Supplementary Table 1. The list of genes of interest for monogenic diabetes used in this study

MODY	KLF11, NEUROD1, WFS1, GCK, PAX4, BLK, CEL, ABCC8, KCNJ11, INS, HNF1A, PDX1, HNF1B, HNF4A
Neonatal diabetes	SLC19A2, EIF2AK3, SLC2A2, PLAGL1, RFX6, ZFP57, GATA4, GLIS3, PTF1A, NEUROG3, FOXP3, PAX6, IER3IP1, GATA6
MIDD	mtDNA 1-16568
Lipodystrophy	LMNA

MODY, maturity-onset diabetes of the young; MIDD, maternally inherited deafness and diabetes.

Supplementary Table 2. Criteria for classifying pathogenic variants

Very strong	PVS1	Null variant in a gene where loss of function is a known mechanism of disease
Strong	PS1	Same amino acid change as a previously established pathogenic variant regardless of nucleotide change in ClinVar (two or more gold stars as review) or HGMD database (high-confidence disease-causing mutation)
	PS2	*De novo* (both maternity and paternity confirmed) in a patient with the disease and no family history
	PS3	Well-established in vitro or in vivo functional studies supportive of a damaging effect on the gene or gene product
	PS4	The prevalence of the variant in affected individuals is significantly increased compared to the prevalence in controls
Moderate	PM1	Located in a mutational hot spot and/or critical and well-established functional domain which contained only pathogenic or likely pathogenic variants without benign or common (Intervar was used)
	PM2	Absent from controls or at extremely low frequency in controls in public databases (minor allele frequency less than 0.0001)

	PM3	For recessive disorders, detected in trans with a pathogenic variant
	PM4	Protein length change as a result of in-frame deletions/insertions in a nonrepeat region or stop-loss variant
	PM5	Novel missense change at an amino acid residue where a different missense change determined to be pathogenic has been seen before
	PM6	Assumed de novo, but without confirmation of paternity and maternity
Supporting	PP1	Cosegregation with disease in multiple affected family members in a gene definitively known to cause the disease
	PP2	Missense variant in a gene that has a low rate of benign missense variation and where missense variants are a common mechanism of disease (>80% pathogenic variants are missense and <10% of missense variants are benign in ClinVar)
	PP3	Multiple lines of computational evidence support a deleterious effect on the gene or gene product. MetaSVM and GERP++ were used (cutoff to 0.0 for MetaSVM scores, 2.0 for GERP++)
	PP4	Patient's phenotype or family history is highly specific for a disease with a single genetic etiology

PP5	Reputable database reports variant as pathogenic but the evidence is not available to the laboratoryto perform an independent evaluation

Supplementary Table 3. Genes included in targeted panel sequencing and their percent coverage at each frequency

Abbreviation	Gene access number	Gene name	Chromosome	30 X coverage	100 X coverage	Average depth of coverage
LMNA	NM_001282625	Lamin A	1	100	99	444.48
SLC19A2	NM_006996	Solute carrier family 19 member 2	1	99.9	98.6	642.45
KLF11	NM_003597	Krueppel-like factor 11	2	98.3	91.2	695.11
EIF2AK3	NM_001313915	Eukaryotic translation initiation factor 2 alpha kinase 3	2	99.8	98.7	784.83
NEUROD1	NM_002500	Neurogenic differentiation 1	2	99.6	95.8	831.08
SLC2A2	NM_000340	Solute carrier family member 2	3	100	100	850.33
WFS1	NM_001145853	Wolframin ER transmembrane glycoprotein	4	99.9	99.3	1067.61

PLAGL1	NM_001289048	PLAG1 like zinc finger 1	6	100	100	979.13
RFX6	NM_173560	Regulatory factor X6	6	100	99.7	761.66
ZFP57	NM_001109809	ZFP57 zinc finger protein	6	100	100	876.93
GCK	NM_000162	Glucokinase	7	100	100	1142.11
PAX4	NM_006193	Paired box gene 4	7	100	100	972.55
BLK	NM_001330465	Mutated B lymphocyte tyrosine kinase	8	100	99.6	940.61
GATA4	NM_001308093	GATA binding protein 4	8	87	72.3	706.37
GLIS3	NM_152629	GlIS family zinc finger 3	9	100	99.7	1216.39
CEL	NM_001807	Carboxyl ester lipase	9	91.9	85.7	709.67
PTF1A	NM_178161	Pancreas specific transcription factor, 1A	10	96.6	86.7	570.18
NEUROG3	NM_020999	Neurogenin 3	10	99.9	98.8	444.48

ABCC8	NM_000352	ATP binding cassette transporter sub-family C member 8	11	99.9	99.3	584.26
KCNJ11	NM_000525	Potassium inwardly-recitifying channel, subfamily J, member 11	11	95.6	91.7	583.04
FOXP3	NM_001114377	Forkhead boxP3	11	99.6	91.8	250.41
INS	NM_001185098	Insulin	11	99.8	96.3	352.05
PAX6	NM_001310160	Paired box 6	11	100	98.6	562.55
HNF1A	NM_001306179	Hepatoyte nuclear factor 1 homeobox A	12	100	99.6	1407.04
PDX1	NM_000209	Pancreatic and duodenal homeobox 1	13	99.8	96.8	962.82
HNF1B	NM_000458	Hepatoyte nuclear factor 1	17	100	99.4	633.81

		homeobox B				
IER3IP1	NM_016097	Immediate early response 3 interacting protein 1	18	99.8	99	471.32
GATA6	NM_005257	GATA binding protein 6	18	91.8	75.9	258.37
HNF4A	NM_001030003	Hepatoyte nuclear factor 4 homeobox A	20	100	99.9	634.17
mtDNA 1-16568		Mitochondria DNA 1-16568	Mt	100	100	

Average depth is sum of total read depth of each position divided by target region length. Chr, chromosome.