SUPPLEMENTAL MATERIAL

Supplemental Table 1:

Supplemental Table 1. Risk of Recurrence During the Blanking Period (<90 Days) According to Risk Allele Status

			Combined		VU		HCL		MGH	
SNP	**Locus**	**Risk Allele**	**OR**	***P***	**OR**	***P***	**OR**	***P***	**OR**	***P***
rs13376333	1q21	T	1.5 (1.2-2.0)	0.002	1.5 (0.8-2.6)	0.130	1.6 (1.2-2.2)	0.004	1.0 (0.4-2.4)	0.938
rs2200733	4q25	T	1.6 (1.2-2.1)	0.000	2.0 (1.1-3.4)	0.016	1.5 (1.1-2.1)	0.007	1.1 (0.5-2.7)	0.782
rs10033464	4q25	T	1.0 (0.8-1.4)	0.815	0.8 (0.4-1.6)	0.503	1.0 (0.7-1.5)	0.793	1.6 (0.6-4.2)	0.317
rs7193343	16q22	T	0.9 (0.7-1.2)	0.696	1.2 (0.7-2.0)	0.579	0.9 (0.6-1.2)	0.323	1.3 (0.5-2.9)	0.609

Recurrence includes AF, atrial flutter, or atrial tachycardia during the 3-month blanking period. 95% confidence intervals are presented in parentheses. Dominant genetic modeling is used for all SNPs. The reference genotype is CC for rs2200733, rs7193343, and rs13376333. The reference genotype is GG for rs10033464.

Supplemental Table 2:

Supplemental Table 2. Univariate Analysis: Risk of Recurrence According to Risk Allele Status

SNP	Locus	Risk Allele	Combined		VU		HCL		MGH	
			HR	*P*	HR	*P*	HR	*P*	HR	*P*
rs13376333	1q21	T	1.1 (0.9-1.3)	0.345	1.2 (0.8-1.7)	0.384	1.1 (0.9-1.4)	0.377	0.8 (0.4-1.5)	0.419
rs2200733	4q25	T	1.2 (1.0-1.5)	0.026	1.5 (1.0-2.2)	0.027	1.1 (0.9-1.4)	0.326	1.6 (0.8-3.1)	0.216
rs10033464	4q25	T	0.8 (0.7-1.0)	0.114	0.7 (0.4-1.2)	0.181	0.9 (0.7-1.1)	0.314	0.7 (0.3-1.7)	0.478
rs7193343	16q22	T	0.9 (0.7-1.1)	0.285	1.3 (0.9-1.9)	0.133	0.8 (0.6-1.0)	0.056	0.7 (0.3-1.4)	0.292

Recurrence includes AF, atrial flutter, or atrial tachycardia. Dominant genetic modeling is used for all SNPs. CC for rs2200733, rs7193343, and rs13376333. The reference genotype is GG for rs10033464.

Supplemental Table 3

Supplemental Table 3. Subgroup Analysis of Subjects with an Atrial Fibrillation Recurrence

SNP	Locus	Risk Allele	VU Adj. HR	VU *P*	HCL Adj. OR	HCL *P*	MGH Adj. HR	MGH *P*
rs13376333	1q21	T	1.4 (0.9-2.1)	0.147	1.0 (0.6-1.5)	0.860	0.8 (0.3-1.9)	0.557
rs2200733	4q25	T	1.7 (1.1-2.7)	0.015	1.3 (0.9-2.0)	0.167	0.4 (0.1-1.2)	0.111
rs10033464	4q25	T	0.7 (0.4-1.2)	0.189	1.3 (0.8-2.1)	0.213	0.9 (0.3-2.6)	0.794
rs7193343	16q22	T	1.2 (0.8-1.8)	0.430	0.7 (0.5-1.2)	0.195	0.7 (0.3-1.8)	0.420

Subgroup analysis includes only patients with AF recurrence. Dominant genetic modeling is used for all SNPs. VU and HCL models are adjusted for age, gender, paroxysmal AF status, hypertension, BMI, LA diameter, and LVEF. The MGH model is adjusted for age and gender. The reference genotype is CC for rs2200733, rs7193343, and rs13376333. The reference genotype is GG for rs10033464.