Supplementary Information for:

Genome-wide association study identifies a susceptibility locus at 21q21 for ventricular fibrillation in acute myocardial infarction

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Supplementary Table 1. Most Significant Associations between Single Nucleotide Polymorphisms (SNPs) and Ventricular Fibrillation in the AGNES case-control set.

SNP	Chromosome Position	Position *	Location	Minor Allele	Major Allele	Frequency Minor Allele †	Imputed (yes/no)	Rsq	Odds Ratio Per Copy of Minor Allele (95% CI) ∫	P Value ‡
rs2824293	21	17709385	Intergenic	G	A	0.47	yes	1.00	1.78 (1.47,2.13)	3.34×10^{-10}
rs2824292	21	17709047	Intergenic	G	A	0.47	no	1.00	1.78 (1.47,2.13)	3.36×10^{-10}
rs208910	21	17708105	Intergenic	C	T	0.47	yes	0.99	1.77 (1.48,2.13)	4.42×10^{-10}
rs12483129	21	17711037	Intergenic	C	T	0.49	yes	0.96	0.58 (0.48,0.70)	6.07×10^{-09}
rs9978331	21	17714804	Intergenic	G	A	0.48	yes	0.97	0.59 (0.49,0.70)	1.35×10^{-08}
rs2824294	21	17709789	Intergenic	T	C	0.48	no	1.00	0.60 (0.50,0.72)	3.61×10^{-08}
rs13050588	21	17721619	Intergenic	T	C	0.37	yes	0.96	1.69 (1.40,2.04)	4.84×10^{-08}
rs4818351	21	17720626	Intergenic	C	T	0.37	yes	0.96	1.69 (1.40,2.05)	4.92×10^{-08}
rs1493100	21	17713763	Intergenic	G	A	0.37	yes	0.97	1.69 (1.39,2.04)	6.07×10^{-08}
rs8130544	21	17708212	Intergenic	C	T	0.36	no	1.00	1.63 (1.35,1.97)	3.22×10^{-07}
rs2824290	21	17707528	Intergenic	A	G	0.64	yes	0.99	0.61 (0.51,0.74)	3.31×10^{-07}
rs2824289	21	17706394	Intergenic	A	T	0.36	yes	0.99	1.63 (1.35,1.97)	3.33×10^{-07}
rs1353342	9	78064589	Intergenic	A	C	0.11	no	1.00	0.46 (0.34,0.63)	3.34×10^{-07}
rs208918	21	17719150	Intergenic	T	A	0.49	yes	0.97	1.59 (1.33,1.92)	3.57×10^{-07}
rs2824288	21	17702254	Intergenic	G	C	0.36	yes	0.98	1.61 (1.33,1.96)	4.69×10^{-07}
rs208926	21	17722200	Intergenic	C	A	0.48	no	1.00	1.56 (1.31,1.88)	5.13×10^{-07}
rs12090554	1	183818971	Intergenic	A	G	0.23	no	1.00	0.58 (0.47,0.72)	7.89×10^{-07}

* Based on Build 36.2. † Allele Frequency was based on the total AGNES sample. ∫ Odds ratios are adjusted for age and sex. ‡ The P-values are corrected for genomic control factor. Rsq estimates the squared correlation between imputed and true genotypes.

Supplementary Table 2. Genotype distributions in the patient samples studied and in a sample of the general population.

Sample	N	Frequencies (95% CI)		
		rs2824292		
		AA	**AG**	**GG**
AGNES cases	513	0.22(0.19-0.26)	0.48(0.44-0.52)	0.30(0.26-0.34)
AGNES controls	457	0.37(0.32-0.41)	0.48(0.43-0.52)	0.15(0.12-0.19)
ARREST-MI (cases)	146	0.25(0.18-0.32)	0.47(0.39-0.55)	0.27(0.20-0.35)
GENDER-MI (controls)	391	0.35(0.30-0.40)	0.48(0.43-0.53)	0.17(0.13-0.21)
General Population	492	0.29(0.25-0.33)	0.52(0.48-0.57)	0.19(0.16-0.23)
		rs1353342		
		GG	**GT**	**TT**
AGNES cases	514	0.86(0.83-0.89)	0.13(0.10-0.16)	0.01(0.00-0.01)
AGNES controls	457	0.73(0.69-0.77)	0.25(0.21-0.29)	0.02(0.01-0.03)
ARREST-MI (cases)	146	0.82(0.76-0.88)	0.17(0.11-0.23)	0.01(-0.01-0.02)
GENDER-MI (controls)	391	0.79(0.75-0.83)	0.2(0.16-0.24)	0.01(0.0-0.02)
General Population	488	0.79(0.75-0.83)	0.2(0.16-0.23)	0.01(0.0-0.02)
		rs12090554		
		GG	**AG**	**AA**
AGNES cases	515	0.67(0.63-0.71)	0.29(0.25-0.33)	0.04(0.02-0.06)
AGNES controls	455	0.51(0.46-0.56)	0.42(0.38-0.47)	0.07(0.04-0.09)
ARREST-MI (cases)	143	0.66(0.59-0.74)	0.31(0.24-0.39)	0.02(0.0-0.04)
GENDER-MI (controls)	391	0.58(0.53-0.62)	0.38(0.34-0.43)	0.04(0.02-0.06)
General Population	477	0.57(0.52-0.61)	0.39(0.34-0.43)	0.05(0.03-0.06)

Supplementary Table 3. Genotype frequencies and Odds Ratio (95% CI) for rs2824292 based on time-to-VF from onset of complaints.

	Homozygous for major allele	**Heterozygous**	**Homozygous for minor allele**	**Odds ratio for VF (95% CI) additive model***	**P value***	**P value §**
No VF	168(36.8%)	219(48.0%)	69(15.1%)	1.00 (ref)		
Early onset VF†	30(25.2%)	51(42.9%)	38(31.9%)	1.79(1.34-2.40)	$7.4{\times}10^{-5}$	0.76
Late onset VF‡	51(25.0%)	92(45.1%)	61(29.9%)	1.71(1.35-2.17)	$1.0{\times}10^{-5}$	

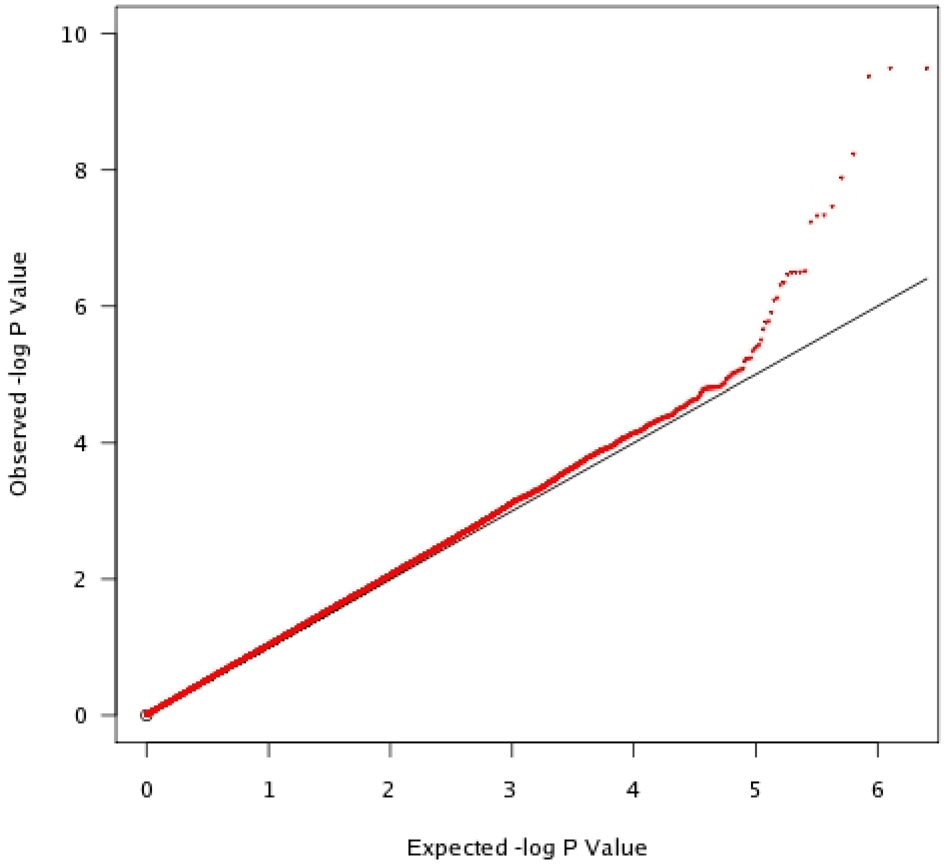
† VF occurring within 5 minutes of onset of chest pain

‡ VF occurring after more than 30 minutes of onset of chest pain

* Compares early onset or late onset VF against controls adjusted for age and sex

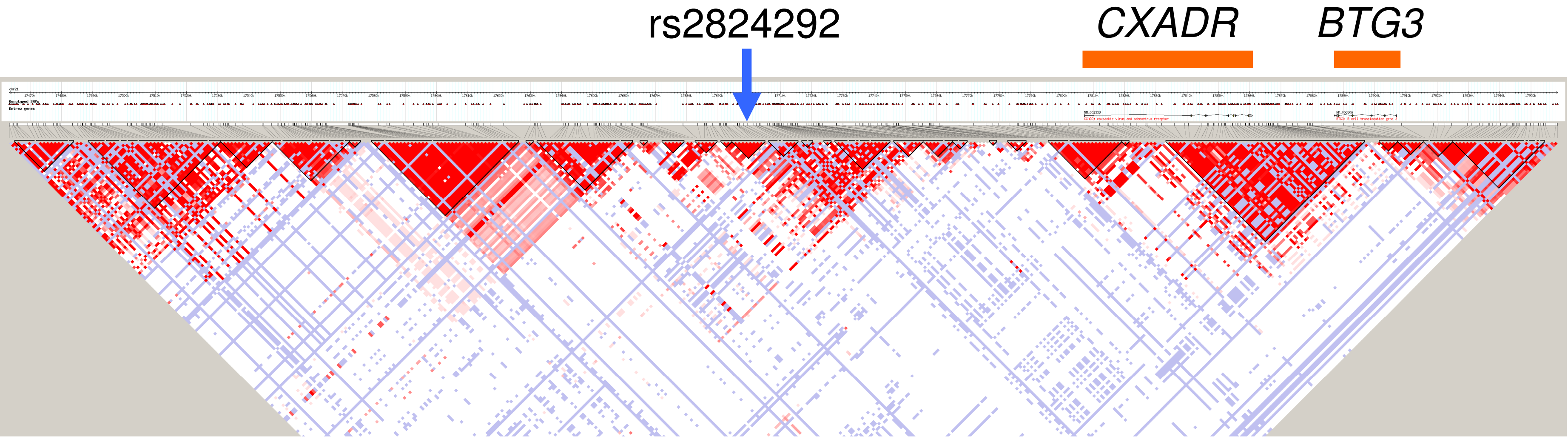
§ Compares early onset vs. late onset VF; adjusted for age and sex

Supplementary Figure 1



Supplementary Figure 1. Quantile-Quantile Plot of Test Statistics (P-values) for the Associations of Single-Nucleotide Polymorphisms with Ventricular Fibrillation in the AGNES Population. Under the null hypothesis of no association, the data points would be expected to fall on the black line. P-values corrected for possible population stratification by means of the genomic control method are presented (λ=1.026).

Supplementary Figure 2



Supplementary Figure 2. Haploview plot of linkage disequilibrium (D') for all CEU HapMap SNPs in a 500 Kb region spanning rs2824292. Colour scheme: D′<1 and LOD<2 = white, D′ =1 and LOD<2 = blue, D′ <1 and LOD≥2 = shades of pink/red, D′ =1 and LOD≥2 = bright red.