Supplemental Table 1. Primer pairs for plasmid constructs

Construct	Forward primer	Reverse primer
rs978906A-allele	5’-CTAGTGTGGATCCCAGTCGCTCACACTACAATGGTCAGTCGCTCACACTACAATGGTCAGTCGCTCACACTACAATGA-3’	5’-CGCGTCATTGTAGTGTGAGCGACTGACCATTGTAGTGTGAGCGACTGACCATTGTAGTGTGAGCGACTGGGATCCACA-3’
rs978906G-allele	5’-CTAGTGTGGATCCCAGTCGCTCACACTACAGTGGTCAGTCGCTCACACTACAGTGGTCAGTCGCTCACACTACAGTGA-3’	5’-CGCGTCACTGTAGTGTGAGCGACTGACCACTGTAGTGTGAGCGACTGACCACTGTAGTGTGAGCGACTGGGATCCACA-3’
rs978906 mutant	5’-CTAGTGTGGATCCCAGTCGCTCACACGCACCGAGTCAGTCGCTCACACGCACCGAGTCAGTCGCTCACACGCACCGAA-3’	5’-CGCGTTCGGTGCGTGTGAGCGACTGACTCGGTGCGTGTGAGCGACTGACTCGGTGCGTGTGAGCGACTGGGATCCACA-3’

rs9808232A-allele	5’-CTCCATCTTGTAGAGAAAATGATTCCATACAATCAAGG-3’	5’-CCTTGATTGTATGGAATCATTTTCTCTACAAGATGGAG -3’

Supplemental Table 2. The association between ROCK2 SNPs and stiffness parameters in the screening data (mean ± SD)

SNPs	Adj Ep	Adj β	Adj PWV	SNPs	Adj Ep	Adj β	Adj PWV
rs9808232 (Thr431Asn)				rs4669700			
CC (N = 305)	105.2 ± 31.7	8.0 ± 2.4	6.1 ± 0.9	CC (N = 256)	105.1 ± 32.2	8.1 ± 2.4	6.1 ± 0.9
AC (N = 393)	103.0 ± 30.8	7.8 ± 2.2	6.1 ± 0.9	CT (N = 413)	102.9 ± 30.2	7.8 ± 2.1	6.1 ± 0.8
AA (N = 141)	98.1 ± 27.4	7.6 ± 2.0	6.0 ± 0.8	TT (N = 171)	98.8 ± 29.6	7.7 ± 2.1	6.0 ± 0.9
Additive model	p = 0.027	p = 0.046	p = 0.037	Additive model	p = 0.042	p = 0.064	p = 0.060
rs978906				rs12479227			
AA (N = 307)	105.1 ± 31.6	8.0 ± 2.4	6.1 ± 0.9	CC (N = 623)	102.5 ± 31.5	7.9 ± 2.3	6.1 ± 0.9
AG (N = 390)	102.4 ± 30.5	7.8 ± 2.1	6.1 ± 0.8	CT (N = 203)	103.1 ± 28.6	7.9 ±2.1	6.1 ± 0.8
GG (N = 144)	98.5 ± 27.2	7.6 ± 2.0	6.0 ± 0.8	TT (N = 16)	103.7 ± 29.8	8.0 ± 2.5	6.1 ± 0.8

Additive model	p = 0.031	p = 0.063	p = 0.038	Additive model	p = 0.798	p = 0.836	p = 0.698
rs10167277				rs1515223			
AA (N = 265)	105.6 ± 32.0	8.1 ± 2.4	6.2 ± 0.9	CC (N = 719)	102.5 ± 30.2	7.8 ± 2.2	6.1 ± 0.8
AT (N = 406)	102.7 ± 30.1	7.8 ± 2.1	6.1 ± 0.8	CT (N = 122)	105.1 ± 32.0	8.1 ± 2.5	6.1 ± 0.9
TT (N = 164)	99.3 ± 29.7	7.7 ± 2.2	6.0 ± 0.9	TT (N = 4)	117.3 ± 40.0	8.7 ± 2.7	6.5 ± 1.1
Additive model	p = 0.041	p = 0.056	p = 0.062	Additive model	p = 0.254	p = 0.215	p = 0.321
rs10168084							
TT (N = 308)	105.2 ± 31.6	8.0 ± 2.3	6.1 ± 0.9				
TC (N = 384)	102.9 ± 30.9	7.8 ± 2.2	6.1 ± 0.9				
CC (N = 135)	98.7 ± 28.1	7.7 ± 2.1	6.0 ± 0.8				
Additive model	p = 0.045	p = 0.087	p = 0.064				

Adjusted Ep, β , and PWV were average values of the raw data pulse the residuals in the multivariate regression model. Covariates in the multivariate regression model included age, sex, diabetes, hypertension, hypercholesterolemia, smoking and body mass index (BMI).

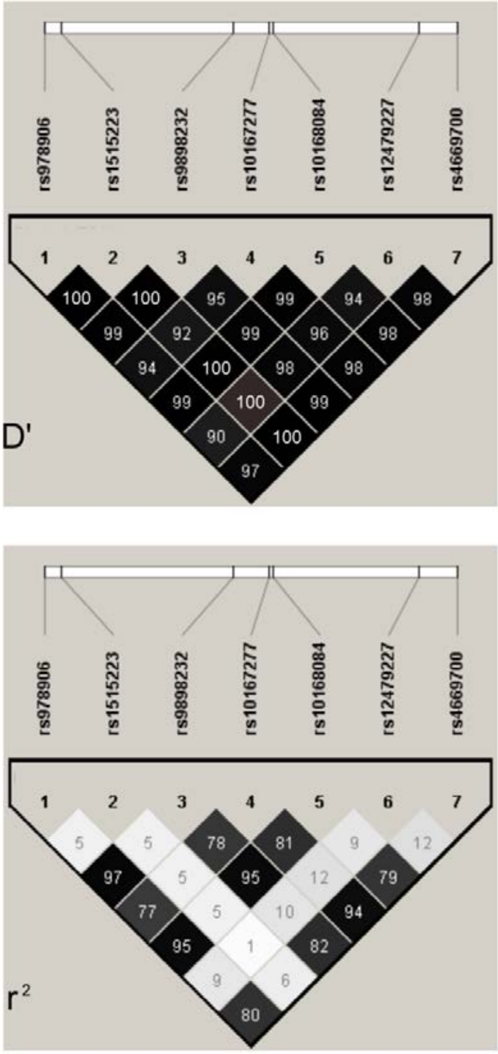
Supplemental Table 3. Relationship between cardiovascular risk factors and leukocyte ROCK activity (N = 52)

Risk factors	Pearson correlation coefficient (γ)	p value
age	-0.23	p = 0.10
Ep	-0.21	p = 0.15
beta	-0.24	p = 0.86
PWV	-0.22	p = 0.12

	Leukocyte ROCK activity (mean ± SD)		
	Absence	Presence	p value
Male	163.3 ± 132.0	135.2 ± 98.9	p = 0.41
Hypertension	163.2 ± 127.3	116.9 ± 74.7	p = 0.28
Diabetes	153.5 ± 119.1	46.0 (N=1)	p = 0.38

Hyperlipidemia	154.2 ± 119.3	142.9 ± 122.0	p = 0.77
Ever and current smoker	149.8 ± 125.4	160.0 ± 78.7	p = 0.83

Supplemental Fig 1. The linkage disequilibrium (LD) plots for the seven tagging SNPs.



The upper plot shows the D' and the lower plot r^2 (%) between any pair of SNPs. The dark gray cells in the upper plot indicate strong LD and log of odds (LOD) of 2 or greater. In the lower panel, the color spectrum indicates pairwise r^2 value ranging from black (r^2=100%) to white (r^2=0%).