

Supporting Information Table S2. Validation study results: SNP associations with ventricular dysfunction after primary coronary artery bypass graft surgery in 786 European ancestry men from the CABG Genomics Study Cohort. (63 SNPs were selected from 34 genetic loci identified to be associated with ventricular dysfunction in the GWAS)

SNP	Chr #, Location NCBI hg36	Gene	GWAS or Additional SNP	Minor Allele/ Major Allele	MAF VnD Cases (n=71)*/ Controls (n=715)	Genetic Model	Unadjusted Odds Ratio	Univariate Asymptotic P value	Univariate Permuted Point-wise P value	MV Adjusted Odds Ratio	MV Adjusted Asymptotic P value	MV Adjusted Point-wise P value
rs7549755	Chr 1, 91,930,396	<i>TGFBR3</i>	GWAS	C/T	0.32/0.21 GWAS 0.33/0.19	Allelic Additive Dominant Recessive	1.78 1.81 2.23 1.67	0.002 0.002 0.002 0.30	0.003 0.003 0.002 0.31	1.65 2.14 1.16	0.02 0.005 0.78	0.02 0.005 0.75
rs2765888	Chr 1, 91,934,880		Additional	T/C	0.08/0.11	Allelic Additive Dominant Recessive	0.68 0.68 0.63 1.25	0.24 0.24 0.19 0.83	0.26 0.26 0.17 0.37	0.84 0.77 1.96	0.61 0.48 0.54	0.61 0.50 0.20
rs6690388	Chr 1, 153,041,071	<i>KCNN3</i>	Additional	C/T	0.30/0.20	Allelic Additive Dominant Recessive	1.78 1.75 2.16 1.62	0.003 0.004 0.002 0.33	0.002 0.003 0.001 0.31	1.70 2.24 1.20	0.01 0.003 0.74	0.008 0.002 0.62
rs6426944	Chr 1, 153,043,036	<i>KCNN3</i>	Additional	A/G	0.37/0.25	Allelic Additive Dominant Recessive	1.76 1.77 2.35 1.56	0.002 0.002 0.001 0.30	0.002 0.002 0.001 0.26	1.81 2.12 2.00	0.005 0.007 0.15	0.006 0.007 0.12
rs1702176	Chr 1, 153,043,781	<i>KCNN3</i>	Additional	T/C	0.25/0.27	Allelic Additive Dominant Recessive	0.94 0.94 1.03 0.54	0.74 0.74 0.90 0.31	0.78 0.71 0.98 0.23	0.83 0.87 0.53	0.41 0.61 0.32	0.41 0.62 0.33
rs2798601	Chr 1, 153,046,309	<i>KCNN3</i>	GWAS	A/G	0.30/0.18 GWAS 0.29/0.16	Allelic Additive Dominant Recessive	1.94 1.92 2.16 2.66	0.0006 0.0009 0.002 0.04	0.001 0.001 0.002 0.04	1.95 2.11 2.92	0.003 0.006 0.05	0.002 0.004 0.04
rs1013219	Chr 1, 175,479,499	<i>FAM5B</i>	Additional	A/G	0.36/0.40	Allelic Additive Dominant Recessive	0.85 0.85 1.10 0.38	0.38 0.38 0.72 0.04	0.43 0.42 0.73 0.03	0.81 1.01 0.36	0.28 0.97 0.04	0.27 1.00 0.04
rs12744134	Chr 1, 175,490,296	<i>FAM5B</i>	GWAS	A/G	0.11/0.23 GWAS 0.11/0.25	Allelic Additive Dominant Recessive	0.42 0.42 0.43 -	0.001 0.002 0.004 1.00	0.001 0.0008 0.003 0.98	0.39 0.39 -	0.002 0.003 1.00	0.001 0.002 0.98
rs10752878	Chr 1, 180,848,998	<i>RGS16</i>	GWAS	G/T	0.25/0.14 GWAS 0.27/0.13	Allelic Additive Dominant Recessive	2.09 1.98 2.16 3.38	0.0003 0.0007 0.003 0.01	0.0006 0.0008 0.002 0.01	2.10 2.29 3.86	0.001 0.003 0.02	0.0008 0.004 0.01

rs1287820	Chr 1, 180,855,954		GWAS	G/C	0.32/0.20 GWAS 0.34/0.20	Allelic Additive Dominant Recessive	1.96 2.00 2.19 3.02	0.0004 0.0004 0.002 0.01	0.001 0.0004 0.001 0.02	2.26 2.53 3.70	0.0002 0.0008 0.008	0.0004 0.0002 0.008
rs7646796	Chr 3, 6,615,547		Additional	T/C	0.45/0.43	Allelic Additive Dominant Recessive	1.08 1.07 0.79 1.66	0.68 0.69 0.36 0.07	0.72 0.71 0.36 0.07	1.00 0.74 1.45	0.99 0.28 0.23	0.99 0.29 0.24
rs7430827	Chr 3, 6,617,993		GWAS	C/A	0.42/0.36 GWAS 0.42/0.34	Allelic Additive Dominant Recessive	1.29 1.28 0.86 2.76	0.16 0.17 0.53 0.0004	0.17 0.16 0.62 0.001	1.45 1.08 3.03	0.05 0.77 0.0005	0.05 0.78 0.0002
rs17691914	Chr 3, 34,937,807		GWAS	G/A	0.19/0.08 GWAS 0.21/0.07	Allelic Additive Dominant Recessive	2.74 2.74 3.53 -	9.3X10 ⁻⁶ 2.7X10 ⁻⁵ 2.2X10 ⁻⁶ 1.00	<0.0001 0.0002 0.0002 0.60	2.96 3.76 -	6.0X10 ⁻⁵ 1.1X10 ⁻⁵ 1.00	0.0002 0.0002 0.98
rs9835451	Chr 3, 34,946,568		GWAS	G/A	0.22/0.11 GWAS 0.23/0.11	Allelic Additive Dominant Recessive	2.17 2.14 2.76 0.77	0.0003 0.0005 8.1X10 ⁻⁵ 0.80	0.0005 0.0006 0.0002 0.44	2.29 2.62 1.75	0.001 0.0007 0.60	0.0008 0.0008 0.33
rs17358517	Chr 3, 59,660,772		GWAS	T/C	0.38/0.23 GWAS 0.38/0.22	Allelic Additive Dominant Recessive	2.07 2.07 2.57 2.52	5.8X10 ⁻⁵ 9.6X10 ⁻⁵ 0.0003 0.02	0.0005 0.0002 0.0002 0.009	2.14 2.72 2.61	0.0002 0.0004 0.02	0.0004 0.0004 0.01
rs17061085	Chr 3, 59,666,765		Additional	A/G	0.26/0.13	Allelic Additive Dominant Recessive	2.42 2.04 2.69 2.59	1.2X10 ⁻⁵ 0.0001 0.0001 0.03	0.0003 0.0004 0.0004 0.03	2.07 2.76 2.61	0.0004 0.0003 0.05	0.0004 0.0002 0.04
rs6774674	Chr 3, 67,263,367		Additional	C/T	0.32/0.39	Allelic Additive Dominant Recessive	0.71 0.71 0.62 0.72	0.07 0.07 0.05 0.39	0.07 0.07 0.05 0.42	0.67 0.56 0.73	0.06 0.03 0.44	0.05 0.04 0.43
rs6766797	Chr 3, 67,266,318		GWAS	A/T	0.27/0.36 GWAS 0.24/0.41	Allelic Additive Dominant Recessive	0.64 0.63 0.51 0.75	0.02 0.02 0.007 0.49	0.02 0.02 0.01 0.51	0.60 0.46 0.82	0.02 0.004 0.66	0.02 0.005 0.70
rs9863767	Chr 3, 75,164,647		GWAS	A/C	0.33/0.22 GWAS 0.34/0.20	Allelic Additive Dominant Recessive	1.72 1.79 1.88 2.68	0.004 0.003 0.01 0.03	0.004 0.004 0.01 0.02	1.86 1.92 3.06	0.004 0.02 0.02	0.004 0.01 0.02
rs9831754	Chr 3, 78,436,281		GWAS	G/T	0.29/0.20 GWAS 0.30/0.18	Allelic Additive Dominant Recessive	1.65 1.67 1.53 3.82	0.01 0.01 0.09 0.002	0.01 0.01 0.06 0.003	1.53 1.48 2.81	0.05 0.15 0.03	0.05 0.16 0.02
rs9837024	Chr 3,		GWAS	G/A	0.36/0.22	Allelic	1.99	0.0002	0.0003			

	78,534,327					GWAS 0.36/0.21	Additive 2.09 Dominant 2.01 Recessive 4.51	0.0002 0.006 0.0001	0.0002 0.006 0.001	1.95 2.06 3.27	0.002 0.008 0.10	0.001 0.008 0.009
rs501833	Chr 3, 184,360,620	<i>LAMP3</i>	Additional	C/G	0.13/0.11	Allelic Additive 1.22 1.23 Dominant 1.21 Recessive 2.02	1.22 1.23 1.21 2.02	0.46 0.45 0.51 0.52	0.46 0.44 0.52 0.35	1.10 1.11 1.20	0.74 0.75 0.88	0.76 0.75 0.44
rs500910	Chr 3, 184,360,726	<i>LAMP3</i>	GWAS	A/T	0.19/0.32 GWAS 0.20/0.37	Allelic Additive 0.51 Dominant 0.41 Recessive 0.59	0.51 0.51 0.41 0.59	0.002 0.002 0.0007 0.32	0.002 0.002 0.0004 0.29	0.52 0.43 0.53	0.005 0.003 0.26	0.007 0.001 0.24
rs1965484	Chr 3, 184,361,591	<i>LAMP3</i>	GWAS	A/C	0.32/0.42 GWAS 0.32/0.48	Allelic Additive 0.64 Dominant 0.46 Recessive 0.87	0.64 0.64 0.46 0.87	0.02 0.02 0.002 0.67	0.02 0.01 0.002 0.72	0.63 0.45 0.75	0.02 0.004 0.44	0.02 0.003 0.44
rs522838	Chr 3, 184,365,224	<i>LAMP3</i>	Additional	G/C	0.13/0.21	Allelic Additive 0.57 Dominant 0.55 Recessive 0.30	0.57 0.57 0.55 0.30	0.02 0.03 0.03 0.23	0.03 0.02 0.04 0.15	0.58 0.56 0.28	0.04 0.06 0.22	0.04 0.05 0.15
rs17597256	Chr 3, 198,252,251	<i>DLG1</i>	GWAS	T/C	0.46/0.40 GWAS 0.47/0.35	Allelic Additive 1.27 1.26 Dominant 0.90 Recessive 2.25	1.27 1.26 0.90 2.25	0.21 0.23 0.69 0.007	0.22 0.22 0.70 0.005	1.11 0.79 1.87	0.60 0.44 0.06	0.60 0.45 0.05
rs4242051	Chr 5, 54,234,532		GWAS	T/C	0.40/0.28 GWAS 0.38/0.26	Allelic Additive 1.71 1.68 Dominant 1.47 Recessive 3.30	1.71 1.68 1.47 3.30	0.003 0.004 0.13 0.0002	0.005 0.003 0.11 0.0004	1.41 1.16 2.73	0.08 0.59 0.005	0.08 0.59 0.004
rs10223133^	Chr5, 80,469,216	<i>RASGRF2</i>	Additional	A/G	0.18/0.20	Allelic Additive 0.86 0.85 Dominant 0.81 Recessive 1.12	0.86 0.85 0.81 1.12	0.51 0.49 0.42 0.88	0.52 0.52 0.41 0.86	0.89 0.82 1.54	0.64 0.50 0.60	0.65 0.51 0.46
rs248989^	Chr 5, 80,472,340	<i>RASGRF2</i>	Additional	C/T	0.54/0.44	Allelic Additive 1.53 1.50 Dominant 1.72 Recessive 1.75	1.53 1.50 1.72 1.75	0.01 0.02 0.07 0.04	0.02 0.02 0.07 0.05	1.43 1.84 1.50	0.05 0.06 0.18	0.05 0.06 0.17
rs17213955^	Chr 5, 80,472,997	<i>RASGRF2</i>	Additional	T/C	0.18/0.24	Allelic Additive 0.69 0.67 Dominant 0.64 Recessive 0.59	0.69 0.67 0.64 0.59	0.10 0.09 0.09 0.47	0.09 0.09 0.09 0.48	0.69 0.66 0.58	0.14 0.15 0.49	0.15 0.16 0.54
rs369844^	Chr 5, 80,483,382	<i>RASGRF2</i>	Additional	T/C	0.25/0.29	Allelic Additive 0.83 0.82 Dominant 0.83 Recessive 0.57	0.83 0.82 0.83 0.57	0.35 0.33 0.46 0.36	0.35 0.34 0.49 0.42	0.78 0.80 0.51	0.27 0.41 0.29	0.27 0.42 0.32
rs4836493	Chr 5, 129,499,621	<i>CSS3</i>	GWAS	A/G	0.11/0.07	Allelic Additive 1.69 1.68	1.69 1.68	0.06 0.07	0.07 0.05	1.87	0.04	0.04

					GWAS 0.13/0.04	Dominant Recessive	1.73 2.54	0.08 0.41	0.06 0.17	1.95 2.84	0.05 0.38	0.05 0.13
rs1017213	Chr 5, 163,281,156		GWAS	T/C	0.44/0.31	Allelic Additive	1.77 1.70	0.001 0.002	0.002 0.0008	1.54	0.02	0.02
					GWAS 0.46/0.29	Dominant Recessive	2.00 2.14	0.009 0.02	0.009 0.009	1.83 1.70	0.03 0.14	0.03 0.12
rs6459959	Chr 7, 155,390,912		GWAS	C/G	0.51/0.36	Allelic Additive	1.89 1.88	0.0003 0.0004	0.0003 0.001	1.78	0.002	0.003
					GWAS 0.47/0.33	Dominant Recessive	2.04 2.66	0.01 0.0007	0.01 0.0008	2.08 2.30	0.02 0.008	0.02 0.005
rs6459961	Chr 7, 155,391,016		GWAS	C/A	0.51/0.36	Allelic Additive	1.89 1.88	0.0003 0.0004	0.0003 0.001	1.78	0.002	0.003
					GWAS 0.49/0.32	Dominant Recessive	2.04 2.66	0.01 0.0007	0.01 0.0008	2.07 2.30	0.02 0.008	0.01 0.005
rs10104640	Chr 8, 40,762,563	ZMAT4	GWAS	A/C	0.38/0.27	Allelic Additive	1.66 1.58	0.006 0.009	0.007 0.007	1.63	0.01	0.007
					GWAS 0.37/0.25	Dominant Recessive	1.29 3.43	0.32 6.7X10 ⁻⁵	0.31 0.0002	1.39 3.51	0.23 0.0003	0.23 0.0004
rs4736880	Chr 8, 40,772,063	ZMAT4	Additional	T/G	0.56/0.46	Allelic Additive	1.48 1.44	0.03 0.03	0.04 0.04	1.51	0.03	0.03
						Dominant Recessive	1.19 2.16	0.54 0.003	0.49 0.003	1.22 2.38	0.51 0.003	0.51 0.002
rs11782961 [@]	Chr 8, 124,369,839		r ² =0.96 with GWAS SNP rs1044714	A/G	0.37/0.23 GWAS rs1044714 0.37/0.22	Allelic Additive	1.97 1.91	0.0002 0.0004	0.0006 0.0008	1.87	0.001	0.001
						Dominant Recessive	1.85 3.78	0.01 0.0001	0.01 0.0006	1.98 3.26	0.01 0.003	0.01 0.003
rs6470145	Chr 8, 124,391,920		Additional	A/G	0.14/0.07	Allelic Additive	2.11 2.09	0.008 0.01	0.006 0.007	1.83	0.06	0.06
						Dominant Recessive	2.23 3.07	0.01 0.32	0.006 0.06	1.83 4.46	0.09 0.19	0.09 0.07
rs6477941	Chr 9, 114,292,170	KIAA1958	GWAS	T/C	0.12/0.05	Allelic Additive	2.46 2.40	0.001 0.002	0.003 0.0008	2.20	0.01	0.01
					GWAS 0.12/0.04	Dominant Recessive	2.60 3.39	0.002 0.29	0.0008 0.18	2.27 4.72	0.02 0.22	0.01 0.05
rs10857508	Chr 10, 50,443,270		GWAS	C/G	0.14/0.10	Allelic Additive	1.54 1.49	0.10 0.11	0.12 0.11	1.48	0.13	0.13
					GWAS 0.16/0.09	Dominant Recessive	1.21 6.70	0.54 0.001	0.60 0.005	1.30 4.73	0.43 0.02	0.42 0.02
rs10832607	Chr 11, 16,419,343	SOX6	GWAS	T/C	0.28/0.19	Allelic Additive	1.69 1.68	0.007 0.009	0.01 0.007	1.81	0.006	0.006
					GWAS 0.29/0.20	Dominant Recessive	1.30 6.06	0.30 5.3X10 ⁻⁶	0.31 0.0002	1.40 7.66	0.22 1.2X10 ⁻⁵	0.24 0.0002
rs10500830	Chr 11, 16,441,827	SOX6	GWAS	A/G	0.28/0.19	Allelic Additive	1.71 1.71	0.006 0.007	0.008 0.007	1.83	0.005	0.005

					GWAS 0.29/0.20	Dominant Recessive	1.40 5.37 [^]	0.18 3.6X10 ⁻⁵	0.17 0.0002	1.54 6.18	0.12 0.0001	0.13 0.0002
rs12279572	Chr 11, 117,458,170	<i>TMPRSS4</i>	GWAS	G/A	0.36/0.29	Allelic Additive	1.39 1.37	0.07 0.08	0.08 0.08	1.44 1.06	0.06 0.84	0.05 0.85
					GWAS 0.36/0.28	Dominant Recessive	0.94 3.61	0.79 3.5X10 ⁻⁵	0.78 0.0004	3.61	0.0002	0.0006
rs10892210	Chr 11, 117,461,548	<i>TMPRSS4</i>	Additional	T/G	0.44/0.39	Allelic Additive	1.24 1.23	0.22 0.23	0.26 0.23	1.19 1.06	0.35 0.84	0.33 0.86
						Dominant Recessive	1.15 1.59	0.60 0.12	0.60 0.12	1.61	0.14	0.12
rs7975290	Chr 12, 26,505,185	<i>ITPR2</i>	GWAS	G/A	0.14/0.05	Allelic Additive	2.96 2.91	2.5X10 ⁻⁵ 8.4X10 ⁻⁵	0.0004 0.0004	3.53 4.23	4.5X10 ⁻⁵ 1.4X10 ⁻⁵	0.0006 0.0002
					GWAS 0.13/0.05	Dominant Recessive	3.56 -	1.4X10 ⁻⁵ 1.00	0.0002 0.91	4.23 -	1.4X10 ⁻⁵ 1.00	0.0002 0.34
rs10773689	Chr 12, 128,686,079	<i>TMEM132D</i>	GWAS	A/C	0.24/0.39	Allelic Additive	0.50 0.50	0.0005 0.0007	0.001 0.0004	0.47 0.45	0.0005 0.004	0.0008 0.004
					GWAS 0.23/0.41	Dominant Recessive	0.48 0.24	0.003 0.02	0.002 0.01	0.19	0.008	0.003
rs11060480	Chr 12, 128,692,468	<i>TMEM132D</i>	GWAS	G/A	0.65/0.48	Allelic Additive	1.96 1.99	0.0002 0.0002	0.0003 0.0004	2.23 3.59	0.0001 0.003	0.0004 0.003
					GWAS 0.34/0.48	Dominant Recessive	3.26 2.17	0.004 0.003	0.004 0.003	2.51	0.002	0.001
rs10519861	Chr 15, 31,773,350	<i>RYR3</i>	GWAS	T/G	0.56/0.40	Allelic Additive	1.96 2.00	0.0001 0.0001	<0.0001 0.0002	2.18 2.90	0.0001 0.002	0.0002 0.002
					GWAS 0.44/0.39	Dominant Recessive	2.74 2.34	0.002 0.002	0.0006 0.003	2.67	0.002	0.002
rs8027394	Chr 15, 76,404,968		GWAS	T/C	0.48/0.30	Allelic Additive	2.12 2.06	1.8X10 ⁻⁵ 4.2X10 ⁻⁵	<0.0001 0.0002	2.12 2.24	0.0002 0.006	0.0004 0.006
					GWAS 0.47/0.31	Dominant Recessive	2.49 2.86	0.0009 0.0006	0.001 0.001	3.44	0.0004	0.0008
rs925987	Chr 15, 76,406,948		Additional	C/T	0.49/0.33	Allelic Additive	1.96 1.93	0.0001 0.0002	0.0002 0.001	1.91 1.98	0.001 0.02	0.001 0.02
						Dominant Recessive	2.26 2.62	0.003 0.001	0.003 0.001	2.88	0.002	0.003
rs12593362	Chr 15, 76,421,786	<i>CRABP1</i>	Additional	T/G	0.47/0.31	Allelic Additive	1.99 1.99	8.4X10 ⁻⁵ 0.0001	<0.0001 0.0002	2.10 2.82	0.0002 0.0007	0.0004 0.0006
						Dominant Recessive	2.70 2.26	0.0004 0.01	0.0004 0.005	2.40	0.02	0.01
rs2437788	Chr 15, 84,987,337		Additional	T/C	0.44/0.38	Allelic Additive	1.26 1.25	0.19 0.20	0.20 0.19	1.23 1.48	0.28 0.17	0.27 0.17
						Dominant Recessive	1.42 1.26	0.19 0.48	0.19 0.42	1.10	0.79	0.82
rs2469182 [±]	Chr 15, 84,990,324		r2=0.86 with GWAS	A/T	0.18/0.10 GWAS rs7183919	Allelic Additive	1.93 1.88	0.004 0.006	0.006 0.004	1.81 2.06	0.02 0.01	0.02 0.01
						Dominant	2.14	0.005	0.002			

			SNP rs7183919		0.22/0.11	Recessive	1.86	0.43	0.17	1.66	0.56	0.35
rs8058644	Chr 16, 48,454,181		GWAS	T/C	0.18/0.07	Allelic	2.72	1.9×10^{-5}	0.0002			
					GWAS	Additive	2.61	6.8×10^{-5}	0.0004	2.86	8.7×10^{-5}	0.0004
					0.16/0.06	Dominant	3.02	6.3×10^{-5}	0.0004	3.50	5.8×10^{-5}	0.0006
						Recessive	3.42	0.14	0.03	3.33	0.17	0.13
rs17212151	Chr 16, 48,472,935		Additional	T/C	0.18/0.10	Allelic	2.03	0.002	0.005			
						Additive	1.96	0.004	0.003	2.23	0.001	0.0008
						Dominant	2.24	0.003	0.003	2.85	0.0006	0.0004
						Recessive	2.04	0.36	0.20	1.93	0.42	0.24
rs12968495	Chr 18, 10,267,737		Additional	C/T	0.31/0.36	Allelic	0.81	0.27	0.29			
						Additive	0.82	0.28	0.29	0.90	0.60	0.60
						Dominant	0.84	0.48	0.49	0.87	0.62	0.61
						Recessive	0.60	0.25	0.22	0.86	0.76	0.77
rs16974035	Chr 18, 10,269,356		GWAS	G/A	0.49/0.34	Allelic	1.86	0.0004	0.0005			
						Additive	1.86	0.0005	0.0004	1.96	0.0005	0.001
						Dominant	2.00	0.01	0.008	2.08	0.01	0.009
						Recessive	2.68	0.001	0.001	3.07	0.0008	0.0006
rs9959544	Chr 18, 55,478,330	<i>CCBE1</i>	Additional	G/A	0.25/0.36	Allelic	0.58	0.006	0.008			
						Additive	0.58	0.007	0.006	0.66	0.06	0.06
						Dominant	0.47	0.003	0.002	0.54	0.02	0.02
						Recessive	0.63	0.29	0.28	0.84	0.71	0.70
rs8093323 [Ⓢ]	Chr 18, 55,479,651	<i>CCBE1</i>	r2=0.84 with GWAS SNP rs6567111	G/A	0.25/0.36	Allelic	0.59	0.008	0.01			
						Additive	0.59	0.009	0.007	0.68	0.08	0.08
						Dominant	0.48	0.004	0.003	0.55	0.03	0.03
						Recessive	0.65	0.34	0.29	0.91	0.84	0.84
rs2062980	Chr 18, 60,573,886		GWAS	T/G	0.52/0.41	Allelic	1.58	0.009	0.01			
						Additive	1.57	0.01	0.009	1.43	0.07	0.07
						Dominant	1.72	0.06	0.06	1.46	0.22	0.22
						Recessive	1.94	0.02	0.02	1.77	0.07	0.07
rs1011636	Chr 20, 50,264,021		Additional	G/C	0.46/0.41	Allelic	1.25	0.20	0.22			
						Additive	1.24	0.21	0.20	1.27	0.21	0.21
						Dominant	1.33	0.29	0.31	1.31	0.36	0.36
						Recessive	1.35	0.32	0.28	1.46	0.25	0.25
rs2016367	Chr 20, 50,276,712		GWAS	C/G	0.30/0.22	Allelic	1.48	0.04	0.05			
						Additive	1.46	0.05	0.04	1.40	0.11	0.10
						Dominant	1.25	0.37	0.35	1.13	0.66	0.65
						Recessive	3.28	0.002	0.004	3.64	0.002	0.003

Chr = chromosome; GWAS = genome wide association study; MAF = minor allele frequency; MV = multivariable; SNP = single nucleotide polymorphism; VnD = ventricular dysfunction;

* 71 VnD cases are a successfully genotyped subset of the 76 VnD cases in the initial GWAS.

SNPs in bold font are 19 SNPs (from 15 genetic loci) that were selected for replication study efforts in both the Vanderbilt cohort (Supporting Information Table S3) and in new VnD cases from the CABG Genomics cohort (Supporting Information Table S4).

^ rs42430 GWAS lead SNP failed Sequenom genotyping but 4 alternate additional SNPs were genotyped to represent the linkage disequilibrium blocks in the region.

@ rs1044714 GWAS lead SNP failed Sequenom genotyping but rs11782961 which is in strong linkage disequilibrium with rs1044714 and was genotyped successfully.

± rs7183919 GWAS lead SNP failed primer formation for Sequenom genotyping but rs2469182 which is in linkage disequilibrium with rs7183919 was genotyped successfully.

© rs6567111 GWAS lead SNP failed primer formation for Sequenom genotyping but rs8093323 which is in linkage disequilibrium with rs6567111 was genotyped successfully.