

**Supplementary Table 1. Study sample characteristics and genotyping.**

**(a) Metabochip meta-analysis**

Study	Country of origin	T2D status	Sample characteristics					Genotyping array
			Sample size (males/females)	Age (years) mean (SD)	Age of diagnosis (years) mean (SD)	Fasting glucose (mmol/l) mean (SD)	BMI (kg/m <sup>2</sup> ) mean (SD)	
InterACT-CMC	France, Germany, Greece, Italy, Netherlands, Norway, Spain, Sweden, UK	Cases	3,553 (1,731/2,069)	N/A	N/A	N/A	N/A	Metabochip
		Controls	5,887 (2,069/3,818)	N/A		N/A	N/A	
PMB	Finland, Sweden	Cases	4,976 (2,908/2,064)	58.8 (12.5)	N/A	N/A	28.2 (8.7)	Metabochip
		Controls	3,500 (1,701/1,798)	58.3 (8.4)		N/A	26.4 (4.4)	
GoDARTS	UK	Cases	3,298 (1,940/1,358)	63.5 (9.6)	55.9 (8.9)	N/A	31.9 (6.3)	Metabochip
		Controls	3,708 (1,918/1,790)	59.1 (11.3)		4.9 (0.5)	27.0 (4.5)	
DANISH	Denmark	Cases	1,892 (1,188/707)	60.8 (11.1)	53.0 (10.7)	N/A	30.2 (5.5)	Metabochip
		Controls	6,603 (2,953/3,650)	46.3 (10.0)		5.5 (1.1)	25.5 (4.2)	
DGDG	France	Cases	2,019 (1,231/788)	59.4 (10.7)	49.7 (10.7)	N/A	28.0 (3.8)	Metabochip
		Controls	3,188 (1,441/1,747)	52.2 (8.4)		5.3 (0.4)	25.2 (3.7)	
KORA	Germany	Cases	1,207 (662/545)	62.9 (9.9)	N/A	N/A	30.9 (5.3)	Metabochip
		Controls	5,673 (2,718/2,955)	55.9 (13.0)		N/A	27.3 (4.5)	
Warren2/58BC	UK	Cases	1,117 (647/470)	N/A	45.5 (11.0)	N/A	32.2 (6.6)	Metabochip
		Controls	4,224 (2,394/1,830)	N/A		N/A	N/A	
IMPROVE	Sweden	Cases	904 (517/387)	64.3 (5.6)	N/A	7.7 (2.2)	29.2 (4.6)	Metabochip
		Controls	2,525 (1,140/1,385)	64.2 (5.3)		5.3 (0.7)	26.5 (3.9)	
HUNT/TROMSO	Norway	Cases	1,239 (628/611)	64.0 (12.9)	61.9 (11.9)	N/A	29.2 (4.8)	Metabochip
		Controls	1,375 (691/684)	63.5 (13.9)		N/A	26.5 (4.0)	
FUSION2	Finland	Cases	1,037 (584/453)	59.7 (8.4)	54.7 (7.4)	7.7 (2.3)	30.8 (5.4)	Metabochip
		Controls	1,154 (689/465)	59.0 (7.6)		5.4 (0.4)	26.9 (3.9)	
EMIL-Ulm	Germany	Cases	755 (510/245)	48.7 (12.0)	45.5 (10.8)	N/A	28.6 (7.1)	Metabochip
		Controls	1,632 (765/867)	45.1 (10.9)		N/A	26.7 (5.0)	
DILGOM	Finland	Cases	541 (298/243)	60.5 (10.3)	N/A	N/A	30.1 (5.6)	Metabochip
		Controls	3,357 (1,482/1,875)	50.9 (13.5)		N/A	26.5 (4.5)	
HNR	Germany	Cases	520 (315/205)	62.6 (7.2)	N/A	N/A	30.4 (5.2)	Metabochip
		Controls	3,932 (1,911/2,021)	59.2 (7.8)		N/A	27.5 (4.4)	
EGCUT	Estonia	Cases	912 (342/570)	64.1 (10.5)	N/A	N/A	33.4 (5.4)	Metabochip
		Controls	889 (326/563)	51.7 (10.7)		N/A	22.3 (2.5)	
METSIM	Finland	Cases	1,167 (1,167/0)	60.5 (6.6)	57.0 (8.0)	7.5 (2.0)	30.2 (5.2)	Metabochip
		Controls	651 (651/0)	53.8 (5.0)		5.5 (0.3)	25.9 (3.1)	
D2D2007	Finland	Cases	454 (269/185)	63.4 (7.6)	55.7 (9.7)	7.7 (1.8)	30.6 (5.6)	Metabochip
		Controls	1,229 (455/774)	58.1 (8.2)		5.6 (0.3)	26.2 (4.3)	
SCARFSHEEP	Sweden	Cases	314 (227/87)	59.6 (7.0)	N/A	8.12(5.4)	27.4 (8.4)	Metabochip
		Controls	2,906 (2,079/827)	57.9 (7.3)		4.0 (3.8)	25.4 (6.1)	

DIAGEN	Germany	Cases	437 (218/219)	66.0 (11.9)	66.0 (11.9)	9.0 (2.6)	30.1 (6.2)	MetaboChip
		Controls	586 (235/351)	58.6 (14.1)		5.2 (0.4)	26.7 (4.4)	
STR	Sweden	Cases	286 (137/149)	75.2 (8.4)	N/A	8.1 (4.3)	26.5 (4.3)	MetaboChip
		Controls	1,301 (549/752)	76.4 (9.6)		5.4 (0.6)	24.7 (3.8)	
Leipzig	Germany	Cases	200 (88/112)	52.5 (13.0)	N/A	N/A	45.0 (11.7)	MetaboChip
		Controls	701 (283/418)	40.9 (16.6)		N/A	34.2 (11.4)	
ULSAM	Sweden	Cases	166 (166/0)	71.0 (0.6)	N/A	N/A	27.7 (3.8)	MetaboChip
		Controls	953 (953/0)	71.0 (0.6)		N/A	25.9 (3.2)	
PIVUS	Sweden	Cases	111 (65/46)	70.2 (0.2)	N/A	N/A	29.5 (5.1)	MetaboChip
		Controls	838 (409/429)	70.2 (0.2)		N/A	26.8 (4.2)	
DRsEXTRA	Finland	Cases	101 (50/51)	68.0 (5.8)	N/A	6.7 (0.8)	30.8 (5.6)	MetaboChip
		Controls	762 (331/431)	66.0 (5.3)		5.4 (0.4)	26.7 (4.0)	

### (b) Validation meta-analysis

Study	Country of origin	T2D status	Sample characteristics					Genotyping array
			Sample size (males/females)	Age (years) mean (SD)	Age of diagnosis (years) mean (SD)	Fasting glucose (mmol/l) mean (SD)	BMI (kg/m <sup>2</sup> ) mean (SD)	
deCODE	Iceland	Cases	7,249 (3,892/3,357)	63.4 (15.3)	N/A	N/A	30.7 (6.0)	Illumina (various)
		Controls	83,049 (35,946/47,103)	51.5 (18.7)		N/A	26.5 (4.9)	
InterACT-GWAS	France, Germany, Italy, Netherlands, Spain, Sweden, UK	Cases	4,624 (2,229/2,395)	N/A	N/A	N/A	30.0 (4.8)	Illumina HumanHap 660
		Controls	4,668 (1,673/2,995)	N/A		N/A	25.9 (4.2)	
WTCCC	UK	Cases	1,924 (1,118/806)	58.6 (9.2)	50.3 (9.2)	N/A	30.7 (6.1)	Affymetrix GeneChip 500K
		Controls	2,938 (1,446/1,492)	N/A		N/A	N/A	
NHS	USA	Cases	1,467 (0/1,467)	53.4 (6.7)	N/A	N/A	27.4 (5.0)	Affymetrix 6.0
		Controls	1,754 (0/1,754)	53.2 (6.7)		N/A	23.5 (3.9)	
ARIC	USA	Cases	755 (408/347)	56.1 (5.6)	N/A	N/A	30.4 (5.5)	Affymetrix 6.0
		Controls	7,009 (3,098/3,911)	54.0 (5.7)		N/A	26.4 (4.5)	
FHS	USA	Cases	673 (386/287)	63.7 (12.4)	N/A	8.6 (2.8)	31.4 (6.5)	Affymetrix GeneChip 500K MIPS 50K
		Controls	7,660 (3,441/4,219)	52.3 (16.0)		5.3 (0.5)	27.0 (5.1)	
HPFS	USA	Cases	1,124 (1,124/0)	55.6 (8.6)	N/A	N/A	27.8 (4.0)	Affymetrix 6.0
		Controls	1,298 (1,298/0)	55.5 (8.4)		N/A	25.0 (2.7)	
Rotterdam Study	Netherlands	Cases	654	N/A	N/A	N/A	N/A	Illumina Human 550K
		Controls	5,219	N/A		N/A	N/A	
FUSION	Finland	Cases	1,060	N/A	N/A	N/A	N/A	Illumina HumanHap 300
		Controls	1,090	N/A		N/A	N/A	
BioMe-Illumina	USA	Cases	255 (181/74)	69.1 (9.0)	N/A	N/A	30.7 (6.2)	Illumina OMNI-ExpressExome
		Controls	1,647 (801/846)	67.6 (9.4)		5.1 (1.0)	26.3 (5.0)	
BioMe-Affy	USA	Cases	132 (97/35)	66.0 (10.7)	N/A	N/A	31.3 (6.3)	Affymetrix 6.0
		Controls	455 (297/158)	59.4 (16.0)		5.1 (1.1)	26.5 (5.2)	

**Supplementary Table 2. Summary of study-specific quality control, imputation and analysis.**

**(a) Metabochip meta-analysis**

Study	Sample QC		Variant QC			Imputation			Association analysis			
	Call rate	Exclusions	Call rate	HWE	MAF	QC+ variants	Software	Quality	QC+ variants	Software	Covariates (if any)	$\lambda_{GT}$
InterACT-CMC	≥0.97	IBD check and ethnic outliers	≥0.95	$p>10^{-4}$	≥0.01	113,924	IMPUTEv2	info≥0.4	341,751	SNPTEST	3 PCs	1.01
PMB	≥0.95	IBD check and ethnic outliers	≥0.95	$p>10^{-6}$	≥0.01	114,574	IMPUTEv2	info≥0.4	274,571	SNPTEST	Sex, 10 PCs	1.07
GoDARTS	≥0.95	IBD check and ethnic outliers	≥0.95	$p>5.7\times 10^{-7}$	≥0.01	115,548	IMPUTEv2	info≥0.4	289,250	SNPTEST	3 PCs	1.07
DANISH	≥0.90	IBD check and ethnic outliers	≥0.95	$p>10^{-4}$	≥0.01	118,622	IMPUTEv2	info≥0.4	294,141	SNPTEST		1.03
DGDG	≥0.90	IBD check and ethnic outliers	≥0.95	$p>10^{-4}$	≥0.01	119,227	IMPUTEv2	info≥0.4	270,645	SNPTEST	Age, Sex, BMI, 2 PCs	1.13
KORA	≥0.95	IBD check	≥0.95	$p>10^{-6}$	≥0.01	115,784	IMPUTEv2	info≥0.4	279,527	SNPTEST	Age, Sex	1.05
Warren2/58BC	≥0.95	IBD check and ethnic outliers	≥0.95	$p>10^{-6}$	≥0.01	115,043	IMPUTEv2	info≥0.4	284,944	SNPTEST		1.07
IMPROVE	≥0.95	IBD check and ethnic outliers	≥0.95	$p>10^{-6}$	≥0.01	105,663	minimac	$r^2\geq 0.3$	212,360	mach2dat	Age, Sex, 3 PCs	1.12
HUNT/TROMSO	≥0.98	IBD check	≥0.98	$p>10^{-5}$	≥0.01	119,658	minimac	$r^2\geq 0.3$	198,043	mach2dat	Age, Study origin	1.08
FUSION2	≥0.98	IBD check	≥0.98	$p>10^{-5}$	≥0.01	116,942	minimac	$r^2\geq 0.3$	190,480	mach2dat	Age, Place of birth	0.97
EMIL-Ulm	≥0.95	IBD check	≥0.95	$p>10^{-6}$	≥0.01	116,795	IMPUTEv2	info≥0.4	251,219	SNPTEST	Age, Sex, 10 PCs	1.13
DILGOM	≥0.95	IBD check	≥0.95	$p>10^{-6}$	≥0.01	115,398	IMPUTEv2	info≥0.4	234,196	SNPTEST	Sex	0.97
HNR	≥0.97	IBD check and ethnic outliers	≥0.95	$p>10^{-4}$	≥0.01	120,219	IMPUTEv2	info≥0.4	269,933	SNPTEST	Age, Sex	0.99
EGCUT	≥0.95	IBD check and ethnic outliers	≥0.95	$p>10^{-6}$	≥0.01	115,469	IMPUTEv2	info≥0.4	221,762	SNPTEST	Age, Sex	1.02
METSIM	≥0.98	IBD check	≥0.98	$p>10^{-5}$	≥0.01	116,075	minimac	$r^2\geq 0.3$	183,195	mach2dat	Age	1.02
D2D2007	≥0.98	IBD check	≥0.98	$p>10^{-5}$	≥0.01	116,585	minimac	$r^2\geq 0.3$	184,582	mach2dat	Age	0.99
SCARFSHEEP	≥0.95	IBD check	≥0.95	$p>10^{-6}$	≥0.01	106,723	minimac	$r^2\geq 0.3$	187,784	mach2dat	Age, Sex, Cohort, CAD, Swedish birth	0.98
DIAGEN	≥0.98	IBD check	≥0.98	$p>10^{-5}$	≥0.01	119,267	minimac	$r^2\geq 0.3$	184,830	mach2dat	Age	1.07
STR	≥0.95	IBD check	≥0.95	$p>10^{-4}$	≥0.01	115,246	IMPUTEv2	info≥0.4	220,186	SNPTEST	Age, Sex	1.09
Leipzig	≥0.95	IBD check and ethnic outliers	≥0.95	$p>5.7\times 10^{-7}$	≥0.01	116,954	IMPUTEv2	info≥0.4	212,700	SNPTEST	Age	1.03
ULSAM	≥0.95	IBD check and ethnic outliers	≥0.98	$p>10^{-4}$	≥0.01	113,580	IMPUTEv2	info≥0.4	209,549	SNPTEST	2 PCs	0.97
PIVUS	≥0.95	IBD check and ethnic outliers	≥0.95	$p>10^{-6}$	≥0.01	117,487	IMPUTEv2	info≥0.4	204,014	SNPTEST	Age, Sex, 2 PCs	0.97
DR-extra	≥0.98	IBD check	≥0.98	$p>10^{-5}$	≥0.01	115,865	minimac	$r^2\geq 0.3$	161,772	mach2dat	Age	1.03

**(b) Validation meta-analysis**

Study	Sample QC		Variant QC			Imputation			Association analysis			
	Call rate	Exclusions	Call rate	HWE	MAF	QC+ variants	Software	Quality	QC+ variants	Software	Covariates (if any)	$\lambda_{GC}$
deCODE	≥0.97	Ethnic outliers	≥0.95	$p>10^{-6}$	≥0.01	699,107	In-house	info≥0.4	<i>in silico</i>	SNPTEST	Age, Sex	1.30
InterACT-GWAS	≥0.98	IBD check and ethnic outliers	≥0.95	$p>5.7\times 10^{-7}$	≥0.01	541,471	IMPUTEv2	info≥0.4	<i>in silico</i>	SNPTEST	Sex, 10 PCs	0.98
WTCCC	≥0.97	IBD check and ethnic outliers	≥0.95	$p>10^{-3}$	≥0.01	N/A	IMPUTEv2	info≥0.4	<i>in silico</i>	SNPTEST		1.00
NHS	≥0.97	IBD check and ethnic outliers	≥0.97	$p>10^{-6}$	≥0.01	606,626	MACH	$r^2\geq 0.3$	<i>in silico</i>	SNPTEST		1.01
ARIC	≥0.95	IBD check and ethnic outliers	≥0.95	$p>10^{-5}$	≥0.01	695,783	IMPUTEv2	info≥0.4	<i>in silico</i>	SNPTEST	Age, Sex, Study Centre, 1 PC	1.01
FHS	≥0.97	Mendelian errors	≥0.95	$p>10^{-6}$	≥0.01	412,053	minimac	$r^2\geq 0.3$	<i>in silico</i>	R geepack	Age, Sex, Cohort, 10 PCs	1.03
HPFS	≥0.97	IBD check and ethnic outliers	≥0.97	$p>10^{-6}$	≥0.01	607,569	MACH	$r^2\geq 0.3$	<i>in silico</i>	SNPTEST		1.01

Rotterdam Study	≥0.975	IBD check	≥0.98	$p>10^{-6}$	≥0.01	N/A	minimac	$r^2\geq 0.3$	<i>in silico</i>	mach2dat		1.02
FUSION	≥0.95	IBD check	≥0.95	$p>10^{-6}$	≥0.01	N/A	minimac	$r^2\geq 0.3$	<i>in silico</i>	mach2dat		1.00
BioMe-Illumina	≥0.98	IBD check and ethnic outliers	≥0.95	$p>5\times 10^{-5}$	≥0.01	845,969	IMPUTE	info≥0.4	<i>in silico</i>	SNPTEST	Age, Sex, 4 PCs	1.01
BioMe-Affy	≥0.95	IBD check and ethnic outliers	≥0.95	$p>10^{-4}$	≥0.01	683,891	IMPUTE	info≥0.4	<i>in silico</i>	SNPTEST	Age, Sex, 5 PCs	1.01

PCs: principal components. BMI: body-mass index. CAD: coronary artery disease status (case-control).

**Supplementary Table 3. Summary of fine-mapping regions on Metabochip that overlap established T2D susceptibility loci.**

Locus	Chr	Fine-mapping region (b37)		Selected trait(s)	Priority <sup>b</sup>	Previously reported lead SNP in European ancestry populations				
		Start position	Stop position			SNP	Position (b37)	p-value	OR (95% CI)	Reference(s)
<i>NOTCH2</i>	1	120,437,717	120,615,600	T2D	S	rs10923931	120,517,959	0.00061	1.07 (1.03-1.12)	Voight <i>et al.</i> (2010) <sup>4</sup> ; Morris <i>et al.</i> (2012) <sup>5</sup>
<i>PROX1</i>	1	214,124,817	214,167,508	FG	G	rs2075423	214,154,719	1.9x10 <sup>-7</sup>	1.07 (1.04-1.10)	Morris <i>et al.</i> (2012) <sup>5</sup>
<i>GCKR</i>	2	27,386,798	28,670,981	TG/FG	G/B	rs780094	27,741,237	8.5x10 <sup>-10</sup>	1.08 (1.06-1.11)	Dupuis <i>et al.</i> (2010) <sup>20</sup> ; Morris <i>et al.</i> (2012) <sup>5</sup>
<i>THADA</i>	2	43,449,384	43,893,878	T2D	B	rs10203174	43,690,030	1.0x10 <sup>-9</sup>	1.14 (1.09-1.19)	Morris <i>et al.</i> (2012) <sup>5</sup>
<i>BCL11A</i>	2	60,557,030	60,601,376	T2D	B	rs243088	60,568,745	6.5x10 <sup>-6</sup>	1.06 (1.03-1.09)	Morris <i>et al.</i> (2012) <sup>5</sup>
<i>GRB14-COBL1</i>	2	165,499,547	165,732,418	HDL/WHR	G/B	rs13389219	165,528,876	1.2x10 <sup>-13</sup>	1.10 (1.07-1.13)	Morris <i>et al.</i> (2012) <sup>5</sup>
<i>IRS1</i>	2	227,007,409	227,190,673	T2D	G	rs2943640	227,093,585	1.1x10 <sup>-14</sup>	1.11 (1.08-1.14)	Morris <i>et al.</i> (2012) <sup>5</sup>
<i>PPARG</i>	3	12,207,460	12,470,239	T2D	B	rs1801282	12,393,125	8.0x10 <sup>-8</sup>	1.11 (1.07-1.15)	Morris <i>et al.</i> (2012) <sup>5</sup>
<i>ADAMTS9</i>	3	64,691,378	64,733,440	T2D	S	rs6795735	64,705,365	1.3x10 <sup>-7</sup>	1.07 (1.04-1.10)	Voight <i>et al.</i> (2010) <sup>4</sup> ; Morris <i>et al.</i> (2012) <sup>5</sup>
<i>ADCY5</i>	3	122,976,417	123,207,012	FG/T2D	G	rs11717195	123,082,398	3.4x10 <sup>-13</sup>	1.12 (1.09-1.15)	Morris <i>et al.</i> (2012) <sup>5</sup>
<i>IGF2BP2</i>	3	185,337,787	185,596,778	T2D	G/S	rs4402960	185,511,687	1.8x10 <sup>-19</sup>	1.13 (1.10-1.16)	Morris <i>et al.</i> (2012) <sup>5</sup>
<i>WFS1</i>	4	6,262,591	6,336,127	T2D	G	rs4458523	6,289,986	2.0x10 <sup>-10</sup>	1.09 (1.06-1.11)	Morris <i>et al.</i> (2012) <sup>5</sup>
<i>ZBED3</i>	5	76,420,789	76,437,700	T2D	S	rs6878122	76,427,311	6.6x10 <sup>-10</sup>	1.09 (1.06-1.12)	Morris <i>et al.</i> (2012) <sup>5</sup>
<i>CDKAL1</i>	6	20,393,906	21,191,928	T2D	G/S	rs7756992	20,679,709	3.2x10 <sup>-22</sup>	1.14 (1.11-1.18)	Morris <i>et al.</i> (2012) <sup>5</sup>
<i>DGKB</i>	7	14,185,087	15,145,681	FG	G/S	rs17168486	14,898,282	0.000024	1.07 (1.04-1.11)	Morris <i>et al.</i> (2012) <sup>5</sup>
<i>JAZF1</i>	7	27,783,994	28,282,062	T2D	G/S	rs849135	28,196,413	5.0x10 <sup>-12</sup>	1.09 (1.07-1.12)	Morris <i>et al.</i> (2012) <sup>5</sup>
<i>GCK</i>	7	44,222,002	44,266,077	FG/HbA1c	S/B	rs10278336	44,245,363	9.6x10 <sup>-7</sup>	1.07 (1.04-1.09)	Morris <i>et al.</i> (2012) <sup>5</sup>
<i>KLF14</i>	7	130,421,158	130,468,190	T2D/HDL	S/B	rs13233731	13,0437,689	0.19	1.02 (0.99-1.04)	Morris <i>et al.</i> (2012) <sup>5</sup>
<i>SLC30A8</i>	8	118,182,117	118,223,955	T2D	B	rs3802177	11,8185,025	1.4x10 <sup>-18</sup>	1.13 (1.10-1.16)	Voight <i>et al.</i> (2010) <sup>4</sup> ; Morris <i>et al.</i> (2012) <sup>5</sup>
<i>GLIS3</i>	9	4,243,161	4,310,558	FG	G	rs10758593	4,292,083	1.1x10 <sup>-6</sup>	1.06 (1.04-1.09)	Morris <i>et al.</i> (2012) <sup>5</sup>
<i>CDKN2A-B</i>	9	21,950,408	22,159,982	T2D/MICAD	G/S	rs10811661	22,134,094	1.1x10 <sup>-27</sup>	1.21 (1.17-1.25)	Morris <i>et al.</i> (2012) <sup>5</sup>
<i>CDC123</i>	10	12,160,444	12,338,626	T2D	G	rs11257655	12,307,894	3.9x10 <sup>-10</sup>	1.10 (1.07-1.13)	Morris <i>et al.</i> (2012) <sup>5</sup>
<i>HHEX-IDE</i>	10	94,200,768	94,498,975	T2D	G	rs1111875	94,462,882	3.0x10 <sup>-14</sup>	1.10 (1.08-1.13)	Morris <i>et al.</i> (2012) <sup>5</sup>
<i>TCF7L2</i>	10	114,746,579	114,822,739	T2D	G	rs7903146	114,758,349	5.8x10 <sup>-120</sup>	1.39 (1.35-1.43)	Voight <i>et al.</i> (2010) <sup>4</sup> ; Morris <i>et al.</i> (2012) <sup>5</sup>
<i>KCNQ1</i>	11	2,443,937	2,943,115	T2D/QT	G/S	rs163184	2,847,069	9.5x10 <sup>-18</sup>	1.12 (1.09-1.14)	Morris <i>et al.</i> (2012) <sup>5</sup>
<i>KCNJ11</i>	11	17,038,776	17,424,926	T2D	B	rs5215	17,408,630	1.5x10 <sup>-10</sup>	1.09 (1.06-1.12)	Voight <i>et al.</i> (2010) <sup>4</sup> ; Morris <i>et al.</i> (2012) <sup>5</sup>
<i>CENTD2</i>	11	72,391,642	72,880,613	T2D	B	rs1552224	72,433,098	3.7x10 <sup>-7</sup>	1.09 (1.05-1.13)	Voight <i>et al.</i> (2010) <sup>4</sup> ; Morris <i>et al.</i> (2012) <sup>5</sup>
<i>MTNR1B</i>	11	92,667,046	92,725,521	FG/HbA1c/T2D	G/S/B	rs10830963	92,708,710	2.9x10 <sup>-12</sup>	1.10 (1.07-1.13)	Morris <i>et al.</i> (2012) <sup>5</sup>
<i>HMG2</i>	12	66,164,516	66,303,735	T2D	G	rs2261181	66,212,318	1.3x10 <sup>-8</sup>	1.13 (1.09-1.18)	Morris <i>et al.</i> (2012) <sup>5</sup>
<i>TSPAN8</i>	12	71,543,070	71,667,022	T2D	G	rs4760790	71,634,794	7.4x10 <sup>-6</sup>	1.07 (1.04-1.10)	Voight <i>et al.</i> (2010) <sup>4</sup> ; Morris <i>et al.</i> (2012) <sup>5</sup>
<i>HNF1A</i>	12	121,157,534	121,490,565	T2D/MICAD/LDL	G/S	rs12427353	121,426,901	0.00016	1.06 (1.03-1.10)	Morris <i>et al.</i> (2012) <sup>5</sup>
<i>C2CD4A-B</i>	15	62,098,986	62,520,663	FG/2hG	S/B	rs4502156	62,383,155	0.0018	1.04 (1.02-1.07)	Morris <i>et al.</i> (2012) <sup>5</sup>
<i>PRC1</i>	15	91,441,382	91,566,862	T2D	B	rs12899811	91,544,076	3.1x10 <sup>-6</sup>	1.07 (1.04-1.09)	Morris <i>et al.</i> (2012) <sup>5</sup>

<i>FTO</i>	16	53,539,508	54,185,787	BMI	G/S	rs9936385	53,819,169	9.9x10 <sup>-24</sup>	1.14 (1.11-1.17)	Morris <i>et al.</i> (2012) <sup>5</sup>
<i>HNF1B</i>	17	36,090,544	36,108,367	T2D	G	rs11651052	36,102,381	1.0x10 <sup>-11</sup>	1.09 (1.06-1.12)	Morris <i>et al.</i> (2012) <sup>5</sup>
<i>MC4R</i>	18	57,727,146	58,094,636	BMI	G/S	rs12970134	57,884,750	0.0019	1.05 (1.02-1.08)	Morris <i>et al.</i> (2012) <sup>5</sup>
<i>CILP2</i>	19	19,301,231	19,792,250	LDL	G	rs10401969	19,407,718	2.5x10 <sup>-11</sup>	1.17 (1.12-1.22)	Morris <i>et al.</i> (2012) <sup>5</sup>
<i>GIPR</i>	19	46,136,486	46,408,041	2hG	G/S	rs8108269	46,158,513	7.1x10 <sup>-8</sup>	1.08 (1.05-1.11)	Morris <i>et al.</i> (2012) <sup>5</sup>
<i>HNF4A</i>	20	43,038,558	43,058,096	HDL	S	rs4812829 <sup>a</sup>	42,989,267	N/A	N/A	Kooner <i>et al.</i> (2011) <sup>2</sup> ; Morris <i>et al.</i> (2012) <sup>5</sup>

Association summary statistics are based on the meta-analysis of Metabochip studies in 27,206 cases and 57,574 controls of European ancestry.

Chr: chromosome. RAF: risk allele frequency. OR: odds-ratio for risk allele. CI: confidence interval.

T2D: type 2 diabetes. FG: fasting glucose. TG: triglycerides. HDL: high-density lipoprotein cholesterol. WHR: waist-hip ratio. HbA1c: haemoglobin A1c. MICAD: myocardial infarction and/or coronary artery disease. QT: QT interval. LDL: low-density lipoprotein cholesterol. 2hG: two-hour glucose. BMI: body-mass index.

<sup>a</sup>The previously reported lead SNP for T2D at the *HNF4A* locus maps outside the fine-mapping region.

<sup>b</sup>Priority for fine-mapping classified as: gold (G); silver (S); or bronze (B).

**Supplementary Table 4. Imputation quality metrics across MetaboChip fine-mapping regions.**

Study	Sample size (cases/controls)	Imputation software	High-quality <sup>a</sup> imputed variants amongst those polymorphic in European ancestry haplotypes from the 1000 Genomes Project Consortium phase 1 integrated reference panel					
			Common (MAF≥5%)		Low-frequency (0.5%≤MAF<5%)		Rare (0%<MAF<0.5%)	
			N (%)	Mean info/ <i>r</i> <sup>2</sup>	N (%)	Mean info/ <i>r</i> <sup>2</sup>	N (%)	Mean info/ <i>r</i> <sup>2</sup>
InterACT-CMC	9,440 (3,553/5,887)	IMPUTEv2	94,815 (99.9)	0.977	65,583 (97.3)	0.855	67,658 (68.5)	0.696
DANISH	8,495 (1,892/6,603)	IMPUTEv2	94,829 (99.9)	0.979	65,028 (96.5)	0.862	60,265 (61.0)	0.705
PMB	8,476 (4,976/3,500)	IMPUTEv2	94,858 (99.9)	0.979	65,124 (96.6)	0.866	57,233 (57.9)	0.700
GoDARTS	7,006 (3,298/3,708)	IMPUTEv2	94,805 (99.9)	0.978	64,540 (95.8)	0.858	59,179 (59.9)	0.695
KORA	6,880 (1,207/5,673)	IMPUTEv2	93,395 (98.4)	0.975	61,082 (90.6)	0.859	52,822 (53.5)	0.717
Warren2/58BC	5,341 (1,117/4,224)	IMPUTEv2	94,803 (99.9)	0.978	64,468 (95.7)	0.859	58,735 (59.5)	0.708
DGDG	5,207 (2,019/3,188)	IMPUTEv2	94,621 (99.7)	0.975	61,791 (91.7)	0.853	44,930 (45.5)	0.742
HNR	4,452 (520/3,932)	IMPUTEv2	94,845 (99.9)	0.979	64,217 (95.3)	0.866	56,157 (56.9)	0.734
DILGOM	3,898 (541/3,357)	IMPUTEv2	94,860 (99.9)	0.981	62,650 (93.0)	0.877	41,514 (42.0)	0.764
IMPROVE	3,429 (904/2,525)	minimac	93,658 (98.7)	0.965	58,507 (86.8)	0.836	32,898 (33.3)	0.684
SCARFSHEEP	3,220 (314/2,906)	minimac	93,804 (98.8)	0.969	57,808 (85.8)	0.841	24,974 (25.3)	0.668
HUNT/TROMSO	2,614 (1,239/1,375)	minimac	94,189 (99.2)	0.973	60,490 (89.8)	0.846	30,595 (31.0)	0.690
EMIL-Ulm	2,387 (755/1,632)	IMPUTEv2	94,778 (99.9)	0.978	64,137 (95.2)	0.858	51,078 (51.7)	0.717
FUSION2	2,191 (1,037/1,154)	minimac	94,449 (99.5)	0.977	61,097 (90.7)	0.851	27,786 (28.1)	0.698
METSIM	1,818 (1167/651)	minimac	94,449 (99.5)	0.977	59,419 (88.2)	0.853	23,748 (24.0)	0.704
EGCUT	1,801 (912/889)	IMPUTEv2	94,846 (99.9)	0.979	63,387 (94.1)	0.869	39,403 (39.9)	0.739
D2D2007	1,683 (454/1,229)	minimac	94,449 (99.5)	0.977	59,753 (88.7)	0.852	24,316 (24.6)	0.694
STR	1,587 (286/1,301)	IMPUTEv2	94,800 (99.9)	0.979	63,523 (94.3)	0.875	40,729 (41.2)	0.755
ULSAM	1,119 (166/953)	IMPUTEv2	94,806 (99.9)	0.979	62,597 (92.9)	0.881	35,905 (36.4)	0.784
DIAGEN	1,023 (437/586)	minimac	94,005 (99.0)	0.972	57,610 (85.5)	0.842	24,377 (24.7)	0.691
PIVUS	949 (111/838)	IMPUTEv2	94,822 (99.9)	0.979	62,122 (92.2)	0.888	33,396 (33.8)	0.806
Leipzig	901 (200/701)	IMPUTEv2	94,767 (99.8)	0.977	62,134 (92.2)	0.869	35,949 (36.4)	0.760
DR-extra	863 (101/762)	minimac	94,404 (99.5)	0.977	50,274 (74.6)	0.860	14,471 (14.7)	0.724

<sup>a</sup>High-quality variants defined by IMPUTEv2 info≥0.4 or minimac *r*<sup>2</sup>≥0.3.

**Supplementary Table 5. Imputation quality metrics in fine-mapping regions overlapping 39 established T2D susceptibility loci.**

(a) Common variants (MAF $\geq$ 5%)

Locus	Chr	Fine-mapping region (b37)		Priority <sup>a</sup>	Variants in European ancestry haplotypes from the 1000 Genomes Project Consortium phase 1 integrated reference panel		High-quality <sup>b</sup> variants imputed into InterACT-CMC scaffold		High-quality <sup>b</sup> variants imputed into DANISH scaffold		High-quality <sup>b</sup> variants imputed into PMB scaffold		High-quality <sup>b</sup> variants imputed into GoDARTS scaffold	
		Start position	Stop position		N	Typed on Metabochip N (%)	N (%)	Mean info	N (%)	Mean info	N (%)	Mean info	N (%)	Mean info
<i>NOTCH2</i>	1	120,437,717	120,615,600	S	149	74 (49.7)	126 (84.6)	0.837	143 (96.0)	0.791	139 (93.3)	0.802	135 (90.6)	0.812
<i>PROX1</i>	1	214,124,817	214,167,508	G	74	45 (60.8)	74 (100.0)	0.966	74 (100.0)	0.969	74 (100.0)	0.968	74 (100.0)	0.968
<i>GCKR</i>	2	27,386,798	28,670,981	G/B	1,742	831 (47.7)	1,742 (100.0)	0.982	1,742 (100.0)	0.984	1,742 (100.0)	0.984	1,742 (100.0)	0.983
<i>THADA</i>	2	43,449,384	43,893,878	B	1,053	525 (49.9)	1,053 (100.0)	0.989	1,053 (100.0)	0.990	1,053 (100.0)	0.990	1,053 (100.0)	0.990
<i>BCL11A</i>	2	60,557,030	60,601,376	B	118	75 (63.6)	118 (100.0)	0.993	118 (100.0)	0.993	118 (100.0)	0.994	118 (100.0)	0.994
<i>GRB14-COBL1</i>	2	165,499,547	165,732,418	G/B	556	212 (38.1)	556 (100.0)	0.985	556 (100.0)	0.986	555 (99.8)	0.987	555 (99.8)	0.988
<i>IRS1</i>	2	227,007,409	227,190,673	G	313	193 (61.7)	313 (100.0)	0.982	313 (100.0)	0.982	313 (100.0)	0.983	313 (100.0)	0.983
<i>PPARG</i>	3	12,207,460	12,470,239	B	490	178 (36.3)	490 (100.0)	0.985	490 (100.0)	0.986	489 (99.8)	0.988	489 (99.8)	0.987
<i>ADAMTS9</i>	3	64,691,378	64,733,440	S	125	84 (67.2)	125 (100.0)	0.988	125 (100.0)	0.989	125 (100.0)	0.989	125 (100.0)	0.988
<i>ADCY5</i>	3	122,976,417	123,207,012	G	424	268 (63.2)	424 (100.0)	0.977	424 (100.0)	0.979	424 (100.0)	0.980	424 (100.0)	0.979
<i>IGF2BP2</i>	3	185,337,787	185,596,778	G/S	367	154 (42.0)	367 (100.0)	0.971	367 (100.0)	0.973	366 (99.7)	0.974	366 (99.7)	0.970
<i>WFS1</i>	4	6,262,591	6,336,127	G	281	197 (70.1)	281 (100.0)	0.978	281 (100.0)	0.988	281 (100.0)	0.983	281 (100.0)	0.984
<i>ZBED3</i>	5	76,420,789	76,437,700	S	34	29 (85.3)	34 (100.0)	0.996	34 (100.0)	0.997	34 (100.0)	0.997	34 (100.0)	0.996
<i>CDKAL1</i>	6	20,393,906	21,191,928	G/S	2,109	1,021 (48.4)	2,108 (100.0)	0.990	2,108 (100.0)	0.991	2,109 (100.0)	0.991	2,108 (100.0)	0.991
<i>DGKB</i>	7	14,185,087	15,145,681	G/S	2,760	1,604 (58.1)	2,759 (100.0)	0.984	2,759 (100.0)	0.986	2,759 (100.0)	0.985	2,759 (100.0)	0.985
<i>JAZF1</i>	7	27,783,994	28,282,062	G/S	1,022	578 (56.6)	1,022 (100.0)	0.986	1,022 (100.0)	0.988	1,022 (100.0)	0.988	1,022 (100.0)	0.987
<i>GCK</i>	7	44,222,002	44,266,077	S/B	134	71 (53.0)	134 (100.0)	0.986	134 (100.0)	0.988	134 (100.0)	0.990	134 (100.0)	0.987
<i>KLF14</i>	7	130,421,158	130,468,190	S/B	128	61 (47.7)	127 (99.2)	0.990	127 (99.2)	0.991	127 (99.2)	0.991	127 (99.2)	0.990
<i>SLC30A8</i>	8	118,182,117	118,223,955	B	102	42 (41.2)	102 (100.0)	0.977	102 (100.0)	0.977	102 (100.0)	0.977	102 (100.0)	0.977
<i>GLIS3</i>	9	4,243,161	4,310,558	G	292	180 (61.6)	292 (100.0)	0.967	292 (100.0)	0.971	292 (100.0)	0.970	292 (100.0)	0.970
<i>CDKN2A-B</i>	9	21,950,408	22,159,982	G/S	432	264 (61.1)	431 (99.8)	0.971	431 (99.8)	0.972	431 (99.8)	0.973	431 (99.8)	0.972
<i>CDC123</i>	10	12,160,444	12,338,626	G	437	182 (41.6)	437 (100.0)	0.962	437 (100.0)	0.966	437 (100.0)	0.964	437 (100.0)	0.962
<i>HHEX-IDE</i>	10	94,200,768	94,498,975	G	490	214 (43.7)	490 (100.0)	0.981	490 (100.0)	0.982	490 (100.0)	0.982	490 (100.0)	0.981
<i>TCF7L2</i>	10	114,746,579	114,822,739	G	127	81 (63.8)	127 (100.0)	0.993	127 (100.0)	0.995	127 (100.0)	0.994	127 (100.0)	0.994
<i>KCNQ1</i>	11	2,443,937	2,943,115	G/S	1,244	786 (63.2)	1,244 (100.0)	0.970	1,244 (100.0)	0.982	1,244 (100.0)	0.982	1,244 (100.0)	0.980
<i>KCNJ11</i>	11	17,038,776	17,424,926	B	728	247 (33.9)	728 (100.0)	0.975	728 (100.0)	0.978	728 (100.0)	0.977	728 (100.0)	0.977
<i>CENTD2</i>	11	72,391,642	72,880,613	B	546	180 (33.0)	546 (100.0)	0.975	546 (100.0)	0.977	546 (100.0)	0.978	546 (100.0)	0.977
<i>MTNR1B</i>	11	92,667,046	92,725,521	G/S/B	110	59 (53.6)	110 (100.0)	0.960	110 (100.0)	0.961	110 (100.0)	0.962	110 (100.0)	0.961
<i>HMGA2</i>	12	66,164,516	66,303,735	G	172	26 (15.1)	172 (100.0)	0.982	172 (100.0)	0.985	172 (100.0)	0.983	172 (100.0)	0.985
<i>TSPAN8</i>	12	71,543,070	71,667,022	G	215	83 (38.6)	215 (100.0)	0.985	215 (100.0)	0.984	215 (100.0)	0.982	215 (100.0)	0.983
<i>HNF1A</i>	12	121,157,534	121,490,565	G/S	948	306 (32.3)	947 (99.9)	0.966	947 (99.9)	0.967	947 (99.9)	0.968	947 (99.9)	0.967
<i>C2CD4A-B</i>	15	62,098,986	62,520,663	S/B	925	311 (33.6)	925 (100.0)	0.987	925 (100.0)	0.988	925 (100.0)	0.988	925 (100.0)	0.988



<i>PRC1</i>	15	91,441,382	91,566,862	B	367	153 (41.7)	367 (100.0)	0.981	367 (100.0)	0.983	367 (100.0)	0.985	367 (100.0)	0.983
<i>FTO</i>	16	53,539,508	54,185,787	G/S	1,446	724 (50.1)	1,446 (100.0)	0.984	1,446 (100.0)	0.986	1,446 (100.0)	0.986	1,446 (100.0)	0.985
<i>HNF1B</i>	17	36,090,544	36,108,367	G	42	22 (52.4)	42 (100.0)	0.960	42 (100.0)	0.963	42 (100.0)	0.964	42 (100.0)	0.963
<i>MC4R</i>	18	57,727,146	58,094,636	G/S	679	409 (60.2)	679 (100.0)	0.989	679 (100.0)	0.990	679 (100.0)	0.989	679 (100.0)	0.990
<i>CILP2</i>	19	19,301,231	19,792,250	G	702	362 (51.6)	702 (100.0)	0.983	702 (100.0)	0.984	702 (100.0)	0.985	702 (100.0)	0.985
<i>GIPR</i>	19	46,136,486	46,408,041	G/S	745	240 (32.2)	745 (100.0)	0.980	745 (100.0)	0.981	745 (100.0)	0.982	745 (100.0)	0.981
<i>HNF4A</i>	20	43,038,558	43,058,096	S	58	31 (53.4)	58 (100.0)	0.990	58 (100.0)	0.990	58 (100.0)	0.992	58 (100.0)	0.990

(b) Low-frequency variants (0.5%≤MAF<5%)

Locus	Chr	Fine-mapping region (b37)		Priority <sup>a</sup>	Variants in European ancestry haplotypes from the 1000 Genomes Project Consortium phase 1 integrated reference panel		High-quality <sup>b</sup> variants imputed into InterACT-CMC scaffold		High-quality <sup>b</sup> variants imputed into DANISH scaffold		High-quality <sup>b</sup> variants imputed into PMB scaffold		High-quality <sup>b</sup> variants imputed into GoDARTS scaffold	
		Start position	Stop position		N	Typed on Metachip N (%)	N (%)	Mean info	N (%)	Mean info	N (%)	Mean info	N (%)	Mean info
<i>NOTCH2</i>	1	120,437,717	120,615,600	S	145	39 (26.9)	108 (74.5)	0.809	106 (73.1)	0.813	112 (77.2)	0.785	105 (72.4)	0.809
<i>PROX1</i>	1	214,124,817	214,167,508	G	70	30 (42.9)	68 (97.1)	0.852	69 (98.6)	0.845	70 (100.0)	0.856	69 (98.6)	0.844
<i>GCKR</i>	2	27,386,798	28,670,981	G/B	1,862	373 (20.0)	1,837 (98.7)	0.892	1,841 (98.9)	0.896	1,838 (98.7)	0.899	1,826 (98.1)	0.892
<i>THADA</i>	2	43,449,384	43,893,878	B	669	108 (16.1)	652 (97.5)	0.865	646 (96.6)	0.863	652 (97.5)	0.874	648 (96.9)	0.863
<i>BCL11A</i>	2	60,557,030	60,601,376	B	60	16 (26.7)	59 (98.3)	0.816	58 (96.7)	0.830	60 (100.0)	0.806	60 (100.0)	0.817
<i>GRB14-COBL1</i>	2	165,499,547	165,732,418	G/B	360	95 (26.4)	349 (96.9)	0.861	352 (97.8)	0.865	353 (98.1)	0.859	353 (98.1)	0.869
<i>IRS1</i>	2	227,007,409	227,190,673	G	268	109 (40.7)	259 (96.6)	0.866	258 (96.3)	0.865	260 (97.0)	0.860	259 (96.6)	0.857
<i>PPARG</i>	3	12,207,460	12,470,239	B	361	95 (26.3)	353 (97.8)	0.851	352 (97.5)	0.857	355 (98.3)	0.863	347 (96.1)	0.852
<i>ADAMTS9</i>	3	64,691,378	64,733,440	S	78	24 (30.8)	78 (100.0)	0.869	78 (100.0)	0.875	77 (98.7)	0.887	75 (96.2)	0.869
<i>ADCY5</i>	3	122,976,417	123,207,012	G	354	114 (32.2)	348 (98.3)	0.817	346 (97.7)	0.833	348 (98.3)	0.839	339 (95.8)	0.824
<i>IGF2BP2</i>	3	185,337,787	185,596,778	G/S	322	93 (28.9)	317 (98.4)	0.840	315 (97.8)	0.846	317 (98.4)	0.856	314 (97.5)	0.836
<i>WFS1</i>	4	6,262,591	6,336,127	G	142	47 (33.1)	138 (97.2)	0.798	141 (99.3)	0.819	135 (95.1)	0.820	138 (97.2)	0.812
<i>ZBED3</i>	5	76,420,789	76,437,700	S	28	6 (21.4)	28 (100.0)	0.852	27 (96.4)	0.868	28 (100.0)	0.862	27 (96.4)	0.850
<i>CDKAL1</i>	6	20,393,906	21,191,928	G/S	981	236 (24.1)	969 (98.8)	0.852	952 (97.0)	0.849	956 (97.5)	0.854	967 (98.6)	0.851
<i>DGKB</i>	7	14,185,087	15,145,681	G/S	1,802	556 (30.9)	1,782 (98.9)	0.880	1,779 (98.7)	0.887	1,764 (97.9)	0.888	1,756 (97.4)	0.876
<i>JAZF1</i>	7	27,783,994	28,282,062	G/S	908	304 (33.5)	903 (99.4)	0.878	901 (99.2)	0.882	899 (99.0)	0.893	887 (97.7)	0.875
<i>GCK</i>	7	44,222,002	44,266,077	S/B	49	11 (22.4)	48 (98.0)	0.716	46 (93.9)	0.775	48 (98.0)	0.778	45 (91.8)	0.738
<i>KLF14</i>	7	130,421,158	130,468,190	S/B	54	19 (35.2)	52 (96.3)	0.861	51 (94.4)	0.878	51 (94.4)	0.867	51 (94.4)	0.867
<i>SLC30A8</i>	8	118,182,117	118,223,955	B	45	7 (15.6)	44 (97.8)	0.656	39 (86.7)	0.699	42 (93.3)	0.709	42 (93.3)	0.683
<i>GLIS3</i>	9	4,243,161	4,310,558	G	155	60 (38.7)	153 (98.7)	0.839	150 (96.8)	0.852	151 (97.4)	0.857	151 (97.4)	0.837
<i>CDKN2A-B</i>	9	21,950,408	22,159,982	G/S	230	45 (19.6)	225 (97.8)	0.796	222 (96.5)	0.795	226 (98.3)	0.804	216 (93.9)	0.797
<i>CDC123</i>	10	12,160,444	12,338,626	G	351	64 (18.2)	343 (97.7)	0.830	334 (95.2)	0.833	335 (95.4)	0.845	303 (86.3)	0.802
<i>HHEX-IDE</i>	10	94,200,768	94,498,975	G	662	205 (31.0)	654 (98.8)	0.903	647 (97.7)	0.909	638 (96.4)	0.905	639 (96.5)	0.897
<i>TCF7L2</i>	10	114,746,579	114,822,739	G	111	21 (18.9)	111 (100.0)	0.817	110 (99.1)	0.839	109 (98.2)	0.839	110 (99.1)	0.827
<i>KCNQ1</i>	11	2,443,937	2,943,115	G/S	918	298 (32.5)	908 (98.9)	0.831	899 (97.9)	0.853	906 (98.7)	0.861	889 (96.8)	0.826
<i>KCNJ11</i>	11	17,038,776	17,424,926	B	492	69 (14.0)	479 (97.4)	0.809	472 (95.9)	0.823	481 (97.8)	0.819	473 (96.1)	0.809

<i>CENTD2</i>	11	72,391,642	72,880,613	B	651	78 (12.0)	640 (98.3)	0.813	635 (97.5)	0.814	626 (96.2)	0.825	628 (96.5)	0.821
<i>MTNR1B</i>	11	92,667,046	92,725,521	G/S/B	124	50 (40.3)	124 (100.0)	0.873	124 (100.0)	0.879	121 (97.6)	0.900	124 (100.0)	0.887
<i>HMGA2</i>	12	66,164,516	66,303,735	G	209	88 (42.1)	205 (98.1)	0.861	199 (95.2)	0.891	205 (98.1)	0.882	201 (96.2)	0.873
<i>TSPAN8</i>	12	71,543,070	71,667,022	G	189	55 (29.1)	174 (92.1)	0.835	170 (89.9)	0.840	169 (89.4)	0.842	169 (89.4)	0.827
<i>HNF1A</i>	12	121,157,534	121,490,565	G/S	632	121 (19.1)	614 (97.2)	0.848	613 (97.0)	0.851	598 (94.6)	0.864	603 (95.4)	0.854
<i>C2CD4A-B</i>	15	62,098,986	62,520,663	S/B	742	194 (26.1)	736 (99.2)	0.903	739 (99.6)	0.909	737 (99.3)	0.912	716 (96.5)	0.900
<i>PRC1</i>	15	91,441,382	91,566,862	B	175	43 (24.6)	173 (98.9)	0.827	173 (98.9)	0.836	170 (97.1)	0.849	170 (97.1)	0.823
<i>FTO</i>	16	53,539,508	54,185,787	G/S	1,049	264 (25.2)	1,039 (99.0)	0.871	1,038 (99.0)	0.881	1,037 (98.9)	0.884	1,029 (98.1)	0.866
<i>HNF1B</i>	17	36,090,544	36,108,367	G	17	3 (17.6)	13 (76.5)	0.631	14 (82.4)	0.683	16 (94.1)	0.654	13 (76.5)	0.684
<i>MC4R</i>	18	57,727,146	58,094,636	G/S	535	138 (25.8)	528 (98.7)	0.889	533 (99.6)	0.896	529 (98.9)	0.899	526 (98.3)	0.888
<i>CILP2</i>	19	19,301,231	19,792,250	G	646	154 (23.8)	632 (97.8)	0.854	635 (98.3)	0.856	631 (97.7)	0.851	636 (98.5)	0.858
<i>GIPR</i>	19	46,136,486	46,408,041	G/S	362	49 (13.5)	362 (100.0)	0.807	355 (98.1)	0.801	356 (98.3)	0.823	352 (97.2)	0.815
<i>HNF4A</i>	20	43,038,558	43,058,096	S	17	3 (17.6)	17 (100.0)	0.746	17 (100.0)	0.760	17 (100.0)	0.780	17 (100.0)	0.722

<sup>a</sup>Priority for fine-mapping classified as: gold (G); silver (S); or bronze (B).

<sup>b</sup>High-quality variants defined by IMPUTEv2 info $\geq$ 0.4.

**Supplementary Table 6. Association signals achieving locus-wide significance ( $p_j < 10^{-5}$ ) in established T2D susceptibility loci.**

Locus	Index variant	Chr	Position (b37)	Risk allele	Other allele	MetaboChip GCTA joint model 27,206 cases and 57,574 controls			Validation GCTA joint model 19,662 cases and 115,140 controls			Combined GCTA joint model 46,868 cases and 172,714 controls	
						RAF	OR (95% CI)	$p_j$	RAF	OR (95% CI)	$p_j$	OR (95% CI)	$p_j$
<i>NOTCH2</i>	N/A <sup>a</sup>	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
<i>PROX1</i>	rs340874	1	214,159,256	C	T	0.520	1.07 (1.04-1.10)	$1.1 \times 10^{-7}$	0.573	1.07 (1.04-1.10)	$9.4 \times 10^{-7}$	1.07 (1.05-1.09)	$5.1 \times 10^{-13}$
<i>GCKR</i>	rs780094	2	27,741,237	C	T	0.611	1.08 (1.05-1.11)	$1.6 \times 10^{-9}$	0.637	1.04 (1.01-1.07)	0.0058	1.06 (1.04-1.08)	$3.4 \times 10^{-10}$
<i>THADA</i>	rs77981966	2	43,777,964	C	T	0.934	1.19 (1.13-1.26)	$1.7 \times 10^{-11}$	0.936	1.11 (1.05-1.18)	0.000098	1.16 (1.11-1.20)	$4.1 \times 10^{-14}$
<i>BCL11A</i>	rs243020	2	60,585,028	G	A	0.462	1.06 (1.03-1.09)	$4.6 \times 10^{-6}$	0.475	1.06 (1.03-1.09)	0.000030	1.06 (1.04-1.08)	$5.5 \times 10^{-10}$
<i>GRB14-COBL1</i>	rs75297654	2	165,545,615	C	T	0.876	1.16 (1.11-1.20)	$9.2 \times 10^{-14}$	0.857	1.05 (1.01-1.10)	0.0067	1.11 (1.08-1.14)	$6.3 \times 10^{-13}$
<i>IRS1</i>	rs2972156	2	227,117,778	G	C	0.621	1.11 (1.08-1.14)	$1.4 \times 10^{-15}$	0.606	1.07 (1.04-1.10)	$8.8 \times 10^{-7}$	1.09 (1.07-1.11)	$4.2 \times 10^{-20}$
<i>PPARG</i>	rs11712037	3	12,344,730	C	G	0.862	1.12 (1.08-1.16)	$3.7 \times 10^{-9}$	0.881	1.17 (1.12-1.22)	$2.0 \times 10^{-13}$	1.14 (1.11-1.17)	$1.7 \times 10^{-20}$
<i>ADAMTS9</i>	rs17676309	3	64,730,121	C	T	0.590	1.07 (1.05-1.10)	$7.5 \times 10^{-8}$	0.597	1.06 (1.04-1.09)	$7.6 \times 10^{-6}$	1.07 (1.05-1.09)	$2.8 \times 10^{-12}$
<i>ADCY5</i>	rs11708067	3	123,065,778	A	G	0.786	1.11 (1.08-1.15)	$5.1 \times 10^{-12}$	0.785	1.11 (1.08-1.15)	$1.3 \times 10^{-10}$	1.11 (1.09-1.14)	$4.2 \times 10^{-21}$
<i>IGF2BP2</i>	rs35510946	3	185,518,910	A	G	0.301	1.14 (1.10-1.17)	$3.9 \times 10^{-20}$	0.295	1.15 (1.12-1.18)	$2.7 \times 10^{-21}$	1.14 (1.12-1.16)	$1.1 \times 10^{-39}$
<i>WFS1</i>	rs10937721	4	6,306,763	C	G	0.580	1.08 (1.05-1.11)	$1.2 \times 10^{-9}$	0.572	1.09 (1.06-1.12)	$5.5 \times 10^{-10}$	1.09 (1.07-1.11)	$4.3 \times 10^{-18}$
<i>ZBED3</i>	rs7732130	5	76,435,004	G	A	0.278	1.09 (1.06-1.12)	$7.1 \times 10^{-10}$	0.270	1.06 (1.03-1.09)	0.00028	1.08 (1.05-1.10)	$2.4 \times 10^{-12}$
<i>CDKAL1</i>	rs35261542	6	20,675,792	A	C	0.280	1.15 (1.12-1.18)	$2.2 \times 10^{-24}$	0.239	1.18 (1.15-1.22)	$3.3 \times 10^{-28}$	1.17 (1.14-1.19)	$1.5 \times 10^{-50}$
<i>DGKB</i>	rs10276674	7	14,922,007	C	T	0.183	1.08 (1.04-1.11)	$4.5 \times 10^{-6}$	0.216	1.09 (1.05-1.12)	$1.3 \times 10^{-6}$	1.08 (1.06-1.11)	$2.8 \times 10^{-11}$
	rs1974620	7	15,065,467	T	C	0.519	1.06 (1.04-1.09)	$1.6 \times 10^{-6}$	0.515	1.05 (1.03-1.08)	0.00014	1.06 (1.04-1.08)	$1.0 \times 10^{-9}$
<i>JAZF1</i>	rs1513272	7	28,200,097	C	T	0.518	1.10 (1.07-1.12)	$4.8 \times 10^{-13}$	0.528	1.10 (1.08-1.13)	$2.4 \times 10^{-13}$	1.10 (1.08-1.12)	$7.8 \times 10^{-25}$
<i>GCK</i>	rs878521	7	44,255,643	A	G	0.235	1.10 (1.07-1.13)	$2.6 \times 10^{-10}$	0.227	1.04 (1.01-1.08)	0.010	1.07 (1.05-1.10)	$1.3 \times 10^{-10}$
<i>KLF14</i>	N/A <sup>a</sup>	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
<i>SLC30A8</i>	rs13266634	8	118,184,783	C	T	0.676	1.12 (1.09-1.15)	$1.1 \times 10^{-16}$	0.666	1.11 (1.08-1.15)	$6.4 \times 10^{-13}$	1.12 (1.09-1.14)	$5.0 \times 10^{-28}$
<i>GLIS3</i>	chr9:4294707:l	9	4,294,707	l	R	0.360	1.08 (1.05-1.11)	$1.5 \times 10^{-8}$	0.340	1.05 (1.02-1.08)	0.00026	1.07 (1.05-1.09)	$3.1 \times 10^{-11}$
<i>CDKN2B</i>	rs10811660	9	22,134,068	G	A	0.830	1.32 (1.27-1.38)	$2.4 \times 10^{-44}$	0.817	1.21 (1.17-1.26)	$2.6 \times 10^{-21}$	1.27 (1.23-1.30)	$1.1 \times 10^{-61}$
	rs10757283	9	22,134,172	T	C	0.437	1.14 (1.10-1.17)	$7.4 \times 10^{-18}$	0.436	1.11 (1.07-1.14)	$1.3 \times 10^{-10}$	1.12 (1.10-1.14)	$3.6 \times 10^{-26}$
<i>CDC123</i>	rs11257658	10	12,309,268	A	G	0.217	1.11 (1.08-1.14)	$1.6 \times 10^{-11}$	0.232	1.08 (1.04-1.11)	$5.6 \times 10^{-6}$	1.09 (1.07-1.12)	$1.2 \times 10^{-15}$
<i>HHEX</i>	rs11187140	10	94,466,910	G	A	0.632	1.10 (1.08-1.13)	$5.5 \times 10^{-14}$	0.609	1.13 (1.10-1.17)	$1.4 \times 10^{-19}$	1.12 (1.10-1.14)	$1.5 \times 10^{-31}$
<i>TCF7L2</i>	rs7903146	10	114,758,349	T	C	0.260	1.38 (1.35-1.42)	$3.1 \times 10^{-117}$	0.294	1.33 (1.29-1.37)	$2.1 \times 10^{-80}$	1.36 (1.33-1.38)	$2.7 \times 10^{-195}$
<i>KCNQ1</i>	chr11:2692322:D	11	2,692,322	D	R	0.374	1.08 (1.05-1.10)	$3.5 \times 10^{-8}$	0.413	1.09 (1.06-1.12)	$1.2 \times 10^{-8}$	1.08 (1.06-1.10)	$2.3 \times 10^{-15}$
	rs2283220	11	2,755,548	A	G	0.661	1.06 (1.03-1.09)	0.000016	0.710	1.05 (1.02-1.08)	0.0031	1.06 (1.03-1.08)	$2.4 \times 10^{-7}$
	rs2237895	11	2,857,194	C	A	0.428	1.08 (1.05-1.11)	$6.6 \times 10^{-7}$	0.433	1.07 (1.03-1.10)	$2.8 \times 10^{-4}$	1.07 (1.05-1.10)	$5.3 \times 10^{-10}$
	rs74046911	11	2,858,636	C	T	0.951	1.32 (1.24-1.40)	$1.7 \times 10^{-17}$	0.943	1.25 (1.17-1.34)	$4.8 \times 10^{-10}$	1.29 (1.23-1.35)	$9.6 \times 10^{-26}$
	rs458069	11	2,858,800	G	C	0.707	1.06 (1.03-1.10)	0.00026	0.707	1.07 (1.03-1.11)	0.00085	1.06 (1.04-1.09)	$1.0 \times 10^{-6}$
<i>KCNJ11</i>	rs5215	11	17,408,630	C	T	0.389	1.08 (1.05-1.11)	$1.3 \times 10^{-9}$	0.386	1.06 (1.03-1.09)	0.000034	1.07 (1.05-1.09)	$3.7 \times 10^{-13}$
<i>CENTD2</i>	chr11:72460930:l	11	72,460,930	R	l	0.823	1.10 (1.06-1.13)	$5.9 \times 10^{-8}$	0.826	1.10 (1.06-1.14)	$2.4 \times 10^{-7}$	1.10 (1.07-1.12)	$6.7 \times 10^{-14}$
<i>MTNR1B</i>	rs10830963	11	92,708,710	G	C	0.283	1.10 (1.07-1.13)	$7.9 \times 10^{-12}$	0.248	1.07 (1.03-1.10)	0.000072	1.09 (1.06-1.11)	$8.5 \times 10^{-15}$
<i>HMGGA2</i>	rs2583941	12	66,204,598	A	G	0.090	1.13 (1.08-1.18)	$6.0 \times 10^{-8}$	0.080	1.10 (1.05-1.15)	0.000048	1.11 (1.08-1.15)	$1.6 \times 10^{-11}$
<i>TSPAN8</i>	rs7961581	12	71,663,102	C	T	0.265	1.07 (1.04-1.10)	$1.4 \times 10^{-6}$	0.270	1.04 (1.01-1.07)	0.012	1.06 (1.03-1.08)	$1.8 \times 10^{-7}$

<i>HNF1A</i>	rs1169288	12	121,416,650	C	A	0.334	1.10 (1.07-1.13)	5.4x10 <sup>-10</sup>	0.316	1.08 (1.05-1.12)	2.8x10 <sup>-6</sup>	1.09 (1.07-1.12)	8.1x10 <sup>-15</sup>
	rs1800574	12	121,416,864	T	C	0.027	1.21 (1.11-1.31)	5.2x10 <sup>-6</sup>	0.020	1.23 (1.12-1.35)	0.000026	1.22 (1.14-1.29)	5.1x10 <sup>-10</sup>
	chr12:121440833:D	12	121,440,833	R	D	0.416	1.06 (1.03-1.09)	0.000028	0.382	1.08 (1.04-1.11)	2.5x10 <sup>-6</sup>	1.07 (1.05-1.09)	2.9x10 <sup>-10</sup>
<i>C2CD4B</i>	rs7161785	15	62,395,224	G	C	0.555	1.04 (1.02-1.07)	0.00068	0.551	1.07 (1.04-1.10)	8.2x10 <sup>-7</sup>	1.06 (1.04-1.08)	4.9x10 <sup>-9</sup>
<i>PRC1</i>	rs3803563	15	91,531,352	A	C	0.175	1.11 (1.07-1.15)	2.2x10 <sup>-10</sup>	0.177	1.05 (1.02-1.09)	0.0049	1.08 (1.06-1.11)	5.6x10 <sup>-11</sup>
<i>FTO</i>	rs9927317	16	53,820,996	G	C	0.396	1.14 (1.11-1.17)	6.8x10 <sup>-25</sup>	0.399	1.13 (1.10-1.16)	1.2x10 <sup>-19</sup>	1.14 (1.12-1.16)	7.9x10 <sup>-43</sup>
<i>HNF1B</i>	rs4430796	17	36,098,040	G	A	0.455	1.09 (1.07-1.12)	5.2x10 <sup>-12</sup>	0.482	1.08 (1.05-1.11)	2.0x10 <sup>-7</sup>	1.09 (1.07-1.11)	7.8x10 <sup>-18</sup>
<i>MC4R</i>	chr18:57739289:D	18	57,739,289	D	R	0.234	1.05 (1.02-1.09)	0.00079	0.254	1.07 (1.03-1.10)	0.000059	1.06 (1.04-1.08)	1.9x10 <sup>-7</sup>
	rs17066842	18	58,040,624	G	A	0.961	1.13 (1.06-1.21)	0.00033	0.948	1.11 (1.04-1.19)	0.0012	1.12 (1.07-1.17)	1.4x10 <sup>-6</sup>
<i>CILP2</i>	rs72999033	19	19,366,632	T	C	0.069	1.20 (1.15-1.26)	6.5x10 <sup>-14</sup>	0.065	1.10 (1.04-1.16)	0.00043	1.16 (1.12-1.20)	1.8x10 <sup>-15</sup>
<i>GIPR</i>	rs4399645	19	46,166,073	T	C	0.395	1.07 (1.04-1.10)	4.4x10 <sup>-7</sup>	0.441	1.05 (1.01-1.08)	0.0046	1.06 (1.04-1.08)	1.4x10 <sup>-8</sup>
	rs2238689	19	46,178,661	C	T	0.425	1.09 (1.07-1.12)	9.7x10 <sup>-12</sup>	0.424	1.07 (1.04-1.10)	9.0x10 <sup>-6</sup>	1.08 (1.06-1.11)	8.3x10 <sup>-16</sup>
<i>HNF4A</i>	rs1800961	20	43,042,364	T	C	0.034	1.16 (1.09-1.24)	0.000011	0.041	1.16 (1.08-1.25)	0.000051	1.16 (1.10-1.22)	2.3x10 <sup>-9</sup>

Each association signal was represented by an index variant in the GCTA-COJO joint regression model on the basis of: (i) summary statistics from a combined meta-analysis of 46,868 cases and 172,714 controls of European ancestry; and (ii) reference genotype data from GoDARTS (3,298 cases and 3,708 controls of European ancestry from the UK) to approximate LD across fine-mapping regions.

Chr: chromosome. RAF: risk allele frequency. OR: odds-ratio for risk allele. CI: confidence interval.

<sup>a</sup>No variants achieved locus-wide significance at the *NOTCH2* and *KLF14* loci.

**Supplementary Table 7. Comparison of summary statistics for association signals in established T2D susceptibility loci obtained from meta-analysis of MetaboChip studies: (i) unconditional; (ii) GCTA joint model using GoDARTS as reference; and (iii) exact conditioning after adjusting for all other index variants in the fine-mapping region.**

Locus	Index variant	Chr	Position (b37)	Risk allele	Other allele	RAF	MetaboChip unconditional meta-analysis		MetaboChip GCTA joint model GoDARTS reference study		MetaboChip exact conditional meta-analysis	
							OR (95% CI)	p-value	OR (95% CI)	p-value	OR (95% CI)	p-value
<i>DGKB</i>	rs10276674	7	14,922,007	C	T	0.183	1.07 (1.04-1.11)	0.000013	1.08 (1.04-1.11)	4.5x10 <sup>-6</sup>	1.07 (1.04-1.11)	0.000020
	rs1974620	7	15,065,467	T	C	0.519	1.06 (1.04-1.09)	9.0x10 <sup>-7</sup>	1.06 (1.04-1.09)	1.6x10 <sup>-6</sup>	1.06 (1.04-1.09)	1.4x10 <sup>-6</sup>
<i>CDKN2B</i>	rs10811660	9	22,134,068	G	A	0.830	1.21 (1.17-1.25)	9.7x10 <sup>-28</sup>	1.32 (1.27-1.38)	2.4x10 <sup>-44</sup>	1.31 (1.27-1.37)	7.0x10 <sup>-43</sup>
	rs10757283	9	22,134,172	T	C	0.437	1.03 (1.01-1.06)	0.015	1.14 (1.10-1.17)	7.4x10 <sup>-18</sup>	1.14 (1.11-1.18)	2.8x10 <sup>-19</sup>
<i>KCNQ1</i>	chr11:2692322:D	11	2,692,322	D	R	0.374	1.08 (1.05-1.11)	2.4x10 <sup>-9</sup>	1.08 (1.05-1.10)	3.5x10 <sup>-8</sup>	1.09 (1.06-1.12)	5.2x10 <sup>-10</sup>
	rs2283220	11	2,755,548	A	G	0.661	1.05 (1.03-1.08)	0.00013	1.06 (1.03-1.09)	0.000016	1.05 (1.02-1.08)	0.00032
	rs2237895	11	2,857,194	C	A	0.428	1.12 (1.09-1.15)	8.7x10 <sup>-19</sup>	1.08 (1.05-1.11)	6.6x10 <sup>-7</sup>	1.07 (1.04-1.11)	0.000013
	rs74046911	11	2,858,636	C	T	0.951	1.32 (1.24-1.40)	2.3x10 <sup>-19</sup>	1.32 (1.24-1.40)	1.7x10 <sup>-17</sup>	1.33 (1.24-1.42)	5.9x10 <sup>-18</sup>
<i>HNF1A</i>	rs458069	11	2,858,800	G	C	0.707	1.07 (1.04-1.10)	1.0x10 <sup>-6</sup>	1.06 (1.03-1.10)	0.00026	1.06 (1.02-1.09)	0.0017
	rs1169288	12	121,416,650	C	A	0.334	1.06 (1.03-1.09)	0.000014	1.10 (1.07-1.13)	5.4x10 <sup>-10</sup>	1.09 (1.06-1.12)	9.3x10 <sup>-9</sup>
	rs1800574	12	121,416,864	T	C	0.027	1.15 (1.07-1.25)	0.00039	1.21 (1.11-1.31)	5.2x10 <sup>-6</sup>	1.21 (1.11-1.31)	5.4x10 <sup>-6</sup>
<i>MC4R</i>	chr12:121440833:D	12	121,440,833	R	D	0.416	1.01 (0.99-1.04)	0.29	1.06 (1.03-1.09)	0.000028	1.06 (1.03-1.09)	0.00017
	chr18:57739289:D	18	57,739,289	D	R	0.234	1.06 (1.02-1.09)	0.00044	1.05 (1.02-1.09)	0.00079	1.05 (1.02-1.09)	0.00091
	rs17066842	18	58,040,624	G	A	0.961	1.13 (1.06-1.21)	0.00030	1.13 (1.06-1.21)	0.00033	1.12 (1.05-1.20)	0.00064
<i>GIPR</i>	rs4399645	19	46,166,073	T	C	0.395	1.05 (1.02-1.08)	0.00030	1.07 (1.04-1.10)	4.4x10 <sup>-7</sup>	1.06 (1.04-1.09)	5.7x10 <sup>-6</sup>
	rs2238689	19	46,178,661	C	T	0.425	1.08 (1.05-1.10)	1.7x10 <sup>-8</sup>	1.09 (1.07-1.12)	9.7x10 <sup>-12</sup>	1.09 (1.06-1.12)	2.5x10 <sup>-10</sup>

Each association signal was represented by an index variant in the GCTA-COJO joint regression model on the basis of: (i) summary statistics from the meta-analysis of MetaboChip studies in 27,206 cases and 57,574 controls of European ancestry; and (ii) reference genotype data from GoDARTS (3,298 cases and 3,708 controls of European ancestry from the UK) to approximate LD across fine-mapping regions.

Chr: chromosome. RAF: risk allele frequency. OR: odds-ratio for risk allele. CI: confidence interval.

**Supplementary Table 8. Summary of 99% credible sets for association signals at established T2D susceptibility.**

Locus	Index variant	Chr	Position (b37)	Risk allele	Other allele	RAF	p-value	OR (95% CI)	99% credible set			
									SNPs	Interval (bp)	Interval start (bp)	Interval stop (bp)
<i>NOTCH2</i>	N/A	1	N/A	N/A	N/A	N/A	N/A	N/A	108	116,782	120,437,718	120,554,499
<i>PROX1</i>	rs340874	1	214,159,256	C	T	0.520	1.1x10 <sup>-7</sup>	1.07 (1.04-1.10)	19	17,970	214,145,706	214,163,675
<i>GCKR</i>	rs780094	2	27,741,237	C	T	0.611	8.5x10 <sup>-10</sup>	1.08 (1.06-1.11)	13	154,775	27,598,097	27,752,871
<i>THADA</i>	rs77981966	2	43,777,964	C	T	0.934	1.7x10 <sup>-11</sup>	1.19 (1.13-1.26)	247	403,194	43,451,957	43,855,150
<i>BCL11A</i>	rs243020	2	60,585,028	G	A	0.462	2.5x10 <sup>-6</sup>	1.06 (1.04-1.09)	35	42,171	60,559,206	60,601,376
<i>GRB14-COBL1</i>	rs75297654	2	165,545,615	C	T	0.876	8.9x10 <sup>-14</sup>	1.16 (1.11-1.20)	24	53,691	165,501,849	165,555,539
<i>IRS1</i>	rs2972156	2	227,117,778	G	C	0.621	1.3x10 <sup>-15</sup>	1.11 (1.08-1.14)	65	80,232	227,083,411	227,163,642
<i>PPARG</i>	rs11712037	3	12,344,730	C	G	0.862	4.6x10 <sup>-8</sup>	1.11 (1.07-1.15)	27	67,173	12,329,783	12,396,955
<i>ADAMTS9</i>	rs17676309	3	64,730,121	C	T	0.590	1.2x10 <sup>-7</sup>	1.07 (1.04-1.10)	27	30,677	64,699,445	64,730,121
<i>ADCY5</i>	rs11708067	3	123,065,778	A	G	0.786	1.1x10 <sup>-13</sup>	1.12 (1.09-1.16)	17	42,051	123,054,770	123,096,820
<i>IGF2BP2</i>	rs35510946	3	185,518,910	A	G	0.301	3.7x10 <sup>-20</sup>	1.14 (1.10-1.17)	50	42,317	185,495,320	185,537,636
<i>WFS1</i>	rs10937721	4	6,306,763	C	G	0.580	7.6x10 <sup>-11</sup>	1.09 (1.06-1.12)	82	42,179	6,264,585	6,306,763
<i>ZBED3</i>	rs7732130	5	76,435,004	G	A	0.278	6.4x10 <sup>-10</sup>	1.09 (1.06-1.12)	5	10,056	76,424,949	76,435,004
<i>CDKAL1</i>	rs35261542	6	20,675,792	A	C	0.280	9.6x10 <sup>-23</sup>	1.15 (1.12-1.18)	8	30,073	20,673,880	20,703,952
<i>DGKB</i>	rs10276674	7	14,922,007	C	T	0.183	0.000020	1.07 (1.04-1.11)	4799	960,535	14,185,147	15,145,681
	rs1974620	7	15,065,467	T	C	0.519	1.4x10 <sup>-6</sup>	1.06 (1.04-1.09)	266	953,983	14,187,402	15,141,384
<i>JAZF1</i>	rs1513272	7	28,200,097	C	T	0.518	3.9x10 <sup>-12</sup>	1.09 (1.07-1.12)	16	58,195	28,174,263	28,232,457
<i>GCK</i>	rs878521	7	44,255,643	A	G	0.235	1.2x10 <sup>-9</sup>	1.09 (1.06-1.13)	18	41,459	44,223,721	44,265,179
<i>KLF14</i>	N/A	7	N/A	N/A	N/A	N/A	N/A	N/A	171	46,857	130,421,159	130,468,015
<i>SLC30A8</i>	rs13266634	8	118,184,783	C	T	0.676	1.3x10 <sup>-18</sup>	1.13 (1.10-1.16)	6	33,133	118,184,783	118,217,915
<i>GLIS3</i>	chr9:4294707:I	9	4,294,707	I	R	0.360	6.5x10 <sup>-8</sup>	1.07 (1.05-1.10)	10	15,453	4,283,137	4,298,589
<i>CDKN2A-B</i>	rs10811660	9	22,134,068	G	A	0.830	7.0x10 <sup>-43</sup>	1.32 (1.27-1.37)	6	1,397	22,132,698	22,134,094
	rs10757283	9	22,134,172	T	C	0.437	2.8x10 <sup>-19</sup>	1.14 (1.11-1.18)	5	1,007	22,133,645	22,134,651
<i>CDC123</i>	rs11257658	10	12,309,268	A	G	0.217	2.9x10 <sup>-10</sup>	1.10 (1.07-1.14)	12	77,391	12,250,620	12,328,010
<i>HHEX</i>	rs11187140	10	94,466,910	G	A	0.632	1.7x10 <sup>-14</sup>	1.11 (1.08-1.14)	40	128,798	94,361,377	94,490,174
<i>TCF7L2</i>	rs7903146	10	114,758,349	T	C	0.260	5.8x10 <sup>-120</sup>	1.39 (1.35-1.43)	3	4,279	114,754,071	114,758,349
<i>KCNQ1</i>	chr11:2692322:D	11	2,692,322	D	R	0.374	5.2x10 <sup>-10</sup>	1.09 (1.06-1.11)	12	32,660	2,691,471	2,724,130
	rs2283220	11	2,755,548	A	G	0.661	0.00032	1.05 (1.02-1.08)	2258	498,068	2,444,732	2,942,799
	rs2237895	11	2,857,194	C	A	0.428	0.000013	1.07 (1.04-1.11)	680	496,351	2,446,432	2,942,782
	rs74046911	11	2,858,636	C	T	0.951	5.9x10 <sup>-18</sup>	1.33 (1.25-1.42)	3	197	2,858,440	2,858,636
	rs458069	11	2,858,800	G	C	0.707	0.0017	1.06 (1.02-1.09)	2309	498,706	2,444,094	2,942,799
<i>KCNJ11</i>	rs5215	11	17,408,630	C	T	0.389	1.5x10 <sup>-10</sup>	1.09 (1.06-1.11)	21	53,874	17,368,013	17,421,886
<i>CENTD2</i>	chr11:72460930:I	11	72,460,930	R	I	0.823	8.8x10 <sup>-9</sup>	1.10 (1.07-1.14)	27	380,747	72,429,579	72,810,325

<i>MTNR1B</i>	rs10830963	11	92,708,710	G	C	0.283	$2.9 \times 10^{-12}$	1.10 (1.07-1.13)	1	1	92,708,710	92,708,710
<i>HMG2</i>	rs2583941	12	66,204,598	A	G	0.090	$7.5 \times 10^{-9}$	1.13 (1.09-1.18)	72	95,454	66,165,471	66,260,924
<i>TSPAN8</i>	rs7961581	12	71,663,102	C	T	0.265	$1.1 \times 10^{-6}$	1.07 (1.04-1.10)	76	122,817	71,543,370	71,666,186
<i>HNF1A</i>	rs1169288	12	121,416,650	C	A	0.334	$9.4 \times 10^{-9}$	1.09 (1.06-1.12)	27	99,112	121,380,544	121,479,655
	rs1800574	12	121,416,864	T	C	0.027	$5.4 \times 10^{-6}$	1.21 (1.11-1.31)	899	332,274	121,157,611	121,489,884
	chr12:121440833:D	12	121,440,833	R	D	0.416	0.00017	1.06 (1.03-1.09)	1427	332,888	121,157,611	121,490,498
<i>C2CD4B</i>	rs7161785	15	62,395,224	G	C	0.555	0.00058	1.05 (1.02-1.07)	1851	421,123	62,099,341	62,520,463
<i>PRC1</i>	rs3803563	15	91,531,352	A	C	0.175	$3.6 \times 10^{-10}$	1.11 (1.07-1.14)	51	59,204	91,502,383	91,561,586
<i>FTO</i>	rs9927317	16	53,820,996	G	C	0.396	$1.7 \times 10^{-24}$	1.14 (1.11-1.17)	72	28,560	53,799,507	53,828,066
<i>HNF1B</i>	rs4430796	17	36,098,040	G	A	0.455	$6.3 \times 10^{-12}$	1.09 (1.07-1.12)	7	5,791	36,097,775	36,103,565
<i>MC4R</i>	chr18:57739289:D	18	57,739,289	D	R	0.234	0.00091	1.05 (1.02-1.08)	1343	367,192	57,727,147	58,094,338
	rs17066842	18	58,040,624	G	A	0.961	0.00064	1.12 (1.05-1.20)	1275	367,490	57,727,147	58,094,636
<i>CILP2</i>	rs72999033	19	19,366,632	T	C	0.069	$5.3 \times 10^{-13}$	1.19 (1.14-1.25)	29	350,425	19,366,632	19,717,056
<i>GIPR</i>	rs4399645	19	46,166,073	T	C	0.395	$5.7 \times 10^{-6}$	1.06 (1.03-1.09)	704	270,315	46,137,712	46,408,026
	rs2238689	19	46,178,661	C	T	0.425	$2.5 \times 10^{-10}$	1.09 (1.06-1.11)	26	20,506	46,158,156	46,178,661
<i>HNF4A</i>	rs1800961	20	43,042,364	T	C	0.034	$7.1 \times 10^{-6}$	1.16 (1.09-1.24)	17	16,286	43,041,546	43,057,831

Association summary statistics and credible set construction are based on the meta-analysis of Metabochip studies in 27,206 cases and 57,574 controls of European ancestry. In loci with multiple signals of association, results are presented from exact conditional analysis after adjusting for all other index variants in the fine-mapping region. In loci with a single signal of association, results are presented from unconditional analysis. Chr: chromosome. RAF: risk allele frequency. OR: odds-ratio for risk allele. CI: confidence interval.

**Supplementary Table 9. Membership of 99% credible sets containing no more than ten variants driving distinct association signals at established T2D susceptibility loci.**

Locus	Index variant	99% credible set variants								
		Variant	Chr	Position (b37)	Risk allele	Other allele	RAF	p-value	OR (95% CI)	Posterior probability of driving association signal
<i>MTNR1B</i>	rs10830963	rs10830963	11	92,708,710	G	C	0.283	2.9x10 <sup>-12</sup>	1.10 (1.07-1.13)	99.8%
<i>TCF7L2</i>	rs7903146	rs7903146	10	114,758,349	T	C	0.260	5.8x10 <sup>-120</sup>	1.39 (1.35-1.43)	77.6%
		rs35198068	10	114,754,784	C	T	0.261	3.4x10 <sup>-119</sup>	1.39 (1.35-1.43)	11.9%
		rs34872471	10	114,754,071	C	T	0.261	5.3x10 <sup>-119</sup>	1.39 (1.35-1.43)	10.4%
<i>KCNQ1</i>	rs74046911	rs74046911	11	2,858,636	C	T	0.951	5.9x10 <sup>-18</sup>	1.33 (1.25-1.42)	84.7%
		rs2237897	11	2,858,546	C	T	0.951	5.4x10 <sup>-17</sup>	1.32 (1.24-1.41)	10.0%
		rs2237896	11	2,858,440	G	A	0.952	1.1x10 <sup>-16</sup>	1.32 (1.24-1.41)	5.0%
<i>ZBED3</i>	rs7732130	rs7732130	5	76,435,004	G	A	0.278	6.4x10 <sup>-10</sup>	1.09 (1.06-1.12)	46.1%
		rs6878122	5	76,427,311	G	A	0.278	6.6x10 <sup>-10</sup>	1.09 (1.06-1.12)	44.9%
		rs4457054	5	76,425,060	G	C	0.268	7.8x10 <sup>-9</sup>	1.09 (1.06-1.12)	4.2%
		rs7708285	5	76,425,867	G	A	0.268	1.1x10 <sup>-8</sup>	1.09 (1.06-1.12)	3.0%
		rs4457053	5	76,424,949	G	A	0.277	2.0x10 <sup>-8</sup>	1.08 (1.05-1.11)	1.7%
<i>CDKN2A-B</i>	rs10757283	rs10757283	9	22,134,172	T	C	0.437	2.8x10 <sup>-19</sup>	1.14 (1.11-1.18)	52.7%
		rs10217762	9	22,133,645	C	T	0.435	6.7x10 <sup>-19</sup>	1.14 (1.11-1.18)	21.8%
		rs10757282	9	22,133,984	C	T	0.436	1.3x10 <sup>-18</sup>	1.14 (1.11-1.18)	11.1%
		rs7019437	9	22,134,302	G	C	0.421	1.8x10 <sup>-18</sup>	1.14 (1.11-1.18)	8.4%
		rs7019778	9	22,134,651	C	A	0.440	2.6x10 <sup>-18</sup>	1.14 (1.11-1.17)	5.8%
<i>SLC30A8</i>	rs13266634	rs13266634	8	118,184,783	C	T	0.676	1.3x10 <sup>-18</sup>	1.13 (1.10-1.16)	29.5%
		rs3802177	8	118,185,025	G	A	0.676	1.4x10 <sup>-18</sup>	1.13 (1.10-1.16)	25.7%
		rs11558471	8	118,185,733	A	G	0.670	1.6x10 <sup>-18</sup>	1.13 (1.10-1.16)	24.1%
		rs35859536	8	118,191,475	C	T	0.675	2.3x10 <sup>-18</sup>	1.13 (1.10-1.16)	16.6%
		rs9650069	8	118,204,020	C	T	0.680	1.3x10 <sup>-17</sup>	1.13 (1.10-1.16)	3.1%
		rs4300038	8	118,217,915	G	A	0.677	3.9x10 <sup>-17</sup>	1.12 (1.09-1.16)	1.1%
<i>CDKN2A-B</i>	rs10811660	rs10811661	9	22,134,094	T	C	0.827	3.2x10 <sup>-43</sup>	1.32 (1.27-1.37)	54.5%
		rs10811660	9	22,134,068	G	A	0.830	7.0x10 <sup>-43</sup>	1.32 (1.27-1.37)	24.1%
		rs10965246	9	22,132,698	T	C	0.823	2.3x10 <sup>-42</sup>	1.32 (1.27-1.37)	8.2%
		rs10965248	9	22,132,878	T	C	0.823	2.5x10 <sup>-42</sup>	1.32 (1.26-1.37)	7.1%
		rs10965250	9	22,133,284	G	A	0.829	4.9x10 <sup>-42</sup>	1.31 (1.26-1.37)	3.8%
		rs10965247	9	22,132,729	A	G	0.823	1.4x10 <sup>-41</sup>	1.31 (1.26-1.37)	1.3%



<i>HNF1B</i>	rs4430796	rs4430796	17	36,098,040	G	A	0.455	$6.3 \times 10^{-12}$	1.09 (1.07-1.12)	31.3%
		rs11651052	17	36,102,381	A	G	0.449	$1.1 \times 10^{-11}$	1.09 (1.06-1.12)	19.6%
		rs8064454	17	36,101,586	A	C	0.450	$1.2 \times 10^{-11}$	1.09 (1.06-1.12)	16.5%
		rs11263763	17	36,103,565	G	A	0.450	$1.5 \times 10^{-11}$	1.09 (1.06-1.12)	13.2%
		rs11263761	17	36,097,775	G	A	0.465	$1.9 \times 10^{-11}$	1.09 (1.06-1.12)	10.5%
		rs11651755	17	36,099,840	C	T	0.462	$3.3 \times 10^{-11}$	1.09 (1.06-1.12)	6.2%
		rs10908278	17	36,099,952	T	A	0.443	$9.3 \times 10^{-11}$	1.09 (1.06-1.12)	2.3%
<i>CDKAL1</i>	rs35261542	rs35261542	6	20,675,792	A	C	0.280	$9.6 \times 10^{-23}$	1.15 (1.12-1.18)	24.8%
		rs9368222	6	20,686,996	A	C	0.280	$1.1 \times 10^{-22}$	1.15 (1.12-1.18)	21.6%
		rs7451008	6	20,673,880	C	T	0.280	$1.6 \times 10^{-22}$	1.15 (1.12-1.18)	15.9%
		chr6:20676414:I	6	20,676,414	I	R	0.283	$2.2 \times 10^{-22}$	1.15 (1.11-1.19)	11.8%
		rs9348441	6	20,680,678	A	T	0.279	$2.8 \times 10^{-22}$	1.15 (1.11-1.18)	9.0%
		rs7756992	6	20,679,709	G	A	0.284	$3.2 \times 10^{-22}$	1.14 (1.11-1.18)	7.9%
		rs7766070	6	20,686,573	A	C	0.282	$3.8 \times 10^{-22}$	1.14 (1.11-1.18)	6.4%
		rs6931514	6	20,703,952	A	C	0.280	$1.1 \times 10^{-22}$	1.15 (1.12-1.18)	2.0%
<i>GLIS3</i>	chr9:4294707:I	chr9:4294707:I	9	4,294,707	I	R	0.360	$6.5 \times 10^{-8}$	1.07 (1.05-1.10)	56.3%
		rs10974438	9	4,291,928	C	A	0.360	$1.6 \times 10^{-7}$	1.07 (1.04-1.10)	23.5%
		rs6476839	9	4,290,823	T	A	0.418	$9.5 \times 10^{-7}$	1.07 (1.04-1.09)	4.1%
		rs10116772	9	4,290,541	A	C	0.417	$9.6 \times 10^{-7}$	1.07 (1.04-1.09)	4.0%
		rs4237150	9	4,290,085	C	G	0.418	$1.0 \times 10^{-6}$	1.07 (1.04-1.09)	3.9%
		rs10758593	9	4,292,083	A	G	0.415	$1.1 \times 10^{-6}$	1.06 (1.04-1.09)	3.6%
		rs1574285	9	4,283,137	G	T	0.413	$2.4 \times 10^{-6}$	1.06 (1.04-1.09)	1.7%
		rs10758594	9	4,295,583	A	G	0.433	$5.0 \times 10^{-6}$	1.06 (1.03-1.09)	0.8%
		rs35338539	9	4,298,589	A	G	0.355	$5.7 \times 10^{-6}$	1.06 (1.04-1.09)	0.8%
rs10814915	9	4,290,544	T	C	0.434	$8.4 \times 10^{-6}$	1.06 (1.03-1.09)	0.5%		

Association summary statistics and credible set construction are based on the meta-analysis of Metabochip studies in 27,206 cases and 57,574 controls of European ancestry. In loci with multiple signals of association, results are presented from exact conditional analysis after adjusting for all other index variants in the fine-mapping region. In loci with a single signal of association, results are presented from unconditional analysis.

Chr: chromosome. RAF: risk allele frequency. OR: odds-ratio for risk allele. CI: confidence interval.

**Supplementary Table 10. Coding variants attaining at least 5% posterior probability ( $\pi_c$ ) of driving association signals across fine-mapping regions.**

Locus	Index variant for association signal	Coding variant	Gene	Substitution	Chr	Position (b37)	Risk allele	Other allele	RAF	p-value	OR (95% CI)	Posterior probability ( $\pi_c$ )
<i>HNF4A</i>	rs1800961	rs1800961	<i>HNF4A</i>	p.T139I	20	43,042,364	T	C	0.034	7.1x10 <sup>-6</sup>	1.16 (1.09-1.24)	97.4%
<i>HNF1A</i>	rs1169288	rs1169288	<i>HNF1A</i>	p.I27L	12	121,416,650	C	A	0.334	9.4x10 <sup>-9</sup>	1.09 (1.06-1.12)	75.5%
<i>HNF1A</i>	rs1800574	rs1800574	<i>HNF1A</i>	p.A98V	12	121,416,864	T	C	0.027	5.4x10 <sup>-6</sup>	1.21 (1.11-1.31)	34.0%
<i>SLC30A8</i>	rs13266634	rs13266634	<i>SLC30A8</i>	p.R325W	8	118,184,783	C	T	0.676	1.3x10 <sup>-18</sup>	1.13 (1.10-1.16)	29.5%
<i>KCNJ11-ABCC8</i>	rs5215	rs5215	<i>KCNJ11</i>	p.V337I	11	17,408,630	C	T	0.389	1.5x10 <sup>-10</sup>	1.09 (1.06-1.11)	15.1%
<i>KCNJ11-ABCC8</i>	rs5215	rs5219	<i>KCNJ11</i>	p.E23K	11	17,409,572	T	C	0.389	1.8x10 <sup>-10</sup>	1.09 (1.06-1.11)	12.9%
<i>KCNJ11-ABCC8</i>	rs5215	rs757110	<i>ABCC8</i>	p.A1369S	11	17,418,477	C	A	0.389	2.5x10 <sup>-10</sup>	1.09 (1.06-1.11)	9.0%
<i>GCKR</i>	rs780094	rs1260326	<i>GCKR</i>	p.P446L	2	27,730,940	C	T	0.605	3.7x10 <sup>-9</sup>	1.08 (1.05-1.11)	5.5%
<i>PPARG</i>	rs11712037	rs1801282	<i>PPARG</i>	p.P12A	3	12,393,125	C	G	0.862	8.0x10 <sup>-8</sup>	1.11 (1.07-1.15)	5.2%

Association summary statistics are based on the meta-analysis of Metabochip studies in 27,206 cases and 57,574 controls of European ancestry. In loci with multiple signals of association, results are presented from exact conditional analysis after adjusting for all other index variants in the fine-mapping region.

In loci with a single signal of association, results are presented from unconditional analysis.

Chr: chromosome. RAF: risk allele frequency. OR: odds-ratio for risk allele. CI: confidence interval.

**Supplementary Table 11. DNA-binding regulatory protein ChIP-seq data.**

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ARID3A	EGR1	HDAC8	NFATC1	RFX5	TAL1
ATF1	ELF1	HMGN3	NFE2	RPC155	TBL1XR1
ATF2	ELK1	HNF4A	NFIC	RUNX3	TBP
ATF3	ELK4	HNF4G	NFYA	RXRA	TCF12
BACH1	EP300	HSF1	NFYB	SAP30	TCF3
BATF	ESR1	IKZF1	NKX2.2	SETDB1	TCF7L2
BCL11A	ESRRA	IRF1	NKX6_1	SIN3A	TEAD4
BCL3	ETS1	IRF3	NR2C2	SIN3AK20	TFAP2A
BCLAF1	EZH2	IRF4	NR2F2	SIRT6	TFAP2C
BDP1	FAM48A	JUN	NR3C1	SIX5	THAP1
BHLHE40	FOS	JUNB	NRF1	SMARCA4	TRIM28
BRCA1	FOSL1	JUND	PAX5	SMARCB1	UBTF
BRF1	FOSL2	KAP1	PBX3	SMARCC1	USF1
BRF2	FOXA1	KDM5A	PDX1	SMARCC2	USF2
CBX3	FOXA2	KDM5B	PHF8	SMC3	WRNIP1
CCNT2	FOXM1	MAFB	PML	SP1	YY1
CEBPB	FOXP2	MAFF	POLR2A	SP2	ZBTB33
CEBPD	GABPA	MAFK	POLR3G	SP4	ZBTB7A
CHD1	GATA1	MAX	POU2F2	SPI1	ZEB1
CHD2	GATA2	MAZ	POU5F1	SREBP1	ZKSCAN1
CREB1	GATA3	MBD4	PPARGC1A	SRF	ZNF143
CTBP2	GRp20	MEF2A	PRDM1	STAT1	ZNF217
CTCF	GTF2B	MEF2C	RAD21	STAT2	ZNF263
CTCF1	GTF2F1	MTA3	RBBP5	STAT3	ZNF274
E2F1	GTF3C2	MXI1	RCOR1	STAT5A	ZZZ3
E2F4	HDAC1	MYBL2	RDBP	SUZ12	
E2F6	HDAC2	MYC	RELA	TAF1	
EBF1	HDAC6	NANOG	REST	TAF7	

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**Supplementary Table 12. Credible set variants in FOXA2 sites.**

Variant	Chr	Position (b37)	Alleles		Association signal			Chromatin State
			Risk	Other	Locus	Index variant	Posterior probability	
rs17186372	1	120,500,951	C	G	<i>NOTCH2</i>	rs41463147	0.01114	HepG2-Enhancer
rs78681698	2	43,598,160	A	G	<i>THADA</i>	rs77981966	0.00150	Islet-Enhancer, HepG2-Enhancer
rs57696714	2	43,626,521	T	C	<i>THADA</i>	rs77981966	0.00351	Islet-Enhancer, HepG2-Enhancer
rs17406646	2	43,678,617	C	T	<i>THADA</i>	rs77981966	0.00072	HepG2-Enhancer
rs7599781	2	43,678,726	T	C	<i>THADA</i>	rs77981966	0.00022	HepG2-Enhancer
rs12105626	2	43,678,759	C	G	<i>THADA</i>	rs77981966	0.00026	HepG2-Enhancer
rs17030845	2	43,687,879	C	T	<i>THADA</i>	rs77981966	0.00079	Islet-Enhancer, HepG2-Enhancer
chr2:43839773	2	43,839,773	C	CT	<i>THADA</i>	rs77981966	0.00054	-
rs243018	2	60,586,707	C	G	<i>BCL11A</i>	rs243020	0.06484	Islet-Enhancer
chr2:165545373	2	165,545,373	C	CAA	<i>GRB14</i>	chr2:165501927	0.00199	Islet-Enhancer
rs75297654	2	165,545,615	C	T	<i>GRB14</i>	chr2:165501927	0.07833	Islet-Enhancer
rs4234731	4	6,299,914	A	G	<i>WFS1</i>	rs10937721	0.01888	Islet-Enhancer
rs7732130	5	76,435,004	G	A	<i>ZBED3</i>	rs7732130	0.46107	Islet-Enhancer
rs10950521	7	14,429,350	C	T	<i>DGKB</i>	rs1974620	0.00003	Islet-Enhancer
					<i>DGKB</i>	rs10276674	0.00100	
rs17668488	7	14,727,413	T	C	<i>DGKB</i>	rs10276674	0.00006	Islet-Enhancer
rs62448646	7	15,055,948	A	T	<i>DGKB</i>	rs10276674	0.00009	-
rs7798360	7	15,055,972	A	G	<i>DGKB</i>	rs1974620	0.00334	-
					<i>DGKB</i>	rs10276674	0.00005	
rs849133	7	28,192,280	C	T	<i>JAZF1</i>	rs1513272	0.04169	Islet-Enhancer
rs13266634	8	118,184,783	C	T	<i>SLC30A8</i>	rs13266634	0.29460	Islet-Enhancer
rs4237150	9	4,290,085	G	C	<i>GLIS3</i>	chr9:4294707	0.03875	Islet-Enhancer
rs10757282	9	22,133,984	T	C	<i>CDKN2B</i>	rs10757283	0.11109	Islet-Enhancer

rs10811660	9	22,134,068	G	A	<i>CDKN2B</i>	rs10811660	0.24144	Islet-Enhancer
rs10811661	9	22,134,094	T	C	<i>CDKN2B</i>	rs10811660	0.54511	Islet-Enhancer
rs11257655	10	12,307,894	C	T	<i>CDC123</i>	rs11257658	0.21096	Islet-Enhancer, HepG2-Enhancer
rs7903146	10	114,758,349	C	T	<i>TCF7L2</i>	rs7903146	0.77648	Islet-Enhancer
rs149039886	11	2,677,676	T	C	<i>KCNQ1</i>	rs458069	0.00043	Islet-Enhancer
					<i>KCNQ1</i>	rs2237895	0.00001	
					<i>KCNQ1</i>	rs2283220	0.00032	
rs117134350	11	2,682,645	T	C	<i>KCNQ1</i>	rs2283220	0.00030	-
					<i>KCNQ1</i>	rs458069	0.00037	
rs144222135	11	2,750,055	G	A	<i>KCNQ1</i>	rs2237895	0.00002	HepG2-Enhancer
					<i>KCNQ1</i>	rs2283220	0.00044	
					<i>KCNQ1</i>	rs458069	0.00065	
rs231908	11	2,751,660	A	G	<i>KCNQ1</i>	rs458069	0.00015	HepG2-Enhancer
rs231907	11	2,752,130	A	T	<i>KCNQ1</i>	rs2283220	0.03136	HepG2-Enhancer
					<i>KCNQ1</i>	rs2237895	0.00002	
					<i>KCNQ1</i>	rs458069	0.00085	
rs78688069	11	2,752,183	C	A	<i>KCNQ1</i>	rs2237895	0.00004	HepG2-Enhancer
					<i>KCNQ1</i>	rs2283220	0.00018	
					<i>KCNQ1</i>	rs458069	0.00057	
rs74949850	11	2,752,203	G	A	<i>KCNQ1</i>	rs458069	0.00023	-
					<i>KCNQ1</i>	rs2283220	0.00019	
rs183123047	11	2,763,764	C	T	<i>KCNQ1</i>	rs458069	0.00049	Islet-Enhancer
					<i>KCNQ1</i>	rs2237895	0.00002	
					<i>KCNQ1</i>	rs2283220	0.00056	
rs188455984	11	2,763,765	G	A	<i>KCNQ1</i>	rs458069	0.00049	Islet-Enhancer
					<i>KCNQ1</i>	rs2237895	0.00002	
					<i>KCNQ1</i>	rs2283220	0.00040	

rs231878	11	2,763,777	G	A	<i>KCNQ1</i>	rs458069	0.00013	Islet-Enhancer
rs147561312	11	2,763,990	G	A	<i>KCNQ1</i>	rs458069	0.00026	Islet-Enhancer
					<i>KCNQ1</i>	rs2283220	0.00021	
chr11:2809814	11	2,809,814	C	CT	<i>KCNQ1</i>	rs2283220	0.00005	Islet-Enhancer
					<i>KCNQ1</i>	rs458069	0.00011	
rs190728714	11	2,813,084	G	C	<i>KCNQ1</i>	rs458069	0.00042	Islet-Enhancer
					<i>KCNQ1</i>	rs2237895	0.00001	
					<i>KCNQ1</i>	rs2283220	0.00035	
rs140718439	11	2,860,956	A	G	<i>KCNQ1</i>	rs2283220	0.00068	Islet-Enhancer
					<i>KCNQ1</i>	rs2237895	0.00002	
					<i>KCNQ1</i>	rs458069	0.00179	
rs77919905	11	2,861,068	G	A	<i>KCNQ1</i>	rs458069	0.00046	Islet-Enhancer
					<i>KCNQ1</i>	rs2237895	0.00001	
					<i>KCNQ1</i>	rs2283220	0.00034	
rs117678333	11	2,898,713	G	A	<i>KCNQ1</i>	rs2283220	0.00017	Islet-Enhancer
rs116358948	11	2,898,719	G	A	<i>KCNQ1</i>	rs458069	0.00052	Islet-Enhancer
					<i>KCNQ1</i>	rs2283220	0.00034	
rs5213	11	17,408,404	C	T	<i>KCNJ11</i>	rs5215	0.13417	Islet-Enhancer
rs10830963	11	92,708,710	C	G	<i>MTNR1B</i>	rs10830963	0.99833	Islet-Enhancer, HepG2-Enhancer
rs188713963	12	121,263,372	G	A	<i>HNF1A</i>	chr12:121440833	0.00020	Islet-Enhancer, HepG2-Enhancer
					<i>HNF1A</i>	rs1800574	0.00004	
rs1169285	12	121,419,540	C	T	<i>HNF1A</i>	chr12:121440833	0.00016	Islet-Enhancer, HepG2-Enhancer
					<i>HNF1A</i>	rs1800574	0.00005	
rs148507926	12	121,420,417	C	T	<i>HNF1A</i>	chr12:121440833	0.00025	Islet-Enhancer, HepG2-Enhancer
					<i>HNF1A</i>	rs1800574	0.00005	
rs1169282	12	121,420,430	C	T	<i>HNF1A</i>	chr12:121440833	0.00008	Islet-Enhancer, HepG2-Enhancer







rs55660034	12	121,422,243	G	A	<i>HNF1A</i>	chr12:121440833	0.00031	Islet-Enhancer, HepG2-Enhancer
					<i>HNF1A</i>	rs1800574	0.00007	
rs80137384	12	121,461,798	C	T	<i>HNF1A</i>	rs1800574	0.00004	HepG2-Enhancer
					<i>HNF1A</i>	chr12:121440833	0.00021	
rs151238175	15	62,171,475	G	A	<i>C2CD4B</i>	rs138692931	0.00043	Islet-Enhancer, HepG2-Enhancer
rs1981916	15	62,171,479	T	C	<i>C2CD4B</i>	rs138692931	0.00009	Islet-Enhancer, HepG2-Enhancer
rs1364809	15	62,172,398	G	C	<i>C2CD4B</i>	rs138692931	0.00020	Islet-Enhancer, HepG2-Enhancer
rs2414755	15	62,172,429	C	T	<i>C2CD4B</i>	rs138692931	0.00010	Islet-Enhancer, HepG2-Enhancer
rs182222907	15	62,172,558	G	A	<i>C2CD4B</i>	rs138692931	0.00062	Islet-Enhancer, HepG2-Enhancer
rs12441358	15	62,199,911	T	A	<i>C2CD4B</i>	rs138692931	0.00021	HepG2-Enhancer
rs184969901	15	62,199,939	G	A	<i>C2CD4B</i>	rs138692931	0.00052	HepG2-Enhancer
rs17271256	15	62,228,592	A	G	<i>C2CD4B</i>	rs138692931	0.00025	Islet-Enhancer
rs188586648	15	62,228,616	C	T	<i>C2CD4B</i>	rs138692931	0.00042	Islet-Enhancer
rs11071641	15	62,228,696	G	C	<i>C2CD4B</i>	rs138692931	0.00011	Islet-Enhancer
rs35523559	15	62,228,770	A	C	<i>C2CD4B</i>	rs138692931	0.00010	Islet-Enhancer
rs192210296	15	62,267,155	T	C	<i>C2CD4B</i>	rs138692931	0.00045	Islet-Enhancer
rs10519156	15	62,375,798	T	A	<i>C2CD4B</i>	rs138692931	0.00011	Islet-Enhancer
rs7177711	15	62,379,971	A	G	<i>C2CD4B</i>	rs138692931	0.00012	Islet-Enhancer
rs181017166	15	62,380,027	C	T	<i>C2CD4B</i>	rs138692931	0.00131	Islet-Enhancer
rs7178540	15	62,380,132	G	A	<i>C2CD4B</i>	rs138692931	0.00012	Islet-Enhancer
rs17205498	15	62,405,255	G	A	<i>C2CD4B</i>	rs138692931	0.00020	Islet-Enhancer
rs17271521	15	62,437,363	T	A	<i>C2CD4B</i>	rs138692931	0.00012	Islet-Enhancer
rs8038542	15	62,437,453	T	C	<i>C2CD4B</i>	rs138692931	0.00012	Islet-Enhancer
rs77058171	15	62,437,471	T	C	<i>C2CD4B</i>	rs138692931	0.00028	Islet-Enhancer
rs184547776	15	62,460,046	C	T	<i>C2CD4B</i>	rs138692931	0.00104	Islet-Enhancer
rs189010722	15	62,503,693	G	C	<i>C2CD4B</i>	rs138692931	0.00044	HepG2-Enhancer
rs181325342	15	62,503,735	C	G	<i>C2CD4B</i>	rs138692931	0.00044	HepG2-Enhancer







rs9939973	16	53,800,568	G	A	<i>FTO</i>	rs9927317	0.02503	Islet-Enhancer, HepG2-Enhancer
rs9940646	16	53,800,629	C	G	<i>FTO</i>	rs9927317	0.02523	Islet-Enhancer, HepG2-Enhancer
rs9940128	16	53,800,754	G	A	<i>FTO</i>	rs9927317	0.02668	Islet-Enhancer, HepG2-Enhancer
rs10401969	19	19,407,718	T	C	<i>CILP2</i>	rs72999033	0.01314	Islet-Enhancer
rs60500622	19	46,161,305	G	T	<i>GIPR</i>	rs4399645	0.00257	Islet-Enhancer, HepG2-Enhancer
rs8104845	19	46,161,326	A	G	<i>GIPR</i>	rs4399645	0.00015	Islet-Enhancer, HepG2-Enhancer
					<i>GIPR</i>	rs2238689	0.00280	
chr19:46172396	19	46,172,396	T	TG	<i>GIPR</i>	rs4399645	0.00006	-
rs182357861	19	46,184,783	A	C	<i>GIPR</i>	rs4399645	0.00009	Islet-Enhancer, HepG2-Enhancer
rs113815244	19	46,220,716	G	A	<i>GIPR</i>	rs4399645	0.00007	-
rs76353548	19	46,224,089	G	T	<i>GIPR</i>	rs4399645	0.00012	HepG2-Enhancer
rs35732815	19	46,224,156	A	G	<i>GIPR</i>	rs4399645	0.00011	HepG2-Enhancer
rs148507178	19	46,224,166	C	A	<i>GIPR</i>	rs4399645	0.00006	HepG2-Enhancer
rs182144573	19	46,283,781	C	T	<i>GIPR</i>	rs4399645	0.00016	Islet-Enhancer, HepG2-Enhancer
rs183752479	19	46,384,359	C	T	<i>GIPR</i>	rs4399645	0.00013	Islet-Enhancer, HepG2-Enhancer
rs147046831	19	46,384,600	C	T	<i>GIPR</i>	rs4399645	0.00006	Islet-Enhancer, HepG2-Enhancer
chr19:46398907	19	46,398,907	CACA	C	<i>GIPR</i>	rs4399645	0.00006	HepG2-Enhancer

Chr: chromosome.



**Supplementary Table 13. FOXA2 site credible set variants disrupting *de novo* motifs.**

Variant	Chr	Position (b37)	Association signal			Motif prediction <sup>a</sup>		
			Locus	Index variant	Posterior probability	Allele	Motif	Top matching <sup>b</sup>
rs10830963	11	92,708,710	<i>MTNR1B</i>	rs10830963	0.998	G		TAL1::TCF3, TAL1_known2, Olig2, OLIG1_1, Atoh1, OLIG2_2, NeuroD1, BHLHA15_1
rs7903146	10	114,758,349	<i>TCF7L2</i>	rs7903146	0.776	T		NFIL3, NFIL3_1, TEF_3, DBP_2, DBP_4
rs13266634	8	118,184,783	<i>SLC30A8</i>	rs13266634	0.295	T		Tcf12, E2A, TCF3_1, MyoD, TFAP4_4, ASCL2_1
rs10811660	9	22,134,068	<i>CDKN2B</i>	rs10811660	0.241	A		-
rs11257655	10	12,307,894	<i>CDC123</i>	rs11257658	0.211	T		FOXA1:AR, HDAC2_disc2, FOXD2_2, FOXD3_4, EP300_disc3, FOXP3_2, FOXA1, FOXL1_4, FOXC2_3
rs849133	7	28,192,280	<i>JAZF1</i>	rs1513272	0.0417	T		Bach1, AP-1, NF-E2, Nrf2, NFE2L2_2, AP1_known8, EP300_disc1

rs231907	11	2,752,130	<i>KCNQ1</i>	rs2283220	0.0310	T		AMYB
rs9940128	16	53,800,754	<i>FTO</i>	rs9927317	0.027	G		ETS_known12, ELK3_1, ERF_1, FEV_2, ELK4, ETS_known2, EHF_1, ETV4_2, ETS_known1, ETS_disc2
rs9939973	16	53,800,568	<i>FTO</i>	rs9927317	0.025	G		-
rs78688069	11	2,752,183	<i>KCNQ1</i>	rs458069	0.0006	A		-
rs190728714	11	2,813,084	<i>KCNQ1</i>	rs458069	0.00042	G		BCL_disc1, ETS_disc2, Elk1, ETS_known2, ELK3_1, ERF_1, FEV_2, Elk4, ETS_known12, ETV4_2
rs7798360	7	15,055,972	<i>DGKB</i>	rs10276674	0.00005	G		RHOXF1_1, RHOXF1_7

<sup>a</sup>Only most disrupted motif prediction reported.

<sup>b</sup>Motifs with  $q$ -value < 0.001, only top 10 matches listed

Chr: chromosome.

**Supplementary Table 14. Genes down-regulated in *Foxa1/2* knock-out mice at FOXA2-enriched signals.**

<b>Gene</b>	<b>Locus</b>	<b>Percent change</b>	<b>p-value</b>
<i>REG4</i>	<i>NOTCH2</i>	1,415.2%	0.15
<i>IGF2</i>	<i>KCNQ1</i>	135.3%	0.083
<i>SLC30A8</i>	<i>SLC30A8</i>	134.7%	0.048
<i>ABCC8</i>	<i>KCNJ11</i>	81.5%	0.22
<i>CAMK1D</i>	<i>CDC123</i>	81.2%	0.13
<i>TCF7L2</i>	<i>TCF7L2</i>	57.2%	0.28
<i>INS</i>	<i>KCNQ1</i>	47.7%	0.89
<i>SLC22A18</i>	<i>KCNQ1</i>	45.8%	0.53
<i>KCNJ11</i>	<i>KCNJ11</i>	38.1%	0.30
<i>PBX4</i>	<i>CILP2</i>	37.9%	0.50
<i>PROSER2</i>	<i>CDC123</i>	35.5%	0.31
<i>CARS</i>	<i>KCNQ1</i>	34.6%	0.33
<i>WFS1</i>	<i>WFS1</i>	29.4%	0.57
<i>AGGF1</i>	<i>ZBED3</i>	21.8%	0.39
<i>ETV1</i>	<i>DGKB</i>	19.6%	0.70
<i>RCL1</i>	<i>GLIS3</i>	17.6%	0.58
<i>MTAP</i>	<i>CDKN2A/B</i>	10.5%	0.76
<i>GDF1</i>	<i>CILP2</i>	9.9%	0.90
<i>GLIS3</i>	<i>GLIS3</i>	6.8%	0.93
<i>BLOC1S4</i>	<i>WFS1</i>	6.7%	0.94
<i>HSD3B2</i>	<i>NOTCH2</i>	3.7%	0.94
<i>HOMER3</i>	<i>CILP2</i>	0.4%	0.99
<i>NOTCH2</i>	<i>NOTCH2</i>	0.2%	0.99
<i>RFXANK</i>	<i>CILP2</i>	0.2%	0.99

**Supplementary Table 15. Comparison of summary statistics for association signals in established T2D susceptibility loci obtained from meta-analysis of Metabochip studies: (i) unconditional; (ii) GCTA joint model using GoDARTS as reference; and (iii) GCTA joint model using FUSION as reference.**

Locus	Index variant	Chr	Position (b37)	Risk allele	Other allele	RAF	Metabochip unconditional meta-analysis		Metabochip GCTA joint model GoDARTS reference study		Metabochip GCTA joint model FUSION reference study	
							OR (95% CI)	p-value	OR (95% CI)	p <sub>i</sub>	OR (95% CI)	p <sub>i</sub>
<i>PROX1</i>	rs340874	1	214,159,256	C	T	0.520	1.07 (1.04-1.10)	1.1x10 <sup>-7</sup>	1.07 (1.04-1.10)	1.1x10 <sup>-7</sup>	1.07 (1.04-1.10)	1.1x10 <sup>-7</sup>
<i>GCKR</i>	rs780094	2	27,741,237	C	T	0.611	1.08 (1.06-1.11)	8.5x10 <sup>-10</sup>	1.08 (1.05-1.11)	1.6x10 <sup>-9</sup>	1.08 (1.06-1.11)	8.7x10 <sup>-10</sup>
<i>THADA</i>	rs77981966	2	43,777,964	C	T	0.934	1.20 (1.13-1.26)	1.7x10 <sup>-11</sup>	1.19 (1.13-1.26)	1.7x10 <sup>-11</sup>	1.19 (1.13-1.26)	1.8x10 <sup>-11</sup>
<i>BCL11A</i>	rs243020	2	60,585,028	G	A	0.462	1.06 (1.04-1.09)	2.5x10 <sup>-6</sup>	1.06 (1.03-1.09)	4.6x10 <sup>-6</sup>	1.06 (1.04-1.09)	2.5x10 <sup>-6</sup>
<i>GRB14-COBL1</i>	rs75297654	2	165,545,615	C	T	0.876	1.16 (1.11-1.20)	8.9x10 <sup>-14</sup>	1.16 (1.11-1.20)	9.2x10 <sup>-14</sup>	1.16 (1.11-1.20)	9.2x10 <sup>-14</sup>
<i>IRS1</i>	rs2972156	2	227,117,778	G	C	0.621	1.11 (1.08-1.14)	1.3x10 <sup>-15</sup>	1.11 (1.08-1.14)	1.4x10 <sup>-15</sup>	1.11 (1.08-1.14)	1.4x10 <sup>-15</sup>
<i>PPARG</i>	rs11712037	3	12,344,730	C	G	0.862	1.11 (1.07-1.15)	4.6x10 <sup>-8</sup>	1.12 (1.08-1.16)	3.7x10 <sup>-9</sup>	1.11 (1.07-1.15)	4.6x10 <sup>-8</sup>
<i>ADAMTS9</i>	rs17676309	3	64,730,121	C	T	0.590	1.07 (1.04-1.10)	1.2x10 <sup>-7</sup>	1.07 (1.05-1.10)	7.5x10 <sup>-8</sup>	1.07 (1.04-1.10)	1.2x10 <sup>-7</sup>
<i>ADCY5</i>	rs11708067	3	123,065,778	A	G	0.786	1.12 (1.09-1.16)	1.1x10 <sup>-13</sup>	1.11 (1.08-1.15)	5.1x10 <sup>-12</sup>	1.12 (1.09-1.16)	1.2x10 <sup>-13</sup>
<i>IGF2BP2</i>	rs35510946	3	185,518,910	A	G	0.301	1.14 (1.11-1.17)	3.7x10 <sup>-20</sup>	1.14 (1.10-1.17)	3.9x10 <sup>-20</sup>	1.14 (1.10-1.17)	3.9x10 <sup>-20</sup>
<i>WFS1</i>	rs10937721	4	6,306,763	C	G	0.580	1.09 (1.06-1.12)	7.6x10 <sup>-11</sup>	1.08 (1.05-1.11)	1.2x10 <sup>-9</sup>	1.09 (1.06-1.12)	7.6x10 <sup>-11</sup>
<i>ZBED3</i>	rs7732130	5	76,435,004	G	A	0.278	1.09 (1.06-1.12)	6.4x10 <sup>-10</sup>	1.09 (1.06-1.12)	7.1x10 <sup>-10</sup>	1.09 (1.06-1.12)	6.5x10 <sup>-10</sup>
<i>CDKAL1</i>	rs35261542	6	20,675,792	A	C	0.280	1.15 (1.12-1.18)	9.6x10 <sup>-23</sup>	1.15 (1.12-1.18)	2.2x10 <sup>-24</sup>	1.15 (1.12-1.18)	1.0x10 <sup>-22</sup>
<i>DGKB</i>	rs10276674	7	14,922,007	C	T	0.183	1.07 (1.04-1.11)	0.000013	1.08 (1.04-1.11)	4.5x10 <sup>-6</sup>	1.07 (1.04-1.10)	0.000042
	rs1974620	7	15,065,467	T	C	0.519	1.06 (1.04-1.09)	9.0x10 <sup>-7</sup>	1.06 (1.04-1.09)	1.6x10 <sup>-6</sup>	1.06 (1.04-1.09)	2.8x10 <sup>-6</sup>
<i>JAZF1</i>	rs1513272	7	28,200,097	C	T	0.518	1.09 (1.07-1.12)	3.9x10 <sup>-12</sup>	1.10 (1.07-1.12)	4.8x10 <sup>-13</sup>	1.09 (1.07-1.12)	3.9x10 <sup>-12</sup>
<i>GCK</i>	rs878521	7	44,255,643	A	G	0.235	1.10 (1.06-1.13)	1.2x10 <sup>-9</sup>	1.10 (1.07-1.13)	2.6x10 <sup>-10</sup>	1.09 (1.06-1.13)	1.2x10 <sup>-9</sup>
<i>SLC30A8</i>	rs13266634	8	118,184,783	C	T	0.676	1.13 (1.10-1.16)	1.3x10 <sup>-18</sup>	1.12 (1.09-1.15)	1.1x10 <sup>-16</sup>	1.13 (1.10-1.16)	1.3x10 <sup>-18</sup>
<i>GLIS3</i>	chr9:4294707:I	9	4,294,707	I	R	0.360	1.07 (1.05-1.10)	6.5x10 <sup>-8</sup>	1.08 (1.05-1.11)	1.5x10 <sup>-8</sup>	1.07 (1.05-1.10)	6.4x10 <sup>-8</sup>
<i>CDKN2B</i>	rs10811660	9	22,134,068	G	A	0.830	1.21 (1.17-1.25)	9.7x10 <sup>-28</sup>	1.32 (1.27-1.38)	2.4x10 <sup>-44</sup>	1.30 (1.25-1.35)	2.1x10 <sup>-40</sup>
	rs10757283	9	22,134,172	T	C	0.437	1.03 (1.01-1.06)	0.015	1.14 (1.10-1.17)	7.4x10 <sup>-18</sup>	1.12 (1.09-1.16)	1.2x10 <sup>-15</sup>
<i>CDC123</i>	rs11257658	10	12,309,268	A	G	0.217	1.10 (1.07-1.14)	2.9x10 <sup>-10</sup>	1.11 (1.08-1.14)	1.6x10 <sup>-11</sup>	1.10 (1.07-1.14)	2.9x10 <sup>-10</sup>
<i>HHEX</i>	rs11187140	10	94,466,910	G	A	0.632	1.11 (1.08-1.14)	1.7x10 <sup>-14</sup>	1.10 (1.08-1.13)	5.5x10 <sup>-14</sup>	1.11 (1.08-1.14)	1.8x10 <sup>-14</sup>
<i>TCF7L2</i>	rs7903146	10	114,758,349	T	C	0.260	1.39 (1.35-1.43)	5.8x10 <sup>-120</sup>	1.38 (1.35-1.42)	3.1x10 <sup>-117</sup>	1.39 (1.35-1.43)	3.2x10 <sup>-119</sup>
<i>KCNQ1</i>	chr11:2692322:D	11	2,692,322	D	R	0.374	1.08 (1.05-1.11)	2.4x10 <sup>-9</sup>	1.08 (1.05-1.10)	3.5x10 <sup>-8</sup>	1.10 (1.07-1.13)	3.6x10 <sup>-13</sup>
	rs2283220	11	2,755,548	A	G	0.661	1.05 (1.03-1.08)	0.00013	1.06 (1.03-1.09)	0.000016	1.05 (1.02-1.08)	0.00089
	rs2237895	11	2,857,194	C	A	0.428	1.12 (1.09-1.15)	8.7x10 <sup>-19</sup>	1.08 (1.05-1.11)	6.6x10 <sup>-7</sup>	1.06 (1.03-1.10)	0.00019
	rs74046911	11	2,858,636	C	T	0.951	1.32 (1.24-1.40)	2.3x10 <sup>-19</sup>	1.32 (1.24-1.40)	1.7x10 <sup>-17</sup>	1.33 (1.24-1.42)	3.2x10 <sup>-16</sup>
	rs458069	11	2,858,800	G	C	0.707	1.07 (1.04-1.10)	1.0x10 <sup>-6</sup>	1.06 (1.03-1.10)	0.00026	1.06 (1.03-1.10)	0.00059
<i>KCNJ11</i>	rs5215	11	17,408,630	C	T	0.389	1.09 (1.06-1.12)	1.5x10 <sup>-10</sup>	1.08 (1.05-1.11)	1.3x10 <sup>-9</sup>	1.09 (1.06-1.11)	1.5x10 <sup>-10</sup>
<i>CENTD2</i>	chr11:72460930:I	11	72,460,930	R	I	0.823	1.10 (1.07-1.14)	8.8x10 <sup>-9</sup>	1.10 (1.06-1.13)	5.9x10 <sup>-8</sup>	1.10 (1.07-1.14)	8.8x10 <sup>-9</sup>
<i>MTNR1B</i>	rs10830963	11	92,708,710	G	C	0.283	1.10 (1.07-1.13)	2.9x10 <sup>-12</sup>	1.10 (1.07-1.13)	7.9x10 <sup>-12</sup>	1.10 (1.07-1.13)	2.9x10 <sup>-12</sup>
<i>HMGA2</i>	rs2583941	12	66,204,598	A	G	0.090	1.14 (1.09-1.19)	7.5x10 <sup>-9</sup>	1.13 (1.08-1.18)	6.0x10 <sup>-8</sup>	1.14 (1.09-1.18)	7.5x10 <sup>-9</sup>
<i>TSPAN8</i>	rs7961581	12	71,663,102	C	T	0.265	1.07 (1.04-1.10)	1.1x10 <sup>-6</sup>	1.07 (1.04-1.10)	1.4x10 <sup>-6</sup>	1.07 (1.04-1.10)	1.1x10 <sup>-6</sup>

<i>HNFB1A</i>	rs1169288	12	121,416,650	C	A	0.334	1.06 (1.03-1.09)	0.000014	1.10 (1.07-1.13)	5.4x10 <sup>-10</sup>	1.09 (1.06-1.12)	8.3x10 <sup>-9</sup>
	rs1800574	12	121,416,864	T	C	0.027	1.15 (1.07-1.25)	0.00039	1.21 (1.11-1.31)	5.2x10 <sup>-6</sup>	1.22 (1.12-1.32)	2.4x10 <sup>-6</sup>
	chr12:121440833:D	12	121,440,833	R	D	0.416	1.01 (0.99-1.04)	0.29	1.06 (1.03-1.09)	0.000028	1.05 (1.02-1.08)	0.00042
<i>C2CD4B</i>	rs7161785	15	62,395,224	G	C	0.555	1.05 (1.02-1.07)	0.00058	1.04 (1.02-1.07)	0.00068	1.05 (1.02-1.07)	0.00058
<i>PRC1</i>	rs3803563	15	91,531,352	A	C	0.175	1.11 (1.07-1.15)	3.6x10 <sup>-10</sup>	1.11 (1.07-1.15)	2.2x10 <sup>-10</sup>	1.11 (1.07-1.14)	3.6x10 <sup>-10</sup>
<i>FTO</i>	rs9927317	16	53,820,996	G	C	0.396	1.14 (1.11-1.17)	1.7x10 <sup>-24</sup>	1.14 (1.11-1.17)	6.8x10 <sup>-25</sup>	1.14 (1.11-1.17)	1.7x10 <sup>-24</sup>
<i>HNFB1B</i>	rs4430796	17	36,098,040	G	A	0.455	1.09 (1.07-1.12)	6.3x10 <sup>-12</sup>	1.09 (1.07-1.12)	5.2x10 <sup>-12</sup>	1.09 (1.07-1.12)	6.4x10 <sup>-12</sup>
<i>MC4R</i>	chr18:57739289:D	18	57,739,289	D	R	0.234	1.06 (1.02-1.09)	0.00044	1.05 (1.02-1.09)	0.00079	1.05 (1.02-1.09)	0.00086
	rs17066842	18	58,040,624	G	A	0.961	1.13 (1.06-1.21)	0.00030	1.13 (1.06-1.21)	0.00033	1.12 (1.05-1.20)	0.00059
<i>CILP2</i>	rs72999033	19	19,366,632	T	C	0.069	1.19 (1.14-1.25)	5.3x10 <sup>-13</sup>	1.20 (1.15-1.26)	6.5x10 <sup>-14</sup>	1.19 (1.14-1.25)	5.4x10 <sup>-13</sup>
<i>GIPR</i>	rs4399645	19	46,166,073	T	C	0.395	1.05 (1.02-1.08)	0.00030	1.07 (1.04-1.10)	4.4x10 <sup>-7</sup>	1.06 (1.04-1.09)	3.1x10 <sup>-6</sup>
	rs2238689	19	46,178,661	C	T	0.425	1.08 (1.05-1.10)	1.7x10 <sup>-8</sup>	1.09 (1.07-1.12)	9.7x10 <sup>-12</sup>	1.09 (1.06-1.12)	2.1x10 <sup>-10</sup>
<i>HNFB4A</i>	rs1800961	20	43,042,364	T	C	0.034	1.16 (1.09-1.24)	7.1x10 <sup>-6</sup>	1.16 (1.09-1.24)	0.000011	1.16 (1.09-1.24)	7.2x10 <sup>-6</sup>

Each association signal was represented by an index variant in the GCTA-COJO joint regression model on the basis of: (i) summary statistics from the meta-analysis of MetaboChip studies in 27,206 cases and 57,574 controls of European ancestry; and (ii) reference genotype data from GoDARTS (3,298 cases and 3,708 controls of European ancestry from the UK) or FUSION (4,435 cases and 5,757 controls of European ancestry from Scandinavia) to approximate LD across fine-mapping regions.

Chr: chromosome. RAF: risk allele frequency. OR: odds-ratio for risk allele. CI: confidence interval.

**Supplementary Table 16. Recognition Motifs enriched in FOXA2 ChIP-seq sites.**

ID	Consensus sequence	Matching known motifs <sup>a,b</sup>
0	GTAAACA	FOXA1:AR, HDAC2_disc2, FOXD2_2, FOXD3_4, EP300_disc3, FOXP3_2, FOXA1, FOXL1_4, FOXC2_3, FOXJ2_4, TCF12_disc2, FOXJ3_4, FOXJ3_7, FOXC1_7, FOXB1_4, FOXA_known6, FOXO1_3, FOXO6_2, FOXA_known7, FOXJ3_1, FOXL1_3, Fox:Ebox
1	CTAAGTAAACA	FOXA_known6, HDAC2_disc2, EP300_disc3, FOXA1, FOXA_known7, FOXC2_3, FOXD3_4, TCF12_disc2, FOXD2_2, Fox:Ebox, FOXJ3_1, FOXA_known2, FOXO6_2, FOXL1_3, FOXL1_4, FOXC1_1, FOXP3_2
2	TGTTTACTTAGG	FOXA_known6, FOXA1, HDAC2_disc2, Fox:Ebox, EP300_disc3, FOXA_known7, TCF12_disc2, FOXO6_2, FOXC2_3, FOXD3_4, FOXJ3_1, FOXD2_2, FOXC1_1, FOXB1_4, FOXA_known2, FOXL1_3, FOXL1_4, FOXD1_2, FOXD1
3	TCCATGTTTACTTTG	FOXA1, FOXA_known7, FOXA_known6, EP300_disc3, HDAC2_disc2, FOXC2_3, FOXP1, Fox:Ebox, FOXJ3_1, FOXL1_3, FOXD1_2, FOXD1, FOXB1_4, TCF12_disc2, FOXO3_5, FOXO1_3, FOXL1_1, FOXO6_2, FOXD2_2, FOXD3_4, FOXA_known2, FOXA1:AR, NF1:FOXA1, FOXF2, FOXO4_2, FOXI1_1, FOXJ2_4, FOXL1_4, FOXP3_2, FOXJ3_7, FOXC1_1
4	AAAAAGTAAACAAAGAC	FOXA_known7, FOXJ3_1, FOXL1_3, FOXC2_3, FOXC1_1, FOXO4_2, FOXP1, FOXL1_1, FOXF2, FOXO3_5, FOXD3_4, FOXO6_2, FOXO1_3, FOXB1_4, FOXD2_2, FOXJ2_4, FOXJ3_7, FOXA_known6, FOXD1_2, FOXD1, HDAC2_disc2, FOX_1, FOXJ3_2, FOXL1_4, EP300_disc3
5	AAAAAGTAAACAAACCC	FOXJ3_1, FOXA_known7, FOXL1_3, FOXF2, FOXC2_3, FOXJ3_7, FOXO4_2, FOXC1_1, FOXJ2_4, FOXO1_3, FOXP1, FOXL1_1, FOXJ3_2, FOXO3_5
6	AAAGTAAACAAAATT	FOXJ3_1, FOXA_known7, FOXL1_3, FOXC2_3, FOXP1, FOXO4_2, FOXJ2_4, FOXJ3_7, FOXL1_4, FOXO1_3, FOXO1_1
7	AAAATGTAAACAAACAG	FOXL1_3, FOXA_known7, FOXJ3_1, FOXO6_2, FOXC2_3, FOXO4_2, FOXF2, FOXO1_3, FOXJ2_4, FOXJ3_7, FOXO3_5, FOXL1_1, FOXC1_1, FOXJ3_2, FOXB1_4, FOXP1, FOXD1_2, FOXD1, FOXO3_3, FOXO3
8	GTAACAT	FOXD1_2, FOXD1, FOXO3_5, FOXO1_3, FOXB1_4, FOXO6_2
9	TAAATGTAAACAAAGGT	FOXL1_3, FOXA_known7, FOXJ3_1, FOXC2_3, FOXJ3_7, FOXJ2_4, FOXO1_3, FOXO4_2, FOXL1_1, FOXJ3_2, FOXB1_4, FOXF2, FOXO3_5, FOXP1
10	TGTCAACA	
11	TCCTGTTTACA	FOXP1, Foxo1, FOXO6_2
12	AAGTAAACAAA	FOXP1, FOXO6_2, FOXJ3_1, FOXA_known7, FOXC2_3, FOXL1_3, Foxo1, Fox:Ebox, FOXA_known6
13	CAAACGTAAACAAT	FOXF2, FOXJ3_1, FOXO1_3, FOXJ2_4, FOXJ3_7, FOXO3_5, FOXO6_2, FOXA_known7, FOXO4_2, FOXL1_3, FOXD1_2, FOXD1, FOXC2_3, FOXJ3_2, FOXL1_4, FOXD2_2, FOXP3_2, FOXO1_1
14	CAAAGTAAACAAAG	FOXJ3_1, FOXA_known7, FOXL1_3, FOXO6_2, FOXC2_3, FOXF2, FOXP1, FOXD2_2, FOXJ3_7, FOXJ2_4, FOXO4_2, FOXO1_3, FOXL1_4, FOXP3_2, EP300_disc3, FOXA_known6, HDAC2_disc2, FOXC1_1, FOXJ3_2
15	TGTAAACA	FOXO3_3, FOXO3
16	GTTTACTT	FOXA_known6
17	TATTGTTTATT	FOXQ1_2, Foxq1
18	TGATTGTTAACAGTTGG	

19	GGATGTTTGT	FOXI1_2, FOXI1, FOXI1_1, FOXD3_1, FOX_1, Foxd3, NF1:FOXA1, FOXL1_1
20	TGTGTACA	
21	TCCAATCCACA	Foxh1
22	AGGAAA	
23	GTAACAAT	SRY_3, SRY, SRY_2
24	GAATGTTTGT	Foxd3, FOXD3_1, FOX_1, Foxa2, FOXI1_2, FOXI1, FOXI1_1
25	TGAGTCAT	Bach1, AP-1, NF-E2, Nrf2, NFE2L2_2, AP1_known8, EP300_disc1
26	TGTATATATACC	
27	CTCTGT	
28	CTTTGT	SOX10
29	AGAGTCCAAAGTCCA	HNf4a, HNF4_known14, HNF4A, HNF4_known1, HNF4_known9, HNF4_known2, HNF4_known13, NR2F1, PPARA_4, HNF4_known21, NR2C2_known1, HNF4_known19, HNF4_known17, TR4, NR2F6_3, RXRA_known7, RXRA_known10, HNF4_known7, RXRA_known12, RXR, PPARG::RXRA, RXRB_1, PPARE, PPARA_3, RXRA_known1, NR1H2::RXRA
30	CAAAGTCC	HNf4a, HNF4_known9, HNF4_known14, HNF4A
31	CTGGACTTTGGACTC	HNf4a, HNF4_known9, HNF4_known14, HNF4A, HNF4_known1, HNF4_known2, HNF4_known13, NR2F1, HNF4_known17, HNF4_known21, PPARA_4, NR2C2_known1, HNF4_known19, TR4, NR2F6_3, RXRA_known7, RXRA_known10, RXRA_known12, RXR, HNF4_known7, PPARA_3, RXRB_1, PPARE, PPARG::RXRA, Erra
32	ACACAG	
33	TACATGTGCACATAAAA	
34	CCTCCC	
35	GGTAAGTA	FOXC1, FOXC1_1
36	AACAACAACAAGAG	ZNF35_1
37	CAGATGTGCACATACGT	
38	TATTGCACAAT	CEBPB_known1
39	TGACCTTTGAACCT	HNf4_known2, HNF4_known13, NR2F1, HNF4_known1, HNF4_known14, HNF4A, PPARA_4, NR2C2_known1, HNF4_known9, HNF4a, HNF4_known7, HNF4_known19, NR2F6_3, HNF4_known21, RXRA_known12, TR4, RXRA_known10, RXRB_1, PPARG::RXRA, PPARA_3, NR1H2::RXRA, PPARE, RXRA_known1, RXR, RXRA_known7, Erra, RARA_1, Nur77
40	ATACTTA	NKX3-1_2, NKX3-1, NKX3-1_1
41	CAAAGGTCAGA	Erra, HNF4_known1
42	CAGATG	
43	ATTGCACAATA	CEBPB_known1
44	TCACGGAACAATAGGTG	SOX7_1, SOX15_1, SOX9_1, SOX18_1, SOX13_1, Sox6, SOX11_1, SOX4_1, SRY_2, SOX9_2, SOX9, SOX17_1
45	CTCACACAATGGCGC	
46	GTGGTTCAATAATTTTG	
47	TCTCAAAGGTCACCTG	RARA_1, NR2F2_2, Nur77, HNF4_known1, RARA_8, RXRA_known1, RARB_2, Erra

48	AATCAACA	
49	TTACACAA	
50	TGCAAAAGTCCAATAT	
51	TCTCAAAGGTCACGAG	NR2F2_2, RARA_1, Nur77, RARA_8, HNF4_known1, RXRA_known9, RARA_6, RARB_2, RXRA_known1
52	TATTC AAGGTCATGCGA	ESRRG_3, ESRRRA_known7, NR2F2_2, ESRRB_1, Esrrb, RARA_1, Nr5a2, ESRRRA_known11, ESRRRA_disc2, NR5A1_2, RORA_1, ESRRRA_known9
53	GGTTACGTAATA	HLF, HLF_1, DBP_2, DBP_4, HLF_4, TEF_3, NFIL3_1, CEBPB_known9, CEBPB_known10
54	GCCTGG	
55	TGACTCA	AP1_known10, AP1
56	AGCTCAAGGTCA	ESRRB_1, Esrrb, ESRRRA_disc2, Nr5a2, ESRRRA_known7, NR5A1_2, ESRRG_3, ESRRRA_known9, ESRRG_1, ESRRRA_known11, RARg, Nur77
57	AGAAGAACAAAGGACTA	SOX4_1, SOX11_1, SOX15_1, SOX9_1, NANOG_disc2, SOX7_1, TCF7_1
58	ATAAGAACAAAGGACTA	SOX11_1, SOX4_1, SOX15_1, SOX9_1, SOX7_1, TCF7_1, NANOG_disc2, SOX18_1
59	TAAATG	
60	CCAAGGTCACA	ESRRRA_disc2, ESRRG_3, NR5A1_2, ESRRRA_known7
61	AGGACGCTGTAAAGGGA	RHOXF1_1, RHOXF1_7
62	CCATTGTTC	SOX9_2, SOX9, SOX9_1
63	ACAACAC	BRCA1
64	AAGGTCA	
65	AAGACGCTGTAAAGCGA	RHOXF1_1, RHOXF1_7
66	AGCTGTAACTAGCCGT	HNF1A_2, HNF1A_3, HMBOX1_2, PAX4_6
67	ATCAAGGTCA	RORA_4, RORA_1
68	TTTAAACA	
69	AAAAATAACAAACGG	
70	CCTTAGTAACTAAAAT	HNF1A_3, HNF1A_2
71	CCATTGTTTT	Sox3, Sox6, NANOG_disc2, SOX9_1, SOX9_2, SOX9, SOX11_1, SOX4_1
72	CGAAGCACACAAAATA	
73	TTCATTGTC	Sox17
74	AGATAA	
75	GGTGACTCATG	Jun-AP1, PRDM1_disc2, Atf3, AP-1, BATF, EP300_disc1, STAT_disc2, TRIM28_disc1, Fos, BCL_disc2, NFE2_known2, AP1_known4, IRF_disc2, BATF_disc1, AP1_known8, AP1_known10, AP1
76	ATATCAAAACAAAACA	
77	GGATGACTCAT	Jun-AP1, Atf3, TRIM28_disc1, PRDM1_disc2, BATF, STAT_disc2, AP-1, EP300_disc1, BCL_disc2, BATF_disc1, Fos, NFE2, IRF_disc2, AP1_known8, NFE2_known2, NFAT:AP1, AP1_known4, BACH1_1, AP1_known2, AP1_known10, AP1, Bach2
78	CCTTTGTT	Sox3, SOX2_1, Sox2



79	TGTGACTCATT	Atf3, Jun-AP1, AP-1, EP300_disc1, BCL_disc2, BATF, STAT_disc2, PRDM1_disc2, IRF_disc2, BATF_disc1, TRIM28_disc1, NFE2_known2, NFAT:AP1, NF-E2, AP1_known10, AP1, Fos
80	ATTGAACAATGGAATT	SOX7_1, SOX15_1, SOX9_1, SOX11_1, SOX4_1, SOX18_1, SOX9_2, SOX9, Sox6, SOX13_1
81	ACTTAGTAACTAAAAA	HNFA1A_2, HNF1A_3
82	AGGAGATGACTCAT	BATF, STAT_disc2, PRDM1_disc2, BCL_disc2, Atf3, Jun-AP1, EP300_disc1, BATF_disc1, TRIM28_disc1, AP-1, IRF_disc2, NFAT:AP1, NFE2_known2, AP1_known8, Fos, BACH1_1, NF-E2, AP1_known10, AP1
83	AAGGTCAC	NR4A2, RARG_9, THRB_2, RARA_1, RARG_1
84	CTTCAGGGGTCAATTGA	RXRA_known9
85	TATACATA	FOXL1_2, FOXL1, FOXL1_1
86	TAATTGTTCTAAAC	SOX18_1, SOX13_1, SOX7_1, SOX15_1
87	TACCCTAGTTACCGA	
88	AATCCCTTTGATCTATC	TCF7_1, Tcf4, TCF7L2_known7, SOX11_1, TCF7L1_2, SOX4_1, Tcf3, TCFL2
89	TATATACATGTAAAATT	IRX4_1, IRX3_1, IRX6_1
90	CAGGGC	
91	TGTCGTGACCCCTTAAT	RXRA_known9, NR2F2_2
92	AAGTTCAAGGTCAGC	Nr5a2, ESRRR_disc2, RARg, ESRRB_1, Esrrb, NR5A1_2, ESRRR_known7, ESRRG_3, ESRRR_known11, PAX6_2
93	TCGCGAAGGTTGTACT	
94	AGGGGTGAGAGGTCA	TR4, NR2C2_known1, NR2F6_3, RXRA_known10, RXRA_known12, RXRB_1, HNF4_known19, RXRA_known1, PPARG::RXRA, HNF4_known7, PPARA_4, RXRA_known7, HNF4_known1, NR1H2::RXRA, RXR, PPARE, HNF4_known14, HNF4A, HNF4_known2, HNF4_known13, NR2F1, PPARA_3, HNF4a, HNF4_known9, HNF4_known17, HNF4_known21
95	CACGTGG	MYC_known15, MAX, USF1, CLOCK, MYC_known7, Mycn, BMAL1, MYC_known3, MYC_known21, MYC_known22, MYCN_1
96	GCAAAACATTACTA	
97	GAAATGACTCA	BATF_disc1, TRIM28_disc1, BCL_disc2, IRF_disc2, BATF, Atf3, Jun-AP1, STAT_disc2, EP300_disc1, AP-1, NFAT:AP1, PRDM1_disc2
98	GTAAAAAATAATTT	
99	TTGTATGCAAATTAGA	POU2F3_1, POU2F2_known4, POU3F1_2, POU2F2_known8, POU2F2_2, POU2F3_2, POU2F2_known15, POU3F3_2, POU2F2_known12, Oct4, POU2F2_known10, Oct2, POU2F2_known13, POU2F2_known9
100	ATTTCTTTGATCTATA	TCF7_1, Tcf4, TCF7L2_known7, SOX11_1, SOX4_1, Tcf3, TCF7L1_2, TCFL2, TCF7L2_known4
101	AACACCAAAACAAAGGA	
102	AAATAGACAAAGGAAT	
103	GTGCTAATTGTGTGTACGCT	
104	GGATGACTCAT	
105	AAAATACATGTAATACT	IRX3_1, IRX4_1, IRX6_1
106	CAGCCTG	
107	GGGCCGTGTGCAAAAA	MTF1_3, MTF1_1

108	TAAATACATGTAAAATT	IRX6_1, IRX3_1, IRX4_1
109	AATTACCTGTCAATAC	MEIS3_1, PKNOX2_1, TGIF1_2
110	GGTGACTCATC	Jun-AP1, Atf3, AP-1, PRDM1_disc2, BATF, STAT_disc2, EP300_disc1, NFE2_known2, BCL_disc2, IRF_disc2, BACH1_1, TRIM28_disc1, BATF_disc1, AP1_known10, AP1
111	TGGCCACCAGGGGGCGCTA	CTCF_known1, CTCF, SMC3_disc1, BORIS, CTCF_disc9
112	GTAGGGCAAAGGTCA	RXRA_known7, PPARE, RXR, PPARA_3, PPARA_4, HNF4_known14, HNF4A, HNF4_known1, HNF4_known7, HNF4_known9, TR4, NR2C2_known1, NR2F6_3, RXRA_known10, HNF4_known2, HNF4_known13, RXRA_known12, NR2F1, HNF4_known19, RXRB_1, HNF4a, Nur77, Erra, PPARG::RXRA
113	AACTAGCTGTCAATAC	MEIS3_1, PKNOX2_1, TGIF1_2
114	AATATACATGTAAAACA	IRX4_1, IRX3_1, IRX6_1
115	CAGCATGACTCAGCA	NF-E2, Nrf2, NFE2L2_2, NFE2L2, Bach2, Bach1, MAF_known2
116	ACTGACGCTTGGTTACCACAAAG	
117	ACACACAC	
118	ATTGATGAGTCACCAA	Jun-AP1, Atf3, PRDM1_disc2, TRIM28_disc1, AP-1, BATF, STAT_disc2, EP300_disc1, BATF_disc1, BACH1_1, BCL_disc2, NFE2_known2, Fos, IRF_disc2, Bach2
119	TTGTATGCAAATTAGA	POU2F3_1, POU2F2_known8, POU2F2_known4, POU2F3_2, POU2F2_2, POU3F1_2, POU2F2_known15, Oct4, POU3F3_2, POU2F2_known12, POU2F2_known10, Oct2, POU2F2_known13, POU2F2_known9
120	CACATTCCTCCG	TEAD1_2, TEAD1
121	AAATTTGCTGACTTAGC	MAF_known4, MafF, NRL_1, MAF_known7, MAFG_1
122	TTATGTAACAT	NFIL3, NFIL3_1, TEF_3, DBP_2, DBP_4
123	TTAATATTTAAC	HNF1B_1, HNF1B, Hnf1, HNF1A_4, HNF1B_4, HNF1_3, HNF1A_1, HNF1A, HNF1_4, HNF1_1
124	AGCGGCACACACGCAA	
125	AATATACATGTAATATT	IRX3_1, IRX4_1, IRX6_1
126	GAAGAACAGGTGTCCG	MYF6_1, TCF3_2, TCF3_1, Ptf1a, Myf5, ASCL2_1, MyoD
127	CCGATGACGTCATCGT	ATF7_1, JDP2_3, JDP2_5, JDP2_7, JunD, CREB3_1, c-Jun-CRE, Atf1, BATF_known1, ATF3_known12, E2F_disc1, ATF3_known8, ATF3_known2, CRE, ATF2_3, ATF3_known14
128	TGTTCCCATTTGTGTA	
129	AAAGGTCAAAGGTCAAC	NR1H2::RXRA, NR2F6_3, NR2C2_known1, PPARG::RXRA, RXRA_known1, TR4, RXRA_known10, RXRA_known12, RXRB_1, HNF4_known19, HNF4_known7, PPARA_4, HNF4_known1, HNF4_known2, HNF4_known13, NR2F1, HNF4_known14, HNF4A, HNF4_known9, RXR, PPARE, PPARA_3, HNF4a, RXRA_known7, HNF4_known21, TCF7L1_2
130	TTCAATTGTTCTAAAA	SOX18_1, SOX7_1, SOX15_1, SOX13_1, SOX9_1, Sox6, SRY_2
131	ATGACTCAGCAATTT	Bach1, Nrf2, NF-E2, NFE2L2, NFE2L2_2, Bach2, MAFG_1, MAF_known7, MAF_known2, MafA, MAF_known11, MafK
132	CATCAATTGTTCCGCTA	SOX15_1, SOX7_1, SOX13_1, SOX18_1, SOX9_1, SOX11_1, SOX4_1
133	ATGGGATATATCCGCCT	
134	TGCGTG	AHR::ARNT_3, Arnt::Ahr, AHR::ARNT_1
135	ATTGTTA	Sox5

136	AAAATACATGAAAAAT	IRX6_1, IRX3_1, IRX4_1
137	CCATGTGCTT	MYC::MAX, Max, n-Myc
138	TAGTGAACAATAGATTT	SOX15_1, SOX7_1, SOX13_1, SOX9_1, SOX18_1, SOX11_1, SOX4_1, SRY_2
139	AAGGAGCTGTCAATAC	MEIS3_1, PKNOX2_1, TGIF1_2
140	AGAACAGAATGTTCT	NR3C1_disc1, ARE, GRE, PR, NR3C2_1, NR3C1_known4, NR3C1_known6, NR3C1_known3, NR3C1, NR3C1_known10, NR3C1_known8, Ar, NR3C1_known1, NR3C1_known17, NR3C1_known15, NR3C1_known2
141	GGCGAGGGGTCAAGGGC	RXRA_known9, NR2F2_2
142	CAATACCGGAAGTGTA	ETS_known12, ELK3_1, ERF_1, FEV_2, ELK4, ETS_known2, EHF_1, ETV4_2, ETS_known1, ETS_disc2, ETS, ETV1, Elk1, BCL_disc1, ELF1, ETS_known3, Elk4, ETV2_1, GABPA, ELF1_known2, ELF1_disc1, ELF4_1, Fli1, ELF5_3, ELF5_4, ERG, SPDEF_1
143	CGACCATCTGTT	TAL1::TCF3, TAL1_known2, Olig2, OLIG1_1, Atoh1, OLIG2_2, NeuroD1, BHLHA15_1
144	GCTGAGTCAGCAATTTTT	MAF_known4, MafF, MAFG_1, MAF_known7, MafA, MafK, Bach1, MAF_known9, MAF_known11, NRL_1, MAF_disc2, Bach2, NF-E2
145	ACATGCCCAGACATG	p63, TP73_1, TP53_4, TP53, TP63_1, TP53_1, p53
146	AAAGACCTGTCAATAC	MEIS3_1, PKNOX2_1, TGIF1_2
147	GATATTGACAGCTGCGT	TGIF1_2, PKNOX2_1, MEIS3_1
148	AATAAAGAACAATAGAATTTCA	SOX7_1, SOX15_1, SOX18_1, SOX9_1, SOX13_1, SOX11_1, SRY_2, SOX4_1, SOX9_2, SOX9, Sox6
149	TGACCTAAAGTAACCTCTG	LXRE, RARG_3, RARA_2, TRa, RARB_2, RARA_6, RARA_8, RARG_9
150	ACGATGACGTCATCGA	ATF7_1, CREB3_1, JunD, JDP2_7, JDP2_5, JDP2_3, Atf1, c-Jun-CRE, E2F_disc1, ATF3_known12, CRE, ATF3_known8, BATF_known1, ATF3_known14, ATF3_known2, ATF2_3, ATF3_known10, ATF3_disc2, ATF2_2, ARNT_2
151	AAGATGATGTCAT	c-Jun-CRE, JunD
152	AGCCGAAAAAAAAAAT	
153	AAGCACATGG	
154	AAAGATCAAAGGAA	Tcf4, TCF7_1, TCF7L2_known7, Tcf3, TCFL2, TCF7L1_2, TCF7L2_known4
155	CCAAGTCCA	AMYB
156	GGGTGGGGTGGAG	
157	AAAGACCTGTCAATCC	MEIS3_1, PKNOX2_1, TGIF1_2
158	GGGTTTAAATAAATTC	ARID3A_2, LMX1B_1, LHX5_1, LHX1_1, PROP1_1, ALX1_3, LHX3_3, HOXB4_1, PAX7_1, UNCX_1, HOXC4_1, HOXC6_1, LHX9_1, HOXA4_2, NOBOX_2, POU3F2_4, DBX2_1, POU2F2_known14, VAX2_1, PHOX2A_1, RHOXF2_1, PAX4_6, POU3F4_1, LHX4_2, PRRX2_1, HOXD13_1, HOXD3_1, HOXA7_3
159	TATAGATCAAAGGAAAA	TCF7_1, Tcf4, TCF7L2_known7, Tcf3, SOX11_1, SOX4_1, TCFL2, TCF7L2_known4, TCF7L1_2
160	CCGCCAAGGGCAG	TFAP2_known14, TFAP2_known11, TFAP2_known20
161	GAGCACGTGGT	MYC::MAX, MYC_known1, MYC_known13, Max, MYC_known19, MYC_known21, n-Myc, MYC_known18, Myc, c-Myc, MNT_1, MYC_known15, MAX, Mycn, MYC_known3, USF1, Arnt
162	AAGCACCTGTCAATAT	PKNOX2_1, MEIS3_1, TGIF1_2
163	TAAAAATGCTGACTT	MafF, MAF_known4, MAF_disc2, NRL_1

164	TTGAAAACCGTTAATTT	MYB_6, MYBL2_3, MYBL1_4
165	TCACCCATCAATAATCA	
166	TATAGATCAAAGGAAAA	TCF7_1, Tcf4, TCF7L2_known7, Tcf3, SOX11_1, SOX4_1, TCFL2, TCF7L1_2, TCF7L2_known4
167	CTATAATTGTTATCG	
168	AAAGATGATGTCATC	c-Jun-CRE, JunD, ATF7_1, JDP2_7, JDP2_3, JDP2_5, CREB3_1, Atf1, BATF_known1
169	AGGATGACTCAGCAC	NF-E2, Nrf2, NFE2L2_2, Bach1, NFE2L2, Bach2, MAF_known2, MAF_known9, MafK, MAF_known11, MafA, MAF_known7, BACH1_1, MAFG_1, AP-1
170	ATCCACAGGTGCGAAAA	TCF3_6, TCF3_2, TCF3_7, ASCL2_1, ZEB1_known3, LMO2_1, ID4_1, TCF4_2, E2A-nearPU.1
171	AGGTCACCCTGACCT	ESRRA_disc1, ESR2, ERE, ESR1, PPARG, ESRRA_disc3
172	CGACCAACTGCCATGC	AMYB
173	AGATAAGA	
174	GCGGAGGTGTGCGCTC	
175	TAACGTCCGC	MIZF
176	TGACCACGTGGTCGGG	MYC_known19, Max, MYC_known1, MYC_known21, MYC::MAX, n-Myc, MYC_known3, MYC_known13, MYC_known15, MNT_1, MAX, MYC_known12, c-Myc, MYCN_1, MYC_known5, USF1, ARNT_2, Mycn, TCF3_2, MYC_known11, Arnt, MYC_known18, Myc, TCF3_6, Usf2, MYC_known7, BHLHE40_known2, BMAL1
177	CCTTTGTTTT	NANOG_disc2, SOX4_1, SOX11_1, Sox3
178	AACAGTGCAG	MyoD, MyoG, Tcf12, ASCL2_1, Ptf1a, E2A, ASCL2_2, MYOD1_2, Ap4, Myf5
179	GAGCACAGCAGGACA	
180	GAGTGTACGTACGATGG	GMEB1_1
181	CACAGTGCAG	Tcf12, E2A, TCF3_1, MyoD, TFAP4_4, ASCL2_1
182	ATGGAAACCGTTATTTT	MYB_6, MYBL1_4, MYBL2_3
183	TATTGGTAATTACCTT	HOXB6_1, HOXA6_1, HOXC6_1, HOXA2_1, HOXD3_1, BARX1_1, MEOX1_1, PDX1_4, BSX_1, DLX4_1, DLX2_1, MEOX1_2, HOXC4_1, PAX7_1, HOXA2_2
184	GAAGATCAATCACTTA	
185	TTCTTATCTGT	GATA_known15, Gata2, GATA_known16, HDAC2_disc1, GATA_known18, Gata4, CCNT2_disc1, GATA_known6
186	TAAGTAATTAGTTATA	DBX2_1, MNX1_1, PHOX2A_1, HOXC6_1, ALX3_1, POU3F2_4, BARX1_1, HOXA7_3, EVX1_1, VAX2_1, PAX7_1, POU2F2_known14, PRRX2_3, HOXB4_1, BARHL1_1, PRRX2_1, EN2_1, GBX1_1, LHX9_1, HOXC4_1, ALX1_3, EMX2_1, LHX3_3, NOBOX_2, BSX_1, PDX1_4, NKX6-1_3, UNCX_1, LHX6_3, ARX_1, RHOXF2_1, HOXA4_2, HOXA2_3, POU3F4_1, Pax7-longest, LHX5_1, LMX1B_1, LHX1_1, ISX_1, DLX4_1, LHX2_2, HOXB6_1, PAX4_6, LHX3_2, Lhx3, LHX6_2, MSX2_1, PROP1_1, GBX1_2, NKX6-2_1, HOXA3_2, ESX1_3, HOXB3_2, Nobox, GBX1_3, NKX1-1_1, MEOX1_2, GSX1_1, HOXD3_1, DLX2_1, HOXA6_1, ALX3_2, LHX4_2, HESX1_1, HOXA2_2, Lhx2, HMX1_1, PRRX1_3, HOXA2_1, MIXL1_1, VAX1_2, VSX1_2, HMX3_2, DLX1_2, PDX1_6, RAX2_1, SHOX_1, MEOX1_1, LHX8_3, PRRX2_4, NOTO_1, DLX5_2, ISX_4, EMX2_3, HOXB8_1, LHX3_1, EVX2_2, VSX2_2, DLX3_2, DLX2_3, LMX1B_2, HOXC9_1
187	CAATCACTGGCAGAAT	
188	TTATGTACTAATAA	

189	CGACCAACTGCCGTG	AMYB
190	GAAAAGTAACTGTTAACATC	
191	AAGGCCAGATGGTCCGG	TAL1_known2, Atoh1, YY1_known2, TAL1::TCF3, ZBTB18_3, TCF3_1, ZBTB18_1
192	TGACGTCA	ATF3_known8, ATF3_known2, ATF3_known14, E2F_disc1, Atf1, JDP2_7, JDP2_3, JDP2_5, CRE, ATF7_1, CREB3_1, JunD, BATF_known1, ATF2_3, ATF3_known10, c-Jun-CRE, ATF3_known12, ATF2_2
193	GGAATAATTACTTCAG	DLX2_1, MEOX1_1, BSX_1, HOXD3_1, PDX1_4, HOXA2_1, HOXA6_1, BARX1_1, DLX4_1, HOXA3_2, PRRX2_1, HOXC6_1, DLX5_2, PAX4_6, DLX1_2, HOXA2_3, MEOX1_2, ALX3_1, HOXB6_1, PAX7_1, EVX1_1, GBX1_1, EVX2_2, Pax7-longest, DLX2_3, UNCX_2, VAX2_1, DBX2_1, PRRX2_3, ESX1_3, DLX3_2, ALX3_2, HOXA2_2, NOBOX_2, NKX6-2_1, ALX1_3, MIXL1_1, EN2_1, HOXB4_1, HOXB3_2, HESX1_1, MNX1_1, HOXC4_1
194	CAAACAACAACACCT	
195	ACCGGTTGATCACCTGA	
196	CACGTG	Arnt, Mycn, MNT_1, bHLHE40, MYC::MAX, CREB3L1_2, MYC_known12, USF1, BMAL1, CLOCK, c-Myc, BHLHE40_known2, NFE2_disc2, BHLHE40_disc1, MYC_known15, BHLHE41_1, BHLHE40_known4, MYC_known21, MLXIPL_1, MLX_2, SREBP_known5, MAX, n-Myc
197	AGTCACGC	PAX2_3, Pax2
198	CCACTTCCGGC	BCL_disc1, ETS_disc2, Elk1, ETS_known2, ELK3_1, ERF_1, FEV_2, Elk4, ETS_known12, ETV4_2, EHF_1, ETS_known3, Fli1, GABPA, ELF1, ETS, ELF5_3, ELF5_4, ELK4, ERG, ETV1, ELF1_known2, ELF4_1, ELF1_disc1, ETS_known15

<sup>a</sup>Tomtom  $q$ -value < 0.001.

<sup>b</sup>Motifs with no entries had no matching known motif at this threshold.

**Supplementary Table 17. Forward strand probe sequences used in electrophoretic mobility shift assays.**

rs10830963-C	5' TTCACACCATCT <u>C</u> CTATCCAGAACC 3'
rs10830963-G	5' TTCACACCATCT <u>G</u> CTATCCAGAACC 3'
NEUROD1	5' AAATCTGGCCAGCTGCTGATCCAAA 3'

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