Supplementary Table 1. The presence of a shared haplotype supports a founder effect in the genetically isolated population. For all samples, fetuses and parents, of which enough DNA was available, genotyping was performed for eight STR markers and eight SNPs by standard methods. SNPs were genotyped by Sanger sequencing. SNPs were selected on the basis of the SNP array data from two fetuses. SNPs which were homozygous for the minor allele with a relative low frequency in controls were selected. Allele numbers for STR markers are derived from Centre d'Étude du Polymorphisme Humain; CEPH (www.cephb.fr). As a control DNA from CEPH sample 1347-2 was included.The shared haplotype is indicated in orange. If no data was obtained, cells are left empty.

Marker name	Marker type	Genomic location (chromosome 9; Hg19)	Individual >	father fetus 1		mother fetus 1		fetus 1		father fetus 2 and 3		mother fetus 2 and 3		fetus 4		fetus 5	
			Affection status >	U		U		A		U		U		A		A	
D9S1784	STR	108,038,745		6	11	8	7			8	8	12	5	12	7	3	5
D9S1677	STR	111,937,590		8	1	8	9			8	2	8	4	8	8	8	8
D9S131	STR	113,043,030		7	7	7	10	7	7	7	8	7	8	7	7	7	7
rs10816965	SNP	113,069,090		G	G	G	A			G	A	G	A	G	G		
rs992886	SNP	113,142,009		G	T	G	T			G	G	G	T	G	G		
rs10980448	SNP	113,325,361		T	T	T	T			T	T	T	T	T	T	T	T
D9S1828	STR	113,332,715		7	2	7	2			7	2	7	2	7	7	7	7
rs10817052	SNP	113,373,423		A	G	A	A			A	G	A	G	A	A		
p.(Ile575Thr)	mutation	113,547,944		+	-	+	-	+	+	+	-	+	-	+	+	+	+
rs1326890	SNP	113,686,353		C	T	C	T			C	T	C	C	C	C		
rs17382569	SNP	113,747,491		T	C	T	C			T	C	T	C	T	T	T	T
rs10980705	SNP	113,803,185		T	T	T	C			T	C	T	C	T	T	T	T
D9S1683	STR	113,863,336		1	1	1	5			1	5	1	1	1	1	1	1
rs10126017	SNP	113,918,933		G	G	G	A			G	A	G	G	G	G		
D9S1856	STR	114,943,296		10	8	10	4			10	6	10	1	10	2	10	10
D9S174	STR	115,821,385		2	2	2	1			2	2	2	1	2	3	2	2
D9S1776	STR	117,959,434		7	2	4	2			6	11	1	7	1	7	6	7

Marker name	father fetus 6		mother fetus 6		fetus 6		father fetus 7		fetus 7		father fetus 8		mother fetus 8		sibling fetus 8	
	U		U		A		U		A		U		U		U	
D9S1784	12	11	11	5	12	11	12	5	12	5	4	8	12	8	12	8
D9S1677	8	2	8	2	8	8	8	11			8	4	8	9	8	4
D9S131	7	3	7	10	7	7	7	3	7	7	7	8	7	5	7	8
rs10816965	G	A	G	A	G	G	G	A			G	A	G	A	G	A
rs992886	G	G	G	T	G	G	G	T			G	T	G	T	G	T
rs10980448	T	T	T	T	T	T	T	T			T	T	T	C	T	T
D9S1828	7	9	7	1	7	7	7	2	7	7	7	4	7	3	7	4
rs10817052	A	G	A	G	A	A	A	G			A	G	A	G	A	G
p.(Ile575Thr)	+	-	+	-	+	+	+	-	+	+	+	-	+	-	+	-
rs1326890	C	T	C	T	C	C	C	C			C	T	C	T	C	T
rs17382569	T	C	T	C	T	T	T	T	T	T	T	C	T	C	T	C
rs10980705	T	T	T	C	T	T	T	C			T	C	T	C	T	C
D9S1683	1	2	1	5	1	1	1	4	1	1	1	4	1	2	1	4
rs10126017	G	G	G	A	G	G	G	A			G	G	G	A	G	G
D9S1856	10	8	10	8	10	10	10	8	10	10	10	1	10	1	10	1
D9S174	2	2	2	4	2	2	2	4	2	2	2	2	2	2	2	2
D9S1776	1	6	6	2	1	2	1	6	4	1	1	1	1	6	1	1

Marker name	father fetus 9		mother fetus 9		father fetus 10 and 11		mother fetus 10 and 11		fetus 10		fetus 11		fetus 12		control CEPH 1347-2	
	U		U		U		U		A		A		A		U	
D9S1784	8	3	7	5	12	4	4	8	12	4	12	4	8	5	4	13
D9S1677	8	1	8	4	8	1	8	4	8	8	8	8	8	8	5	10
D9S131	7	9	7	9	7	8	7	6	7	7	7	7	7	7	8	9
rs10816965	G	A	G	A	G	A	G	A	G	G	G	G			A	A
rs992886	G	G	G	T	G	T	G	T	G	G	G	G	G	G	G	T
rs10980448	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T
D9S1828	7	2	7	4	7	4	7	1	7	7	7	7	7	7	9	1
rs10817052	A	G	A	G	A	G	A	A	A	A	A	A			A	G
p.(Ile575Thr)	+	-	+	-	+	-	+	-	+	+	+	+	+	+		
rs1326890	C	T	T	T	C	T	C	T	C	C	C	C	C	C	T	T
rs17382569	T	C	C	C	T	C	T	C	T	T	T	T	T	T	C	C
rs10980705	T	T	T	C	T	C	T	C	T	T	T	T	T	T	C	C
D9S1683	1	2	1	2	1	4	1	4	1	1	1	1	1	1	2	1
rs10126017	G	A	G	A	G	G	G	G	G	G	G	G			A	G
D9S1856	10	1	8	3	10	1	10	8	10	10	10	10	10	10	6	6
D9S174	2	2	2	1	2	2	2	2	2	2	2	2	2	2	3	2
D9S1776	1	6	1	3	1	1	7	2	1	7	1	7	6	2	4	1