ONLINE DATA SUPPLEMENTS

EXTENDED METHODS

Genetic Analyses

Genotyping for the common variants in LQTS and *NOS1AP* genes was performed using Sequenom MALDI-TOF mass spectrometry (MassArray Compact Analyzer, Sequenom Inc, San Diego, CA, U.S.A.) according to manufacturer's instructions. The following variants were genotyped using iPLEX chemistry: *KCNH2* (NM_000238) rs3807375 G/A, *SCN5A* (NM_198056) **R190G C>G,** H558R (rs1805124, A/G), *SCN5A* A572D C/A, *KCNE1* (NM_000219) D85N (rs1805128, G/A), *KCNE1* G38S (rs1805127, G/A), *KCNE2* (NM_172201) T8A (rs2234916, A/G), *NOS1AP* (NM_014697) rs10494366 T/G, rs10918594 C/G, rs2880058 A/G and rs4657139 T/A. Genotyping for *KCNH2* R1047L (rs36210421, G/T) was completed using the homogeneous MassEXTEND method. Sequences were reviewed using the ProxSNP and PreXTEND software packages (www.realsnp.com), and the reactions were designed utilizing Sequenom Assay Designer 3.1 software. The PCR primer and extension primer sequences are available in the supplementary data (online Data Supplement Table 1). Prior to genotyping, reaction conditions were tested with 32 test DNA samples. The results were evaluated using SpectroAnalyzer 3.4 software. *KCNH2* K897T (rs1805123, A/C) was genotyped with Applied Biosystems TaqMan SNP Genotyping Assay C_11631103_10 and 7900HT Real Time PCR System (Applied Biosystems, Foster City, CA, U.S.A.) according to standard protocols. SDS2.2 software (Applied Biosystems, Foster City, CA, U.S.A.) was used in the evaluation of the genotyping results for *KCNH2* K897T (rs1805123). Previously identified heterozygous and homozygous DNA samples (1) served as positive controls in the genotyping process.

REFERENCE SECTION

1. Fodstad H, Swan H, Laitinen P, et al. Four potassium channel mutations account for 73% of the genetic spectrum underlying long-QT syndrome (LQTS) and provide evidence for a strong founder effect in Finland. Ann Med 2004;36:53-63.