SDC Text 1 Haplotype based CGI-S association of markers from ADCK1 region using directly genotyped markers

SNPs from ADCK1 regions directly tiled on Illumina 1MDuo and PsychArray (surrounding rs56240334 and rs10147707, Table S1) are used to phase haplotype for CGI-S analysis. A haplotype sliding window approach was used for each of the three cohorts (Table S2, S3, and S4). The haplotype association was performed using PLINK v1.07.

Table S1 the list of Markers directly genotyped in Illumina 1MDuo and PsychArray used for the haplotype analysis. SNP directly genotyped are represented by X, while SNP not tiled on the genotyping platform was marked by "-". The two SNPs highlighted in the paper are bolded.

CHR	SNP		POS	A1	A2	1M	PsychArray
14	rs2364747	0	78368390	A	G	X	X
14	rs12433276	0	78368610	G	A	X	-
14	rs11623841	0	78370261	C	T	X	-
14	rs8017520	0	78370882	T	C	X	-
14	rs10140793	0	78371389	C	T	X	-
14	**rs56240334**	**0**	**78371403**	**A**	**G**	**-**	**-**
14	rs17094040	0	78371946	T	C	X	-
14	rs13379143	0	78373092	G	A	X	-
14	rs6574411	0	78374327	A	G	X	-
14	rs2364748	0	78378375	C	A	X	-
14	rs1549118	0	78379684	T	C	X	-
14	rs4533193	0	78380168	T	C	X	-
14	rs8015618	0	78380390	G	A	X	X
14	**rs10147707**	**0**	**78380555**	**T**	**C**	**X**	**-**

14	rs8006523	0	78382375	C	A	X	-
14	rs11628968	0	78388706	G	A	X	-
14	rs7144239	0	78389173	T	G	X	X
14	rs17106616	0	78390060	A	G	-	X
14	rs2302944	0	78390880	C	T	X	-
14	rs11850022	0	78392008	T	C	X	-
14	rs7152398	0	78392555	T	G	-	X
14	rs7141578	0	78394473	A	G	X	-
14	rs3783952	0	78397193	A	G	X	-
14	rs2287652	0	78397448	G	A	X	-
14	rs2287653	0	78397627	T	C	X	-
14	rs10438027	0	78398317	T	C	X	-
14	rs11159309	0	78398891	T	C	X	X
14	rs3087972	0	78399867	C	T	X	X

Table S2 in Cohort 1, the directly genotyped marker rs10147707 is highlighted in blue and the alleles making up the haplotype are aligned vertically (2 SNPs not directly genotyped in 1M are represented by dot (.) in the haplotype sequence. Only haplotype markers with CGI-S association p-value than less 0.001 are shown.

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NSNP NHAP  CHR         BP1         BP2        SNP1        SNP2    HAPLOTYPE                F     BETA     STAT        P
   1    2   14    78380555    78380555  rs10147707  rs10147707            T           0.0916    0.405     12.7 0.000405
   1    2   14    78380555    78380555  rs10147707  rs10147707            C           0.908    -0.405     12.7 0.000405
   2    3   14    78380390    78380555   rs8015618  rs10147707           AT           0.0917     0.41       13 0.000339
   3    4   14    78380168    78380555   rs4533193  rs10147707          CAT           0.0916    0.405     12.7 0.000405
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4	5	14	78379684	78380555	rs1549118	rs10147707	TCAT	0.0916	0.405	12.7	0.000405
5	6	14	78378375	78380555	rs2364748	rs10147707	CTCAT	0.0916	0.405	12.7	0.000405
6	6	14	78374327	78380555	rs6574411	rs10147707	GCTCAT	0.0916	0.405	12.7	0.000405
6	10	14	78378375	78382375	rs2364748	rs8006523	CTCATA	0.0458	0.6	12.6	0.000416
7	6	14	78373092	78380555	rs13379143	rs10147707	GGCTCAT	0.0916	0.405	12.7	0.000405
8	6	14	78371946	78380555	rs17094040	rs10147707	CGGCTCAT	0.0916	0.405	12.7	0.000405
9	9	14	78371389	78380555	rs10140793	rs10147707	TCGGCTCAT	0.084	0.455	14.3	0.000178
10	10	14	78370882	78380555	rs8017520	rs10147707	CTCGGCTCAT	0.0834	0.456	14.5	0.000157
10	23	14	78374327	78390880	rs6574411	rs2302944	GCTCATAAT.T	0.0105	1.15	13.9	0.00022
11	15	14	78370882	78382375	rs8017520	rs8006523	CTCGGCTCATA	0.0484	0.555	11.8	0.000644
11	24	14	78374327	78392008	rs6574411	rs11850022	GCTCATAAT.TC	0.0105	1.16	14	0.000205
12	15	14	78370882	78388706	rs8017520	rs11628968	CTCGGCTCATAA	0.0485	0.546	12.1	0.00056
12	26	14	78374327	78394473	rs6574411	rs7141578	GCTCATAAT.TC.A	0.0103	1.16	14	0.000206
13	26	14	78374327	78397193	rs6574411	rs3783952	GCTCATAAT.TC.AA	0.0103	1.15	13.9	0.000212
14	28	14	78374327	78397448	rs6574411	rs2287652	GCTCATAAT.TC.AAA	0.0103	1.15	13.9	0.000212
15	28	14	78374327	78397627	rs6574411	rs2287653	GCTCATAAT.TC.AAAC	0.0103	1.15	13.9	0.000216
16	25	14	78374327	78398317	rs6574411	rs10438027	GCTCATAAT.TC.AAACC	0.0103	1.15	13.9	0.000214
17	25	14	78374327	78398891	rs6574411	rs11159309	GCTCATAAT.TC.AAACCC	0.0103	1.15	13.9	0.000214
18	25	14	78374327	78399867	rs6574411	rs3087972	GCTCATAAT.TC.AAACCCT	0.0103	1.15	13.9	0.000214

Table S3 in Cohort 2, the directly genotyped marker rs10147707 is highlighted in blue and the alleles making up the haplotype are aligned vertically (2 SNPs not directly genotyped in 1M are represented by dot (.) in the haplotype sequence. Only haplotype markers with CGI-S association p-value than less 0.001 are shown.

NSNP	NHAP	CHR	BP1	BP2	SNP1	SNP2	HAPLOTYPE	F	BETA	STAT	P
5	9	14	78380555	78390880	rs10147707	rs2302944	TAAG.T	0.0222	0.869	11.5	0.000753
6	11	14	78380555	78392008	rs10147707	rs11850022	TAAG.TC	0.0184	0.839	11	0.000995

10	10	14	78370882	78380555	rs8017520	rs10147707	CTCGGCTCAT	0.0834	0.378	11.5	0.000761
11	15	14	78370882	78382375	rs8017520	rs8006523	CTCGGCTCATA	0.0484	0.503	11.2	0.000891
11	20	14	78373092	78390880	rs13379143	rs2302944	GGCTCATAAG.T	0.0276	0.727	12.6	0.000409
11	13	14	78380555	78398317	rs10147707	rs10438027	TAAG.TC.GGACT	0.0174	0.813	11.3	0.000821
12	18	14	78371946	78390880	rs17094040	rs2302944	CGGCTCATAAG.T	0.0188	0.894	12	0.000569
12	19	14	78373092	78392008	rs13379143	rs11850022	GGCTCATAAG.TC	0.024	0.734	12	0.00057
12	15	14	78380390	78398317	rs8015618	rs10438027	ATAAG.TC.GGACT	0.0171	0.849	12.1	0.000551
12	13	14	78380555	78398891	rs10147707	rs11159309	TAAG.TC.GGACTC	0.0174	0.813	11.3	0.00082
13	19	14	78371389	78390880	rs10140793	rs2302944	TCGGCTCATAAG.T	0.0156	1.1	15.5	9.48e-05
13	21	14	78371946	78392008	rs17094040	rs11850022	CGGCTCATAAG.TC	0.0164	0.879	11.5	0.000749
3	6	14	78371389	78373092	rs10140793	rs13379143	TCG	0.157	0.298	11.2	0.000868
4	8	14	78370882	78373092	rs8017520	rs13379143	TCG	0.157	0.301	11.6	0.000722
4	6	14	78371389	78374327	rs10140793	rs6574411	TCGG	0.156	0.296	11.1	0.00091
5	8	14	78370882	78374327	rs8017520	rs6574411	CTCGG	0.156	0.299	11.4	0.000774
5	7	14	78371389	78378375	rs10140793	rs2364748	TCGGC	0.154	0.297	11.2	0.000876
13	20	14	78373092	78394473	rs13379143	rs7141578	GGCTCATAAG.TC.G	0.0233	0.73	12.2	0.000518
13	18	14	78380168	78398317	rs4533193	rs10438027	CATAAG.TC.GGACT	0.0169	0.856	12.1	0.000558
13	15	14	78380390	78398891	rs8015618	rs11159309	ATAAG.TC.GGACTC	0.0171	0.849	12.1	0.000551
13	13	14	78380555	78399867	rs10147707	rs3087972	TAAG.TC.GGACTCC	0.0174	0.813	11.3	0.00082
14	22	14	78370882	78390880	rs8017520	rs2302944	CTCGGCTCATAAG.T	0.0248	0.808	14.7	0.000138
14	21	14	78371389	78392008	rs10140793	rs11850022	TCGGCTCATAAG.TC	0.0132	1.14	15.2	0.000107
14	20	14	78373092	78397193	rs13379143	rs3783952	GGCTCATAAG.TC.GG	0.0233	0.731	12.2	0.000514
14	21	14	78379684	78398317	rs1549118	rs10438027	TCATAAG.TC.GGACT	0.0173	0.836	12	0.000587
14	18	14	78380168	78398891	rs4533193	rs11159309	CATAAG.TC.GGACTC	0.017	0.855	12.1	0.000559
14	15	14	78380390	78399867	rs8015618	rs3087972	ATAAG.TC.GGACTCC	0.0171	0.849	12.1	0.000551

15	23	14	78370882	78392008	rs8017520	rs11850022	CTCGGCTCATAAG.TC	0.0216	0.832	14.2	0.000183
15	22	14	78371389	78394473	rs10140793	rs7141578	TCGGCTCATAAG.TC.G	0.0139	1.01	14.9	0.000127
15	21	14	78373092	78397448	rs13379143	rs2287652	GGCTCATAAG.TC.GGA	0.0232	0.737	12.4	0.000476
15	21	14	78379684	78398891	rs1549118	rs11159309	TCATAAG.TC.GGACTC	0.0173	0.836	12	0.000585
15	18	14	78380168	78399867	rs4533193	rs3087972	CATAAG.TC.GGACTCC	0.017	0.855	12.1	0.000559
16	16	14	78368610	78390880	rs12433276	rs2302944	ACCTCGGCTCATAAG.T	0.015	0.958	11.3	0.00081
16	22	14	78370882	78394473	rs8017520	rs7141578	CTCGGCTCATAAG.TC.G	0.0213	0.824	14.2	0.000179
16	22	14	78371389	78397193	rs10140793	rs3783952	TCGGCTCATAAG.TC.GG	0.0139	1.01	14.9	0.000127
16	21	14	78371946	78397448	rs17094040	rs2287652	CGGCTCATAAG.TC.GGA	0.0168	0.801	11	0.000975
16	21	14	78373092	78397627	rs13379143	rs2287653	GGCTCATAAG.TC.GGAC	0.0233	0.737	12.4	0.000466
16	21	14	78379684	78399867	rs1549118	rs3087972	TCATAAG.TC.GGACTCC	0.0173	0.836	12	0.000585
17	17	14	78368610	78392008	rs12433276	rs11850022	ACCTCGGCTCATAAG.TC	0.015	0.985	13.2	0.000314
17	22	14	78370882	78397193	rs8017520	rs3783952	CTCGGCTCATAAG.TC.GG	0.0214	0.826	14.4	0.000165
17	21	14	78371389	78397448	rs10140793	rs2287652	TCGGCTCATAAG.TC.GGA	0.0138	0.995	14.8	0.000137
17	21	14	78371946	78397627	rs17094040	rs2287653	CGGCTCATAAG.TC.GGAC	0.0168	0.801	11.1	0.000945
17	20	14	78373092	78398317	rs13379143	rs10438027	GGCTCATAAG.TC.GGACT	0.0181	0.862	12.8	0.000381
18	17	14	78368610	78394473	rs12433276	rs7141578	ACCTCGGCTCATAAG.TC.G	0.0153	0.896	12	0.000561
18	21	14	78370882	78397448	rs8017520	rs2287652	CTCGGCTCATAAG.TC.GGA	0.0213	0.824	14.4	0.000167
18	22	14	78371389	78397627	rs10140793	rs2287653	TCGGCTCATAAG.TC.GGAC	0.0138	0.993	14.8	0.000137
18	21	14	78371946	78398317	rs17094040	rs10438027	CGGCTCATAAG.TC.GGACT	0.0155	0.972	14.8	0.000136
18	20	14	78373092	78398891	rs13379143	rs11159309	GGCTCATAAG.TC.GGACTC	0.0181	0.862	12.8	0.000381
19	17	14	78368610	78397193	rs12433276	rs3783952	ACCTCGGCTCATAAG.TC.GG	0.0153	0.896	12	0.000561
19	21	14	78370882	78397627	rs8017520	rs2287653	CTCGGCTCATAAG.TC.GGAC	0.0213	0.824	14.4	0.000164
19	22	14	78371389	78398317	rs10140793	rs10438027	TCGGCTCATAAG.TC.GGACT	0.0132	0.976	14.5	0.000153
19	21	14	78371946	78398891	rs17094040	rs11159309	CGGCTCATAAG.TC.GGACTC	0.0155	0.972	14.8	0.000136

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  19   20   14     78373092     78399867  rs13379143   rs3087972      GGCTCATAAG.TC.GGACTCC       0.0181    0.862     12.8 0.000381
  20   18   14     78368610     78397448  rs12433276   rs2287652 ACCTCGGCTCATAAG.TC.GGA           0.0153    0.894       12 0.000564
  20   22   14     78371389     78398891  rs10140793  rs11159309    TCGGCTCATAAG.TC.GGACTC        0.0132    0.976     14.5 0.000153
  20   21   14     78371946     78399867  rs17094040   rs3087972     CGGCTCATAAG.TC.GGACTCC       0.0155    0.972     14.8 0.000136
  21   18   14     78368610     78397627  rs12433276   rs2287653 ACCTCGGCTCATAAG.TC.GGAC          0.0154    0.891       12 0.000576
  21   22   14     78371389     78399867  rs10140793   rs3087972    TCGGCTCATAAG.TC.GGACTCC       0.0132    0.976     14.5 0.000153
  22   17   14     78368610     78398317  rs12433276  rs10438027 ACCTCGGCTCATAAG.TC.GGACT         0.0138    0.901     11.6 0.000712
  23   17   14     78368610     78398891  rs12433276  rs11159309 ACCTCGGCTCATAAG.TC.GGACTC        0.0138    0.901     11.6 0.000713
  24   17   14     78368610     78399867  rs12433276   rs3087972 ACCTCGGCTCATAAG.TC.GGACTCC       0.0138    0.901     11.6 0.000713
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Table S4 in Cohort 3, the alleles making up the haplotype are aligned vertically (SNPs not directly genotyped in PsychArray are represented by dot (.) in the haplotype sequence. Only haplotype markers with CGI-S association p-value than less 0.001 are shown.

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SNP NHAP  CHR         BP1          BP2        SNP1        SNP2     HAPLOTYPE                    F     BETA     STAT          P
   1    2   14     78398891     78398891  rs11159309  rs11159309                            T     0.104    0.339     8.08  0.00475
   1    2   14     78398891     78398891  rs11159309  rs11159309                            C     0.896   -0.339     8.08  0.00475
   2    3   14     78392555     78398891   rs7152398  rs11159309                      G.....T     0.104    0.339     8.08  0.00475
   2    3   14     78398891     78399867  rs11159309   rs3087972                            TC    0.104    0.339     8.08  0.00475
   3    4   14     78390060     78398891  rs17106616  rs11159309                   G..G.....T     0.104     0.34     8.14  0.00461
   3    4   14     78392555     78399867   rs7152398   rs3087972                   G.....TC       0.104     0.34     8.14  0.00461
   4    6   14     78389173     78398891   rs7144239  rs11159309               GG..G.....T        0.0808     0.35     7.05  0.00829
   4    5   14     78390060     78399867  rs17106616   rs3087972                   G..G.....TC    0.104     0.34     8.14  0.00461
   5    7   14     78389173     78399867   rs7144239   rs3087972               GG..G.....TC       0.0809    0.349     7.01  0.00847
   6   15   14     78368390     78398891   rs2364747 rs11159309 G..........A...GG..G.....T        0.0191     0.81     6.96   0.0087
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