

S4 Table. 113 cis-meQTLs with FDR<0.05 that are associated with Genetic Risk Score of 18 Hcy-associated variants in a sample size of 9,894.

The CpGs are sorted in chromosomes and base pairs.

Rank	CpG	Sample Size	Effect	StdErr	Pvalue	FDR	HetISq	HetPVal	Genes Associated	Chr	Bp	Enhancer	Promoter
43	cg17514528	9,894	0.022	0.003	6.43E-14	6.51E-10	25	1.99E-01	CLCN6 (-3275), MTHFR (+3228)	1	11862907	-	-
78	cg17745097	9,894	0.006	0.001	1.93E-07	1.06E-03	7.7	3.70E-01	CLCN6 (-2817), MTHFR (+2770)	1	11863365	-	TRUE
31	cg05228408	9,894	-0.016	0.002	4.45E-18	6.28E-14	0	5.19E-01	CLCN6 (-878), MTHFR (+831)	1	11865352	-	-
25	cg20202438	9,894	0.016	0.002	2.77E-21	4.96E-17	57	7.45E-03	NPPA (-123)	1	11907986	TRUE	-
24	cg25341925	9,894	0.014	0.001	2.23E-21	4.15E-17	20.2	2.45E-01	NPPA (-243)	1	11908058	TRUE	-
18	cg05396397	9,894	0.031	0.003	1.74E-26	4.26E-22	8.3	3.64E-01	NPPA (-301)	1	11908164	TRUE	-
7	cg06193043	9,894	0.049	0.004	4.14E-39	2.41E-34	69.8	1.43E-04	NPPA (-384)	1	11908199	TRUE	-
16	cg14194983	9,894	0.029	0.003	2.05E-27	5.62E-23	64.4	1.16E-03	NPPA (-483)	1	11908298	TRUE	-
4	cg24844545	9,894	0.050	0.003	5.25E-54	6.11E-49	67.9	3.30E-04	NPPA (-484)	1	11908347	TRUE	-
26	cg00299820	9,334	-0.014	0.002	1.91E-20	3.29E-16	55.5	1.66E-02	NPPB (-24139), KIAA2013 (+43354)	1	11943154	TRUE	-
63	cg03321020	9,894	-0.016	0.003	5.19E-09	3.50E-05	20	2.47E-01	NPPB (-39359), KIAA2013 (+28134)	1	11958326	-	-
23	cg27432085	9,894	-0.037	0.004	3.21E-22	6.23E-18	34.9	1.11E-01	NPPB (-39557), KIAA2013 (+27936)	1	11958572	-	-
79	cg23086274	9,173	-0.006	0.001	2.02E-07	1.09E-03	70.1	7.72E-04	NPPB (-49192), KIAA2013 (+18301)	1	11968159	-	TRUE
69	cg03532363	9,334	-0.009	0.002	2.14E-08	1.33E-04	35.8	1.22E-01	NPPB (-50656), KIAA2013 (+16837)	1	11969623	-	TRUE
32	cg07603449	6,837	0.027	0.003	1.31E-17	1.79E-13	0	4.47E-01	-	1	11986842	-	TRUE
54	cg02156723	9,894	-0.014	0.002	1.77E-10	1.37E-06	56.8	7.87E-03	TNFRSF8 (-22778), MFN2 (+60418)	1	12100631	TRUE	-
29	cg11803389	6,837	0.051	0.006	3.42E-18	5.14E-14	4.5	3.92E-01	-	1	45965020	-	TRUE
46	cg17297354	9,894	0.007	0.001	8.83E-13	8.22E-09	33.4	1.23E-01	RYR2 (-149036), MTR (+98085)	1	237056641	TRUE	-
112	cg07061783	6,277	-0.018	0.004	1.40E-05	4.72E-02	0	9.66E-01	HOXB9 (-1827)	6	25882402	-	-
101	cg03264133	9,894	-0.040	0.009	2.62E-06	1.04E-02	15.4	2.93E-01	SLC17A3 (-8017), SLC17A2 (+48458)	6	25882463	-	-
93	cg12310025	9,894	-0.050	0.010	1.67E-06	7.27E-03	33.5	1.22E-01	SLC17A3 (-8035), SLC17A2 (+48440)	6	25882481	-	-
92	cg03517284	9,894	-0.041	0.009	1.31E-06	5.76E-03	21.4	2.33E-01	SLC17A3 (-8096), SLC17A2 (+48379)	6	25882590	-	-
108	cg08501292	6,754	0.006	0.001	8.40E-06	3.01E-02	18.6	2.77E-01	TRIM38 (-107)	6	25962987	TRUE	TRUE
104	cg06035815	9,894	0.008	0.002	4.73E-06	1.81E-02	0	7.06E-01	HIST1H4D (-270)	6	26189597	-	TRUE
39	cg14345882	9,894	0.039	0.005	8.29E-15	9.19E-11	0	6.18E-01	BTN3A2 (-3636)	6	26364793	TRUE	TRUE
102	cg27626102	9,334	-0.008	0.002	3.62E-06	1.40E-02	0	6.54E-01	STEAP2 (-244)	7	89840731	-	-

96	cg27367526	9,894	-0.014	0.003	1.69E-06	7.09E-03	10.6	3.42E-01	STEAP2 (+717)	7	89841692	-	-
94	cg01887633	6,754	0.009	0.002	1.67E-06	7.20E-03	0	5.56E-01	GTPBP10 (-26371), C7orf63 (+75120)	7	89949631	-	-
91	cg25739043	9,894	-0.010	0.002	1.26E-06	5.59E-03	0	5.35E-01	GTPBP10 (-25496), C7orf63 (+75995)	7	89950458	-	-
88	cg12445565	9,894	0.014	0.003	1.04E-06	4.75E-03	38.5	8.44E-02	GTPBP10 (-24264), C7orf63 (+77227)	7	89951738	-	-
75	cg25638870	7,535	0.027	0.005	1.44E-07	8.18E-04	0	6.56E-01	NOX4 (-89)	11	89224717	-	-
107	cg25542007	6,277	-0.060	0.013	6.51E-06	2.41E-02	0	5.66E-01	FLRT1 (-18527), OTUB1 (+99510)	11	89323282	-	-
109	cg05041596	8,095	-0.026	0.006	9.32E-06	3.26E-02	9.7	3.51E-01	NAALAD2 (-408)	11	89867385	-	-
113	cg21721566	9,894	0.014	0.003	1.53E-05	4.98E-02	32.9	1.27E-01	ACADS (-402)	12	121163144	TRUE	TRUE
81	cg13567169	9,894	-0.014	0.003	2.35E-07	1.22E-03	35.5	1.06E-01	SPPL3 (-68677), HNF1A (-5717)	12	121410855	-	-
59	cg14101638	8,095	0.009	0.002	3.44E-09	2.46E-05	22.2	2.32E-01	HNF1A (+88)	12	121416612	-	-
111	cg25615068	9,894	-0.011	0.003	1.15E-05	3.97E-02	54.6	1.19E-02	HNF1A (+26737), OASL (+33494)	12	121443309	-	-
106	cg02403541	9,894	0.002	0.000	6.29E-06	2.34E-02	55.9	9.26E-03	OASL (+22467), HNF1A (+37764)	12	121454288	-	TRUE
51	cg19788934	6,837	-0.018	0.003	9.92E-11	8.10E-07	0	8.48E-01	MSRA (-149089), TNKS (+349296)	12	121455706	-	-
62	cg08335008	9,334	0.027	0.005	4.52E-09	3.10E-05	41	8.45E-02	CDH15 (-12643), ACSF3 (+65303)	16	89225495	-	-
97	cg02648441	9,894	-0.008	0.002	2.11E-06	8.77E-03	0	8.30E-01	CDH15 (+4689), SLC22A31 (+23677)	16	89242827	-	-
66	cg09164168	9,894	0.015	0.003	1.32E-08	8.54E-05	44.1	4.98E-02	ZNF778 (+100635), ANKRD11 (+172223)	16	89384721	-	-
73	cg26536240	9,894	0.014	0.003	8.65E-08	5.04E-04	2.1	4.23E-01	ANKRD11 (+47232), ZNF778 (+225626)	16	89509760	TRUE	-
76	cg15206445	9,894	-0.012	0.002	1.63E-07	9.15E-04	19.9	2.48E-01	SPG7 (-1468)	16	89573312	TRUE	-
105	cg16428612	9,894	-0.004	0.001	6.29E-06	2.36E-02	22.2	2.25E-01	SPG7 (-1293)	16	89573535	-	-
77	cg07924503	9,894	-0.016	0.003	1.85E-07	1.03E-03	20.3	2.44E-01	SPG7 (-1197)	16	89573631	-	-
50	cg02244288	9,894	-0.012	0.002	5.00E-11	4.23E-07	8.7	3.60E-01	SPG7 (-873)	16	89573955	-	-
95	cg08845973	9,894	-0.010	0.002	1.69E-06	7.15E-03	16.8	2.79E-01	RPL13 (-35017), SPG7 (+17243)	16	89592071	-	-
99	cg03169557	9,894	-0.011	0.002	2.45E-06	9.92E-03	0	5.04E-01	RPL13 (-28090), SPG7 (+24170)	16	89598950	-	-
82	cg08784311	5,330	0.053	0.011	4.22E-07	2.16E-03	0	5.05E-01	CPNE7 (-9427), RPL13 (+5684)	16	89632724	-	-
60	cg16616467	9,894	-0.013	0.002	3.77E-09	2.66E-05	15.8	2.89E-01	CPNE7 (+715)	16	89642914	-	-
55	cg26217441	9,894	-0.016	0.003	2.65E-10	2.02E-06	23.4	2.13E-01	DPEP1 (-43561), CPNE7 (+1263)	16	89643414	-	-
84	cg04080022	9,894	0.010	0.002	4.79E-07	2.37E-03	0	8.36E-01	DPEP1 (-38489), CPNE7 (+6335)	16	89648534	TRUE	-
110	cg02628002	9,894	-0.003	0.001	1.04E-05	3.61E-02	9.9	3.48E-01	DPEP1 (-37367), CPNE7 (+7457)	16	89649608	-	-
58	cg02848750	9,894	-0.010	0.002	2.11E-09	1.54E-05	36.3	1.01E-01	DPEP1 (-18569), CPNE7 (+26255)	16	89668406	TRUE	-
1	cg01097406	9,894	0.232	0.011	9.57E-104	4.46E-98	81.3	1.58E-08	-	16	89675127	-	-

103	cg20972466	9,334	0.010	0.002	4.41E-06	1.70E-02	10.4	3.47E-01	DPEP1 (-7380), CPNE7 (+37444)	16	89679595	-	-
42	cg06082883	9,894	-0.015	0.002	6.40E-14	6.62E-10	54.2	1.26E-02	DPEP1 (-279)	16	89686744	-	-
71	cg05059843	9,894	0.007	0.001	5.76E-08	3.48E-04	16.8	2.79E-01	DPEP1 (-62)	16	89686913	-	-
13	cg01749904	9,334	0.042	0.004	1.08E-30	3.59E-26	65.3	2.07E-03	DPEP1 (+29)	16	89687052	-	-
83	cg00996377	9,894	0.004	0.001	4.23E-07	2.14E-03	58	6.03E-03	DPEP1 (+2782), CHMP1A (+34347)	16	89689757	-	-
15	cg02393727	9,334	-0.043	0.004	9.36E-29	2.72E-24	66.5	1.45E-03	DPEP1 (+3113), CHMP1A (+34016)	16	89690088	-	-
9	cg05347456	9,334	-0.047	0.004	1.01E-34	4.70E-30	75.6	2.70E-05	DPEP1 (+3287), CHMP1A (+33842)	16	89690262	-	-
48	cg09869502	9,894	-0.015	0.002	1.18E-11	1.04E-07	69.3	1.84E-04	DPEP1 (+3827), CHMP1A (+33302)	16	89690802	TRUE	-
49	cg01747591	9,894	0.008	0.001	2.09E-11	1.80E-07	37.4	9.18E-02	DPEP1 (+16589), CHMP1A (+20540)	16	89703612	-	-
44	cg06047934	9,894	0.007	0.001	1.22E-13	1.18E-09	29.3	1.58E-01	CHMP1A (+11635), DPEP1 (+25494)	16	89712517	-	-
17	cg27134767	9,894	0.020	0.002	8.62E-27	2.23E-22	51.6	1.92E-02	CHMP1A (+10765), DPEP1 (+26364)	16	89713339	-	-
98	cg26681017	9,894	0.015	0.003	2.41E-06	9.84E-03	7.7	3.70E-01	-	16	89723193	-	-
8	cg07835443	6,837	0.050	0.004	1.17E-38	6.05E-34	38.8	1.33E-01	ABL1 (-48359), EXOSC2 (+93314)	16	89734986	-	-
10	cg16725984	9,334	0.048	0.004	3.03E-34	1.28E-29	62.7	4.10E-03	CDK10 (-17867), CHMP1A (-11080)	16	89735184	-	-
28	cg00574278	9,894	0.008	0.001	1.36E-18	2.11E-14	11.5	3.33E-01	CDK10 (-17221), CHMP1A (-11726)	16	89735878	-	-
100	cg16570414	9,894	0.005	0.001	2.61E-06	1.05E-02	16.2	2.85E-01	CDK10 (-16261), CHMP1A (-12686)	16	89736790	TRUE	-
5	cg03605463	9,894	0.074	0.005	1.86E-49	1.44E-44	51.1	2.10E-02	CHMP1A (-16460), CDK10 (-12487)	16	89740564	-	-
14	cg09827496	6,837	0.049	0.004	2.16E-30	6.71E-26	0	5.93E-01	GALNT9 (+53539), NOC4L (+223373)	16	89740639	-	-
35	cg04747957	6,837	-0.004	0.000	2.32E-16	2.84E-12	74.2	7.07E-04	ENPP5 (-149975), RCAN2 (+170368)	16	89751896	-	-
2	cg04155793	9,894	0.054	0.003	3.46E-61	8.06E-56	82.3	3.46E-09	CDK10 (-204)	16	89752847	-	TRUE
3	cg12119029	9,894	0.047	0.003	1.59E-55	2.47E-50	72.9	2.87E-05	CDK10 (-220)	16	89752879	-	TRUE
56	cg00796364	9,334	0.004	0.001	6.63E-10	4.98E-06	28.7	1.80E-01	CDK10 (+473)	16	89753572	-	TRUE
53	cg27113347	9,894	-0.014	0.002	1.76E-10	1.39E-06	57.5	6.73E-03	CDK10 (+7534), C16orf7 (+26784)	16	89760585	-	-
36	cg04544017	9,894	-0.011	0.001	3.03E-16	3.62E-12	8.6	3.61E-01	CDK10 (+10271), C16orf7 (+24047)	16	89763370	-	-
74	cg26822161	9,894	-0.002	0.000	1.23E-07	7.07E-04	62.9	1.80E-03	C16orf7 (+14805), CDK10 (+19513)	16	89772612	-	-
6	cg00261912	8,095	-0.046	0.004	6.64E-40	4.42E-35	69	3.58E-04	C16orf7 (+9654), CDK10 (+24664)	16	89777763	-	-
41	cg03809021	9,894	-0.030	0.004	3.33E-14	3.52E-10	27.6	1.73E-01	ZNF276 (+43196), FANCA (+51917)	16	89831123	-	-
40	cg05795554	8,095	-0.009	0.001	2.69E-14	2.91E-10	48.1	3.70E-02	FANCA (-124)	16	89883212	-	TRUE
57	cg04287289	8,095	-0.014	0.002	1.11E-09	8.21E-06	42.3	6.73E-02	FANCA (-152)	16	89883240	-	TRUE
65	cg26513180	8,095	-0.011	0.002	7.55E-09	4.95E-05	49.7	3.04E-02	SCNN1A (-2185)	16	89883248	-	TRUE

70	cg05139061	9,894	-0.010	0.002	2.18E-08	1.34E-04	5.3	3.93E-01	SPIRE2 (-3395)	16	89891535	-	-
38	cg07402062	9,894	-0.035	0.005	5.87E-15	6.67E-11	28.7	1.64E-01	SPIRE2 (-832)	16	89894098	-	-
19	cg21285383	9,894	-0.022	0.002	2.58E-26	6.01E-22	50.6	2.24E-02	SPIRE2 (-622)	16	89894308	-	-
11	cg03388025	9,894	-0.035	0.003	3.75E-32	1.46E-27	59.8	4.05E-03	SPIRE2 (-601)	16	89894329	-	-
68	cg05500240	9,894	-0.011	0.002	1.97E-08	1.24E-04	56.1	8.97E-03	TCF25 (-14360), SPIRE2 (+30727)	16	89925609	-	-
85	cg05941025	9,894	-0.011	0.002	5.21E-07	2.53E-03	54.7	1.17E-02	TCF25 (-12373), SPIRE2 (+32714)	16	89927596	-	-
67	cg19635926	6,277	-0.009	0.002	1.50E-08	9.57E-05	11	3.43E-01	-	16	89946313	-	-
37	cg06558623	6,837	-0.022	0.003	5.93E-16	6.90E-12	20.4	2.74E-01	BSPH1 (-2629), ELSPBP1 (+148)	16	89946397	-	-
61	cg09569215	9,894	0.010	0.002	4.36E-09	3.03E-05	38.6	8.36E-02	TUBB3 (-22969), TCF25 (+26724)	16	89966693	-	-
86	cg06017697	9,894	0.007	0.001	7.00E-07	3.29E-03	0	6.63E-01	TUBB3 (-12995), TCF25 (+36698)	16	89976667	TRUE	-
21	cg05749642	9,334	-0.019	0.002	6.35E-24	1.34E-19	30.4	1.66E-01	TUBB3 (-7442), TCF25 (+42251)	16	89982268	-	-
34	cg01768446	9,894	-0.012	0.002	1.09E-16	1.37E-12	46.1	4.00E-02	TUBB3 (-7243), TCF25 (+42450)	16	89982419	-	-
27	cg01023759	5,038	0.050	0.006	1.12E-18	1.80E-14	73.1	2.30E-03	-	16	89983766	-	-
33	cg08627397	5,472	0.043	0.005	7.50E-17	9.98E-13	54.8	5.03E-02	TUBB3 (-5634), TCF25 (+44059)	16	89984028	-	-
80	cg00534858	6,277	0.022	0.004	2.33E-07	1.22E-03	44.3	1.27E-01	-	16	90074520	-	-
64	cg06907930	7,535	-0.052	0.009	6.49E-09	4.32E-05	0	4.46E-01	C16orf3 (-14514), LOC100130015 (+3368)	16	90110798	-	-
87	cg07800524	9,894	0.007	0.002	9.19E-07	4.24E-03	0	5.36E-01	FUT1 (-830), FGF21 (+329)	19	49259452	TRUE	-
12	cg15157241	9,334	-0.052	0.004	4.39E-32	1.57E-27	73.4	9.53E-05	PKNOX1 (+1586), CBS (+100243)	21	44396204	-	-
22	cg08751406	9,334	0.027	0.003	9.79E-23	1.98E-18	17.8	2.79E-01	CBS (+25595), PKNOX1 (+76234)	21	44470900	-	-
89	cg07211972	8,095	0.014	0.003	1.05E-06	4.75E-03	0	7.50E-01	CBS (+22999), PKNOX1 (+78830)	21	44473496	-	-
52	cg01788910	9,894	0.022	0.003	1.16E-10	9.31E-07	0	4.63E-01	CBS (+22927), PKNOX1 (+78902)	21	44473568	-	-
72	cg14171527	9,894	-0.010	0.002	6.32E-08	3.77E-04	43.3	5.41E-02	CBS (+22655), PKNOX1 (+79174)	21	44473840	-	-
30	cg19312314	9,334	0.034	0.004	3.56E-18	5.18E-14	0	6.34E-01	CBS (+22485), PKNOX1 (+79344)	21	44473962	-	-
47	cg02644491	9,894	0.021	0.003	3.09E-12	2.82E-08	0	6.26E-01	CBS (+22428), PKNOX1 (+79401)	21	44474019	-	-
90	cg09128751	9,894	0.006	0.001	1.13E-06	5.06E-03	21.4	2.33E-01	CBS (+10290), PKNOX1 (+91539)	21	44486205	-	-
45	cg22633722	9,894	-0.012	0.002	8.49E-13	8.07E-09	16.1	2.86E-01	CBS (-296)	21	44496743	-	-
20	cg15300856	9,894	-0.015	0.001	3.18E-26	7.05E-22	68.7	2.35E-04	-	21	44497019	-	-

Effect: Regression coefficients

FDR: False discovery Rate adjusted P-value, threshold = 0.05

HetISq: Heterogeneity I^2 parameter

HetPVal: Heterogeneity p-value

Enhancer & promoter annotations from Illumina 450k annotation