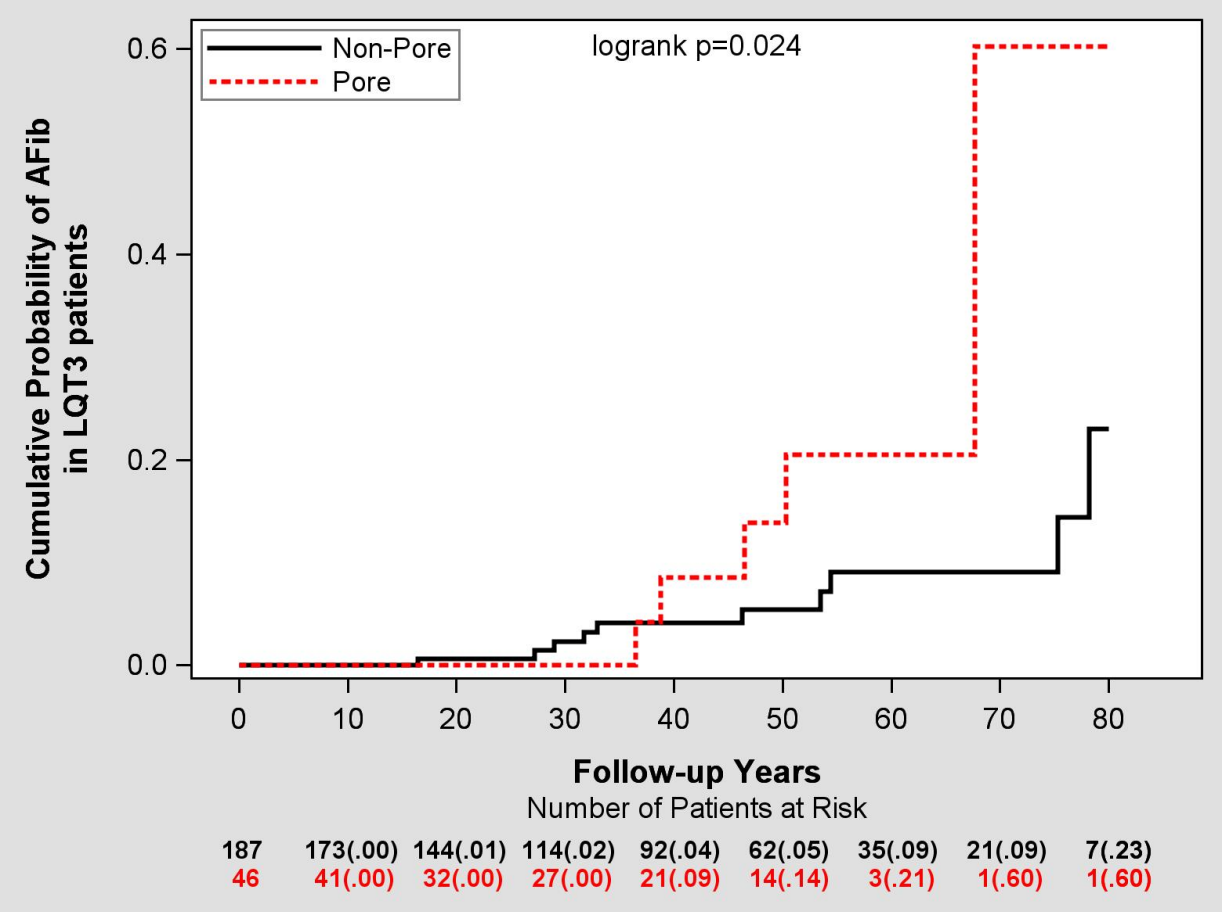
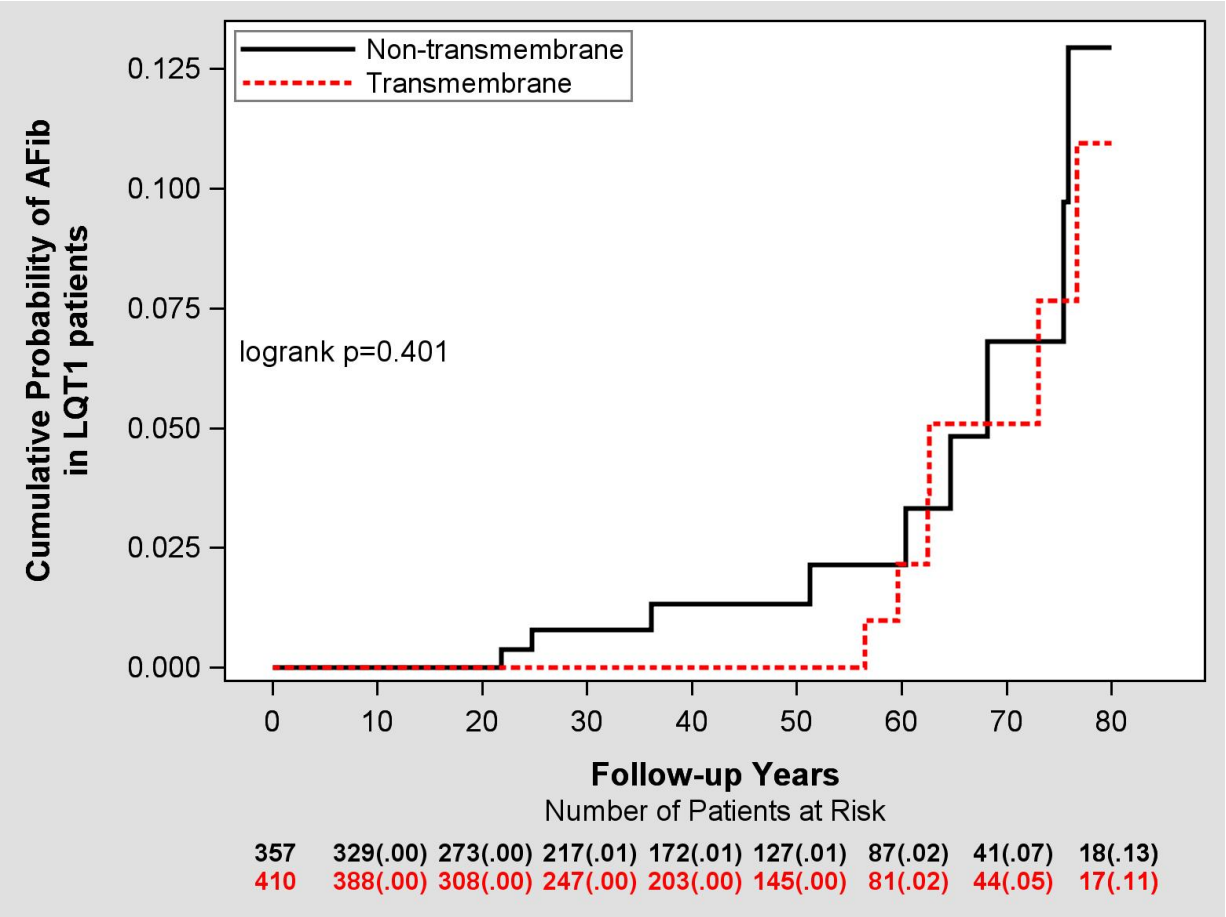
SUPPLEMENTAL MATERIAL

Supplementary Table 1: *Distrubution of mutation types by their location in the LQT1, LQT2 and LQT3 genes and their relationship to AF.*

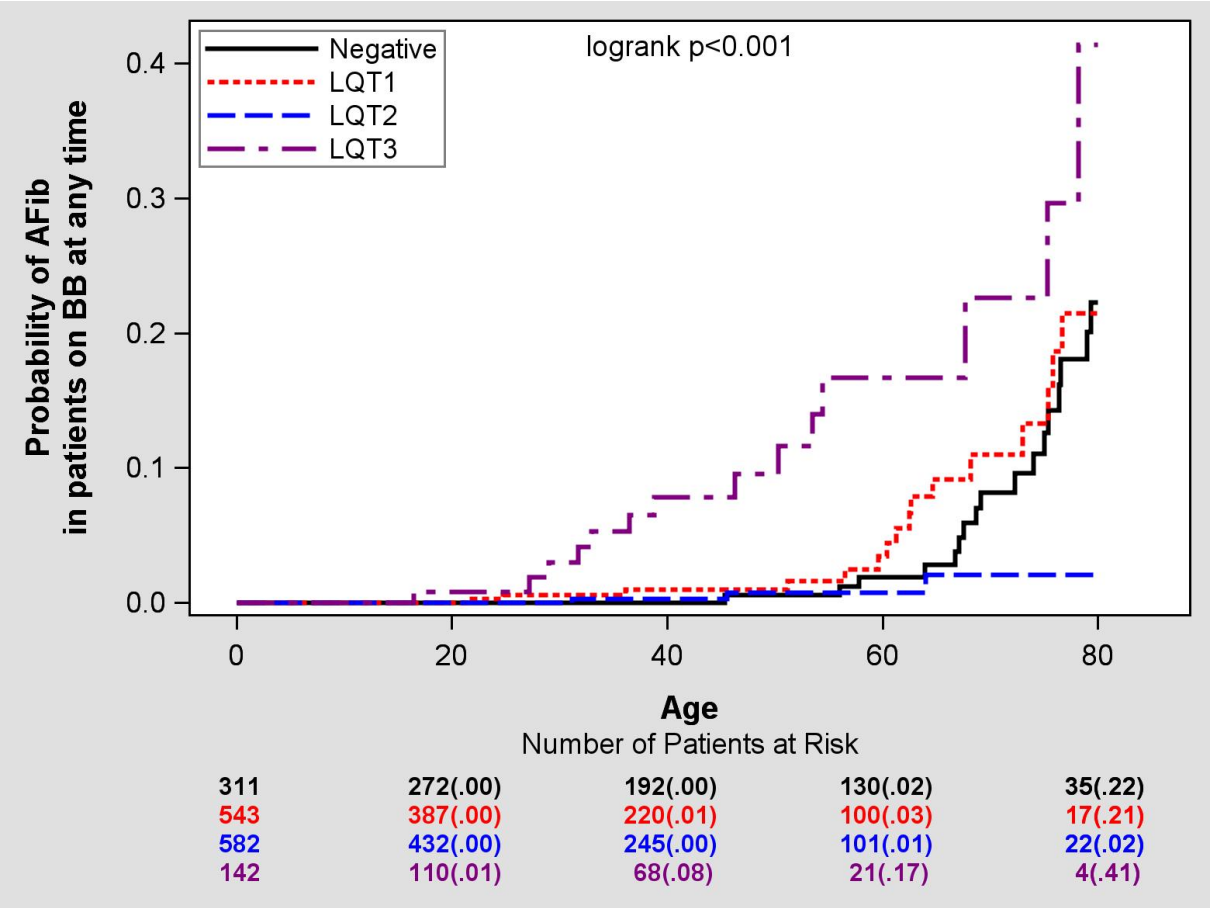
	AF	No AF	p-value
LQT1: Transmembrane mutations, n(%)	6(38)	404(53)	0.231
LQT2: Pore mutations, n(%)	0(0)	170(23)	1.000
LQT3: Pore mutations, n(%)	6(35)	40(19)	0.113



Supplementary Figure 1A: *Cumulative life-time risk of new onset AF among LQT3 patients by the type of SCN5A mutations (pore vs non-pore). Note the increased AF hazard associated with the pore mutations.*



Supplementary Figure 1B: *Cumulative life-time risk of new-onset AF among LQT1 patients by the type of KCNQ1 mutation (transmembrane vs non-transmebrane)*



Supplementary Figure 2: *The results of sensitivity analysis demonstrating cumulative lifetime risk of AF among patients with LQTS by genotype compared with genotype-negative controls. The analysis is limited to patients who were treated with beta-blockers at any time. Observe that curve distribution is similar to the entire cohort presented in the Figure 1 thus suggesting that differences in the AF risk between genotypes are not dependent on the beta-blocker use.*