

S Table 1. List of hypermethylation candidates in colon cancer

#	Primary Annotation	ID	Location	HCT116			LS180		
				Norm IP Signal	Norm WCE Signal	Log Ratio	Norm IP Signal	Norm WCE Signal	Log Ratio
1	CA4	A_17_P17002046	chr17:55573378-55573422	15677.90	3595.67	2.12	14385.75	3461.79	2.06
2	DMN	A_17_P16831699	chr15:97463381-97463425	2138.09	327.72	2.71	3664.88	527.42	2.80
3	POU3F3	A_17_P01379433	chr2:104834955-104835014	808.16	135.58	2.58	3710.21	811.73	2.19
4	FAM43A	A_17_P02873231	chr3:195888914-195888958	4794.16	863.25	2.47	11320.65	2548.99	2.15
5	KCNK12	A_17_P15240926	chr2:47601700-47601744	5176.80	935.12	2.47	6080.86	1535.16	1.99
6	ALK	A_17_P15230137	chr2:29996596-29996640	4110.83	749.16	2.46	18664.56	4409.01	2.08
7	SLC6A17	A_17_P00452527	chr1:110495285-110495330	2725.85	500.45	2.45	8459.23	2171.92	1.96
8	CHRD12	A_17_P16473985	chr11:74120144-74120188	6540.84	1207.95	2.44	7582.24	1394.86	2.44
9	GSC2	A_17_P17254687	chr22:17516541-17516585	5825.43	1076.89	2.44	6882.04	1020.06	2.75
10	SLC6A7	A_17_P15752136	chr5:149549821-149549865	9985.67	1895.10	2.40	7729.66	1407.37	2.46
11	DHH	A_17_P08340657	chr12:47769915-47769959	3899.96	741.36	2.40	11745.13	2282.19	2.36
12	BHLHB5	A_17_P26457915	chr8:65650952-65651011	2258.60	429.50	2.39	4977.22	1099.84	2.18
13	HOXC12	A_17_P08362004	chr12:52631311-52631361	5480.11	1044.61	2.39	3871.86	838.20	2.21
14	BMP2	A_17_P17171054	chr20:6696468-6696512	2890.38	553.25	2.39	9094.61	1852.81	2.30
15	NEUROG3	A_17_P07298070	chr10:71002136-71002180	3369.92	645.32	2.38	12215.75	3367.16	1.86
16	CYP26A1	A_17_P16373180	chr10:94818426-94818470	7355.02	1413.22	2.38	7675.69	1407.86	2.45
17	VSX2	A_17_P09390380	chr14:73776099-73776143	8886.14	1726.00	2.36	8874.54	2073.08	2.10
18	PNMA1	A_17_P09388148	chr14:73249297-73249356	4994.87	971.62	2.36	5774.08	1240.33	2.22
19	CXCL12	A_17_P07195009	chr10:44199558-44199602	4671.25	912.16	2.36	3232.85	982.82	1.72
20	OVOL2	A_17_P31738797	chr20:17984153-17984202	5313.73	1043.27	2.35	6581.23	1142.81	2.53
21	ADAMTS18	A_17_P10126493	chr16:76025881-76025925	8222.03	1636.27	2.33	9788.70	1844.93	2.41
22	ADAM32	A_17_P06081915	chr8:39084112-39084165	7585.22	1516.05	2.32	2752.13	677.84	2.02
23	OXTR	A_17_P22181173	chr3:8784008-8784052	7415.61	1482.16	2.32	9776.01	1795.80	2.44
24	ADAMTS5	A_17_P11329584	chr21:27259649-27259693	3843.73	770.56	2.32	4157.97	851.47	2.29
25	ALPP	A_17_P01962868	chr2:232960106-232960150	9286.86	1863.32	2.32	10115.24	1706.45	2.57
26	TAL1	A_17_P15057700	chr1:47463782-47463826	4192.22	842.34	2.32	5733.64	1304.91	2.14
27	HAND2	A_17_P15639260	chr4:174674475-174674519	6154.33	1236.70	2.32	11760.92	2955.44	1.99
28	EVC	A_17_P02905150	chr4:5764267-5764311	6221.80	1257.52	2.31	7405.53	1337.30	2.47

29	EGR4	A_17_P01276999	chr2:73372162-73372206	4772.11	965.16	2.31	4465.49	969.02	2.20
30	DNAJC6	A_17_P15068201	chr1:65504171-65504215	7149.72	1446.51	2.31	4002.94	929.87	2.11
31	HS3ST3A1	A_17_P16945172	chr17:13444692-13444736	5969.43	1211.69	2.30	7149.98	1320.08	2.44
32	NPY2R	A_17_P03546584	chr4:156348707-156348751	13691.39	2780.36	2.30	15940.83	2941.73	2.44
33	ADCY2	A_17_P03746288	chr5:7448253-7448303	4225.07	858.34	2.30	4917.47	1067.35	2.20
34	FAM148B	A_17_P16796481	chr15:60243755-60243799	8108.78	1653.93	2.29	8452.13	1522.36	2.47
35	DLX3	A_17_P10356564	chr17:45425743-45425787	8724.61	1781.84	2.29	10881.52	2964.68	1.88
36	ADCY8	A_17_P16135982	chr8:132121426-132121470	14812.39	3030.00	2.29	11836.39	2266.29	2.38
37	ACTN2	A_17_P15195221	chr1:234916614-234916659	6625.09	1356.48	2.29	10808.74	2756.04	1.97
38	WIT1	A_17_P07734878	chr11:32415138-32415197	4771.76	977.90	2.29	5007.62	1015.01	2.30
39	CDH13	A_17_P10151824	chr16:81218128-81218172	11224.38	2305.31	2.28	8515.74	1875.03	2.18
40	ZIC5	A_17_P09077668	chr13:99406079-99406123	3026.33	622.79	2.28	18237.15	4165.22	2.13
41	EMX2	A_17_P07511888	chr10:119283977-119284026	11732.29	2417.12	2.28	7334.07	1861.17	1.98
42	HDGFRP3	A_17_P16818821	chr15:81666697-81666741	6268.29	1292.39	2.28	5912.45	1496.79	1.98
43	KHDRBS2	A_17_P04769084	chr6:63053750-63053802	8966.26	1850.35	2.28	4032.82	767.74	2.39
44	GFRA4	A_17_P17169149	chr20:3589174-3589218	6940.89	1437.43	2.27	8617.13	1787.26	2.27
45	FLT3	A_17_P08741734	chr13:27572113-27572171	6001.76	1243.47	2.27	3880.87	957.70	2.02
46	NXPH4	A_17_P28812042	chr12:55904917-55904961	6636.77	1375.47	2.27	7106.60	1567.27	2.18
47	NRG3	A_17_P07351407	chr10:83624202-83624246	6296.62	1305.17	2.27	6808.73	1555.35	2.13
48	MT1A	A_17_P16899456	chr16:55227112-55227156	6984.57	1448.90	2.27	8216.21	1648.65	2.32
49	FGF4	A_17_P16468527	chr11:69298250-69298294	6856.53	1424.57	2.27	7368.96	1452.89	2.34
50	SFRP1	A_17_P26372259	chr8:41284779-41284838	5202.12	1081.85	2.27	3877.15	823.32	2.24
51	PAX2	A_17_P07429885	chr10:102487511-102487558	7798.88	1628.31	2.26	8015.35	1882.02	2.09
52	MDGA2	A_17_P09273026	chr14:47213199-47213243	6040.46	1261.98	2.26	8306.89	1458.62	2.51
53	FAT4	A_17_P03413760	chr4:126456920-126456972	11122.77	2329.34	2.26	4862.80	1232.17	1.98
54	FBXL5	A_17_P02945674	chr4:15266618-15266662	4077.93	855.78	2.25	5721.61	848.65	2.75
55	ITGA9	A_17_P02175229	chr3:37469002-37469046	9646.16	2024.35	2.25	11889.09	1989.78	2.58
56	SIGLEC15	A_17_P17064365	chr18:41671477-41671521	3303.40	693.84	2.25	14323.03	3704.85	1.95
57	AGTR1	A_17_P15498946	chr3:149898414-149898458	4572.18	960.81	2.25	20979.67	5181.47	2.02
58	MAP9	A_17_P23708977	chr4:156516993-156517052	6762.74	1421.62	2.25	8599.62	1484.61	2.53
59	HPSE2	A_17_P07423642	chr10:100982157-100982201	5678.99	1193.92	2.25	6516.97	1540.05	2.08
60	WASF3	A_17_P16620570	chr13:26030368-26030412	5461.03	1149.01	2.25	4133.72	959.56	2.11
61	MGC52498	A_17_P15060739	chr1:52871339-52871383	5974.81	1257.30	2.25	11033.28	2279.90	2.27
62	BCL2L10	A_17_P09656336	chr15:50191487-50191531	5312.59	1118.04	2.25	5982.17	1177.99	2.34

63	DGKE	A_17_P16998871	chr17:52266826-52266870	9463.41	1991.74	2.25	11832.50	3014.90	1.97
64	FLJ40125	A_17_P10974944	chr19:50693802-50693846	12074.32	2548.15	2.24	12519.25	2572.02	2.28
65	DPP10	A_17_P01414269	chr2:115136512-115136556	7337.60	1549.46	2.24	12304.42	3427.91	1.84
66	PLCB1	A_17_P17171712	chr20:8061281-8061325	5790.67	1223.75	2.24	10581.85	2515.25	2.07
67	CRHBP	A_17_P04029430	chr5:76285128-76285177	5954.31	1258.67	2.24	13136.56	3275.25	2.00
68	PSTPIP2	A_17_P15810363	chr6:42803015-42803059	1780.00	376.34	2.24	7760.47	2009.37	1.95
69	NKX2-5	A_17_P15764253	chr5:172588525-172588569	2907.31	615.33	2.24	6762.92	1858.29	1.86
70	SPHKAP	A_17_P15389965	chr2:228754221-228754265	6404.94	1357.54	2.24	14352.05	3319.67	2.11
71	CITED1	A_17_P11786540	chrX:71441453-71441503	4050.86	859.68	2.24	5357.81	1116.06	2.26
72	ATP1B2	A_17_P10214352	chr17:7495094-7495138	5762.59	1223.42	2.24	5142.51	1282.06	2.00
73	OR10AD1	A_17_P16555479	chr12:46878762-46878806	13423.89	2851.17	2.24	12422.33	3066.54	2.02
74	IMPA2	A_17_P17039793	chr18:12028439-12028483	7585.35	1611.59	2.23	8167.43	1771.82	2.20
75	TTC9B	A_17_P10961333	chr19:45415863-45415907	10154.99	2158.01	2.23	4698.64	1158.05	2.02
76	LBH	A_17_P01077838	chr2:30307042-30307088	6614.53	1406.78	2.23	8300.23	1520.59	2.45
77	TMEM155	A_17_P03397283	chr4:122905253-122905297	10947.45	2329.47	2.23	12839.17	2567.81	2.32
78	RCCD1	A_17_P16826742	chr15:89301083-89301127	9647.88	2053.17	2.23	12339.67	2188.51	2.50
79	ARHGAP9	A_17_P08377684	chr12:56155367-56155411	5164.03	1099.21	2.23	5268.79	1127.10	2.22
80	ZNF804B	A_17_P05596892	chr7:88226095-88226154	3085.18	657.24	2.23	9331.66	2018.02	2.21
81	PAX9	A_17_P09227703	chr14:36186557-36186601	14808.05	3159.55	2.23	7549.17	1555.40	2.28
82	DCDC2	A_17_P04616484	chr6:24465811-24465855	5312.14	1134.23	2.23	4985.53	1205.34	2.05
83	RPESP	A_17_P16106203	chr8:74167593-74167637	19157.79	4091.52	2.23	13023.23	2934.96	2.15
84	LHX2	A_17_P06954321	chr9:125811152-125811199	8225.62	1762.24	2.22	6081.31	1436.67	2.08
85	KLHL14	A_17_P17056028	chr18:28603767-28603811	12480.94	2676.05	2.22	6983.84	1700.53	2.04
86	COL12A1	A_17_P15831794	chr6:75851578-75851622	3210.01	688.79	2.22	12447.71	2266.81	2.46
87	RASL11A	A_17_P08737989	chr13:26743701-26743760	3903.14	837.70	2.22	7604.65	1921.42	1.98
88	ALPL	A_17_P00083294	chr1:21708570-21708614	7308.03	1572.38	2.22	7012.02	1683.60	2.06
89	GHSR	A_17_P02770971	chr3:173648321-173648366	12985.90	2795.86	2.22	14146.44	3392.27	2.06
90	LHX1	A_17_P10305315	chr17:32363515-32363572	8164.02	1759.97	2.21	4578.82	1104.13	2.05
91	PTGER4	A_17_P03892456	chr5:40716754-40716803	9753.01	2106.32	2.21	4360.64	1032.43	2.08
92	DCHS2	A_17_P15628832	chr4:155473621-155473665	9568.00	2066.82	2.21	12027.39	2542.65	2.24
93	EPHA6	A_17_P02431902	chr3:98014715-98014759	4398.30	950.29	2.21	5927.65	1066.34	2.47
94	SST	A_17_P15520723	chr3:188870730-188870774	7914.97	1710.75	2.21	8004.94	1732.18	2.21
95	RELN	A_17_P05659047	chr7:103416714-103416758	2067.53	446.96	2.21	8418.53	2010.27	2.07
96	CD14	A_17_P04324142	chr5:139991833-139991877	6437.56	1392.58	2.21	8275.44	1989.65	2.06

97	KIAA1576	A_17_P10128091	chr16:76380237-76380281	10811.38	2343.34	2.21	12685.91	2621.26	2.27
98	DLX2	A_17_P01675521	chr2:172669835-172669880	5592.89	1212.63	2.21	6701.03	1601.77	2.06
99	HIST1H3C	A_17_P04624478	chr6:26153543-26153602	4890.89	1060.84	2.20	9012.99	2638.20	1.77
100	CD38	A_17_P23098726	chr4:15389187-15389231	5767.59	1251.95	2.20	6924.53	1307.98	2.40
101	CEBPA	A_17_P10940198	chr19:38483953-38483997	11741.25	2551.34	2.20	13923.19	3013.29	2.21
102	SFRP4	A_17_P15930800	chr7:37922235-37922279	9285.29	2019.32	2.20	5456.08	1135.62	2.26
103	NLRP1	A_17_P10205494	chr17:5343928-5343972	8526.79	1854.60	2.20	10252.71	2169.29	2.24
104	ANKRD57	A_17_P15299985	chr2:109729812-109729856	5469.44	1189.66	2.20	8016.72	1260.66	2.67
105	HMX3	A_17_P16392328	chr10:124883217-124883261	18644.84	4057.29	2.20	6243.64	1333.34	2.23
106	ABHD12B	A_17_P29744328	chr14:50408391-50408450	1432.70	311.83	2.20	1670.79	284.15	2.56
107	LHX4	A_17_P00633093	chr1:178464653-178464699	2554.72	556.47	2.20	6471.79	1490.26	2.12
108	GRM5	A_17_P07934456	chr11:87881421-87881476	7515.15	1637.80	2.20	9224.24	1774.24	2.38
109	RASGRF1	A_17_P09777982	chr15:77168828-77168872	1516.25	330.66	2.20	2154.78	566.54	1.93
110	STK32B	A_17_P02902963	chr4:5103821-5103876	7202.20	1570.80	2.20	6972.22	1510.82	2.21
111	ADHFE1	A_17_P06182970	chr8:67507330-67507374	6347.24	1384.67	2.20	4758.43	1329.37	1.84
112	HOXB13	A_17_P10350887	chr17:44157688-44157735	10141.63	2213.04	2.20	8277.58	1534.23	2.43
113	ABTB2	A_17_P16434575	chr11:34334852-34334896	5339.07	1165.83	2.20	10129.77	2773.31	1.87
114	LRRC3B	A_17_P22261298	chr3:26639280-26639324	6831.93	1491.94	2.20	7093.76	1769.56	2.00
115	MGC42105	A_17_P03902927	chr5:43227686-43227730	8868.01	1937.96	2.19	10192.41	2504.66	2.02
116	TADA1L	A_17_P00574127	chr1:165120176-165120221	10369.24	2266.24	2.19	10733.45	2542.90	2.08
117	ALX3	A_17_P15098863	chr1:110411841-110411885	6437.40	1410.32	2.19	8581.92	1715.15	2.32
118	FOXF2	A_17_P04506710	chr6:1326708-1326752	5577.82	1223.01	2.19	8846.79	1979.96	2.16
119	TMEM145	A_17_P10967723	chr19:47519598-47519642	4579.56	1004.78	2.19	5023.93	1048.30	2.26
120	ICAM4	A_17_P10880930	chr19:10258681-10258725	10973.70	2408.03	2.19	11323.48	2722.59	2.06
121	POU4F1	A_17_P16651500	chr13:78068126-78068170	6745.89	1480.88	2.19	6633.60	1467.95	2.18
122	HEXIM1	A_17_P30911154	chr17:40577430-40577475	5459.53	1199.02	2.19	5715.36	1366.79	2.06
123	NTRK2	A_17_P06786547	chr9:86473485-86473529	6539.68	1436.41	2.19	6092.65	1054.63	2.53
124	FLJ45803	A_17_P08028282	chr11:110674500-110674544	8535.95	1874.91	2.19	8608.67	2039.52	2.08
125	KCNMA1	A_17_P07335242	chr10:79066764-79066808	5906.08	1297.66	2.19	12818.03	2872.45	2.16
126	VEGFC	A_17_P23805910	chr4:177950119-177950178	3465.33	762.59	2.18	3675.46	762.40	2.27
127	MYCN	A_17_P15220680	chr2:15998193-15998237	7111.62	1565.85	2.18	9637.98	2115.62	2.19
128	GSX2	A_17_P03104041	chr4:54660958-54661002	3574.54	787.20	2.18	7138.12	1778.97	2.00
129	SHOX2	A_17_P02705740	chr3:159294817-159294861	7080.48	1559.44	2.18	9034.47	1633.04	2.47
130	CENTA2	A_17_P10281606	chr17:26273837-26273881	5372.55	1183.41	2.18	5632.68	1298.56	2.12

131	BAALC	A_17_P06347189	chr8:104222344-104222390	11815.42	2603.50	2.18	10173.99	2140.51	2.25
132	HIST1H3F	A_17_P04625489	chr6:26358356-26358405	5333.49	1176.76	2.18	6599.96	1188.61	2.47
133	NKX2-8	A_17_P09227336	chr14:36119033-36119077	7767.66	1714.30	2.18	7859.57	1809.16	2.12
134	SFXN3	A_17_P16378345	chr10:102797842-102797886	6729.45	1486.62	2.18	5915.33	1467.96	2.01
135	FGF14	A_17_P09087542	chr13:101366823-101366867	6710.89	1482.79	2.18	8780.72	1610.46	2.45
136	MAFB	A_17_P17192197	chr20:38745255-38745299	5018.76	1109.74	2.18	5423.94	1358.61	2.00
137	CLDN11	A_17_P02760437	chr3:171618829-171618888	7911.52	1751.63	2.18	8318.94	1804.59	2.20
138	FGF19	A_17_P16468453	chr11:69229458-69229512	5844.38	1295.03	2.17	5279.14	1205.49	2.13
139	SH3MD4	A_17_P01396743	chr2:109111179-109111223	5357.70	1187.75	2.17	11350.14	2541.33	2.16
140	MTNR1B	A_17_P28375979	chr11:92342263-92342307	6914.23	1533.32	2.17	6264.75	1718.33	1.87
141	SNTG1	A_17_P16093541	chr8:50984848-50984892	3389.00	751.60	2.17	4070.10	1006.66	2.02
142	OTP	A_17_P15712738	chr5:76959667-76959711	5760.95	1278.62	2.17	7181.50	1587.80	2.18
143	DOCK2	A_17_P15761770	chr5:168996916-168996960	7118.19	1581.50	2.17	8999.32	1827.43	2.30
144	VLDLR	A_17_P06549907	chr9:2611182-2611228	3994.55	887.58	2.17	5172.59	1230.77	2.07
145	CCDC13	A_17_P02198421	chr3:42789664-42789708	6673.67	1484.07	2.17	7810.17	1559.30	2.32
146	EVX2	A_17_P02905133	chr4:5760855-5760899	6960.28	1548.16	2.17	7824.90	1822.47	2.10
147	SORCS1	A_17_P16382342	chr10:108914002-108914046	5928.81	1318.83	2.17	8922.40	2152.00	2.05
148	SLC5A8	A_17_P16585698	chr12:100127561-100127605	16892.34	3759.90	2.17	18639.31	4734.95	1.98
149	TLX1	A_17_P07432192	chr10:102873089-102873133	15842.62	3526.45	2.17	13270.41	2642.14	2.33
150	PAP2D	A_17_P00407957	chr1:99242457-99242501	7202.27	1603.23	2.17	8698.80	1750.85	2.31
151	MKX	A_17_P16304674	chr10:28070210-28070254	5229.94	1164.66	2.17	6489.67	1181.32	2.46
152	PURA	A_17_P15746088	chr5:139474356-139474400	2561.58	570.55	2.17	10005.97	2071.84	2.27
153	FAM135B	A_17_P16139838	chr8:139578146-139578190	7220.41	1608.60	2.17	6358.72	1410.92	2.17
154	SLC6A5	A_17_P07681907	chr11:20574334-20574378	6466.08	1441.96	2.16	6363.12	1568.03	2.02
155	SOCS2	A_17_P08540771	chr12:92490709-92490753	6574.69	1466.70	2.16	6314.96	1536.12	2.04
156	TRPC4	A_17_P08788156	chr13:37341544-37341595	6229.66	1391.11	2.16	3713.35	860.40	2.11
157	PLCD1	A_17_P02178508	chr3:38045421-38045465	13704.79	3062.79	2.16	9347.37	2167.06	2.11
158	LPHN2	A_17_P20358477	chr1:82038485-82038544	2629.40	587.68	2.16	5830.24	1212.27	2.27
159	CCDC140	A_17_P01917003	chr2:222868082-222868126	4902.71	1096.64	2.16	8187.64	1595.71	2.36
160	KIAA0644	A_17_P05388031	chr7:28961824-28961868	6540.44	1463.52	2.16	8416.38	1669.49	2.33
161	SLC38A4	A_17_P08331001	chr12:45511749-45511796	6142.80	1374.66	2.16	11254.82	2701.05	2.06
162	LEFTY1	A_17_P00835619	chr1:224141941-224141985	11442.04	2562.20	2.16	14157.47	2448.54	2.53
163	UNC5C	A_17_P23441506	chr4:96688208-96688252	4236.12	949.26	2.16	9798.25	2309.31	2.09
164	VWCE	A_17_P07827091	chr11:60818245-60818289	12192.79	2732.27	2.16	16561.89	3574.04	2.21

165	NKX2-4	A_17_P11110115	chr20:21324408-21324452	5751.20	1288.99	2.16	7961.29	1700.00	2.23
166	FOXL2	A_17_P02617790	chr3:140139324-140139368	4411.88	988.85	2.16	4931.51	1087.20	2.18
167	WNT6	A_17_P01898994	chr2:219444428-219444472	8969.29	2011.86	2.16	6943.01	1565.00	2.15
168	RALYL	A_17_P06263125	chr8:85259383-85259431	10122.09	2271.11	2.16	8554.23	1655.76	2.37
169	DLEC1	A_17_P02178556	chr3:38055852-38055896	6743.76	1514.34	2.15	4691.98	1122.28	2.06
170	LOC152573	A_17_P03065727	chr4:42093960-42094004	5372.17	1207.14	2.15	19275.02	4957.38	1.96
171	IGFBP7	A_17_P03116376	chr4:57670798-57670842	10736.79	2412.97	2.15	9265.45	2245.10	2.05
172	MCHR2	A_17_P04933303	chr6:100548591-100548635	3348.52	752.71	2.15	3925.62	748.86	2.39
173	TYRO3	A_17_P16782541	chr15:39664718-39664762	7388.86	1661.05	2.15	8146.62	1620.36	2.33
174	SLC6A2	A_17_P10031333	chr16:54247076-54247120	5457.93	1227.44	2.15	7054.48	1390.19	2.34
175	ADAM19	A_17_P04397750	chr5:156934066-156934110	3443.81	774.58	2.15	4478.02	819.31	2.45
176	STOX2	A_17_P03680332	chr4:185063179-185063238	3564.66	801.79	2.15	11003.32	2769.02	1.99
177	UBD	A_17_P04636978	chr6:29629146-29629190	5503.45	1238.47	2.15	7307.47	1437.10	2.35
178	KCNAB1	A_17_P15502976	chr3:157491831-157491875	10155.69	2285.80	2.15	9320.06	2309.15	2.01
179	HIC1	A_17_P09511079	chr14:99181063-99181107	6725.17	1513.82	2.15	8772.23	1934.65	2.18
180	GRIA4	A_17_P28430634	chr11:104986175-104986219	5496.02	1238.33	2.15	17629.47	4313.67	2.03
181	LIN28B	A_17_P04956088	chr6:105507751-105507795	8743.33	1971.70	2.15	9673.68	2219.22	2.12
182	CDH6	A_17_P03851289	chr5:31229774-31229833	2296.10	518.03	2.15	14670.23	3662.31	2.00
183	TWIST1	A_17_P05340617	chr7:19112565-19112610	4372.63	989.46	2.14	10117.99	2690.55	1.91
184	SIM2	A_17_P11375309	chr21:36987241-36987285	9103.08	2059.91	2.14	5127.48	1112.57	2.20
185	ST8SIA3	A_17_P17072660	chr18:53171076-53171120	7957.81	1801.16	2.14	10739.84	2176.84	2.30
186	CCDC11	A_17_P17067860	chr18:46046858-46046902	11139.16	2522.96	2.14	3257.92	631.44	2.37
187	GRIA2	A_17_P03556492	chr4:158360866-158360913	3150.14	713.68	2.14	4780.04	996.95	2.26
188	SNRPF	A_17_P08550157	chr12:94776044-94776094	5630.06	1276.16	2.14	5762.37	1223.04	2.24
189	ASAM	A_17_P08085830	chr11:122571846-122571890	7204.51	1633.27	2.14	14789.79	3561.18	2.05
190	GNB4	A_17_P15515577	chr3:180651402-180651446	4233.44	959.95	2.14	3514.04	664.19	2.40
191	TLE4	A_17_P06764253	chr9:81375480-81375524	12444.27	2822.11	2.14	7820.42	1820.90	2.10
192	EDIL3	A_17_P15716379	chr5:83713867-83713911	5768.15	1308.28	2.14	10210.59	2228.82	2.20
193	ZNF580	A_17_P11003375	chr19:60843274-60843318	4565.73	1036.88	2.14	5334.67	1308.84	2.03
194	FCRLB	A_17_P00550511	chr1:159962304-159962348	9344.73	2122.35	2.14	16025.75	4127.39	1.96
195	CIDEB	A_17_P16686802	chr14:23849805-23849849	10197.70	2317.06	2.14	10039.45	2447.73	2.04
196	DMRT1	A_17_P26829912	chr9:831434-831478	10083.18	2291.99	2.14	8297.75	1823.43	2.19
197	IRX5	A_17_P10027987	chr16:53522602-53522646	7923.98	1801.85	2.14	5905.40	1466.15	2.01
198	CA10	A_17_P16996333	chr17:47590389-47590433	13192.16	3002.12	2.14	13743.24	3656.05	1.91

199	HIST1H3G	A_17_P04625552	chr6:26379571-26379615	7306.50	1662.85	2.14	5993.86	1403.50	2.09
200	TACR3	A_17_P03316565	chr4:104860384-104860435	2863.58	651.72	2.14	10871.24	2260.72	2.27
201	CREB5	A_17_P05384574	chr7:28414755-28414800	7204.59	1640.17	2.14	11391.82	2536.92	2.17
202	ADAM11	A_17_P10335674	chr17:40191386-40191430	13745.63	3129.47	2.13	15282.20	3274.49	2.22
203	ELOVL4	A_17_P25044778	chr6:80713638-80713682	5427.35	1236.29	2.13	6230.77	1284.40	2.28
204	CNTN4	A_17_P15407069	chr3:2115033-2115077	7748.59	1765.46	2.13	9583.54	1962.61	2.29
205	LOC387856	A_17_P16555461	chr12:46864003-46864047	8500.51	1937.61	2.13	6331.40	1443.61	2.13
206	HTR1E	A_17_P04872782	chr6:87704126-87704175	4499.80	1026.21	2.13	6150.63	1147.08	2.42
207	IGF2AS	A_17_P07601672	chr11:2117611-2117655	8283.28	1889.39	2.13	4177.33	712.43	2.55
208	TBX18	A_17_P04865550	chr6:85539342-85539386	3835.07	875.27	2.13	11507.96	2030.89	2.50
209	TMEFF2	A_17_P21896975	chr2:192766424-192766468	6584.52	1503.63	2.13	9104.01	1631.86	2.48
210	VSX1	A_17_P11126995	chr20:25006487-25006531	5682.69	1298.72	2.13	15257.25	3267.81	2.22
211	GALC	A_17_P29917408	chr14:87528775-87528829	12494.52	2855.95	2.13	13316.46	3616.68	1.88
212	ELMO1	A_17_P15930576	chr7:37454667-37454711	3033.63	693.62	2.13	7892.09	1859.24	2.09
213	HOXD13	A_17_P01695065	chr2:176664854-176664898	3107.54	710.57	2.13	2837.89	640.96	2.15
214	EMID2	A_17_P25903993	chr7:100792708-100792752	16893.53	3865.12	2.13	24633.99	4905.54	2.33
215	KAL1	A_17_P17316584	chrX:8658895-8658939	4687.80	1072.87	2.13	3137.36	789.85	1.99
216	NKX2-1	A_17_P09227052	chr14:36056228-36056272	5348.26	1224.31	2.13	6528.63	1394.33	2.23
217	JAM3	A_17_P16520052	chr11:133444171-133444215	4239.15	971.07	2.13	4464.43	819.46	2.45
218	AVPR1A	A_17_P08402456	chr12:61829945-61829989	4997.65	1144.83	2.13	4885.96	1126.08	2.12
219	WIPF1	A_17_P01688145	chr2:175255313-175255357	7804.65	1788.13	2.13	5924.31	1249.43	2.25
220	ADCY4	A_17_P09171603	chr14:23871385-23871430	6544.54	1499.76	2.13	6430.45	1613.58	1.99
221	SSH2	A_17_P16967042	chr17:25112218-25112262	4901.35	1123.65	2.12	5372.46	1224.52	2.13
222	MYOZ3	A_17_P15752579	chr5:150031522-150031566	8025.24	1839.91	2.12	16607.33	4696.10	1.82
223	SLC6A15	A_17_P08501301	chr12:83829441-83829495	10145.43	2328.93	2.12	4244.28	1089.48	1.96
224	LRRC2	A_17_P02214927	chr3:46582356-46582400	12842.54	2949.06	2.12	8777.02	1820.91	2.27
225	LOC401498	A_17_P16171063	chr9:32772951-32772996	2165.06	497.69	2.12	8726.26	2133.87	2.03
226	SOX13	A_17_P20801486	chr1:202310990-202311034	10696.56	2460.04	2.12	7369.45	1717.03	2.10
227	SGCZ	A_17_P05972670	chr8:15138940-15138984	7271.48	1672.66	2.12	9029.52	2064.25	2.13
228	FOXB2	A_17_P16228653	chr9:78818902-78818946	16878.26	3884.85	2.12	20430.49	4770.00	2.10
229	GPR149	A_17_P02689350	chr3:155629104-155629151	6540.85	1506.12	2.12	8533.85	1689.47	2.34
230	GJD2	A_17_P16778023	chr15:32833907-32833951	9029.40	2080.25	2.12	10093.04	2359.58	2.10
231	TFPI2	A_17_P15989745	chr7:93357314-93357358	5268.75	1214.37	2.12	6183.87	1465.95	2.08
232	THY1	A_17_P08067806	chr11:118797919-118797963	5826.52	1343.04	2.12	7263.65	1756.27	2.05

233	NKX2-3	A_17_P07424786	chr10:101277195-101277239	18486.83	4261.49	2.12	6187.67	1305.14	2.25
234	LECT1	A_17_P08854647	chr13:52211161-52211205	6888.20	1589.54	2.12	9792.35	1730.97	2.50
235	DNER	A_17_P01952268	chr2:230286473-230286517	5066.53	1169.24	2.12	6008.42	1356.13	2.15
236	CAMK2N1	A_17_P00079582	chr1:20683118-20683166	2635.90	608.34	2.12	8601.37	2028.59	2.08
237	EPHA5	A_17_P15573612	chr4:66217922-66217966	10476.09	2419.26	2.11	12839.09	2715.78	2.24
238	CRHR1	A_17_P16987846	chr17:41216563-41216607	4904.75	1133.06	2.11	6107.79	1410.88	2.11
239	FSTL4	A_17_P15741775	chr5:132974878-132974922	4195.11	969.17	2.11	7661.16	1894.74	2.02
240	VMO1	A_17_P10202831	chr17:4635315-4635364	7155.74	1654.09	2.11	9165.58	1871.91	2.29
241	OPRM1	A_17_P05184354	chr6:154402396-154402440	8481.97	1961.29	2.11	2512.93	763.37	1.72
242	ACOT4	A_17_P09387845	chr14:73128063-73128121	5163.95	1194.13	2.11	5235.87	1217.82	2.10
243	SOX21	A_17_P09052763	chr13:94152208-94152252	7356.27	1701.49	2.11	8683.84	1949.93	2.15
244	PRDM14	A_17_P06198993	chr8:71144338-71144382	12605.39	2915.95	2.11	7495.20	1860.85	2.01
245	TRIM36	A_17_P04207671	chr5:114534381-114534425	6121.50	1416.80	2.11	13366.60	3302.75	2.02
246	ADCY1	A_17_P15936884	chr7:45579951-45579995	3185.34	738.19	2.11	4128.66	813.76	2.34
247	WDR69	A_17_P22069796	chr2:228444414-228444458	6795.70	1575.03	2.11	8007.80	1956.93	2.03
248	CRISPLD1	A_17_P16107229	chr8:76059078-76059122	11002.62	2550.79	2.11	6594.16	2346.80	1.49
249	CHODL	A_17_P17222691	chr21:18539100-18539145	14681.65	3404.93	2.11	18991.30	3645.66	2.38
250	ZNF583	A_17_P11005866	chr19:61607108-61607152	9611.32	2229.63	2.11	11419.84	2539.12	2.17
251	HADHA	A_17_P15227319	chr2:26260951-26260995	2443.62	566.93	2.11	2884.64	492.23	2.55
252	FRZB	A_17_P15362864	chr2:183439119-183439163	6327.43	1468.05	2.11	7144.04	1662.27	2.10
253	DAB1	A_17_P00221111	chr1:57660585-57660629	6735.08	1562.76	2.11	7601.18	1836.49	2.05
254	GUCY1A3	A_17_P03548560	chr4:156807786-156807830	6443.25	1495.43	2.11	11083.43	2587.01	2.10
255	SLC12A8	A_17_P02561391	chr3:126343425-126343469	10500.70	2437.49	2.11	13544.15	2779.13	2.28
256	DMRTA1	A_17_P06642798	chr9:22436784-22436829	5865.81	1361.98	2.11	7602.56	1553.97	2.29
257	ZNF528	A_17_P31635216	chr19:57592688-57592745	2484.22	577.32	2.11	2809.70	670.10	2.07
258	PRKD1	A_17_P09197351	chr14:29466199-29466243	8604.58	1999.72	2.11	4905.11	1156.61	2.08
259	L3MBTL2	A_17_P11511383	chr22:39963482-39963526	6946.00	1615.79	2.10	6452.78	1605.32	2.01
260	MAL	A_17_P21436562	chr2:95054561-95054605	6598.02	1535.58	2.10	6837.48	1729.10	1.98
261	RAB3C	A_17_P03953324	chr5:57913954-57914006	4818.85	1121.71	2.10	5283.60	1177.54	2.17
262	DLX1	A_17_P01675412	chr2:172654359-172654403	9819.52	2285.90	2.10	6561.58	1385.39	2.24
263	BVES	A_17_P25156254	chr6:105690751-105690810	6893.59	1605.97	2.10	5282.35	1670.61	1.66
264	FREM2	A_17_P08791441	chr13:38159205-38159249	4620.54	1076.44	2.10	10787.76	2602.11	2.05
265	AMH	A_17_P17096702	chr19:2201856-2201900	7415.96	1728.75	2.10	5737.32	1341.74	2.10
266	OAT	A_17_P16393149	chr10:126067493-126067537	14674.03	3421.50	2.10	12395.23	2632.54	2.24

267	GAS1	A_17_P16235814	chr9:88750476-88750520	10521.88	2453.42	2.10	13538.74	2925.23	2.21
268	TOX	A_17_P06149870	chr8:60192729-60192782	7679.46	1791.66	2.10	13224.33	2911.29	2.18
269	LHFPL3	A_17_P05660391	chr7:103756673-103756717	10299.73	2403.01	2.10	9200.78	2237.42	2.04
270	ATOH1	A_17_P03273698	chr4:94969650-94969700	9396.85	2192.37	2.10	5254.25	1051.17	2.32
271	TEPP	A_17_P10041275	chr16:56575948-56575992	7828.46	1826.74	2.10	9272.45	1913.97	2.28
272	RSPO2	A_17_P06371123	chr8:109163666-109163710	10325.27	2409.89	2.10	8136.10	1978.23	2.04
273	LOC645191	A_17_P17096828	chr19:2240899-2240943	9070.60	2118.41	2.10	5261.38	1055.67	2.32
274	DNAH11	A_17_P05351949	chr7:21548902-21548949	5479.83	1279.88	2.10	10759.52	2335.99	2.20
275	GPR158	A_17_P16302119	chr10:25504531-25504575	4889.87	1142.28	2.10	6410.29	1418.72	2.18
276	RARA	A_17_P16980033	chr17:35752277-35752321	5537.15	1294.46	2.10	6575.02	1352.93	2.28
277	SLC35F1	A_17_P05014176	chr6:118335090-118335134	2905.85	679.69	2.10	3693.97	720.76	2.36
278	ABCC9	A_17_P16539923	chr12:21985239-21985290	2779.25	650.11	2.10	4198.19	968.89	2.12
279	IFITM1	A_17_P16405638	chr11:305807-305851	6228.75	1458.29	2.09	7652.26	1479.94	2.37
280	CAB39	A_17_P15391685	chr2:231401040-231401084	8227.05	1927.92	2.09	8241.72	2059.14	2.00
281	AMPH	A_17_P05430131	chr7:38636880-38636932	9059.76	2124.67	2.09	9882.07	2667.25	1.89
282	SYT14	A_17_P15170351	chr1:208177841-208177885	4697.27	1101.63	2.09	5854.60	1176.37	2.32
283	CXCR7	A_17_P01983113	chr2:237141436-237141491	12877.41	3020.22	2.09	12304.12	2962.33	2.05
284	MEIS2	A_17_P09590765	chr15:35190452-35190502	6192.04	1452.50	2.09	9024.75	1950.47	2.21
285	HIST1H4H	A_17_P24813897	chr6:26392652-26392711	3685.64	864.65	2.09	343.47	71.35	2.27
286	TRIM72	A_17_P09986042	chr16:31134711-31134755	5995.31	1406.61	2.09	5719.75	1110.35	2.36
287	GSC	A_17_P09486469	chr14:94304437-94304481	7215.81	1693.81	2.09	7867.06	1707.34	2.20
288	ISL2	A_17_P09767147	chr15:74414548-74414592	7371.75	1731.24	2.09	8329.04	1974.85	2.08
289	GAD1	A_17_P15355012	chr2:171383186-171383230	6564.24	1542.55	2.09	6484.19	2063.45	1.65
290	FLJ45983	A_17_P16289656	chr10:8131442-8131492	5019.11	1179.58	2.09	6860.93	1466.25	2.23
291	ZNF582	A_17_P11005840	chr19:61596483-61596527	6841.68	1608.99	2.09	8028.78	1723.83	2.22
292	LAMB1	A_17_P05676515	chr7:107429063-107429107	9625.09	2263.63	2.09	11703.13	2531.84	2.21
293	TCF21	A_17_P05091092	chr6:134252275-134252328	8156.67	1918.41	2.09	10106.57	2339.72	2.11
294	ZBPB	A_17_P05480583	chr7:50103062-50103121	2056.43	483.81	2.09	8406.57	1813.17	2.21
295	MSX1	A_17_P15538994	chr4:4905597-4905641	3916.52	921.48	2.09	2335.56	486.24	2.26
296	RUNDC3B	A_17_P05592084	chr7:87094849-87094893	8336.32	1962.65	2.09	8472.78	2050.17	2.05
297	HIST1H2BB	A_17_P04624467	chr6:26152188-26152241	5819.78	1370.70	2.09	6723.17	1335.57	2.33
298	EN1	A_17_P15314989	chr2:119309122-119309166	3557.32	838.18	2.09	15013.80	3393.96	2.15
299	DACH2	A_17_P11813503	chrX:85289823-85289867	3581.17	844.27	2.08	8909.75	2227.53	2.00
300	EBF1	A_17_P04405739	chr5:158456554-158456598	7480.77	1763.76	2.08	8502.11	1896.02	2.16

301	NKX2-2	A_17_P11110573	chr20:21436519-21436563	7379.71	1740.48	2.08	3949.90	986.48	2.00
302	FGF12	A_17_P15523102	chr3:193608539-193608583	6528.65	1540.45	2.08	8467.42	1976.81	2.10
303	INSRR	A_17_P00530277	chr1:155081556-155081600	17287.19	4079.09	2.08	7049.90	1694.04	2.06
304	GPR176	A_17_P09604625	chr15:37999187-37999234	9182.95	2167.35	2.08	6044.05	1386.22	2.12
305	MARCKS	A_17_P25196718	chr6:114283653-114283709	3882.89	916.70	2.08	7906.20	1590.60	2.31
306	NPBWR1	A_17_P26406641	chr8:54014472-54014517	4403.42	1039.91	2.08	7249.57	1612.12	2.17
307	SOX5	A_17_P08252048	chr12:24606506-24606552	9426.66	2226.36	2.08	11744.71	2929.93	2.00
308	GALNT13	A_17_P01587244	chr2:154436256-154436300	8239.65	1946.33	2.08	6500.71	1356.44	2.26
309	TMEM176B	A_17_P16037980	chr7:150127916-150127960	16158.23	3817.69	2.08	8789.27	2106.50	2.06
310	FOLH1	A_17_P28208619	chr11:49186497-49186541	6895.53	1629.72	2.08	16764.34	4190.87	2.00
311	ST6GALNAC5	A_17_P15074278	chr1:77106078-77106122	7639.00	1805.86	2.08	4507.88	1051.34	2.10
312	NELL1	A_17_P07682393	chr11:20647143-20647187	5878.08	1389.67	2.08	7153.55	1475.21	2.28
313	RUNX1T1	A_17_P16116038	chr8:93183257-93183301	11596.30	2741.67	2.08	10122.25	2395.60	2.08
314	MT1G	A_17_P16899554	chr16:55259474-55259518	6730.70	1591.38	2.08	5261.02	964.58	2.45
315	LOC388931	A_17_P15225852	chr2:24086173-24086217	9281.95	2195.28	2.08	9853.74	2201.28	2.16
316	ZNF578	A_17_P10996137	chr19:57648585-57648629	6677.65	1579.51	2.08	8888.30	1788.93	2.31
317	KCTD8	A_17_P03074893	chr4:44144330-44144379	11219.75	2653.90	2.08	9807.55	2282.06	2.10
318	ELF3	A_17_P15162241	chr1:200248997-200249041	11478.02	2715.27	2.08	16740.04	3981.38	2.07
319	TRPC6	A_17_P16495770	chr11:100958655-100958699	6818.66	1614.01	2.08	7582.35	1944.75	1.96
320	MYF6	A_17_P16575924	chr12:79626517-79626562	8639.92	2045.53	2.08	22406.40	6364.13	1.82
321	TCF4	A_17_P10726942	chr18:51407955-51408014	1938.93	459.12	2.08	1911.31	441.40	2.11
322	TBX20	A_17_P05414694	chr7:35259472-35259520	6111.79	1447.98	2.08	8314.17	2023.54	2.04
323	GRIK1	A_17_P17229741	chr21:30233321-30233365	9282.22	2200.06	2.08	9946.25	2304.89	2.11
324	FAM150A	A_17_P26405123	chr8:53639645-53639692	5943.77	1408.94	2.08	5758.45	1291.04	2.16
325	SYT7	A_17_P16457707	chr11:61033157-61033201	1765.19	418.47	2.08	4386.38	907.55	2.27
326	TBX15	A_17_P15105625	chr1:119323912-119323956	7432.43	1762.13	2.08	10951.71	2028.86	2.43
327	SCRT2	A_17_P17167035	chr20:592351-592395	3607.15	855.21	2.08	4395.36	1045.05	2.07
328	ZAR1	A_17_P15565313	chr4:48186817-48186867	4884.34	1158.53	2.08	4572.90	1072.54	2.09
329	NODAL	A_17_P07302069	chr10:71870077-71870121	8649.76	2052.10	2.08	5719.18	1445.22	1.98
330	EMX1	A_17_P15255667	chr2:72998607-72998651	3761.98	892.79	2.08	8063.08	2153.20	1.90
331	OLIG3	A_17_P05108669	chr6:137851012-137851058	5867.05	1393.53	2.07	6990.11	1608.44	2.12
332	PHACTR1	A_17_P04561150	chr6:12857954-12857998	5995.77	1424.62	2.07	6326.09	1393.15	2.18
333	TMEM55A	A_17_P16115473	chr8:92066496-92066540	5552.95	1319.77	2.07	8664.96	1967.45	2.14
334	PRMT8	A_17_P16524864	chr12:3470352-3470396	10507.54	2497.70	2.07	6931.54	2091.37	1.73

335	TBC1D10C	A_17_P16464739	chr11:66933556-66933600	5162.64	1227.30	2.07	5681.92	1321.56	2.10
336	CHRM1	A_17_P16459392	chr11:62447789-62447833	5672.75	1349.05	2.07	5976.11	1414.68	2.08
337	NPTX2	A_17_P15993072	chr7:98083692-98083736	5324.27	1266.47	2.07	6148.50	1450.17	2.08
338	HOXC11	A_17_P08362192	chr12:52653134-52653190	5731.07	1364.04	2.07	9629.57	2395.59	2.01
339	FBN1	A_17_P09641905	chr15:46724138-46724182	8983.44	2138.93	2.07	11200.34	2458.42	2.19
340	NXPH2	A_17_P15336134	chr2:139254150-139254194	3876.85	923.13	2.07	7597.31	1714.00	2.15
341	VWC2	A_17_P15940391	chr7:49783516-49783560	5812.50	1384.33	2.07	10843.23	2873.39	1.92
342	PDGFD	A_17_P07998316	chr11:103539768-103539812	4864.26	1158.82	2.07	5155.73	1307.90	1.98
343	RUSC1	A_17_P15132026	chr1:153557270-153557314	7543.12	1797.48	2.07	9787.51	2388.42	2.03
344	ZNF292	A_17_P15837440	chr6:87918333-87918377	3675.50	876.21	2.07	19482.82	4877.05	2.00
345	CREB3L1	A_17_P16441860	chr11:46256307-46256351	9562.83	2279.80	2.07	9437.91	2087.61	2.18
346	CACNA2D1	A_17_P05566466	chr7:81910280-81910328	5331.36	1271.09	2.07	8780.87	2213.94	1.99
347	NOS2A	A_17_P10269531	chr17:23144490-23144534	8387.94	1999.86	2.07	9965.78	1994.21	2.32
348	CCNO	A_17_P15691599	chr5:54554908-54554952	8570.96	2043.64	2.07	11189.13	2451.85	2.19
349	SIX1	A_17_P16707843	chr14:60173749-60173793	6100.84	1455.64	2.07	6568.44	1371.25	2.26
350	FAM26F	A_17_P15854422	chr6:116889810-116889854	9261.28	2210.13	2.07	20012.21	4090.90	2.29
351	PRKCE	A_17_P15239550	chr2:45732845-45732889	6746.35	1610.24	2.07	7094.14	1570.98	2.17
352	ADCYAP1R1	A_17_P15923446	chr7:31059024-31059068	6830.65	1630.41	2.07	7985.47	1850.90	2.11
353	BSX	A_17_P08084964	chr11:122353213-122353260	12916.74	3084.12	2.07	15475.14	3559.48	2.12
354	RGS20	A_17_P06126585	chr8:54952251-54952296	7222.26	1725.05	2.07	12750.26	3233.27	1.98
355	VSTM2A	A_17_P05499935	chr7:54577464-54577509	5587.08	1335.37	2.06	10661.14	2550.09	2.06
356	RUVBL1	A_17_P15486584	chr3:129278201-129278245	6307.77	1508.56	2.06	7047.82	1460.16	2.27
357	LPL	A_17_P16076100	chr8:19841172-19841216	6444.20	1541.55	2.06	17562.62	5591.00	1.65
358	HPDL	A_17_P00174845	chr1:45565136-45565180	10620.26	2543.79	2.06	15568.60	3206.60	2.28
359	KY	A_17_P15491934	chr3:135852352-135852396	3080.18	738.15	2.06	6029.11	1677.66	1.85
360	SEC61A1	A_17_P02572602	chr3:129277470-129277514	6039.06	1447.55	2.06	5980.18	1497.34	2.00
361	KCTD12	A_17_P08969788	chr13:76357436-76357480	7350.83	1762.43	2.06	6343.58	1422.38	2.16
362	ZNF829	A_17_P17135371	chr19:42098836-42098880	12564.79	3014.18	2.06	4870.88	1177.02	2.05
363	SLC16A11	A_17_P10211813	chr17:6886410-6886454	7109.78	1705.71	2.06	9197.91	1855.59	2.31
364	IRX4	A_17_P15657031	chr5:1927993-1928037	4220.69	1013.08	2.06	14157.13	2891.56	2.29
365	CYYR1	A_17_P11327639	chr21:26867052-26867096	4681.31	1123.68	2.06	5527.76	1306.46	2.08
366	SH3GL2	A_17_P16162587	chr9:17568951-17568995	4638.79	1113.63	2.06	3312.41	763.67	2.12
367	P2RY1	A_17_P15501314	chr3:154036243-154036287	10905.34	2619.93	2.06	17578.76	4193.42	2.07
368	TRIM15	A_17_P15798908	chr6:30247735-30247779	2804.43	674.00	2.06	3668.64	732.44	2.32

369	WNT9B	A_17_P10342562	chr17:42283520-42283564	17474.43	4201.46	2.06	6864.89	1719.77	2.00
370	UNCX	A_17_P15899025	chr7:1230080-1230124	8953.68	2153.18	2.06	4078.39	1047.94	1.96
371	SCUBE3	A_17_P04658851	chr6:35289189-35289233	3684.76	886.16	2.06	22353.68	5348.56	2.06
372	DLX4	A_17_P10356359	chr17:45396209-45396253	18908.39	4550.25	2.06	15387.89	3296.38	2.22
373	ABCB6	A_17_P01900712	chr2:219792233-219792281	4258.12	1024.85	2.05	8208.85	1895.70	2.11
374	CD1D	A_17_P00535880	chr1:156417222-156417270	2377.84	572.34	2.05	9499.38	2275.29	2.06
375	NHLH2	A_17_P00476183	chr1:116172394-116172438	14265.92	3434.54	2.05	18810.19	3753.76	2.33
376	KIAA1383	A_17_P00865691	chr1:231007633-231007677	15212.78	3664.10	2.05	17835.59	4490.32	1.99
377	PDE4D	A_17_P03960860	chr5:59224841-59224885	5015.39	1209.08	2.05	7527.34	1534.03	2.29
378	TACC1	A_17_P16088143	chr8:38764279-38764323	7454.08	1797.36	2.05	10396.08	2347.56	2.15
379	RAX	A_17_P10745202	chr18:55083010-55083055	7151.32	1724.55	2.05	7614.07	1862.05	2.03
380	GMPPA	A_17_P01902071	chr2:220069908-220069952	12505.93	3016.40	2.05	15384.56	2848.61	2.43
381	SPAG17	A_17_P00486623	chr1:118529433-118529477	5317.56	1282.64	2.05	6395.71	1342.33	2.25
382	HIST1H2BI	A_17_P04625559	chr6:26380396-26380440	2889.14	696.90	2.05	3757.08	724.56	2.37
383	FAM19A2	A_17_P16565704	chr12:60871209-60871253	4457.40	1075.22	2.05	14176.97	3316.35	2.10
384	KIAA1199	A_17_P16813001	chr15:78859571-78859615	7461.69	1800.37	2.05	11521.20	2438.33	2.24
385	GLT25D2	A_17_P00650450	chr1:182272120-182272165	5199.75	1255.23	2.05	10082.75	2527.62	2.00
386	KLF4	A_17_P06881136	chr9:109289633-109289677	11017.91	2660.25	2.05	12423.04	3419.96	1.86
387	GAL7	A_17_P17137318	chr19:43975354-43975398	9458.87	2284.13	2.05	11124.19	2550.87	2.12
388	CBLN4	A_17_P11228534	chr20:54011874-54011928	2860.10	690.89	2.05	8449.38	1857.60	2.19
389	FOXC2	A_17_P16923135	chr16:85156831-85156875	13175.70	3183.64	2.05	6730.44	1645.98	2.03
390	CALCA	A_17_P07656160	chr11:14951739-14951783	15345.71	3711.34	2.05	9107.25	2209.74	2.04
391	STAT5A	A_17_P16983281	chr17:37693718-37693762	8614.92	2086.25	2.05	12069.26	2801.53	2.11
392	STAC2	A_17_P16979035	chr17:34619760-34619804	8788.10	2128.68	2.05	3809.10	912.75	2.06
393	FLRT2	A_17_P16723891	chr14:85066350-85066394	5153.16	1248.40	2.05	10655.86	2293.18	2.22
394	G0S2	A_17_P00766809	chr1:207914979-207915025	4375.02	1060.62	2.04	4933.02	1299.41	1.92
395	HIF1AN	A_17_P16377783	chr10:102312154-102312198	8834.11	2142.12	2.04	5549.17	1272.21	2.12
396	TNFRSF8	A_17_P15024281	chr1:12046115-12046159	10178.55	2469.44	2.04	11573.16	2516.58	2.20
397	MFAP3L	A_17_P23775277	chr4:171183299-171183358	4026.57	977.21	2.04	3364.72	857.65	1.97
398	HIST4H4	A_17_P08206542	chr12:14813328-14813381	8082.57	1961.81	2.04	9828.02	2276.53	2.11
399	SLC7A14	A_17_P02761375	chr3:171785612-171785656	6000.22	1456.49	2.04	7313.85	1630.41	2.17
400	CLEC14A	A_17_P09235378	chr14:37794156-37794200	5170.40	1255.11	2.04	6425.11	1408.57	2.19

Supplementary Table 2. Clinicopathological characteristics and CA4 methylation status in tumor tissues of colon cancer patients

	Methylated		Non-methylated	
	(n=87)	%	(n=28)	%
Age	54.4±26.5		58.5±28.5	
Gender				
M	51	71.83	20	28.17
F	36	81.82	8	18.18
TNM				
I	0	0	0	0
II	25	75.76	8	24.24
III	62	75.61	20	24.39
IV	0	0	0	0
Localization				
Colon	36	69.23	16	30.77
Rectum	51	80.95	12	19.05
Differentiation				
Low	20	71.43	6	28.57
Moderate /or high	67	77.01	20	22.99

Supplementary Table 3. DNA Sequences of primers

Primer names	Sequence (5'->3')
PCR	
CA4-F	CCGGCTCAGAGGACTCTT
CA4-R	GTTGGAGGACTCGGCTTGAA
WTAP-F	CCTCCCTTCACCTTTCCTC
WTAP-R	TGGGAAGAGGTTCTTCGTTG
TBL1-F	GTAACCTGGCCAGCACCTTA
TBL1-R	GGCAAAGGTCGTGTTGTTCT
β -actin-F	GTCTTCCCCTCCATCGTG
β -actin-R	AGGGTGAGGATGCCTCTCTT
COBRA	
CA4-cobra-F	TATAGGGTAAGAGGTGGTTAGGTAGG
CA4-cobra-R	CATCCTTATCAAAAACCTCCCAACT
MSP	
CA4-methylated-F	GTCGTTGTTGAGTGGAGAGGACGC
CA4-methylated-R	CGCGAATACAACGATCCTACCG
CA4-unmethylated-F	GTTGTTGTTGAGTGGAGAGGATGT
CA4-unmethylated-R	CACCACAAATACAACAATCCTACCA

Supplementary Table 4. A list shows the antibodies used

Antibody name	Company	Catalog No.	Dilution
CA4	Santa cruz	sc-74527	1:500
GAPDH	Santa cruz	sc-25778	1:2,000
P27	Cell Signaling Technology	#2552	1:1,000
P15	Santa cruz	sc-612	1:1,000
Cyclin-D1	Santa cruz	sc-246	1:1,000
p21	Santa cruz	sc-6246	1:1,000
Cleaved caspase-3	Cell Signaling Technology	#9661	1:500
Cleaved caspase-7	Cell Signaling Technology	#9491	1:800
Cleaved caspase-8	Cell Signaling Technology	#9496L	1:800
Cleaved PARP	Cell Signaling Technology	#9541	1:800
E-cadherin	Cell Signaling Technology	#3195	1:500
N-cadherin	Cell Signaling Technology	#13116	1:500
Vimentin	Cell Signaling Technology	#5741	1:500
WTAP	Santa cruz	sc-374280	1:500
WT1	Novus	NB110-60011	1:500
Active β -catenin	Millipore	2189941	1:800
β -catenin	Cell Signaling Technology	#9562	1:1,000
Lamin A/C	BD Bioscience	612162	1:1,000
Ubiquitin	Cell Signaling Technology	#3936	1:800