739.12	0.070	1670.43	116.53
A_68_P23232644	chr4:116805889-116805940	NM_013807:643	Plk3	INSIDE	0.098	1.433	2102.86	3012.87	0.140	1484.68	208.44
A_68_P32238979	chrX:7151677-7151727	NM_138605:-456	Ppp1r3f	DIVERGENT_PROMOTER	0.098	1.949	2287.73	4458.78	0.191	834.31	159.24
A_68_P28519207	chr12:71328317-71328361	NM_133198:332	Pygl	INSIDE	0.098	0.733	2449.40	1795.97	0.072	1678.78	120.54
A_68_P28535622	chr12:74213314-74213358	NM_011382:896	Six4	INSIDE	0.098	0.458	5157.11	2363.02	0.045	4099.58	183.87
A_68_P24179198	chr5:149211250-149211294	NM_007513:208	Slc7a1	INSIDE	0.098	0.678	2631.10	1784.16	0.066	1868.57	124.19
A_68_P23749448	chr5:64550705-64550749	NM_019636:-723	Tbc1d1	PROMOTER	0.098	0.588	2519.70	1480.59	0.058	2083.97	119.96
A_68_P20184658	chr1:42752112-42752171	NR_027826:-471	2610017I09Rik	DIVERGENT_PROMOTER	0.097	2.128	723.64	1539.94	0.207	577.58	119.60
A_68_P21631946	chr2:130665493-130665537	NM_029432:332	4930402H24Rik	INSIDE	0.097	0.579	2842.83	1647.26	0.056	2115.54	118.97
A_68_P27756958	chr11:44433864-44433908	NM_007897:2251	Ebf1	INSIDE	0.097	0.602	2795.45	1682.18	0.058	2017.61	117.38
A_68_P24295385	chr6:23197965-23198012	NM_028462:276	Fezf1	INSIDE	0.097	0.674	2733.93	1843.83	0.066	1863.56	122.39
A_68_P30347594	chr15:76161371-76161427	NM_010331:-325	Gpaa1	PROMOTER	0.097	1.732	3798.95	6579.07	0.168	2617.21	439.45
A_68_P28153291	chr11:115265419-115265463	NM_026729:361	Ict1	INSIDE	0.097	0.611	3100.80	1893.09	0.059	2044.59	121.42
A_68_P23088445	chr4:87678149-87678193	NM_027326:1141	Mllt3	INSIDE	0.097	1.463	1250.70	1829.75	0.142	851.33	121.23
A_68_P23615749	chr5:38218796-38218844	NM_010835:-2996	Msx1	PROMOTER	0.097	0.700	2498.75	1748.87	0.068	1757.86	119.86
A_68_P31117691	chr17:27792800-27792847	NM_011861:197	Pacsin1	INSIDE	0.097	1.781	2537.19	4517.62	0.173	1782.84	309.16
A_68_P24428256	chr6:48551764-48551808	NM_001079901:7905	Repin1	DOWNSTREAM	0.097	0.571	3897.33	2224.12	0.056	2850.56	158.25
A_68_P21085997	chr2:27532005-27532049	NM_011305:-694	Rxra	PROMOTER	0.097	0.539	3354.66	1807.88	0.052	2324.06	121.18
A_68_P22319130	chr3:89199983-89200027	NM_009565:-2879	Zbtb7b	PROMOTER	0.097	1.370	3604.55	4939.84	0.132	2314.19	306.42
A_68_P24972086	chr7:13063602-13063648	NM_001039951:-29	Zfp606	PROMOTER	0.097	0.731	2191.81	1602.35	0.071	1688.84	120.13
A_68_P20859036	chr1:179269190-179269235			Unknown	0.097	0.593	3275.94	1942.36	0.057	2291.85	131.49
A_68_P26600190	chr9:67481095-67481139			Unknown	0.097	0.687	2446.79	1681.82	0.066	1788.83	118.88
A_68_P25505909	chr7:134655506-134655551	NR_024331:855	1700008J07Rik	INSIDE	0.096	0.686	2461.44	1688.69	0.066	1760.20	115.85
A_68_P24818074	chr6:124947113-124947157	NM_001145927:-1320	C530028O21Rik	PROMOTER	0.096	0.584	3975.60	2320.86	0.056	2612.11	145.96
A_68_P29737944	chr14:77557089-77557133	NM_172813:488	Enox1	INSIDE	0.096	0.619	2862.54	1772.12	0.060	2050.29	122.15
A_68_P31344185	chr17:73457680-73457725	NM_001081071:378	Lclat1	INSIDE	0.096	0.605	2613.75	1580.26	0.058	2063.89	119.58
A_68_P31074433	chr17:17762462-17762506	NM_172827:-1031	Lnpep	PROMOTER	0.096	1.541	4977.27	7669.21	0.149	3293.10	489.09
A_68_P23417961	chr4:151689896-151689940	NM_001033489:2816	Rnf207	INSIDE	0.096	1.485	1945.18	2888.13	0.142	1178.34	167.47
A_68_P32117790	chr19:41970534-41970578	NM_199447:87	Rrp12	INSIDE	0.096	1.475	5616.48	8284.03	0.141	3624.66	511.70
A_68_P26983378	chr10:19571100-19571144	NM_029529:143	Slc35d3	INSIDE	0.096	0.615	2845.12	1750.59	0.059	2155.76	127.27
A_68_P32036084	chr19:26680907-26680951	NM_011416:1279	Smarca2	INSIDE	0.096	0.602	2879.04	1733.99	0.058	2012.12	116.74
A_68_P28047901	chr11:96839052-96839100	NM_001080964:-74	Sp2	PROMOTER	0.096	2.050	940.01	1927.24	0.198	612.72	121.04
A_68_P30296502	chr15:67007203-67007248	NM_009177:1219	St3gal1	INSIDE	0.096	0.590	2928.70	1727.49	0.057	2120.27	120.20
A_68_P27846980	chr11:60988451-60988495	NM_001004143:89	Usp22	INSIDE	0.096	0.605	2922.75	1769.03	0.058	2122.12	122.84
A_68_P23440510	chr4:155144347-155144391	NM_147776:4302	Vwa1	INSIDE	0.096	1.780	4304.34	7660.18	0.171	2725.87	465.45
A_68_P30476324	chr15:98593039-98593083	NM_007478:489	Arf3	INSIDE	0.095	1.584	2749.81	4356.37	0.151	1835.59	277.20
A_68_P27685427	chr11:31771207-31771257	NM_026252:-978	Cpeb4	PROMOTER	0.095	1.649	1143.34	1885.26	0.157	760.29	119.28
A_68_P27541863	chr10:127962197-127962241	NM_011843:697	Esyt1	INSIDE	0.095	0.484	3415.01	1653.85	0.046	2501.62	115.69
A_68_P32746467	chrX:148238346-148238395	NM_021523:546	Huwe1	INSIDE	0.095	2.035	1820.13	3704.42	0.194	592.67	115.02
A_68_P29348448	chr13:115608501-115608545	NM_001113374:78	Mocs2	INSIDE	0.095	0.685	3500.56	2396.99	0.065	2555.47	166.97
A_68_P25375581	chr7:108966881-108966925	NM_008887:76	Phox2a	INSIDE	0.095	0.713	2481.75	1769.57	0.068	1898.03	128.44
A_68_P24043181	chr5:121654660-121654704	NM_011290:173	Rpl6	INSIDE	0.095	0.538	2971.47	1598.61	0.051	2277.71	116.39
A_68_P23271976	chr4:124744252-124744296	NM_175246:338	Snip1	INSIDE	0.095	0.656	2594.54	1702.23	0.062	1892.47	117.77
A_68_P28936823	chr13:34222460-34222504	NM_023716:-259	Tubb2b	PROMOTER	0.095	1.885	9046.41	17054.26	0.179	5512.25	986.47
A_68_P31420724	chr17:87424991-87425037	NM_019936:114	Cript	INSIDE	0.094	1.411	2658.36	3751.73	0.133	1895.95	251.82
A_68_P22941966	chr4:56878242-56878286	NM_018761:-181	Ctnnal1	PROMOTER	0.094	0.737	3378.25	2490.28	0.069	2376.21	164.66
A_68_P28033990	chr11:94491386-94491430	NM_133807:271	Lrrc59	INSIDE	0.094	0.437	4001.82	1747.53	0.041	2873.50	118.49
A_68_P27922357	chr11:74584686-74584730	NM_026197:344	Mettl16	INSIDE	0.094	1.562	1192.86	1863.45	0.147	942.42	138.16
A_68_P32691812	chrX:135449017-135449063	NM_013724:72	Nrk	INSIDE	0.094	3.143	1481.01	4654.61	0.294	570.56	167.80
A_68_P24815138	chr6:124364754-124364798	NM_008995:309	Pex5	INSIDE	0.094	0.726	2860.12	2077.77	0.068	1976.67	135.04

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P32790799	chrX:159199053-159199097	NM_009031:771	Rbbp7	INSIDE	0.094	2.219	4538.78	10072.80	0.208	2097.62	435.96
A_68_P24785568	chr6:118147500-118147544	NM_001080780:240	Ret	INSIDE	0.094	2.388	10979.76	26219.25	0.225	6636.61	1490.45
A_68_P25091604	chr7:52431430-52431474	NM_182993:12162	Slc17a7	INSIDE	0.094	2.939	8630.71	25361.52	0.277	4801.50	1331.85
A_68_P21783932	chr2:158437350-158437394	NM_009508:879	Slc32a1	INSIDE	0.094	0.748	6245.23	4670.35	0.071	4035.16	285.01
A_68_P30510786	chr16:4558818-4558862	NM_031182:880	Tcfap4	INSIDE	0.094	0.496	3581.30	1774.60	0.046	2543.23	118.19
A_68_P22708706	chr4:6918269-6918313	NM_145711:-420	Tox	PROMOTER	0.094	0.752	5768.87	4337.10	0.071	3833.26	270.81
A_68_P24295386	chr6:23198116-23198160	NM_028462:126	Fezf1	INSIDE	0.093	0.733	3157.65	2316.08	0.069	2097.79	143.85
A_68_P31259698	chr17:57171184-57171228	NM_010613:-276	Khsrp	PROMOTER	0.093	0.563	3531.04	1987.89	0.052	2623.12	136.68
A_68_P21046080	chr2:19580505-19580552	NM_027715:840	Otud1	INSIDE	0.093	1.398	1215.23	1698.91	0.130	1014.23	131.51
A_68_P32289247	chrX:20195452-20195505	NM_001167776:594	Rbm10	INSIDE	0.093	1.501	2255.84	3386.70	0.139	849.63	118.40
A_68_P22412732	chr3:108248246-108248294	NM_001204979:-93	Sars	PROMOTER	0.093	0.667	2721.42	1816.43	0.062	1934.76	120.72
A_68_P28102660	chr11:106473862-106473908	NM_198292:360	Tex2	INSIDE	0.093	0.613	3115.84	1908.84	0.057	2226.23	127.47
A_68_P29484376	chr14:27783003-27783055	NM_145221:709	Appl1	INSIDE	0.092	0.665	2691.53	1789.55	0.061	1896.03	116.17
A_68_P25093837	chr7:52825440-52825491	NM_009737:-267	Bcat2	PROMOTER	0.092	1.931	1625.10	3138.28	0.177	1068.24	189.09
A_68_P28059225	chr11:98769164-98769211	NM_001025779:-15	Cdc6	PROMOTER	0.092	1.435	3080.32	4421.42	0.132	1984.56	261.01
A_68_P26971597	chr10:17443088-17443132	NM_010828:77	Cited2	INSIDE	0.092	0.727	4990.73	3629.41	0.067	3467.83	230.99
A_68_P21071362	chr2:25174225-25174270	NM_001177656:436	Grin1	INSIDE	0.092	0.738	2525.73	1864.24	0.068	1722.66	116.66
A_68_P32465786	chrX:71211813-71211857	NM_008224:-180	Hcfc1	PROMOTER	0.092	2.410	2382.95	5743.18	0.221	857.36	189.12
A_68_P26216543	chr8:122394587-122394646	NM_146219:8412	Klhl36	INSIDE	0.092	2.460	687.92	1692.01	0.226	562.75	127.29
A_68_P31411765	chr17:86021432-86021477	NM_011381:1281	Six3	INSIDE	0.092	0.658	2687.41	1769.21	0.060	2029.65	122.78
A_68_P29440563	chr14:19726488-19726532	NM_144839:-369	Ube2e2	PROMOTER	0.092	2.790	14911.27	41604.55	0.257	9652.93	2478.26
A_68_P22346424	chr3:95733202-95733246	NM_023210:45	Anp32e	INSIDE	0.091	0.587	3302.07	1939.57	0.053	2484.57	132.32
A_68_P32369309	chrX:46847140-46847184	NM_001081123:23536	Arhgap36	INSIDE	0.091	1.831	3852.82	7054.90	0.166	1444.40	240.23
A_68_P28003593	chr11:88922175-88922219	NM_019505:-134	Dgke	PROMOTER	0.091	0.724	4385.09	3174.27	0.066	3073.38	201.66
A_68_P24156215	chr5:144126161-144126205	NM_133355:596	Grid2ip	INSIDE	0.091	0.658	2795.15	1838.53	0.060	1986.64	118.49
A_68_P32727714	chrX:143397800-143397847	NM_008312:768	Htr2c	INSIDE	0.091	2.948	1053.02	3104.47	0.268	438.49	117.56
A_68_P28037994	chr11:95170942-95170986	NM_001195003:596	Myst2	INSIDE	0.091	0.712	2425.63	1726.09	0.065	1875.50	121.79
A_68_P32118990	chr19:42165379-42165423	NM_145501:476	Pi4k2a	INSIDE	0.091	0.705	3132.84	2209.61	0.064	2332.25	149.57
A_68_P32699217	chrX:136991521-136991565	NM_021463:401	Prps1	INSIDE	0.091	1.930	2446.42	4721.17	0.176	954.07	168.25
A_68_P30670711	chr16:35542576-35542620	NM_013661:1151	Sema5b	INSIDE	0.091	0.449	3881.02	1744.02	0.041	3032.25	123.37
A_68_P27985540	chr11:85646214-85646259	NM_009324:120	Tbx2	INSIDE	0.091	1.680	960.96	1614.69	0.154	766.00	117.73
A_68_P27104119	chr10:43868447-43868491			Unknown	0.091	0.652	3005.45	1959.91	0.060	2046.39	122.05
A_68_P32396639	chrX:53851315-53851359	NM_146234:-240	Mmgt1	PROMOTER	0.090	1.981	2044.38	4050.73	0.179	969.54	173.19
A_68_P27357765	chr10:93610485-93610538	NM_011629:-164	Nr2c1	PROMOTER	0.090	1.434	2855.08	4093.69	0.130	1944.92	252.30
A_68_P23354401	chr4:139377795-139377839	NM_011039:11067	Pax7	INSIDE	0.090	0.624	3088.81	1927.55	0.056	2075.44	117.12
A_68_P26587155	chr9:65194859-65194910	NM_016688:1010	Pdcd7	INSIDE	0.090	0.674	2960.66	1995.37	0.060	2000.98	120.88
A_68_P29587990	chr14:49065856-49065910	NM_172600:-144	6720456H20Rik	PROMOTER	0.089	0.709	2798.46	1982.78	0.063	1907.49	120.25
A_68_P22321220	chr3:89519673-89519729	NM_001038587:757	Adar	INSIDE	0.089	0.692	2887.04	1997.45	0.062	2104.34	130.19
A_68_P26467270	chr9:44187680-44187724	NM_021395:130	Hyou1	INSIDE	0.089	0.715	2770.75	1981.99	0.064	2056.23	131.22
A_68_P21305449	chr2:68699678-68699722	NM_172856:87	Lass6	INSIDE	0.089	0.714	2771.14	1978.10	0.063	1875.64	118.97
A_68_P27982140	chr11:85125306-85125350	NM_016910:573	Ppm1d	INSIDE	0.089	0.734	2455.57	1802.06	0.066	1804.02	118.41
A_68_P28765897	chr12:117316101-117316145	NM_009511:-73	Vipr2	PROMOTER	0.089	0.738	2223.11	1641.65	0.066	1824.72	120.40
A_68_P27268626	chr10:76978772-76978818	NM_133998:-236	1810008A18Rik	PROMOTER	0.088	0.724	2614.28	1893.48	0.064	1833.69	117.28
A_68_P22889568	chr4:46614078-46614122	NM_001164804:701	Coro2a	INSIDE	0.088	0.724	2470.65	1788.66	0.064	1938.06	123.89
A_68_P24135004	chr5:139821148-139821192	NM_197980:-50	Cox19	DIVERGENT_PROMOTER	0.088	0.636	4720.53	3002.72	0.056	3184.38	178.65
A_68_P29681788	chr14:67486601-67486645	NM_009955:815	Dpysl2	INSIDE	0.088	1.990	6312.82	12565.59	0.175	4012.47	701.53
A_68_P20186163	chr1:43010333-43010377	NM_053107:638	Gpr45	INSIDE	0.088	1.770	10255.33	18152.41	0.156	6082.87	951.65
A_68_P26025056	chr8:88017117-88017161	NM_173866:623	Gpt2	INSIDE	0.088	0.679	3052.04	2071.98	0.060	2121.83	126.60
A_68_P20937890	chr1:193221506-193221550	NM_144880:-608	Ppp2r5a	PROMOTER	0.088	0.739	2514.81	1859.29	0.065	1834.82	119.50
A_68_P32479503	chrX:75040859-75040905	NM_016979:417	Prkx	INSIDE	0.088	1.916	1957.16	3750.13	0.169	710.61	120.44
A_68_P30348874	chr15:76350196-76350240	NM_130893:2341	Scrt1	INSIDE	0.088	1.855	10808.14	20049.85	0.163	6370.92	1038.67

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P32036067	chr19:26678985-26679030	NM_011416:-642	Smarca2	PROMOTER	0.088	1.741	5326.76	9275.55	0.153	3434.24	525.22
A_68_P31145137	chr17:32487319-32487363	NM_017476:182	Akap8l	INSIDE	0.087	1.577	3470.55	5473.20	0.137	2299.72	314.37
A_68_P29575956	chr14:47007694-47007740	NM_007554:2558	Bmp4	INSIDE	0.087	2.096	1870.95	3921.78	0.183	1256.59	230.24
A_68_P21605247	chr2:125684679-125684728	NM_009939:51	Cops2	INSIDE	0.087	1.832	1477.37	2707.09	0.159	959.46	152.71
A_68_P32468048	chrX:71674396-71674448	NM_008062:78	G6pdx	INSIDE	0.087	2.031	1862.12	3782.36	0.176	685.10	120.82
A_68_P26465908	chr9:43942942-43942986	NM_023061:224	Mcam	INSIDE	0.087	0.708	3512.73	2485.37	0.062	2331.60	143.60
A_68_P25368570	chr7:107731384-107731428	NM_198831:238	Mrpl48	INSIDE	0.087	0.577	3498.30	2017.03	0.050	2586.56	129.01
A_68_P31983175	chr19:17030736-17030792	NM_181348:157	Prune2	INSIDE	0.087	1.416	1322.36	1872.16	0.124	965.87	119.36
A_68_P29405446	chr14:12386981-12387025	NM_008981:936	Ptprg	INSIDE	0.087	0.565	3968.43	2242.14	0.049	2981.08	147.26
A_68_P24327616	chr6:29559131-29559176	NM_177296:454	Tnpo3	INSIDE	0.087	0.652	2501.68	1630.35	0.056	2038.32	115.08
A_68_P27308092	chr10:84850082-84850126	NM_028709:546	Btbd11	INSIDE	0.086	0.453	4449.39	2016.92	0.039	3007.86	117.16
A_68_P26540068	chr9:56920704-56920750	NM_001110350:-3456	Sin3a	PROMOTER	0.086	0.589	3349.84	1973.10	0.051	2397.22	122.00
A_68_P29102446	chr13:65342785-65342836			Unknown	0.086	1.634	3632.57	5934.77	0.141	2245.85	316.68
A_68_P24039807	chr5:121062809-121062858	NM_029096:-235	1110008J03Rik	DIVERGENT_PROMOTER	0.085	0.741	2716.71	2012.92	0.063	1912.35	120.62
A_68_P32651800	chrX:126284923-126284967	NM_172493:667	Diap2	INSIDE	0.085	1.796	2452.36	4405.13	0.154	978.86	150.28
A_68_P28419968	chr12:50486468-50486512	NM_008241:2497	Foxg1	INSIDE	0.085	0.715	3350.25	2393.93	0.061	2453.86	149.14
A_68_P26844443	chr9:114310274-114310318	NM_009752:60	Glb1	INSIDE	0.085	0.667	4000.44	2667.31	0.056	3204.12	180.90
A_68_P32385499	chrX:50410041-50410085	NR_029756:-2536	Mir322	PROMOTER	0.085	5.460	8292.22	45276.10	0.462	3869.76	1788.41
A_68_P32239400	chrX:7215668-7215712	NM_009305:-15	Syp	PROMOTER	0.085	1.890	8689.40	16423.24	0.161	3233.06	521.89
A_68_P32340124	chrX:39264668-39264712	NM_001033422:388	Thoc2	INSIDE	0.085	2.072	1610.88	3338.30	0.176	677.99	119.38
A_68_P30959121	chr16:90810687-90810731	NM_029497:-50	Urb1	PROMOTER	0.085	0.749	5604.64	4196.73	0.064	3815.21	243.76
A_68_P25581341	chr7:147130605-147130649	NM_009482:872	Utf1	INSIDE	0.085	1.655	11064.98	18312.08	0.141	6853.57	967.55
A_68_P30160396	chr15:40486463-40486507	NM_011766:-103	Zfpm2	PROMOTER	0.085	0.606	3340.84	2023.81	0.052	2247.96	115.78
A_68_P29961850	chr14:122864514-122864560	NM_022987:344	Zic5	INSIDE	0.085	1.788	1092.78	1954.43	0.152	792.19	120.29
A_68_P32470552	chrX:72341213-72341257	NM_001030307:42	Dkc1	INSIDE	0.084	1.365	2697.83	3683.43	0.114	1045.20	119.18
A_68_P25087743	chr7:51752229-51752273	NM_028169:293	Fam71e1	INSIDE	0.084	0.619	4174.24	2584.28	0.052	2598.44	135.66
A_68_P26129630	chr8:107165289-107165337	NM_026753:316	Fam96b	INSIDE	0.084	1.360	1467.13	1995.89	0.114	1021.51	116.42
A_68_P31166955	chr17:37183328-37183372	NM_019439:440	Gabbr1	INSIDE	0.084	1.401	6152.17	8619.26	0.117	4556.94	535.18
A_68_P30347740	chr15:76181682-76181726	NM_001164607:-19	Maf1	DIVERGENT_PROMOTER	0.084	1.888	4164.69	7864.25	0.159	2780.52	442.59
A_68_P21853525	chr2:170336931-170336975	NM_001110152:223	Pfdn4	INSIDE	0.084	0.631	3612.00	2280.58	0.053	2589.43	137.14
A_68_P28513223	chr12:70285038-70285082	NM_025589:-6	Rpl36al	DIVERGENT_PROMOTER	0.084	0.690	2835.31	1956.33	0.058	2031.47	118.31
A_68_P24245776	chr6:13020122-13020168	NM_027992:386	Tmem106b	INSIDE	0.084	1.468	2774.21	4072.07	0.124	1719.67	213.26
A_68_P32460116	chrX:70232552-70232596	NM_001109043:-103	Zfp185	PROMOTER	0.084	1.652	2553.62	4219.84	0.138	1147.58	158.86
A_68_P32262594	chrX:12164926-12164970	NM_027439:64	Atp6ap2	INSIDE	0.083	1.768	3157.66	5582.75	0.147	1146.07	168.05
A_68_P30541580	chr16:10313819-10313863	NM_007929:221	Emp2	INSIDE	0.083	1.402	7452.33	10446.84	0.117	5020.15	586.06
A_68_P25520717	chr7:137409140-137409185	NM_010207:1160	Fgfr2	INSIDE	0.083	1.362	2061.58	2807.24	0.113	1466.40	165.91
A_68_P27260807	chr10:75700398-75700442	NM_001077638:190	Prmt2	INSIDE	0.083	0.601	3581.04	2152.35	0.050	2395.19	119.62
A_68_P32747588	chrX:148451460-148451504	NM_019710:512	Smc1a	INSIDE	0.083	2.064	2069.27	4271.13	0.171	779.51	133.28
A_68_P32488665	chrX:78316348-78316392	NM_138751:388	Tmem47	INSIDE	0.083	2.290	4701.99	10769.55	0.190	1725.36	328.11
A_68_P32289747	chrX:20281555-20281599	NM_145628:542	Usp11	INSIDE	0.083	1.484	3365.04	4992.15	0.123	1300.83	159.74
A_68_P20335677	chr1:72282883-72282927	ENSMUST00000147711:-134		PROMOTER	0.083	1.395	1509.58	2105.80	0.115	1015.93	117.27
A_68_P23756658	chr5:65883543-65883594	NM_133697:506	1110003E01Rik	INSIDE	0.082	1.376	1428.44	1965.72	0.113	1055.44	119.46
A_68_P29863081	chr14:103380685-103380729	NM_177715:1148	Kctd12	INSIDE	0.082	0.624	3074.56	1918.04	0.051	2306.57	117.81
A_68_P24758234	chr6:113187868-113187912	NM_026849:54	Mtmr14	INSIDE	0.082	0.677	2866.59	1939.61	0.055	2176.18	120.56
A_68_P20354544	chr1:75501965-75502010	NM_178884:1040	Obsl1	INSIDE	0.082	0.567	3667.31	2080.00	0.046	2724.69	126.61
A_68_P31096050	chr17:24343435-24343480	NM_001163847:-950	Tbc1d24	PROMOTER	0.082	0.687	3700.30	2541.32	0.056	2675.83	150.10
A_68_P24005588	chr5:115158042-115158088	NM_029992:277	Tchp	INSIDE	0.082	0.733	2868.20	2103.62	0.060	2061.91	124.42
A_68_P31675571	chr18:46358139-46358185	NM_001170855:310	Trim36	INSIDE	0.082	0.694	2673.28	1855.88	0.057	2181.95	123.51
A_68_P31715738	chr18:54022583-54022627	NM_152809:838	Csnk1g3	INSIDE	0.081	1.393	8923.58	12431.41	0.113	5833.60	656.68
A_68_P23807225	chr5:75471780-75471824	NM_133256:177	Gsx2	INSIDE	0.081	0.449	4540.07	2039.43	0.037	3157.80	115.28
A_68_P23334804	chr4:136157993-136158037	NM_133872:624	Kdm1a	INSIDE	0.081	0.574	4248.67	2438.37	0.047	3328.66	155.49

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P21820676	chr2:164774969-164775013	NM_013599:1240	Mmp9	INSIDE	0.081	1.346	3257.25	4385.41	0.110	2138.71	234.40
A_68_P24040027	chr5:121099008-121099052	NM_013832:200	Rasal1	INSIDE	0.081	2.528	1026.21	2594.46	0.204	595.00	121.17
A_68_P27468585	chr10:114688513-114688557	NM_025706:15	Tbc1d15	INSIDE	0.081	1.643	1762.21	2894.45	0.133	1156.78	153.80
A_68_P21104600	chr2:30532803-30532848	ENSMUST00000147959:-7397		PROMOTER	0.081	1.414	3899.92	5513.40	0.115	2549.52	293.41
A_68_P20101397	chr1:25887463-25887509	NM_175642:-934	Bai3	PROMOTER	0.080	0.599	3280.46	1965.75	0.048	2529.25	121.29
A_68_P23103963	chr4:91067208-91067252	NM_207685:-555	Elavl2	PROMOTER	0.080	0.639	3163.57	2021.53	0.051	2263.49	115.40
A_68_P25181447	chr7:72301734-72301778	NM_183087:-342	Fam189a1	PROMOTER	0.080	0.622	4566.13	2839.35	0.050	3019.94	150.74
A_68_P23297198	chr4:129219482-129219532	NM_008228:384	Hdac1	INSIDE	0.080	1.379	1454.66	2006.33	0.110	1059.73	116.49
A_68_P23198686	chr4:108673421-108673465	NM_146150:33	Nrd1	INSIDE	0.080	0.626	3248.33	2032.43	0.050	2490.66	124.05
A_68_P31827294	chr18:73863805-73863852	NM_008540:-433	Smad4	PROMOTER	0.080	0.742	2742.81	2035.67	0.059	2018.84	119.36
A_68_P26872171	chr9:119312063-119312107	NM_007397:466	Acvr2b	INSIDE	0.079	0.717	2617.25	1877.42	0.057	2058.02	117.29
A_68_P21761658	chr2:154483094-154483138	NM_029362:355	Chmp4b	INSIDE	0.079	0.435	4970.80	2162.56	0.034	3535.80	121.94
A_68_P28833511	chr13:12742044-12742088	NR_003568:596	Gpr137b-ps	INSIDE	0.079	0.555	4116.48	2283.77	0.044	3162.14	138.51
A_68_P31487964	chr18:10029653-10029701	NM_001038589:471	Usp14	INSIDE	0.079	1.842	6195.31	11413.37	0.145	4093.49	592.67
A_68_P32363625	chrX:45609838-45609889	NM_028276:-247	Utp14a	PROMOTER	0.079	3.156	1161.87	3666.93	0.248	518.54	128.66
A_68_P30503505	chr15:103153548-103153598	NM_013866:16945	Zfp385a	INSIDE	0.079	2.034	4335.45	8817.79	0.160	2853.66	457.12
A_68_P22546441	chr3:133899193-133899237	NM_001004367:-3897	Cxxc4	PROMOTER	0.078	0.749	4240.34	3178.10	0.058	2918.18	169.53
A_68_P30588475	chr16:20611479-20611531	NM_025462:-169	Ece2	DIVERGENT_PROMOTER	0.078	0.723	3023.77	2184.80	0.056	2057.09	116.13
A_68_P30221120	chr15:53177342-53177386	NM_010162:374	Ext1	INSIDE	0.078	0.582	3731.61	2170.97	0.045	2615.44	118.71
A_68_P28083515	chr11:102993907-102993951	NM_001130516:-724	Hexim2	PROMOTER	0.078	1.695	2730.81	4628.89	0.132	1621.76	214.70
A_68_P31826517	chr18:73733495-73733539	NM_001039214:1158	Mex3c	INSIDE	0.078	1.399	2843.39	3978.71	0.110	1972.83	216.63
A_68_P27838147	chr11:59476518-59476570	NM_012027:548	Mprip	INSIDE	0.078	1.462	1401.86	2049.00	0.114	1050.26	120.02
A_68_P31252241	chr17:55851663-55851707	NM_028370:242	Pot1b	INSIDE	0.078	0.678	4114.54	2791.39	0.053	2979.72	157.39
A_68_P28988730	chr13:43266919-43266963	NM_025935:-212	Tbc1d7	PROMOTER	0.078	0.624	3490.74	2177.97	0.049	2524.62	122.59
A_68_P28729928	chr12:110032252-110032296	NM_009537:754	Yy1	INSIDE	0.078	0.702	3053.77	2143.40	0.054	2223.67	121.00
A_68_P24537469	chr6:71583121-71583165	NM_001038695:-243	Kdm3a	PROMOTER	0.077	1.350	4220.43	5698.05	0.104	2899.62	300.82
A_68_P23298327	chr4:129420133-129420178	NM_011317:-629	Khdrbs1	PROMOTER	0.077	1.406	1879.44	2643.30	0.109	1298.73	141.46
A_68_P32240001	chrX:7327551-7327595	NR_030454:-2642	Mir684-1	DIVERGENT_PROMOTER	0.077	2.605	4060.53	10578.59	0.200	1527.46	304.95
A_68_P22357701	chr3:97817894-97817938	NM_010928:456	Notch2	INSIDE	0.077	0.623	3547.43	2209.09	0.048	2398.52	115.09
A_68_P32465511	chrX:71167531-71167575	NM_001164704:8637	Renbp	INSIDE	0.077	1.563	2571.84	4020.36	0.120	1067.20	127.67
A_68_P32321655	chrX:34625187-34625231	NM_026055:-29	Rpl39	PROMOTER	0.077	1.761	2145.06	3777.63	0.135	881.35	118.80
A_68_P28818473	chr13:9762982-9763026	NM_001199141:1556	Zmynd11	INSIDE	0.077	0.664	5357.19	3558.42	0.051	3894.44	200.43
A_68_P23588844	chr5:33775994-33776042	ENSMUST00000030994:-2174		PROMOTER	0.077	1.547	1438.65	2225.51	0.119	1007.79	120.30
A_68_P27889189	chr11:68213605-68213649	ENSMUST00000108674:699		INSIDE	0.077	0.553	3545.26	1961.80	0.042	2749.14	116.61
A_68_P23576981	chr5:31495306-31495353	NM_001127355:183	Eif2b4	INSIDE	0.076	0.575	3657.33	2104.26	0.044	2694.09	118.19
A_68_P26375217	chr9:27108097-27108141	NM_001033323:1306	Igsf9b	INSIDE	0.076	0.581	3690.51	2144.89	0.044	2698.86	118.66
A_68_P24155791	chr5:144031328-144031372	NM_017467:351	Zfp316	INSIDE	0.076	0.449	4921.70	2209.77	0.034	3505.98	119.72
A_68_P31899539	chr18:86881114-86881158	NM_172633:-1303	Cbln2	PROMOTER	0.075	2.705	5819.18	15742.21	0.203	3236.54	658.59
A_68_P22968878	chr4:62875674-62875718	NM_025685:-749	Col27a1	PROMOTER	0.075	1.634	2729.17	4459.20	0.122	1704.67	207.86
A_68_P32183081	chr19:53604393-53604437	NM_001085390:607	Dusp5	INSIDE	0.075	1.453	1606.62	2334.21	0.110	1087.04	119.17
A_68_P31980262	chr19:16511319-16511363	NM_008137:1184	Gna14	INSIDE	0.075	0.685	3023.98	2070.76	0.051	2280.64	117.31
A_68_P32672782	chrX:131135885-131135929	NM_019868:82	Hnrnph2	INSIDE	0.075	2.992	5115.46	15306.29	0.225	2082.20	468.59
A_68_P23391249	chr4:147279034-147279078	NM_133201:-128	Mfn2	PROMOTER	0.075	0.741	3922.36	2905.25	0.056	2626.60	146.34
A_68_P31023476	chr17:7165875-7165919	NM_147155:-391	Tagap1	PROMOTER	0.075	0.662	10591.97	7015.01	0.050	7779.16	388.33
A_68_P21106324	chr2:30837544-30837588	NM_144885:-105	BC005624	DIVERGENT_PROMOTER	0.074	0.699	4223.37	2950.23	0.052	2853.65	147.36
A_68_P23767820	chr5:67817841-67817885	NM_001164806:1176	Bend4	INSIDE	0.074	2.214	4749.84	10514.43	0.165	2920.32	480.52
A_68_P26555224	chr9:59598868-59598912	NM_173018:-90	Myo9a	DIVERGENT_PROMOTER	0.074	0.531	4461.33	2370.67	0.039	3225.68	126.42
A_68_P32403906	chrX:55284045-55284104	NM_009575:270	Zic3	INSIDE	0.074	4.497	1428.96	6425.88	0.331	542.29	179.57
A_68_P23237067	chr4:117559785-117559829	NM_033617:128	Atp6v0b	INSIDE	0.073	0.749	4477.31	3352.79	0.055	2996.22	163.37
A_68_P28513757	chr12:70398282-70398327	NM_027117:637	Klhdc2	INSIDE	0.073	3.260	3464.37	11292.49	0.239	2091.29	499.84
A_68_P31556969	chr18:23962757-23962801	NM_153058:308	Mapre2	INSIDE	0.073	1.884	6992.76	13172.49	0.138	4524.25	623.56

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P32375460	chrX:48558753-48558797	NM_134163:235	Mbnl3	INSIDE	0.073	1.444	3023.47	4366.83	0.106	1085.52	115.03
A_68_P20560376	chr1:122017920-122017975	NM_001172074:184	3110009E18Rik	INSIDE	0.072	1.646	1745.17	2873.17	0.118	1163.32	137.64
A_68_P32241629	chrX:7651043-7651087	NM_011514:822	Suv39h1	INSIDE	0.072	1.414	2929.62	4142.89	0.102	1185.63	120.42
A_68_P27985539	chr11:85646087-85646145	NM_009324:0	Tbx2	INSIDE	0.072	1.485	1523.17	2261.27	0.107	1092.65	116.97
A_68_P29346589	chr13:115249074-115249124	NM_008046:-160	Fst	PROMOTER	0.071	1.475	1858.64	2741.70	0.105	1247.68	130.53
A_68_P22964956	chr4:62185874-62185918	NM_021498:152	Pole3	INSIDE	0.071	1.756	4791.00	8414.54	0.125	3104.51	389.18
A_68_P27365025	chr10:94878000-94878046	NM_001168657:-105	Socs2	PROMOTER	0.071	1.614	1570.75	2535.47	0.115	1049.86	120.93
A_68_P23332903	chr4:135804530-135804574	NM_011542:681	Tcea3	INSIDE	0.071	1.422	4105.23	5839.24	0.101	2502.04	252.30
A_68_P32589660	chrX:105011451-105011503	NM_025921:197	2610002M06Rik	INSIDE	0.070	2.499	2043.26	5105.76	0.175	685.55	119.65
A_68_P22398706	chr3:105508483-105508532	NM_001163356:132	6530418L21Rik	INSIDE	0.070	1.990	1457.80	2901.24	0.139	890.76	123.87
A_68_P20858579	chr1:179187522-179187574	NM_011785:-8650	Akt3	PROMOTER	0.070	1.543	4336.99	6692.37	0.108	2838.08	305.62
A_68_P32328375	chrX:35918239-35918283	NM_001110142:11113	Cul4b	INSIDE	0.070	2.613	4453.97	11636.75	0.184	1912.55	351.27
A_68_P21433078	chr2:93028237-93028293	NM_001025246:524	Trp53i11	INSIDE	0.070	1.431	1844.01	2638.20	0.100	1150.48	114.97
A_68_P28936822	chr13:34222312-34222356	NM_023716:-111	Tubb2b	PROMOTER	0.070	1.945	5328.16	10364.36	0.137	3246.00	445.09
A_68_P27266466	chr10:76628787-76628837	NM_009929:463	Col18a1	INSIDE	0.069	2.104	3474.49	7308.83	0.145	2390.09	346.92
A_68_P31849792	chr18:78033867-78033918	NM_013831:604	Pstpip2	INSIDE	0.069	1.383	3351.66	4636.44	0.096	2396.56	230.19
A_68_P30343688	chr15:75561991-75562035			Unknown	0.069	1.740	5044.01	8778.76	0.120	3426.96	409.57
A_68_P21977361	chr3:19795434-19795478	NR_027985:586	4632415L05Rik	INSIDE	0.068	0.670	3689.45	2470.52	0.046	2570.35	117.06
A_68_P31097445	chr17:24592379-24592423	NM_007893:-144	E4f1	PROMOTER	0.068	0.746	3145.67	2346.73	0.051	2272.53	115.10
A_68_P27289250	chr10:80840838-80840882	NM_019757:255	Fzr1	INSIDE	0.068	1.874	2237.73	4194.37	0.127	1493.69	189.10
A_68_P29269015	chr13:101322806-101322850	NM_008756:-375	Ocln	PROMOTER	0.068	1.923	3702.50	7119.37	0.132	2243.73	295.18
A_68_P23271503	chr4:124667328-124667372	NM_138683:3677	Rspo1	INSIDE	0.068	1.366	4346.41	5935.84	0.092	2711.92	250.02
A_68_P20880187	chr1:183140858-183140911	NM_145514:1225	Wdr26	INSIDE	0.068	1.852	1729.94	3204.00	0.126	1230.71	155.21
A_68_P32300610	chrX:23270059-23270108	NM_175180:-159	Wdr44	PROMOTER	0.068	1.739	2450.06	4260.32	0.118	1028.19	121.48
A_68_P20002773	chr1:3662046-3662090	NM_001011874:-489	Xkr4	PROMOTER	0.068	0.648	3911.41	2534.36	0.044	2772.36	121.88
A_68_P21866700	chr2:172764763-172764807	NM_007557:1010	Bmp7	INSIDE	0.067	0.581	6091.26	3536.32	0.039	4480.39	175.43
A_68_P31899538	chr18:86881037-86881081	NM_172633:-1381	Cbln2	PROMOTER	0.067	1.702	14900.30	25364.05	0.114	9814.59	1123.72
A_68_P24816271	chr6:124613291-124613335	NM_145130:191	Lpcat3	INSIDE	0.067	0.552	4653.68	2567.20	0.037	3141.69	116.63
A_68_P25989172	chr8:81033404-81033456	NM_029736:197	Slc10a7	INSIDE	0.067	1.382	3021.95	4175.13	0.093	2170.20	202.18
A_68_P29517797	chr14:33276567-33276611	NM_021712:1448	Slc18a3	INSIDE	0.067	0.684	4420.12	3025.44	0.046	3068.08	140.23
A_68_P27911311	chr11:72224533-72224583	NM_177776:657	Smtnl2	INSIDE	0.067	1.615	2028.51	3276.09	0.108	1455.58	157.84
A_68_P28048202	chr11:96883898-96883943	NM_031183:9038	Sp6	INSIDE	0.067	2.296	2943.93	6759.36	0.154	1974.68	304.04
A_68_P32540975	chrX:92391699-92391746	ENSMUST00000113884:438		INSIDE	0.067	1.613	3129.57	5049.41	0.108	1089.45	118.18
A_68_P24129541	chr5:138705342-138705401	NM_153161:-91	BC037034	PROMOTER	0.066	1.555	1655.49	2573.91	0.102	1150.94	117.60
A_68_P27281212	chr10:79601441-79601485	NM_001195268:-1330	Dos	PROMOTER	0.066	1.344	7195.75	9673.17	0.088	4601.83	405.26
A_68_P20849152	chr1:177555795-177555846	NM_010209:-54	Fh1	DIVERGENT_PROMOTER	0.066	1.365	2170.50	2961.80	0.090	1673.46	150.99
A_68_P31063011	chr17:15115516-15115564	NM_001123367:236	Gm3417	INSIDE	0.066	0.493	5097.23	2514.76	0.033	3680.04	120.47
A_68_P32465787	chrX:71211906-71211951	NM_008224:-274	Hcfc1	PROMOTER	0.066	2.773	1632.69	4527.60	0.183	670.10	122.34
A_68_P25678160	chr8:15011568-15011612	NM_029116:566	Kbtbd11	INSIDE	0.066	0.715	3719.89	2659.04	0.047	2653.43	124.50
A_68_P23433043	chr4:154010163-154010214	NM_001177995:794	Prdm16	INSIDE	0.066	0.736	3679.81	2707.03	0.048	2470.24	119.77
A_68_P21628855	chr2:130100231-130100275	NR_028547:-998	Snord110	PROMOTER	0.066	0.675	3651.49	2464.71	0.044	2749.58	121.58
A_68_P31259429	chr17:57129711-57129755	NM_017393:46	Clpp	INSIDE	0.065	1.638	5541.89	9077.77	0.106	3565.52	378.50
A_68_P23401327	chr4:148961132-148961176	NM_023051:408	Clstn1	INSIDE	0.065	0.743	3944.35	2928.84	0.049	2517.93	122.15
A_68_P25577541	chr7:146574687-146574731	NM_001127363:-299	Inpp5a	PROMOTER	0.065	0.647	5097.15	3297.48	0.042	3693.72	155.70
A_68_P32773807	chrX:155694248-155694292	NM_148945:219	Rps6ka3	INSIDE	0.065	1.597	3251.45	5192.77	0.104	1141.61	118.64
A_68_P32786682	chrX:158346088-158346143	NM_001081052:251607	Nhs	INSIDE	0.064	2.986	2136.10	6377.93	0.192	816.00	156.77
A_68_P31631094	chr18:38115681-38115725	NM_153793:490	Rell2	INSIDE	0.064	0.658	3935.67	2591.41	0.042	2784.17	117.36
A_68_P29141940	chr13:73901479-73901523	NM_011390:356	Slc12a7	INSIDE	0.064	0.574	4587.60	2633.57	0.037	3231.45	118.90
A_68_P31247139	chr17:54438039-54438089	NM_022025:295	Slc5a7	INSIDE	0.064	0.690	3657.85	2522.83	0.044	2637.98	116.63
A_68_P30142416	chr15:37065776-37065825			Unknown	0.064	1.796	1274.06	2288.38	0.115	1022.74	117.56
A_68_P27795130	chr11:51464039-51464083	NR_027958:-395	D930048N14Rik	PROMOTER	0.063	0.712	3868.01	2755.52	0.045	2649.21	119.65

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO$_2$-NP/Vehicle)	Sham group			TiO$_2$-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P23756666	chr5:65884517-65884566	NM_133697:-467	1110003E01Rik	PROMOTER	0.062	1.900	2135.45	4057.75	0.119	1475.15	175.18
A_68_P31791363	chr18:67503527-67503573	NR_033214:207	B430212C06Rik	INSIDE	0.062	1.525	1796.39	2738.65	0.095	1274.39	120.93
A_68_P25045779	chr7:35597123-35597172	NM_175140:583	Chst8	INSIDE	0.062	0.700	3530.48	2471.14	0.043	2796.11	121.54
A_68_P32730440	chrX:143988591-143988635	NM_001081173:12	Lrch2	INSIDE	0.062	2.353	2924.30	6880.77	0.146	1103.33	161.60
A_68_P25394540	chr7:112959842-112959886	NM_025301:-263	Mrpl17	PROMOTER	0.062	0.675	4014.69	2708.01	0.042	2894.92	120.14
A_68_P29162267	chr13:78334860-78334904	NM_010151:3361	Nr2f1	INSIDE	0.062	1.413	7189.05	10158.16	0.088	4645.59	408.31
A_68_P21784241	chr2:158493133-158493177	NM_001159662:284	Ppp1r16b	INSIDE	0.062	1.522	5115.00	7784.87	0.095	3433.40	324.83
A_68_P29482226	chr14:27354098-27354142	NM_032008:-894	Slmap	PROMOTER	0.062	0.662	5259.13	3482.21	0.041	3537.96	144.74
A_68_P25113824	chr7:56891950-56892001	NM_001005232:230	Dbx1	INSIDE	0.061	1.479	4110.71	6079.61	0.090	2549.02	229.67
A_68_P25328181	chr7:100229343-100229387	NM_021427:976	Fam181b	INSIDE	0.061	0.716	4535.13	3247.78	0.044	3244.95	142.88
A_68_P21114608	chr2:32167860-32167904	NR_029811:-6097	Mir199b	PROMOTER	0.061	0.545	5383.54	2932.25	0.033	3466.85	115.46
A_68_P32289745	chrX:20281291-20281340	NM_145628:281	Usp11	INSIDE	0.061	3.297	1735.70	5722.13	0.202	648.10	131.15
A_68_P27186311	chr10:61949916-61949968	NM_133672:-389	Vps26a	PROMOTER	0.061	1.371	1933.92	2651.77	0.084	1414.91	118.56
A_68_P24828002	chr6:126593244-126593288	NM_010595:2553	Kcna1	INSIDE	0.060	0.726	3643.30	2644.31	0.043	2703.77	116.95
A_68_P24758833	chr6:113277046-113277100	NM_010957:103	Ogg1	INSIDE	0.060	1.477	1972.22	2912.53	0.088	1364.63	120.44
A_68_P32415812	chrX:58146994-58147038	NM_009237:-411	Sox3	PROMOTER	0.060	1.992	2303.86	4589.02	0.119	996.00	118.31
A_68_P31128446	chr17:29686489-29686534	NM_001162901:27	Tmem217	INSIDE	0.060	1.482	1893.32	2805.17	0.089	1368.66	121.21
A_68_P20618262	chr1:133806972-133807021	NM_001145804:-38	Nucks1	PROMOTER	0.059	0.573	4903.36	2808.04	0.034	3475.83	116.53
A_68_P32240898	chrX:7499680-7499725	NM_013892:2755	Pcsk1n	INSIDE	0.059	2.926	2124.50	6217.11	0.173	806.98	139.48
A_68_P32481890	chrX:75828993-75829037	NM_001164275:107	Prrg1	INSIDE	0.059	1.411	4045.61	5706.80	0.083	1508.92	125.58
A_68_P31620298	chr18:35989480-35989524	NM_133687:31	Cxxc5	INSIDE	0.058	0.711	6141.97	4366.36	0.041	4314.31	177.72
A_68_P28941742	chr13:35086077-35086121	NM_001110331:-85	Eci2	PROMOTER	0.058	1.647	2213.86	3646.81	0.095	1375.37	131.01
A_68_P32239706	chrX:7274518-7274562	NM_173747:281	Gpkow	INSIDE	0.058	3.468	1824.03	6326.36	0.200	618.74	124.05
A_68_P24603555	chr6:85137374-85137418	NM_010131:-528	Emx1	PROMOTER	0.057	0.637	4927.83	3140.04	0.036	3613.56	131.38
A_68_P26134614	chr8:108090464-108090513	NM_013477:-548	Atp6v0d1	PROMOTER	0.056	1.824	1603.00	2924.67	0.103	1152.37	118.29
A_68_P31347824	chr17:74059066-74059113	NM_027864:702	Galnt14	INSIDE	0.056	2.589	4127.46	10686.06	0.144	2551.03	367.54
A_68_P30365876	chr15:79178645-79178689	NM_010755:559	Maff	INSIDE	0.056	0.744	4402.30	3275.28	0.041	2943.95	121.66
A_68_P32569611	chrX:99839237-99839281	NM_008832:327	Phka1	INSIDE	0.056	2.794	4375.23	12225.17	0.156	1577.23	246.39
A_68_P21957616	chr3:14611261-14611305	NM_001099674:-26	1810022K09Rik	PROMOTER	0.055	1.711	8239.94	14100.84	0.094	4815.05	454.13
A_68_P32553707	chrX:96332536-96332580	NM_010110:1090	Efnb1	INSIDE	0.055	2.793	1851.05	5170.11	0.155	777.30	120.18
A_68_P22894260	chr4:47365694-47365738	NM_009370:-460	Tgfbr1	PROMOTER	0.055	1.745	2338.09	4078.79	0.095	1466.34	139.55
A_68_P32578103	chrX:101866009-101866059	NM_175358:369	Zdhhc15	INSIDE	0.055	2.727	2259.62	6162.57	0.149	806.45	120.13
A_68_P27282601	chr10:79805419-79805466	NM_001113548:5749	Adamtsl5	INSIDE	0.054	2.077	5997.11	12454.74	0.113	3739.60	422.49
A_68_P23767821	chr5:67817925-67817969	NM_001164806:1092	Bend4	INSIDE	0.054	2.300	6069.92	13961.59	0.124	3932.74	487.66
A_68_P29531957	chr14:35633864-35633908	NM_008166:565	Grid1	INSIDE	0.054	1.338	4410.16	5899.98	0.073	2791.40	203.22
A_68_P28043737	chr11:96180501-96180545	NM_010459:942	Hoxb4	INSIDE	0.054	0.742	4134.06	3067.29	0.040	2834.86	114.11
A_68_P32141596	chr19:46078435-46078479	NM_176785:489	Hps6	INSIDE	0.054	0.718	5887.53	4228.23	0.039	4128.41	161.27
A_68_P20852905	chr1:178205134-178205178	NM_176916:287	Pld5	INSIDE	0.054	0.732	4045.40	2961.82	0.039	3061.41	120.17
A_68_P31644533	chr18:40378844-40378888	NM_023311:187	Yipf5	INSIDE	0.054	1.878	14054.89	26395.33	0.102	8501.30	866.43
A_68_P32601450	chrX:109009220-109009268			Unknown	0.054	2.484	2369.90	5887.83	0.134	884.27	118.77
A_68_P28593011	chr12:84827402-84827446	NM_058212:1234	Dpf3	INSIDE	0.053	1.542	8286.68	12778.79	0.081	5432.00	442.38
A_68_P29696148	chr14:70008926-70008970	NM_033325:-334	Loxl2	PROMOTER	0.053	1.760	4525.86	7966.21	0.092	2920.66	269.90
A_68_P27541975	chr10:127986066-127986114	NM_018860:134	Rpl41	INSIDE	0.053	1.609	2185.75	3517.88	0.085	1372.94	116.61
A_68_P27567652	chr11:6174705-6174749	NM_134020:114	Tmed4	INSIDE	0.053	1.414	2618.98	3702.34	0.075	1607.48	120.52
A_68_P20804634	chr1:169280619-169280663	NM_019993:519	Aldh9a1	INSIDE	0.052	1.869	4491.55	8394.50	0.097	2920.32	284.26
A_68_P32592615	chrX:106029602-106029650	NM_001081477:68	Brwd3	INSIDE	0.052	2.627	2774.50	7287.86	0.137	861.55	117.82
A_68_P32328377	chrX:35918417-35918470	NM_001110142:10930	Cul4b	INSIDE	0.052	3.025	1745.89	5281.59	0.156	739.79	115.73
A_68_P32798240	chrX:160857773-160857818	NM_011081:77	Piga	INSIDE	0.052	1.666	3449.95	5746.86	0.086	1373.40	118.01
A_68_P30380961	chr15:81846636-81846680	NM_134095:-88	Pppde2	DIVERGENT_PROMOTER	0.052	0.697	7707.50	5372.11	0.036	5343.73	194.99
A_68_P28519208	chr12:71328463-71328507	NM_133198:186	Pygl	INSIDE	0.052	1.798	6304.49	11338.04	0.093	3743.06	346.85
A_68_P23973505	chr5:109106557-109106601	NM_174870:-1910	Slc26a1	PROMOTER	0.052	1.822	1939.53	3534.19	0.094	1277.76	120.45

						Sham group			TiO_2-H group		
ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27534513	chr10:126626792-126626847	NM_001166413:60	Arhgef25	INSIDE	0.051	1.389	2672.40	3710.76	0.071	1699.16	120.72
A_68_P26920732	chr10:7500225-7500275	NM_145418:465	BC013529	INSIDE	0.051	0.720	4171.11	3004.32	0.037	3130.63	114.96
A_68_P31207500	chr17:46683388-46683432	NM_001081335:-73	Cul9	PROMOTER	0.051	2.117	3755.77	7950.94	0.108	2256.59	243.96
A_68_P31545966	chr18:21811604-21811648	NM_001081403:-757	Klhl14	PROMOTER	0.051	1.495	4721.84	7059.15	0.076	3244.50	247.11
A_68_P25091647	chr7:52436916-52436960	NM_053256:574	Pth2	INSIDE	0.051	1.638	5199.99	8515.05	0.083	3282.43	273.82
A_68_P27827732	chr11:57641072-57641118	NM_008213:4555	Hand1	DOWNSTREAM	0.050	1.535	4642.97	7127.85	0.077	2995.31	230.27
A_68_P23088443	chr4:87677902-87677949	NM_027326:1386	Mllt3	INSIDE	0.050	1.378	3132.38	4315.93	0.069	2132.62	147.74
A_68_P24951861	chr7:5012862-5012906	NM_001205231:-860	U2af2	PROMOTER	0.050	1.386	5584.12	7737.96	0.069	3565.50	246.70
A_68_P26234307	chr8:125100918-125100973	NM_009698:-138	Aprt	PROMOTER	0.049	1.853	2008.98	3722.06	0.091	1303.90	119.25
A_68_P32136351	chr19:45155030-45155086	NM_178929:4430	Kazald1	DOWNSTREAM	0.049	1.432	2706.42	3875.13	0.070	1917.99	135.00
A_68_P27899593	chr11:70043429-70043486	NM_007528:-157	Bcl6b	DIVERGENT_PROMOTER	0.048	1.531	2278.22	3486.99	0.073	1668.41	122.14
A_68_P32319275	chrX:34138849-34138893	NM_016783:651	Pgrmc1	INSIDE	0.048	4.730	1509.48	7140.44	0.225	545.32	122.94
A_68_P25411544	chr7:117205106-117205158	NM_009281:-83	Zfp143	PROMOTER	0.048	1.934	1882.54	3640.72	0.092	1349.52	124.02
A_68_P32260272	chrX:11657098-11657142	NM_029510:559	Bcor	INSIDE	0.047	1.527	7364.88	11244.67	0.072	2313.39	167.32
A_68_P20768471	chr1:162722421-162722468	NM_013862:625	Rabgap1l	INSIDE	0.047	1.347	2476.00	3334.55	0.064	1913.93	122.20
A_68_P32240694	chrX:7461707-7461754	NM_001083937:361	Slc35a2	INSIDE	0.047	2.503	2768.65	6928.78	0.116	1019.91	118.76
A_68_P32651796	chrX:126284437-126284481	NM_172493:181	Diap2	INSIDE	0.046	2.019	3296.73	6655.66	0.094	1263.70	118.38
A_68_P31256434	chr17:56615114-56615158	NM_011218:767	Ptprs	INSIDE	0.046	1.406	10793.29	15174.52	0.064	6437.47	412.14
A_68_P29575957	chr14:47007792-47007836	NM_007554:2460	Bmp4	INSIDE	0.045	1.669	5683.48	9482.93	0.075	3733.09	279.16
A_68_P32380515	chrX:49518249-49518293	NM_008150:-170	Gpc4	PROMOTER	0.045	2.950	2257.23	6658.92	0.134	890.06	118.95
A_68_P31631084	chr18:38114429-38114473	NM_010411:192	Hdac3	INSIDE	0.045	2.035	2056.96	4186.80	0.091	1314.65	119.16
A_68_P27992600	chr11:86923122-86923170	NR_029652:-3359	Mir301	PROMOTER	0.045	2.344	1719.34	4029.52	0.107	1095.49	116.69
A_68_P27536452	chr10:126971104-126971148	NM_183297:489	Nxph4	INSIDE	0.045	1.402	12909.02	18098.38	0.064	7582.89	483.68
A_68_P29249243	chr13:97842140-97842199	NM_001100458:572	Fam169a	INSIDE	0.044	1.885	2079.58	3920.02	0.084	1622.84	135.71
A_68_P26022753	chr8:87461135-87461179	NM_019945:96	Mast1	INSIDE	0.044	1.797	5022.41	9027.06	0.078	3037.14	237.70
A_68_P32598389	chrX:108010047-108010091	NM_008901:265	Pou3f4	INSIDE	0.044	5.620	6802.72	38228.22	0.246	2678.51	659.05
A_68_P21566789	chr2:118726839-118726885	NM_001045523:-488	Bahd1	PROMOTER	0.043	4.027	1664.43	6703.31	0.172	953.62	164.43
A_68_P21094090	chr2:28765327-28765371	NM_019446:6593	Barhl1	INSIDE	0.042	1.337	3319.03	4438.08	0.057	2144.44	121.85
A_68_P31259430	chr17:57129793-57129837	NM_017393:128	Clpp	INSIDE	0.042	1.585	6366.32	10088.04	0.067	3872.02	259.37
A_68_P24138250	chr5:140383933-140383977	NM_175522:58	Elfn1	INSIDE	0.042	1.584	2700.46	4277.88	0.066	1760.59	116.87
A_68_P26152542	chr8:111238708-111238758	NM_007496:189	Zfhx3	INSIDE	0.042	1.352	3471.69	4694.99	0.057	2100.28	120.40
A_68_P28271876	chr12:17697378-17697423	NM_016677:-219	Hpcal1	PROMOTER	0.041	1.988	2184.05	4341.67	0.082	1451.54	118.99
A_68_P30633253	chr16:28929529-28929575	NM_177718:232	1600021P15Rik	INSIDE	0.040	3.548	1827.40	6483.44	0.143	1069.02	152.71
A_68_P30381577	chr15:81958707-81958759	NM_172428:381	Ccdc134	INSIDE	0.040	1.497	3033.92	4542.02	0.060	2027.68	122.01
A_68_P32395899	chrX:53708448-53708501	NM_172779:459	Ddx26b	INSIDE	0.039	5.109	2071.50	10583.14	0.199	581.42	115.63
A_68_P31151052	chr17:34067414-34067462	NM_009059:600	Rgl2	INSIDE	0.039	4.551	5324.40	24230.36	0.179	3132.35	559.83
A_68_P22903293	chr4:49072217-49072261	NM_178756:-95	E130309F12Rik	PROMOTER	0.038	1.987	5573.01	11074.82	0.075	3841.46	287.20
A_68_P25289617	chr7:91754287-91754332	NM_010176:143	Fah	INSIDE	0.038	1.364	3888.45	5304.05	0.052	2397.88	124.31
A_68_P25959941	chr8:74685000-74685047	NM_023126:-75	Rab8a	PROMOTER	0.038	1.500	3214.79	4822.37	0.056	2138.57	120.77
A_68_P22129177	chr3:51145110-51145166	ENSMUST00000135496:-558		PROMOTER	0.038	1.817	2836.78	5153.90	0.070	1736.93	120.85
A_68_P32395900	chrX:53708549-53708594	NM_172779:556	Ddx26b	INSIDE	0.037	3.030	3147.19	9535.48	0.111	1084.40	120.86
A_68_P32742985	chrX:147247678-147247726	NM_001199246:544	Maged2	INSIDE	0.037	3.682	2465.96	9080.68	0.135	876.03	117.91
A_68_P32601449	chrX:109009111-109009155			Unknown	0.037	3.293	3989.37	13136.78	0.123	1447.47	178.03
A_68_P31150915	chr17:34046487-34046531	NM_001199733:-37	Daxx	PROMOTER	0.036	1.513	3355.42	5076.31	0.054	2218.99	120.83
A_68_P32746464	chrX:148238102-148238146	NM_021523:300	Huwe1	INSIDE	0.036	2.197	4454.26	9785.52	0.079	1640.12	129.40
A_68_P26348961	chr9:21602785-21602833	NM_145611:182	Kank2	INSIDE	0.035	1.396	6997.57	9770.96	0.049	4304.21	209.97
A_68_P30207180	chr15:50721578-50721632	NM_032000:-17	Trps1	PROMOTER	0.035	1.391	3787.97	5268.18	0.049	2339.62	114.92
A_68_P24951860	chr7:5012759-5012803	NM_001205231:-964	U2af2	PROMOTER	0.035	1.731	3897.00	6746.08	0.061	2578.09	157.88
A_68_P24637122	chr6:91107049-91107096	NM_144919:264	Hdac11	INSIDE	0.034	1.864	2902.03	5408.58	0.064	1920.46	122.60
A_68_P21105302	chr2:30656577-30656621	NM_198000:629	1700001O22Rik	INSIDE	0.033	3.922	16457.71	64553.78	0.130	10033.62	1305.90
A_68_P31899540	chr18:86881200-86881249	NM_172633:-1215	Cbln2	PROMOTER	0.033	3.469	1983.08	6878.59	0.114	1062.30	120.80

ProbeName	Target position of probe on CpG island microarray	TargetID	GeneSymbol	CpG island Description	Ratio of relative methylation (TiO_2-NP/Vehicle)	Sham group			TiO_2-H group		
						Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)	Relative methylation (Cy5/Cy3)	Cy3 signal (Input)	Cy5 signal (MeDIP)
A_68_P27840489	chr11:59859589-59859648	NM_008819:-9277	Pemt	PROMOTER	0.033	2.790	2341.77	6534.34	0.093	1602.80	148.31
A_68_P32698228	chrX:136812874-136812918	ENSMUST00000130153:-495		PROMOTER	0.033	1.896	5612.21	10641.14	0.064	1975.78	125.49
A_68_P32380514	chrX:49518048-49518092	NM_008150:30	Gpc4	INSIDE	0.031	3.509	2434.58	8541.97	0.109	1060.70	115.78
A_68_P28271882	chr12:17698051-17698099	NM_016677:455	Hpcal1	INSIDE	0.031	1.447	3887.70	5626.17	0.045	2651.60	120.63
A_68_P24785569	chr6:118147581-118147630	NM_001080780:157	Ret	INSIDE	0.031	2.450	3790.76	9288.09	0.077	2407.56	184.55
A_68_P22885108	chr4:45811962-45812007	NM_028270:91	Aldh1b1	INSIDE	0.030	1.585	5500.95	8720.82	0.047	3396.99	159.35
A_68_P28025142	chr11:92961341-92961387	NM_028296:761	Car10	INSIDE	0.027	1.596	3914.31	6247.50	0.043	2760.61	119.50
A_68_P31791020	chr18:67449254-67449298	NM_053261:400	Impa2	INSIDE	0.027	1.454	5572.36	8102.62	0.040	3547.63	141.36
A_68_P21061288	chr2:22924783-22924828	NM_001102437:214	Acbd5	INSIDE	0.024	1.918	4351.38	8347.05	0.045	2834.50	128.16
A_68_P23301440	chr4:129985621-129985680	NM_010174:-371	Fabp3	PROMOTER	0.022	2.767	2315.19	6404.98	0.062	1915.62	118.89
A_68_P23236661	chr4:117508209-117508255	NM_008135:370	Slc6a9	INSIDE	0.022	3.433	4780.88	16413.51	0.077	3061.80	235.89
A_68_P24138249	chr5:140383826-140383870	NM_175522:-48	Elfn1	PROMOTER	0.020	1.782	5297.62	9442.53	0.036	3315.72	118.02
A_68_P25371480	chr7:108257652-108257696	NM_001146010:386	Fchsd2	INSIDE	0.018	1.469	6853.58	10064.94	0.026	4417.02	116.42
A_68_P28158445	chr11:116144132-116144186	NM_010254:1906	Galr2	INSIDE	0.018	2.351	4288.22	10083.10	0.043	2941.95	125.80
A_68_P20250392	chr1:57028581-57028634	NR_024325:295	9130024F11Rik	INSIDE	0.016	3.220	3574.32	11508.11	0.052	2359.54	121.70
A_68_P32462127	chrX:70588115-70588159	NM_001160229:177	Zfp275	INSIDE	0.007	8.116	5707.12	46321.67	0.056	2110.42	117.44