Supplementary Online Content

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eTable 1. Comparison of the Included and Excluded Participants

eTable 2. Associations Between the 56 SNPs and Changes in Body Weight Adjusted for Age and Sex During the Intervention

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eFigure. Selection and Genotyping of SNPs

This supplementary material has been provided by the authors to give readers additional information about their work.

eTable 1: Comparison of the included and excluded participants.

	N	Girls/Boys	Age (years)	Body weight (kg)	BMI (kg/m^2)	BMI-SDS
			Mean (SD)	Mean (SD)	Mean (SD)	Mean (SD)
Included	1198	670/528	14.0 (2.2)	92.2 (23.1)	33.8 (5.8)	2.8 (0.5)
Excluded	231	126/105	13.9 (2.4)	91.6 (24.7)	33.9 (7.1)	2.8 (0.6)
p-Value		p=0.70	p=0.40	p=0.72	p=0.83	p=0.99

BMI=body mass index, BMI-SDS=body mass index – standard deviation score, N=number, SD=standard deviation

	N	Girls/Boys	Age (years)	Body weight (kg)	BMI (kg/m^2)	BMI-SDS
			Mean (SD)	Mean (SD)	Mean (SD)	Mean (SD)

eTable 2: Associations between the 56 SNPs and changes in body weight adjusted for age and sex during the intervention (per week).

SNP	Chr	Position	Effect Allele	Other Allele	β-coefficient	Lower CI	Upper CI	p-value	Corr. p-value	Effect Allele Frequency	Gene	N
rs977747	1	47.457.264	T	G	0.009	-0.015	0.034	0.46	1	0.421	TAL1	1197
rs11583200	1	50.332.407	C	T	-0.015	-0.04	0.009	0.22	1	0.426	ELAVL4	1188
rs11165643	1	96.696.685	T	C	0.003	-0.021	0.027	0.80	1	0.557	PTBP2	1187
rs17024393	1	109.956.211	C	T	0.029	-0.032	0.091	0.35	1	0.072	GNAT2	1198
rs543874	1	176.156.103	G	A	-0.02	-0.049	0.01	0.19	1	0.262	SEC16B	1190
rs10182181	2	25.003.800	G	A	0.025	0.002	0.049	0.04	1	0.483	ADCY3	1196
rs11126666	2	26.782.315	A	G	-0.031	-0.057	-0.004	0.02	1	0.343	KCNK3	1190
rs2121279	2	142.759.755	T	C	-0.03	-0.066	0.005	0.09	1	0.207	LRP1B	1195
rs1460676	2	164.275.935	C	T	-0.001	-0.032	0.029	0.92	1	0.26	FIGN	1198
rs1528435	2	181.259.207	T	C	-0.033	-0.058	-0.008	0.01	0.51	0.603	UBE2E3	1197
rs17203016	2	207.963.763	G	A	0.001	-0.029	0.03	0.96	1	0.278	CREB1	1194
rs2176040	2	226.801.046	A	G	0.017	-0.008	0.043	0.19	1	0.407	LOC646736	1184
rs6804842	3	25.081.441	G	A	-0.003	-0.028	0.021	0.78	1	0.574	RARB	1194
rs2365389	3	61.211.502	C	T	0.006	-0.018	0.031	0.60	1	0.571	FHIT	1189
rs13078960	3	85.890.280	G	T	0.032	0	0.064	0.05	1	0.268	CADM2	1047
rs1516725	3	187.306.698	C	T	-0.037	-0.073	-0.001	0.05	1	0.813	ETV5	1193
rs10938397	4	44.877.284	G	A	-0.025	-0.049	-0.001	0.04	1	0.475	GNPDA2	1180
rs17001654	4	77.348.592	G	C	-0.019	-0.05	0.012	0.23	1	0.255	SCARB2	1195
rs13107325	4	103.407.732	T	C	-0.027	-0.069	0.016	0.22	1	0.139	SLC39A8	1191
rs11727676	4	145.878.514	T	C	-0.001	-0.043	0.041	0.96	1	0.85	HHIP	1197

SNP	Chr	Position	Effect Allele	Other Allele	β-coefficient	Lower CI	Upper CI	p-value	Corr. p-value	Effect Allele Frequency	Gene	N
rs205262	6	34.671.142	G	A	0.004	-0.022	0.031	0.75	1	0.35	C6orf106	1186
rs13201877	6	137.717.234	G	A	-0.073	-0.106	-0.039	$2.39*10^{-5}$	0.001	0.21	IFNGR1	1184
rs13191362	6	162.953.340	A	G	-0.023	-0.061	0.015	0.24	1	0.838	PARK2	1193
rs1167827	7	75.001.105	G	A	0.008	-0.017	0.033	0.52	1	0.561	HIP1	1197
rs17405819	8	76.969.139	T	C	0.008	-0.018	0.034	0.55	1	0.65	HNF4G	1177
rs10968576	9	28.404.339	G	A	0.001	-0.025	0.027	0.94	1	0.371	LINGO2	1193
rs6477694	9	110.972.163	C	T	0.02	-0.004	0.045	0.11	1	0.405	EPB41L4B	1190
rs1928295	9	119.418.304	T	C	-0.021	-0.045	0.003	0.08	1	0.538	TLR4	1190
rs10733682	9	128.500.735	A	G	-0.041	-0.065	-0.018	$6.37*10^{-4}$	0.04	0.516	LMX1B	1194
rs7899106	10	87.400.884	G	A	0.024	-0.029	0.077	0.38	1	0.09	GRID1	1159
rs17094222	10	102.385.430	C	T	0	-0.029	0.028	0.99	1	0.278	HIF1AN	1190
rs4256980	11	8.630.515	G	C	-0.014	-0.039	0.01	0.26	1	0.588	TRIM66	1194
rs11030104	11	27.641.093	A	G	-0.017	-0.046	0.012	0.25	1	0.72	BDNF	1189
rs3817334	11	47.607.569	T	C	-0.018	-0.042	0.006	0.15	1	0.443	MTCH2	1194
rs12286929	11	114.527.614	G	A	0.008	-0.017	0.033	0.52	1	0.54	CADM1	1161
rs11170468	12	37.716.315	A	C	0.017	-0.011	0.046	0.24	1	0.7	CPNE8	1197
rs7138803	12	48.533.735	A	G	-0.027	-0.052	-0.003	0.03	1	0.45	BCDIN3D	1191
rs10773049	12	123.072.584	C	T	-0.021	-0.046	0.004	0.10	1	0.447	ZNF664-FAM101A	1170
rs12429545	13	53.000.207	A	G	0.01	-0.025	0.044	0.58	1	0.196	OLFM4	1177
rs1441264	13	78.478.920	A	G	-0.007	-0.032	0.018	0.57	1	0.598	MIR548A2	1176
rs7164727	15	70.881.044	T	C	0.047	0.021	0.073	$4.02*10^{-4}$	0.02	0.633	LOC100287559	1194
rs758747	16	3.567.359	T	C	-0.018	-0.044	0.007	0.16	1	0.359	NLRC3	1197

SNP	Chr	Position	Effect Allele	Other Allele	β-coefficient	Lower CI	Upper CI	p-value	Corr. p-value	Effect Allele Frequency	Gene	N
rs12446632	16	19.842.890	G	A	0.02	-0.017	0.057	0.30	1	0.812	GPRC5B	1191
rs2650492	16	28.240.912	A	G	-0.016	-0.042	0.009	0.21	1	0.368	SBK1	1196
rs3888190	16	28.796.987	A	C	0.021	-0.003	0.045	0.09	1	0.444	ATP2A1	1187
rs4787491	16	29.922.838	G	A	-0.018	-0.042	0.006	0.14	1	0.529	INO80E	1197
rs2080454	16	47.620.091	C	A	0.021	-0.004	0.046	0.09	1	0.422	CBLN1	1142
rs1000940	17	5.223.976	G	A	0.015	-0.01	0.04	0.24	1	0.375	RABEP1	1190
rs12940622	17	76.230.166	G	A	0.054	0.029	0.078	$1.86*10^{-5}$	0.001	0.565	RPTOR	1194
rs6567160	18	55.980.115	C	T	0.003	-0.022	0.028	0.79	1	0.368	MC4R	1194
rs17724992	19	18.315.825	A	G	-0.034	-0.062	-0.007	0.02	0.81	0.689	PGPEP1	1183
rs29941	19	39.001.372	G	A	-0.003	-0.03	0.023	0.81	1	0.638	KCTD15	1192
rs2075650	19	50.087.459	A	G	0.054	0.02	0.088	0.002	0.11	0.777	TOMM40	1198
rs2287019	19	50.894.012	C	T	-0.036	-0.067	-0.006	0.02	0.96	0.733	QPCTL	1189
rs2836754	21	39.213.610	C	T	-0.047	-0.072	-0.023	$1.51*10^{-4}$	0.01	0.575	ETS2	1190

Chr=Chromosome, CI=Confidence Interval, β-coefficient= standardized regression coefficient, N=number, SNP= Single nucleotide polymorphism. Effect Allele, for which we provide the effect estimates against the "other allele", which serves as reference (A=Adenosine, G=Guanine, C=Cytosine, T=Thymine). Genes are provided according to Illumina annotation (http://support.illumina.com/content/dam/illumina-support/documents/downloads/productfiles/cardio-metabochip/metabochip_gene_annotation.zip).

eTable 3: Associations between the 56 SNPs and changes in BMI adjusted for age and sex during the intervention (per week).

SNP	Chr	Position	Effect Allele	Other Allele	β-coefficient	Lower CI	Upper CI	p-value	Corr. p-value	Effect Allele Frequency	Gene	N
rs977747	1	47.457.264	T	G	0.004	-0.004	0.013	0.33	1	0.421	TAL1	1197
rs11583200	1	50.332.407	C	T	-0.002	-0.01	0.007	0.67	1	0.426	ELAVL4	1188
rs11165643	1	96.696.685	T	C	0	-0.008	0.009	0.91	1	0.557	PTBP2	1187
rs17024393	1	109.956.211	C	T	0.011	-0.01	0.032	0.31	1	0.072	GNAT2	1198
rs543874	1	176.156.103	G	A	-0.006	-0.016	0.004	0.25	1	0.262	SEC16B	1190
rs10182181	2	25.003.800	G	A	0.003	-0.005	0.011	0.43	1	0.483	ADCY3	1196
rs11126666	2	26.782.315	A	G	-0.011	-0.02	-0.002	0.02	1	0.343	KCNK3	1190
rs2121279	2	142.759.755	T	C	-0.005	-0.017	0.007	0.45	1	0.207	LRP1B	1195
rs1460676	2	164.275.935	C	T	-0.002	-0.012	0.009	0.75	1	0.26	FIGN	1198
rs1528435	2	181.259.207	T	C	-0.008	-0.017	0	0.05	1	0.603	UBE2E3	1197
rs17203016	2	207.963.763	G	A	0.003	-0.007	0.013	0.57	1	0.278	CREB1	1194
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rs6804842	3	25.081.441	G	A	0.002	-0.006	0.01	0.62	1	0.574	RARB	1194
rs2365389	3	61.211.502	C	T	0.002	-0.007	0.01	0.70	1	0.571	FHIT	1189
rs13078960	3	85.890.280	G	T	0.01	-0.001	0.021	0.06	1	0.268	CADM2	1047
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rs17001654	4	77.348.592	G	C	-0.01	-0.02	0.001	0.06	1	0.255	SCARB2	1195
rs13107325	4	103.407.732	T	C	-0.007	-0.022	0.007	0.32	1	0.139	SLC39A8	1191
rs11727676	4	145.878.514	T	C	-0.004	-0.019	0.01	0.56	1	0.85	HHIP	1197

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rs13201877	6	137.717.234	G	A	-0.022	-0.034	-0.011	$1.48*10^{-4}$	0.01	0.21	IFNGR1	1184
rs13191362	6	162.953.340	A	G	-0.008	-0.021	0.005	0.24	1	0.838	PARK2	1193
rs1167827	7	75.001.105	G	A	0.004	-0.004	0.012	0.36	1	0.561	HIP1	1197
rs17405819	8	76.969.139	T	C	0.005	-0.004	0.014	0.25	1	0.65	HNF4G	1177
rs10968576	9	28.404.339	G	A	0.005	-0.004	0.014	0.25	1	0.371	LINGO2	1193
rs6477694	9	110.972.163	C	T	0.005	-0.003	0.014	0.22	1	0.405	EPB41L4B	1190
rs1928295	9	119.418.304	T	C	-0.005	-0.014	0.003	0.18	1	0.538	TLR4	1190
rs10733682	9	128.500.735	A	G	-0.013	-0.021	-0.005	0.001	0.06	0.516	LMX1B	1194
rs7899106	10	87.400.884	G	A	0.008	-0.01	0.026	0.40	1	0.09	GRID1	1159
rs17094222	10	102.385.430	C	T	-0.002	-0.012	0.007	0.66	1	0.278	HIF1AN	1190
rs4256980	11	8.630.515	G	C	-0.003	-0.011	0.006	0.55	1	0.588	TRIM66	1194
rs11030104	11	27.641.093	A	G	-0.003	-0.013	0.007	0.52	1	0.72	BDNF	1189
rs3817334	11	47.607.569	T	C	-0.006	-0.014	0.002	0.15	1	0.443	MTCH2	1194
rs12286929	11	114.527.614	G	A	0.003	-0.005	0.011	0.48	1	0.54	CADM1	1161
rs11170468	12	37.716.315	A	C	0.007	-0.003	0.016	0.19	1	0.7	CPNE8	1197
rs7138803	12	48.533.735	A	G	-0.006	-0.015	0.002	0.14	1	0.45	BCDIN3D	1191
rs10773049	12	123.072.584	C	T	-0.005	-0.013	0.004	0.27	1	0.447	ZNF664-FAM101A	1170
rs12429545	13	53.000.207	A	G	0.003	-0.008	0.015	0.56	1	0.196	OLFM4	1177
rs1441264	13	78.478.920	A	G	-0.002	-0.01	0.007	0.67	1	0.598	MIR548A2	1176
rs7164727	15	70.881.044	T	C	0.012	0.003	0.021	0.01	0.38	0.633	LOC100287559	1194
rs758747	16	3.567.359	T	C	-0.011	-0.019	-0.002	0.02	0.83	0.359	NLRC3	1197

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rs2650492	16	28.240.912	A	G	0	-0.008	0.009	0.94	1	0.368	SBK1	1196
rs3888190	16	28.796.987	A	C	0.011	0.003	0.019	0.01	0.42	0.444	ATP2A1	1187
rs4787491	16	29.922.838	G	A	-0.008	-0.016	0	0.06	1	0.529	INO80E	1197
rs9925964	16	31.037.396	A	G	-0.008	-0.016	0.001	0.08	1	0.584	KAT8	1186
rs2080454	16	47.620.091	C	A	0.008	-0.001	0.016	0.08	1	0.422	CBLN1	1142
rs1000940	17	5.223.976	G	A	0.004	-0.004	0.013	0.32	1	0.375	RABEP1	1190
rs12940622	17	76.230.166	G	A	0.012	0.004	0.021	0.004	0.23	0.565	RPTOR	1194
rs6567160	18	55.980.115	C	T	0	-0.008	0.009	0.93	1	0.368	MC4R	1194
rs17724992	19	18.315.825	A	G	-0.011	-0.02	-0.001	0.03	1	0.689	PGPEP1	1183
rs29941	19	39.001.372	G	A	0.002	-0.007	0.012	0.60	1	0.638	KCTD15	1192
rs2075650	19	50.087.459	A	G	0.017	0.005	0.028	0.01	0.26	0.777	TOMM40	1198
rs2287019	19	50.894.012	C	T	-0.014	-0.025	-0.004	0.01	0.33	0.733	QPCTL	1189
rs2836754	21	39.213.610	C	T	-0.015	-0.024	-0.007	2.84×10^{-4}	0.02	0.575	ETS2	1190

Chr=Chromosome, CI=Confidence Interval, β-coefficient= standardized regression coefficient, N=number, SNP= Single nucleotide polymorphism. Effect Allele, for which we provide the effect estimates against the "other allele", which serves as reference (A=Adenosine, G=Guanine, C=Cytosine, T=Thymine). Genes are provided according to Illumina annotation (http://support.illumina.com/content/dam/illumina-support/documents/downloads/productfiles/cardio-metabochip/metabochip_gene_annotation.zip).

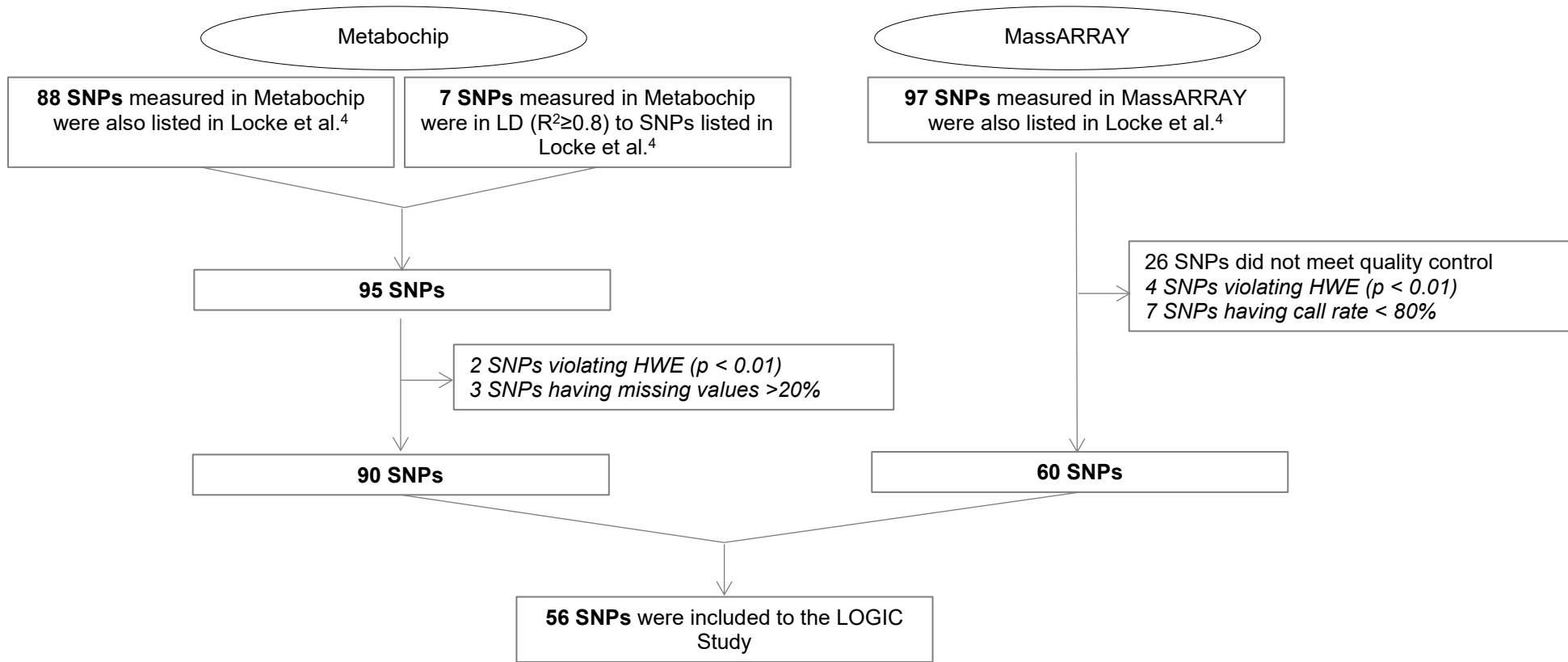**eTable 4: Associations between the 56 SNPs and changes in BMI-SDS during the intervention (per week).**

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rs11583200	1	50.332.407	C	T	0	-0.001	0.001	0.78	1	0.426	ELAVL4	1188
rs11165643	1	96.696.685	T	C	0	-0.001	0.001	0.87	1	0.557	PTBP2	1187
rs17024393	1	109.956.211	C	T	-0.003	-0.005	0	0.08	1	0.072	GNAT2	1198
rs543874	1	176.156.103	G	A	-0.002	-0.003	-0.001	0.004	0.23	0.262	SEC16B	1190
rs10182181	2	25.003.800	G	A	-0.001	-0.002	0.001	0.35	1	0.483	ADCY3	1196
rs11126666	2	26.782.315	A	G	0.001	0	0.003	0.04	1	0.343	KCNK3	1190
rs2121279	2	142.759.755	T	C	0.001	-0.001	0.002	0.46	1	0.207	LRP1B	1195
rs1460676	2	164.275.935	C	T	0	-0.001	0.002	0.65	1	0.26	FIGN	1198
rs1528435	2	181.259.207	T	C	0	-0.002	0.001	0.42	1	0.603	UBE2E3	1197
rs17203016	2	207.963.763	G	A	-0.001	-0.003	0	0.08	1	0.278	CREB1	1194
rs2176040	2	226.801.046	A	G	0	-0.002	0.001	0.62	1	0.407	LOC646736	1184
rs6804842	3	25.081.441	G	A	0.002	0.001	0.003	0.003	0.14	0.574	RARB	1194
rs2365389	3	61.211.502	C	T	0.001	0	0.002	0.06	1	0.571	FHIT	1189
rs13078960	3	85.890.280	G	T	0.003	0.002	0.005	$2.52*10^{-5}$	0.001	0.268	CADM2	1047
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rs10938397	4	44.877.284	G	A	0.001	0	0.002	0.07	1	0.475	GNPDA2	1180
rs17001654	4	77.348.592	G	C	0.001	-0.001	0.002	0.34	1	0.255	SCARB2	1195
rs13107325	4	103.407.732	T	C	0.004	0.002	0.006	$1.67*10^{-4}$	0.01	0.139	SLC39A8	1191
rs11727676	4	145.878.514	T	C	0	-0.002	0.002	0.98	1	0.85	HHIP	1197

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rs13191362	6	162.953.340	A	G	-0.002	-0.004	0	0.02	1	0.838	PARK2	1193
rs1167827	7	75.001.105	G	A	0.001	0	0.003	0.01	0.69	0.561	HIP1	1197
rs17405819	8	76.969.139	T	C	0.001	0	0.002	0.07	1	0.65	HNF4G	1177
rs10968576	9	28.404.339	G	A	0.001	0	0.002	0.04	1	0.371	LINGO2	1193
rs6477694	9	110.972.163	C	T	-0.001	-0.002	0	0.03	1	0.405	EPB41L4B	1190
rs1928295	9	119.418.304	T	C	-0.001	-0.002	0.001	0.36	1	0.538	TLR4	1190
rs10733682	9	128.500.735	A	G	-0.001	-0.002	0	0.12	1	0.516	LMX1B	1194
rs7899106	10	87.400.884	G	A	0.001	-0.001	0.004	0.36	1	0.09	GRID1	1159
rs17094222	10	102.385.430	C	T	-0.001	-0.002	0	0.16	1	0.278	HIF1AN	1190
rs4256980	11	8.630.515	G	C	0	-0.002	0.001	0.45	1	0.588	TRIM66	1194
rs11030104	11	27.641.093	A	G	0.001	0	0.002	0.18	1	0.72	BDNF	1189
rs3817334	11	47.607.569	T	C	0.001	0	0.002	0.25	1	0.443	MTCH2	1194
rs12286929	11	114.527.614	G	A	-0.001	-0.002	0	0.13	1	0.54	CADM1	1161
rs11170468	12	37.716.315	A	C	0.003	0.001	0.004	$1.05*10^{-4}$	0.01	0.7	CPNE8	1197
rs7138803	12	48.533.735	A	G	-0.002	-0.003	0	0.01	0.44	0.45	BCDIN3D	1191
rs10773049	12	123.072.584	C	T	0.002	0	0.003	0.01	0.55	0.447	ZNF664-FAM101A	1170
rs12429545	13	53.000.207	A	G	-0.002	-0.003	0	0.04	1	0.196	OLFM4	1177
rs1441264	13	78.478.920	A	G	0.001	0	0.002	0.18	1	0.598	MIR548A2	1176
rs7164727	15	70.881.044	T	C	0	-0.002	0.001	0.56	1	0.633	LOC100287559	1194

SNP	Chr	Position	Effect Allele	Other Allele	β-coefficient	Lower CI	Upper CI	p-value	Corr. p-value	Effect Allele Frequency	Gene	N
rs758747	16	3.567.359	T	C	0.001	0	0.002	0.09	1	0.359	NLRC3	1197
rs12446632	16	19.842.890	G	A	0	-0.001	0.002	0.72	1	0.812	GPRC5B	1191
rs2650492	16	28.240.912	A	G	0.001	-0.001	0.002	0.33	1	0.368	SBK1	1196
rs3888190	16	28.796.987	A	C	0.002	0	0.003	0.01	0.51	0.444	ATP2A1	1187
rs4787491	16	29.922.838	G	A	0	-0.001	0.001	0.82	1	0.529	INO80E	1197
rs9925964	16	31.037.396	A	G	-0.002	-0.003	-0.001	3.48×10^{-4}	0.02	0.584	KAT8	1186
rs2080454	16	47.620.091	C	A	-0.001	-0.002	0.001	0.33	1	0.422	CBLN1	1142
rs1000940	17	5.223.976	G	A	0.001	0	0.002	0.05	1	0.375	RABEP1	1190
rs12940622	17	76.230.166	G	A	0	-0.002	0.001	0.42	1	0.565	RPTOR	1194
rs6567160	18	55.980.115	C	T	0	-0.001	0.002	0.41	1	0.368	MC4R	1194
rs17724992	19	18.315.825	A	G	0.001	-0.001	0.002	0.31	1	0.689	PGPEP1	1183
rs29941	19	39.001.372	G	A	0.002	0	0.003	0.02	0.83	0.638	KCTD15	1192
rs2075650	19	50.087.459	A	G	0.001	0	0.003	0.10	1	0.777	TOMM40	1198
rs2287019	19	50.894.012	C	T	0	-0.001	0.002	0.72	1	0.733	QPCTL	1189
rs2836754	21	39.213.610	C	T	-0.001	-0.002	0	0.08	1	0.575	ETS2	1190

Chr=Chromosome, CI=Confidence Interval, β-coefficient= standardized regression coefficient, N=number, SNP= Single nucleotide polymorphism. Effect Allele, for which we provide the effect estimates against the "other allele", which serves as reference (A=Adenosine, G=Guanine, C=Cytosine, T=Thymine). Genes are provided according to Illumina annotation (http://support.illumina.com/content/dam/illumina-support/documents/downloads/productfiles/cardio-metabochip/metabochip_gene_annotation.zip).

eFigure: Selection and genotyping of SNPs.

Metabochip

MassARRAY

88 SNPs measured in Metabochip were also listed in Locke et al.[4]

7 SNPs measured in Metabochip were in LD (R^2≥0.8) to SNPs listed in Locke et al.[4]

97 SNPs measured in MassARRAY were also listed in Locke et al.[4]

95 SNPs

26 SNPs did not meet quality control
4 SNPs violating HWE (p < 0.01)
7 SNPs having call rate < 80%

2 SNPs violating HWE (p < 0.01)
3 SNPs having missing values >20%

90 SNPs

60 SNPs

56 SNPs were included to the LOGIC Study

HWE=Hardy Weinberg Equilibrium, LD=Linkage disequilibrium, SNP=Single nucleotide polymorphism.