Supplementary table 1. Effects of individual type 2 diabetes risk variants and the combined genetic scores on the age at diabetes diagnosis in 203 *HNF1A*-MODY unrelated probands (youngest family members). All effect sizes are in years change of age at diagnosis per risk allele. The 203 patients were successfully genotyped for all 15 SNPs that were included in the combined genetic score. Individual SNP effects are based on risk allele count method. *P* values are unadjusted for multiple testing. Results are presented in order of Table 3 adjusted results.

		Unadjusted analysis			Adjusted analysis ‡		
		Effect Size	**Std Error**	***P*-value**	**Effect Size**	**Std Error**	***P*-value**
Individual SNP effects							
Gene region	SNP						
HNF1B (TCF2) *	rs757210 / rs4430796	-0.64	0.74	0.39	-0.37	0.58	0.52
SLC30A8	rs13266634	-2.09	0.82	0.011	-1.29	0.66	0.052
CDKAL1 *	rs10946398 / rs7754840	-0.93	0.79	0.24	-0.64	0.62	0.30
TCF7L2	rs7903146	0.76	0.85	0.37	-0.46	0.69	0.51
ADAMTS9	rs4607103	0.13	0.89	0.89	-0.89	0.70	0.20
TSPAN8	rs7961581	-1.15	0.82	0.16	-0.79	0.64	0.22
JAZF1 †	rs864745	-1.23	0.93	0.19	-1.31	0.74	0.078
FTO *	rs8050136 / rs9939609	0.05	0.81	0.95	-0.38	0.64	0.55
KCNJ11	rs5219	-0.33	0.87	0.71	0.17	0.68	0.81
CDKN2A/2B	rs10811661	-0.54	1.13	0.63	-0.42	0.88	0.64
WFS1	rs10010131	0.35	0.79	0.66	0.05	0.62	0.94
CDC123	rs12779790	0.73	0.96	0.45	0.42	0.76	0.58
HHEX/IDE *	rs1111875 / rs5015480	-0.04	0.78	0.96	-0.33	0.61	0.59
PPARG	rs1801282	-0.99	1.37	0.47	0.46	1.08	0.67
IGF2BP2	rs4402960	0.17	0.83	0.84	0.28	0.66	0.67
THADA	rs7578597	0.65	1.44	0.65	0.67	1.13	0.55
NOTCH2 †	rs2934381	2.41	1.70	0.16	1.70	1.33	0.20
Combined SNP effect							
Allele count score		-0.26	0.21	0.23	-0.28	0.17	0.094

*At 4 loci different SNPs, representing the same signal, were genotyped by the two study centres, in which case they are shown as UK / Norway SNPs.

† Results for *JAZF1* and *NOTCH2* variants were available only for UK samples (N=140 and 139, respectively).

‡ Adjusted results include study, sex, age at study, presence of intrauterine hyperglycaemia, and mutation position (2 groups, according to exon affected, 1-7 or 8-10) as covariates in the regression model.

Supplementary table 2. Effects of individual type 2 diabetes risk variants and the combined genetic scores on the age at diabetes diagnosis in 410 *HNF1A*-MODY patients, in an adjusted analysis excluding age at study. All effect sizes are in years change of age at diagnosis per risk allele. The 410 patients were successfully genotyped for all 15 SNPs that were included in the combined genetic score. All analyses took into account full family relationships and included a random family effect in the regression model. Individual SNP effects are based on risk allele count method. *P* values are unadjusted for multiple testing. Results are presented in order of the Table 3 adjusted effect sizes.

		Adjusted results excluding age at study			**T-test *P* for difference between results with age at study**
		Effect Size	**Std Error**	***P*-value**	
Individual SNP effects					
Gene region	SNP				
HNF1B (TCF2) *	rs757210 / rs4430796	-1.19	0.52	0.023	0.86
SLC30A8	rs13266634	-1.00	0.59	0.092	0.90
CDKAL1 *	rs10946398 / rs7754840	-1.36	0.52	0.0095	0.48
TCF7L2	rs7903146	-0.34	0.57	0.54	0.67
ADAMTS9	rs4607103	0.07	0.62	0.91	0.41
TSPAN8	rs7961581	-0.79	0.56	0.16	0.72
JAZF1 †	rs864745 (n=296)	-0.47	0.64	0.46	0.99
FTO *	rs8050136 / rs9939609	-0.60	0.57	0.29	0.81
KCNJ11	rs5219	0.20	0.56	0.72	0.47
CDKN2A/2B	rs10811661	-0.79	0.78	0.31	0.59
WFS1	rs10010131	-0.36	0.55	0.51	0.83
CDC123	rs12779790	0.22	0.67	0.74	0.86
HHEX/IDE *	rs1111875 / rs5015480	-0.36	0.53	0.50	0.42
PPARG	rs1801282	-0.81	0.90	0.37	0.32
IGF2BP2	rs4402960	0.72	0.58	0.22	0.70
THADA	rs7578597	0.70	0.93	0.45	0.90
NOTCH2 †	rs2934381 (n=297)	1.31	1.15	0.26	0.75
Combined SNP effect					
Allele count score, adjusted		-0.40	0.15	0.0072	0.80

*At 4 loci different SNPs, representing the same signal, were genotyped by the two study centres, in which case they are shown as UK / Norway SNPs.
† Results for *JAZF1* and *NOTCH2* SNPs were available only for UK samples (N=296 and 297, respectively).

Supplementary table 3. Stratified-by-study analysis of non-polygenic factors, individual type 2 diabetes risk variants, and the combined genetic scores on the age at diabetes diagnosis in 410 *HNF1A*-MODY patients. All analyses took into account full family relationships and, except for those marked ‡, included a random family effect in the regression model All effect sizes are in years change of age at diagnosis per risk allele. Individual SNP effects are based on risk allele count method adjusted for sex, age at study, presence of intrauterine hyperglycaemia, and mutation position. All *P* values are unadjusted for multiple testing. Individual SNP results are in the same order as in Table 3.

		UK (N=298)			Norway (N=112)			T-test *P* for difference
		Effect size	**Std Error**	***P*-value**	**Effect size**	**Std Error**	***P*-value**	
Non-polygenic factors (without genetic score)								
Sex (effect w.r.t. females)		-3.63	1.06	6.3×10^{-4}	-1.48	1.49	0.32	0.27
Presence of intrauterine hyperglycaemia		-5.27	0.96	4.1×10^{-8}	-4.58	1.29	4.0×10^{-4}	0.69
Position of *HNF1A* mutation		-5.27	2.34	0.024	-3.11	5.57	0.58	0.67
Age at study (per year increase)		0.29	0.03	3.3×10^{-26}	0.30	0.04	1.1×10^{-13}	0.86
Individual SNP effects								
Gene region	SNP							
HNF1B *	rs757210 / rs4430796	-0.76	0.57	0.18	-1.53	0.65	0.018	0.45
SLC30A8	rs13266634	-0.74	0.60	0.22	-0.83	0.28	0.003	0.93
CDKAL1 *	rs10946398 / rs7754840	-1.18	0.53	0.026	-0.08	0.92	0.93	0.29
TCF7L2	rs7903146	-0.39	0.54	0.48	-1.19	0.55	0.031	0.40
ADAMTS9 ‡	rs4607103	-0.65	0.61	0.29	-0.70	0.86	0.42	0.96
JAZF1 †	rs864745	-0.46	0.53	0.38	*NA*	*NA*	*NA*	*NA*
FTO *	rs8050136 / rs9939609	-0.47	0.57	0.41	-0.24	0.63	0.70	0.81
TSPAN8 ‡	rs7961581	-0.47	0.52	0.37	-0.56	0.82	0.49	0.93
CDKN2A/2B	rs10811661	0.38	0.74	0.61	-1.16	0.40	0.004	0.21
KCNJ11	rs5219	-0.43	0.59	0.46	0.22	0.94	0.82	0.56
WFS1	rs10010131	-0.20	0.55	0.71	-0.56	0.80	0.48	0.72
CDC123 ‡	rs12779790	-0.09	0.64	0.89	0.13	0.96	0.89	0.85
HHEX-IDE *	rs1111875 / rs5015480	-0.002	0.54	1.00	0.34	0.23	0.15	0.70
THADA	rs7578597	0.69	0.87	0.43	-0.45	1.97	0.82	0.54
IGF2BP2	rs4402960	-0.09	0.55	0.88	1.46	0.90	0.10	0.14
PPARG	rs1801282	0.08	0.92	0.93	1.04	1.25	0.41	0.57
NOTCH2 †	rs2934381	0.82	1.00	0.41	*NA*	*NA*	*NA*	*NA*
Combined SNP effects								
Allele count score, unadjusted		-0.43	0.20	0.036	-0.73	0.32	0.021	0.43
Allele count score, adjusted		-0.35	0.15	0.020	-0.43	0.24	0.069	0.78

*At 4 loci different SNPs, representing the same signal, were genotyped by the two study centres, in which case they are shown as UK / Norway SNPs.

† Results for *JAZF1* and *NOTCH2* SNPs were available only for UK samples (N=296 and 297, respectively).

‡ Because of the small sample size relative to the number of covariates, the random family effect could not be fully fitted in the regression model for the Norwegian sample. Therefore, for these 3 variants, this term was excluded from the model in both studies (in the Exeter sample the results with and without the random family term were nearly identical)