Table S1: **Clinical variables**

Number	Variable	Description
1	Age	-
2	Gender	-
3	Systolic BP (mmHg)	Maximum arterial pressure during contraction of the left ventricle of the heart.
4	Diastolic BP (mmHg)	Minimum arterial pressure when the ventricles of the heart fill with blood.
5	BMI (kg/m^2)	A person's weight in kilograms divided by the square of height in meters.
6	Fasting Blood Glucose (mg/dL)	Level of glucose in the blood after an overnight fast.
7	Total Cholesterol (mg/dL)	Calculated as LDL+HDL+Triglycerides/5, used to assess heart disease risk.
8	Triglycerides (mg/dL)	Lipids that are used to store energy and give energy to muscles.
9	HDL Cholesterol	Moves excess cholesterol from the cells to the liver.
10	LDL Cholesterol	Transports lipids around the body within the water outside cells.
11	Fibrinogen	A coagulation factor that is essential for blood clot formation.

Except age and gender, all clinical variables are used for predicting coronary calcium within random forest models in conjunction with SNP predictors.

Table S2: **General statistics of clinical variables among controls and case subjects (89th-99th CAC score percentile) in the ClinSeq® cohort**

Number	Variable	p-value	Cases mean	Cases SD	Controls mean	Controls SD
1	Age	0.82	58.25	4.70	57.88	4.33
2	Gender	-	All males	-	All males	-
3	Systolic BP (mmHg)	0.51	129.91	10.45	126.97	14.18
4	Diastolic BP (mmHg)	0.70	78.06	7.04	76.91	9.33
5	BMI (kg/m^2)	0.09	28.74	5.03	26.17	2.79
6	Fasting Blood Glucose (mg/dL)	0.07	106.44	16.74	97.69	8.34
7	Total Cholesterol (mg/dL)	0.78	190.75	49.02	186.75	30.88
8	Triglycerides (mg/dL)	0.17	127.13	62.69	98.75	49.77
9	HDL Cholesterol (mg/dL)	0.11	49.38	11.59	56.00	11.44
10	LDL Cholesterol (mg/dL)	0.74	115.63	38.28	111.44	30.88
11	Fibrinogen (mg/dL)	0.37	312.38	33.28	299.63	45.61

Mean and standard deviation (SD) values of the clinical variables in the ClinSeq® cohort. Per variable, a p-value is computed using a two-sample t-test (with univariate criterion) by testing the null hypothesis that the case and control vectors are from populations with equal means without making the assumption that the two populations have equal variance values for any predictor.

Table S3: **General statistics of clinical variables among controls and case subjects (89th-99th CAC score percentile) in the FHS cohort**

Number	Variable	p-value	Cases mean	Cases SD	Controls mean	Controls SD
1	Age	0.58	51.28	5.57	50.53	5.98
2	Gender	-	All males	-	All males	-
3	Systolic BP (mmHg)	0.10	125.86	17.07	120.00	12.03
4	Diastolic BP (mmHg)	0.72	78.56	10.32	77.81	6.67
5	BMI (kg/m^2)	0.21	28.41	4.44	27.23	3.38
6	Fasting Blood Glucose (mg/dL)	0.07	102.25	10.78	98.06	8.39
7	Total Cholesterol (mg/dL)	0.97	194.22	36.50	193.89	31.34
8	Triglycerides (mg/dL)	0.65	130.33	72.43	122.89	64.47
9	HDL Cholesterol (mg/dL)	0.86	46.78	13.05	46.25	12.76
10	LDL Cholesterol (mg/dL)	0.81	121.38	32.00	123.06	28.43
11	Fibrinogen (mg/dL)	0.09	361.86	97.01	329.33	58.59

Mean and standard deviation (SD) values of the clinical variables in the FHS cohort. Per variable, a p-value is computed using a two-sample t-test (with univariate criterion) by testing the null hypothesis that the case and control vectors are from populations with equal means without making the assumption that the two populations have equal variance values for any predictor.

Table S4: **List of SNPs associated with CAC in past GWAS and meta-analyses (SNP Set 1)**

Number	SNP	Locus	p-value	GWAS	Number	SNP	Locus	p-value	GWAS
1	rs4456611	BCL2	4.1E-4	[1]	37	rs34014631	C10orf76	4.3E-6	[2]
2	rs3789422	ABCA4	8.5E-5	[1]	38	rs11777747	FLJ43860	7.9E-6	[2]
3	rs13386681	ATOH8	1.6E-4	[1]	39	rs9506514	IFT88 *	4.9E-6	[2]
4	rs10499276	OPRM1 *	6.9E-5	[1]	40	rs7070038	IPMK *	6.6E-6	[2]
5	rs13260	COL4A1	8.7E-5	[1]	41	rs7765175	MARCKS *	4.7E-6	[2]
6	rs6667260	ITPKB	8.0E-5	[1]	42	rs10502575	MCART2 *	1.5E-7	[2]
7	rs3768991	NPAS2	3.7E-4	[1]	43	rs10803016	PLD5	7.4E-6	[2]
8	rs17056112	ADRA1A	3.3E-4	[1]	44	rs16976171	RIT2 *	3.6E-6	[2]
9	rs4977574	CDKN2B-AS1	9.0E-5	[1]	45	rs7856675	SLC1A1	8.3E-6	[2]
10	rs2891168	CDKN2B-AS1	1.7E-4	[1]	46	rs9907236	SOX9 *	1.7E-6	[2]
11	rs10757274	CDKN2B-AS1	2.2E-4	[1]	47	rs2622633	ZFPM2	6.5E-6	[2]
12	rs10757272	CDKN2B-AS1	3.5E-4	[1]	48	rs1537370	CDKN2B-AS1	2.3E-11	[3]
13	rs2834669	RUNX1	3.9E-4	[1]	49	rs9349379	PHACTR1	2.7E-11	[4]
14	rs10483853	NUMB	6.1E-6	[5]	50	rs163189	PRDM6	7.5E-3	[4]
15	rs10519394	PCDH18 *	1.1E-5	[5]	51	rs599839	PSRC1	3.9E-3	[4]
16	rs9321354	TAAR5 *	3.4E-5	[5]	52	rs646776	CELSR2	7.9E-12	[4]
17	rs220457	C17orf79 *	3.8E-4	[5]	53	rs2259816	HNF1A	4.8E-7	[4]
18	rs722208	ESR1	5.0E-3	[5]	54	rs3184504	SH2B3	8.6E-8	[4]
19	rs1365057	CD44 *	7.7E-3	[5]	55	rs9818870	MRAS	7.4E-13	[4]
20	rs1467558	CD44	2.0E-2	[5]	56	rs11206510	PCSK9	9.6E-9	[4]
21	rs2190305	CREB5	1.2E-6	[6]	57	rs12146493	DKFZp761E198	7.4E-3	[4]
22	rs9574536	SPRY2 *	2.4E-6	[6]					
23	rs7158225	FLRT2 *	5.3E-6	[6]					
24	rs17819063	FTO	4.2E-5	[6]					
25	rs432695	CDYL *	2.3E-7	[6]					
26	rs4867326	CDH6 *	4.7E-7	[6]					
27	rs622348	MIR759 *	3.8E-6	[6]					
28	rs16872734	GPR125	7.0E-6	[6]					
29	rs2727551	PRKAG2	5.2E-5	[6]					
30	rs10096362	CDH17 *	2.2E-6	[6]					
31	rs9843942	TGFBR2	3.0E-6	[6]					
32	rs1679195	LPP	3.4E-5	[6]					
33	rs2618157	THBS1 *	5.3E-5	[6]					
34	rs6032769	SLC35C2 *	1.3E-5	[6]					
35	rs1062087	TBC1D4	4.2E-7	[6]					
36	rs3758014	ARHGEF10	7.8E-5	[6]					

Genotypes of these SNPs (previously associated with CAC) are used for predicting the binary CAC state among the ClinSeq® subjects. Nearest genes are listed for intergenic SNPs (marked with asterisk).

Table S5: **List of highly predictive SNPs not previously associated with coronary calcium in past GWAS and meta-analyses (SNP Set 2)**

Number	SNP	Locus	Number	SNP	Locus
1	rs243170	*FOXN3*	37	rs8107904	*EMR2*[*]
2	rs243172	*FOXN3*	38	rs9290557	*NAALADL2*
3	rs328395	*LOC100506172*[*]	39	rs9804449	*FGF3*[*]
4	rs342393	*NRG3*	40	rs9967032	*DOK6*
5	rs480220	*NRG3*	41	rs10036954	*C5orf34*
6	rs514237	*NRG3*	42	rs10054519	*C5orf28*
7	rs571797	*NRG3*	43	rs10059993	*NNT-AS1*
8	rs750582	*C5orf28*[*]	44	rs10065689	*NNT*
9	rs1130329	*RBAK-LOC389458*	45	rs10079672	*AFAP1L1*
10	rs1288331	*SLC1A7*[*]	46	rs10458221	*EEF1E1-BLOC1S5*[*]
11	rs1366410	*NNT*	47	rs11131194	*RPUSD3*
12	rs1389401	*ASB7*[*]	48	rs11575624	*HABP2*
13	rs1505279	*C15orf54*[*]	49	rs11575634	*HABP2*
14	rs1887413	*TTL*[*]	50	rs11674863	*LOC101927701*
15	rs2217855	*FBXO8*[*]	51	rs11767632	*YAE1D1*[*]
16	rs2241097	*TLR5*	52	rs12521249	*PAIP1*[*]
17	rs2390285	*MACC1*	53	rs12645809	*ANTXR2*
18	rs4255867	*DOK6*	54	rs13159307	*FBXL17*[*]
19	rs4410460	*KCNH8*[*]	55	rs13220973	*LOC401324*[*]
20	rs4491835	*SCN11A*[*]	56	rs13429160	*LOC101927701*
21	rs4622486	*C15orf54*[*]			
22	rs4632970	*AGK*			
23	rs4676660	*WDR48*[*]			
24	rs4793853	*MSI2*			
25	rs6014727	*CASS4*			
26	rs6024879	*CASS4*			
27	rs6069753	*CASS4*			
28	rs6451696	*C5orf28*			
29	rs6565484	*RPTOR*			
30	rs6849832	*DDIT4L*[*]			
31	rs6860493	*NNT*			
32	rs7176702	*MEGF11*			
33	rs7225157	*DNAH9*			
34	rs7501899	*C17orf54*[*]			
35	rs7531219	*PPP2R5A*[*]			
36	rs7713479	*NNT-AS1*			

Nearest genes are listed for intergenic SNPs (marked with asterisk [*]).

Table S6: **The network of genes derived by GeneMANIA from a database of 244 studies in humans. The loci of the 21 predictive SNPs are used as the input gene set for network construction. Gene symbols and names are based on the information from the HUGO Gene Nomenclature Committee (HGNC).**

Number	Gene symbol	Gene name
1	*MACC1*	Metastasis Associated In Colon Cancer 1
2	*NRG3*	Neuregulin 3
3	*ANTXR2*	Anthrax Toxin Receptor 2
4	*FBXL17*	F-Box And Leucine-Rich Repeat Protein 17
5	*YAE1D1*	Yae1 Domain Containing 1
6	*PAIP1*	Poly(A) Binding Protein Interacting Protein 1
7	*FOXN3*	Forkhead Box N3
8	*C5orf28*	Chromosome 5 Open Reading Frame 28
9	*EMR2* (*ADGRE2*)	EGF-like module-containing mucin-like hormone receptor-like 2 (Adhesion G Protein-Coupled Receptor E2)
10	*TLR5*	Toll Like Receptor 5
11	*NNT*	Nicotinamide Nucleotide Transhydrogenase
12	*WDR70*	WD repeat domain 70
13	*FASTKD3*	FAST Kinase Domains 3
14	*AIMP1*	Aminoacyl TRNA Synthetase Complex-Interacting Multifunctional Protein 1
15	*EGLN1*	Egl-9 Family Hypoxia Inducible Factor 1
16	*C5orf22*	Chromosome 5 Open Reading Frame 22
17	*MICU2*	Mitochondrial Calcium Uptake 2
18	*NIPBL*	NIPBL, Cohesin Loading Factor
19	*N6AMT1*	N-6 adenine-specific DNA methyltransferase 1
20	*MARCH6*	Membrane Associated Ring-CH-Type Finger 6
21	*ZNF131*	Zinc Finger Protein 131
22	*SRP72*	Signal Recognition Particle 72kDa
23	*ARID5B*	AT-Rich Interaction Domain 5B
24	*CEP72*	Centrosomal Protein 72
25	*TIPRL*	TOR Signaling Pathway Regulator
26	*FAM172A*	Family With Sequence Similarity 172 Member A
27	*EMC2*	ER Membrane Protein Complex Subunit 2
28	*EDEM1*	ER Degradation Enhancing Alpha-Mannosidase Like Protein 1
29	*CYB5R4*	Cytochrome B5 Reductase 4
30	*RETN*	Resistin
31	*FUT3*	Fucosyltransferase 3 (Lewis Blood Group)

Network of genes derived from GeneMANIA based on 244 studies in humans.

Table S7: **Enriched diseases and biological functions in the gene network relevant to cardiovascular disease with p-values ranging between 1.0E-2 and 5.0E-2 (statistically less significant than the diseases and biological functions listed in Table 4) as identified by IPA based on Fisher's exact test.**

Category	Disease or Function	Genes
Cardiovascular System Development and Function	Abnormal morphology of dilated vasculature	*ANTXR2*
Lipid Metabolism	Recognition of lipid	*TLR5*
Connective Tissue Development and Function	Morphology of adipocytes	*ARID5B, RETN*
Endocrine System Development and Function	Insulin sensitivity	*CYB5R4, RETN*
Cell Signaling	Handling of Ca^{2+}	*MICU2*
Organismal Injury and Abnormalities	Infection of kidney	*TLR5*
Metabolic Disease	Susceptibility to type 2 diabetes mellitus	*RETN*
Hematological System Development and Function	Decreased hematocrit of organism	*EGLN1*
Respiratory System Development and Function	Respiratory minute volume	*EGLN1*
Cardiovascular System Development and Function	Morphogenesis of heart	*EGLN1, NIPBL*
Protein Synthesis	Quantity of hemoglobin in blood	*EGLN1*
Tissue Morphology	Morphology of connective tissue	*ARID5B, CYB5R4 RETN, TLR5*
Cellular Movement	Migration of fibroblasts	*AIMP1, ARID5B*
Cardiovascular System Development and Function	Contractility of ventricular myocytes	*TLR5*
Cellular Compromise, Hepatic System Disease	Oxidative stress response of hepatocytes	*CYB5R4*
Cell-To-Cell Signaling and Interaction	Activation of kidney cell lines	*TLR5*
Cellular Assembly and Organization, Inflammatory Response	Formation of neutrophil extracellular trap	*RETN*
Cardiovascular System Development and Function	Functional recovery of heart	*EGLN1*
Free Radical Scavenging	Metabolism of superoxide	*CYB5R4*
Endocrine System Development and Function	Quantity of insulin in blood	*CYB5R4, TLR5*
Cell Morphology, Cellular Function and Maintenance	Autophagy of cytoplasm	*TLR5*
Carbohydrate Metabolism	Synthesis of oligosaccharide	*FUT3*
Cell Death and Survival	Apoptosis of peripheral blood lymphocytes	*AIMP1*
Metabolic Disease	Hypoinsulinemia	*CYB5R4*
Cell-To-Cell Signaling and Interaction	Activation of smooth muscle cells	*RETN*
Cardiovascular Disease, Organismal Injury and Abnormalities	Dysfunction of endothelial tissue	*RETN*
Metabolic Disease	Insulin-dependent diabetes mellitus	*NRG3, RETN, TLR5*
Endocrine System Disorders, Metabolic Disease	Insulin resistance of liver	*RETN*
Protein Synthesis	Quantity of protein in blood	*CYB5R4, EGLN1, TLR5*
Cardiovascular System Development and Function	Morphogenesis of ventricular septum	*EGLN1*
Cell Morphology, Cellular Assembly and Organization	Size of mitochondria	*CYB5R4*
Connective Tissue Development and Function	Mass of adipose tissue	*CYB5R4, TLR5*
Connective Tissue Development and Function	Differentiation of fibroblast cell lines	*EGLN1, RETN*
Molecular Transport, Nucleic Acid Metabolism	Quantity of NADPH	*NNT*
Cellular Assembly and Organization	Activation of mitochondria	*RETN*
Immune Cell Trafficking, Inflammatory Response	Cellular infiltration by monocytes	*RETN*
Cellular Compromise	Stress response of cells	*CYB5R4, RETN*
Connective Tissue Development and Function	Abnormal morphology of adipocytes	*ARID5B*
Cardiovascular System Development and Function	Density of capillary vessel	*EGLN1*
Carbohydrate Metabolism	Disposal of D-glucose	*RETN*

Category	Disease or Function	Genes
Hematological System Development and Function	Hematocrit of blood	*EGLN1*
Immune Cell Trafficking, Inflammatory Response	Cellular infiltration by macrophages	*EGLN1, RETN*
Cardiovascular System Development and Function	Abnormal morphology of trabeculae carne	*EGLN1*
Nutritional Disease	Obesity	*ARID5B, RETN, TLR5*
Hematological System Development and Function	Cell viability of neutrophils	*ADGRE2*
Cell-mediated Immune Response	Development of Th17 cells	*TLR5*
Hematological Disease, Immunological Disease	Growth of lymphoma	*AIMP1*
Cardiovascular System Development and Function	Morphogenesis of cardiac muscle	*EGLN1*
Connective Tissue Development and Function	Function of adipose tissue	*TLR5*
Protein Synthesis	Production of cytokine	*TLR5*
Cardiovascular System Development and Function	QT interval of heart	*NRG3*

Table S8: Interactions within the advanced coronary calcium network generated by GeneMANIA (network shown in Figure 6). The nature of interactions (INT) between gene pairs are based either on co-expression (CE) or genetic interactions (GI). We list the source of the interactions (networks previously published) under "Ref".

#	Gene 1	Gene 2	INT	Ref	#	Gene 1	Gene 2	INT	Ref	#	Gene 1	Gene 2	INT	Ref
1	C5orf28	PAIP1	CE	[7]	48	C5orf22	C5orf28	CE	[8]	95	AIMP1	NNT	CE	[9]
2	WDR70	PAIP1	CE	[7]	49	C5orf22	NNT	CE	[8]	96	C5orf22	PAIP1	CE	[9]
3	WDR70	C5orf28	CE	[7]	50	C5orf22	WDR70	CE	[8]	97	MARCH6	NNT	CE	[9]
4	FASTKD3	PAIP1	CE	[7]	51	C5orf22	FASTKD3	CE	[8]	98	ZNF131	NNT	CE	[9]
5	FASTKD3	C5orf28	CE	[7]	52	MICU2	PAIP1	CE	[8]	99	SRP72	MICU2	CE	[9]
6	FASTKD3	WDR70	CE	[7]	53	MICU2	C5orf28	CE	[8]	100	TIPRL	TLR5	CE	[9]
7	AIMP1	C5orf28	CE	[7]	54	MICU2	AIMP1	CE	[8]	101	EMC2	AIMP1	CE	[9]
8	EGLN1	FOXN3	CE	[7]	55	NIPBL	C5orf28	CE	[8]	102	C5orf28	PAIP1	CE	[10]
9	C5orf22	NNT	CE	[7]	56	NIPBL	C5orf22	CE	[8]	103	C5orf22	NNT	CE	[10]
10	MICU2	PAIP1	CE	[7]	57	N6AMT1	C5orf28	CE	[8]	104	C5orf22	FASTKD3	CE	[10]
11	NIPBL	NNT	CE	[7]	58	N6AMT1	FASTKD3	CE	[8]	105	MICU2	FBXL17	CE	[10]
12	NIPBL	C5orf22	CE	[7]	59	MARCH6	C5orf22	CE	[8]	106	MICU2	PAIP1	CE	[10]
13	N6AMT1	C5orf28	CE	[7]	60	MARCH6	NIPBL	CE	[8]	107	ZNF131	C5orf28	CE	[10]
14	MARCH6	C5orf28	CE	[7]	61	ZNF131	WDR70	CE	[8]	108	EDEM1	ARID5B	CE	[10]
15	MARCH6	FASTKD3	CE	[7]	62	ZNF131	FASTKD3	CE	[8]	109	FBXL17	ANTXR2	GI	[11]
16	MARCH6	C5orf22	CE	[7]	63	ZNF131	C5orf22	CE	[8]	110	YAE1D1	ANTXR2	GI	[11]
17	MARCH6	NIPBL	CE	[7]	64	ARID5B	FOXN3	CE	[8]	111	PAIP1	YAE1D1	GI	[11]
18	ZNF131	PAIP1	CE	[7]	65	CEP72	FASTKD3	CE	[8]	112	FOXN3	FBXL17	GI	[11]
19	ZNF131	WDR70	CE	[7]	66	FAM172A	C5orf28	CE	[8]	113	NNT	ANTXR2	GI	[11]
20	ZNF131	FASTKD3	CE	[7]	67	FAM172A	MARCH6	CE	[8]	114	NNT	FOXN3	GI	[11]
21	ZNF131	C5orf22	CE	[7]	68	EMC2	PAIP1	CE	[8]	115	WDR70	EMR2	GI	[11]
22	ZNF131	MICU2	CE	[7]	69	EDEM1	NNT	CE	[8]	116	AIMP1	MACC1	GI	[11]
23	ZNF131	NIPBL	CE	[7]	70	C5orf28	YAE1D1	CE	[12]	117	AIMP1	YAE1D1	GI	[11]
24	ZNF131	MARCH6	CE	[7]	71	FASTKD3	YAE1D1	CE	[12]	118	AIMP1	PAIP1	GI	[11]
25	SRP72	C5orf28	CE	[7]	72	AIMP1	YAE1D1	CE	[12]	119	EGLN1	FOXN3	GI	[11]
26	SRP72	AIMP1	CE	[7]	73	AIMP1	C5orf28	CE	[12]	120	C5orf22	FOXN3	GI	[11]
27	ARID5B	FOXN3	CE	[7]	74	MICU2	WDR70	CE	[12]	121	MICU2	ANTXR2	GI	[11]
28	CEP72	PAIP1	CE	[7]	75	TIPRL	SRP72	CE	[12]	122	MICU2	FOXN3	GI	[11]
29	CEP72	C5orf28	CE	[7]	76	FAM172A	WDR70	CE	[12]	123	NIPBL	ANTXR2	GI	[11]
30	TIPRL	C5orf28	CE	[7]	77	EMC2	YAE1D1	CE	[12]	124	NIPBL	EMR2	GI	[11]
31	TIPRL	FASTKD3	CE	[7]	78	EMC2	C5orf28	CE	[12]	125	N6AMT1	FBXL17	GI	[11]
32	TIPRL	ZNF131	CE	[7]	79	EMC2	FASTKD3	CE	[12]	126	N6AMT1	FOXN3	GI	[11]
33	FAM172A	FOXN3	CE	[7]	80	CYB5R4	MICU2	CE	[12]	127	MARCH6	FBXL17	GI	[11]
34	EMC2	C5orf28	CE	[7]	81	RETN	EMR2	CE	[12]	128	MARCH6	YAE1D1	GI	[11]
35	EMC2	AIMP1	CE	[7]	82	FUT3	MACC1	CE	[12]	129	SRP72	PAIP1	GI	[11]
36	EMC2	SRP72	CE	[7]	83	NNT	PAIP1	CE	[13]	130	SRP72	FOXN3	GI	[11]
37	EDEM1	EMR2	CE	[7]	84	NIPBL	FOXN3	CE	[13]	131	SRP72	NIPBL	GI	[11]
38	CYB5R4	PAIP1	CE	[7]	85	NIPBL	NNT	CE	[13]	132	FAM172A	MICU2	GI	[11]
39	RETN	TLR5	CE	[7]	86	MARCH6	PAIP1	CE	[13]	133	EMC2	YAE1D1	GI	[11]
40	FUT3	TLR5	CE	[7]	87	MARCH6	NIPBL	CE	[13]	134	EMC2	AIMP1	GI	[11]
41	C5orf28	PAIP1	CE	[8]	88	SRP72	FOXN3	CE	[13]	135	EDEM1	FBXL17	GI	[11]
42	WDR70	C5orf28	CE	[8]	89	TIPRL	NNT	CE	[13]	136	EDEM1	C5orf28	GI	[11]
43	WDR70	NNT	CE	[8]	90	FAM172A	NNT	CE	[13]	137	EDEM1	MARCH6	GI	[11]
44	FASTKD3	PAIP1	CE	[8]	91	FAM172A	NIPBL	CE	[13]	138	CYB5R4	FBXL17	GI	[11]
45	FASTKD3	C5orf28	CE	[8]	92	FAM172A	MARCH6	CE	[13]	139	CYB5R4	FOXN3	GI	[11]
46	EGLN1	NNT	CE	[8]	93	NNT	PAIP1	CE	[9]	140	CYB5R4	NNT	GI	[11]
47	C5orf22	PAIP1	CE	[8]	94	AIMP1	PAIP1	CE	[9]	141	RETN	C5orf28	GI	[11]
										142	FUT3	AIMP1	GI	[11]

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