Table S1. Positively regulated genes of expression in primary ACS versus the control group

Parametric p-value	ACS	Control	Fold-change	Name	Symbol
1.00E-07	1.06	0.64	1.67	Mitofusin-2	MFN2
2.00E-07	2.57	1.36	1.89	Diamine acetyltransferase 1	SAT1
2.00E-07	1.09	0.56	1.93	Transcription factor E2F3	E2F3
2.00E-07	0.23	0.079	2.93	High mobility group protein B2	HMGB2
2.00E-07	1.43	0.37	3.92	SAM domain-containing protein SAMSN-1	SAMSN1
3.00E-07	1.92	1.04	1.84	PHD finger protein 20-like 1 isoform 1	NP_940915.1
4.00E-07	1.32	0.8	1.65	Serine incorporator 3	SERINC3
4.00E-07	0.61	0.35	1.73	Transmembrane protein 165	TMEM165
4.00E-07	3.86	1.62	2.39	Metastasis-associated lung adenocarcinoma transcript 1	MALAT_HUMAN
5.00E-07	0.98	0.54	1.82	H/ACA ribonucleoprotein complex subunit 3	NOLA3
5.00E-07	7.04	3.16	2.23	Dual specificity protein phosphatase 1	DUSP1
6.00E-07	7.78	4.61	1.69	BTG1 protein	BTG1
7.00E-07	1.87	1.08	1.72	Probable cysteinyl-tRNA synthetase, mitochondrial precursor	SYCM_HUMAN
7.00E-07	1.12	0.47	2.39	Complement decay-accelerating factor precursor	CD55
8.00E-07	1.98	0.59	3.36	Annexin A3	ANXA3
9.00E-07	3.55	2.04	1.74	nuclear factor of kappa light polypeptide gene enhancer in B-cells	NFKBIZ
1.00E-06	0.14	0.062	2.22	Thioredoxin (Trx)	TXN
1.20E-06	4.09	2.12	1.93	Beta-2-microglobulin precursor	B2M
1.20E-06	0.58	0.28	2.07	Mitogen-activated protein kinase kinase 1-interacting protein 1	MAP2K1IP1
1.20E-06	1.44	0.63	2.31	Proto-oncogene protein c-fos	FOS

Negatively regulated genes of expression in ACS versus the control group

Parametric p-value	ACS	Control	Fold-change	Name	Symbol
1.00E-06	0.28	0.44	0.63	Nucleolar phosphoprotein p130	NOLC1
3.10E-06	0.16	0.28	0.56	Guanine nucleotide-binding protein G(I)/G(S)/G(O) gamma-3	GNG3
3.40E-06	0.14	0.25	0.57	ATP synthase protein 8	MT-ATP8
4.20E-06	0.14	0.24	0.59	Protein TMEM99 precursor.	TMEM99
4.60E-06	2.19	3.47	0.63	Ephrin type-A receptor 1 precursor	EPHA1
4.90E-06	0.88	1.3	0.68	Trafficking protein particle complex subunit 6A	TRAPPC6A
5.00E-06	0.18	0.31	0.58	Cell division protein kinase 4	CDK4
5.60E-06	0.88	1.48	0.6	Presenilin-2 Presenilin-2 CTF subunit	PSEN2
6.00E-06	0.63	0.95	0.67	Peroxisomal targeting signal 1 receptor import receptor	PEX5
6.00E-06	0.7	1.05	0.67	E3 SUMO-protein ligase PIAS3	PIAS3
6.30E-06	3.56	5.84	0.61	Coiled-coil domain-containing protein 84	CCDC84
8.40E-06	0.44	0.69	0.64	misato	MSTO1
1.19E-05	0.51	0.77	0.66	Protein MYLE	MYLE_HUMAN
1.22E-05	0.61	1.11	0.55	Protein Jade-3 (PHD finger protein 16).	PHF16
1.54E-05	0.54	0.79	0.68	Zinc finger protein 512.	ZNF512
1.81E-05	3.43	5.4	0.63	Orphan sodium- and chloride-dependent neurotransmitter	SLC6A16
2.07E-05	0.36	0.53	0.68	FACT complex subunit SSRP1	SSRP1
2.17E-05	1.06	1.57	0.68	Probable oxidoreductase C10orf33	C10orf33
2.25E-05	1.83	3.22	0.57	Mannosyl-oligosaccharide 1,2-alpha-mannosidase IC	MAN1C1
2.62E-05	2.09	3.95	0.53	Alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3-N-acetyl-	ST6GALNAC4

Univariate t test was done. The first 20 genes that were the most significantly altered were listed.

Table S2-1. Baseline characteristics according to outcome

		TLR		P-value
		Yes (N=7)	**No** (N=23)	
Age, y		67 ± 11	64 ± 13	0.58
Male, n (%)		7 (100)	23 (100)	
Hypertension, n (%)		6 (86)	18 (78)	1.00
Diabetes Mellitus, n (%)		6 (86)	9 (39)	0.08
Smoking, n (%)		6 (86)	16 (70)	0.64
No. of diseased vessels, n				0.060
	1 vessel	0	10	
	2 vessels	4	10	
	3 vessels	3	3	
LMT lesion		1 (14)	4 (17)	1.00
Stent				
	Bare metal stent, n	3	15	0.39
	Drug eluting stent, n	4	8	
LVEF [%]		66 ± 11	54 ± 13	0.04
Max CK [IU/l]		1264 (765-2038)	1735 (1298-3000)	0.25
BNP at day 7 [pg/ml]		98 (59-280)	52 (34-116)	0.40
CCr [ml/min]		57 (51-61)	73 (60-113)	0.22
hsCRP at day 0 [mg/dl]		0.16 (0.06-0.30)	0.18 (0.09-0.42)	0.86
T-Chol [mg/dl]		174 (143-187)	158 (144-217)	0.77
TG [mg/dl]		74 (69-104)	79 (57-116)	0.90
HDL-C [mg/dl]		41 (38-54)	41 (37-45)	0.65
LDL-C [mg/dl]		85 (82-113)	95 (85-130)	0.39
HbA1c, NGSP [%]		6.8 (6.5-7.0)	6.1 (5.8-7.3)	0.12
FPG [mg/dl]		108 (101-139)	115 (99-151)	0.12
FIRI [µU/ml]		3.3 (2.0-5.5)	8.3 (4.5-14.9)	0.02
HOMA-IR		0.84 (0.66-1.40)	2.00 (1.07-5.50)	0.03
Lp(a) [mg/dl]		35 (32-42)	31 (13-43)	0.71
BMI [kg/m^2]		22.8 ± 4.9	24.2 ± 3.2	0.40
Medication at discharge				
	RAS inhibitor, n (%)	5 (71)	19 (83)	0.60
	statin, n (%)	4 (57)	20 (87)	0.12

hsCRP: high-sensitivity C-reactive protein. Data are shown as mean ± standard deviation or the median with interquartile range.

Table S2-2. Baseline characteristics according to outcome

	de novo PCI		P-value
	Yes (N=7)	**No** (N=23)	
Age, y	66 ± 8	64 ± 13	0.62
Male, n (%)	7 (100)	23 (100)	
Hypertension, n (%)	6 (86)	18 (78)	1.00
Diabetes Mellitus, n (%)	4 (57)	11 (48)	1.00
Smoking, n (%)	2 (29)	5 (22)	1.00
No. of diseased vessels, n			0.046
1 vessel	0	10	
2 vessels	6	8	
3 vessels	1	5	
LMT lesion	2 (29)	3 (13)	0.57
LVEF [%]	60 ± 17	56 ± 12	0.43
Max CK [IU/l]	1488 (751-1794)	2027 (1117-3103)	0.16
BNP at day 7 [pg/ml]	85 (72-114)	51 (35-236)	0.45
CCr [ml/min]	62 (51-69)	79 (57-116)	0.20
hsCRP at day 0 [mg/dl]	0.16 (0.06-0.45)	0.18 (0.09-0.34)	0.73
T-Chol [mg/dl]	157 (145-213)	174 (144-198)	0.84
TG [mg/dl]	72 (62-96)	81 (61-117)	0.59
HDL-C [mg/dl]	45 (42-48)	40 (37-45)	0.35
LDL-C [mg/dl]	91 (82-156)	95 (83-125)	0.90
HbA1c, NGSP (%)	6.4 (6.1-6.6)	6.2 (5.9-7.3)	0.98
FPG [mg/dl]	108 (100-120)	115 (100-156)	0.49
FIRI [µU/ml]	3.8 (3.2-6.4)	7.5 (4.4-14.2)	0.12
HOMA-IR	0.89 (0.68-1.58)	2.00 (1.07-5.50)	0.03
Lp(a) [mg/dl]	37 (33-41)	26 (12-44)	0.21
BMI [kg/m^2]	22.9 ± 2.0	24.2 ± 4.0	0.41
Medication at discharge			
RAS inhibitor, n (%)	5 (71)	19 (83)	0.60
statin, n (%)	6 (86)	18 (78)	1.00

hsCRP: high-sensitivity C-reactive protein. Data are shown as mean ± standard deviation or the median with interquartile range.

Table S3. Positively regulated genes of expression in ACS in the secondary non-fatal coronary event (NFE) group

Parametric p-value	Non-event	Event	Fold-change	Name	Symbol
9.47E-05	0.17	0.25	1.47	Deoxyuridine 5'-triphosphate nucleotidohydrolase,	DUT
0.0004995	0.073	0.14	1.92	Dual specificity protein phosphatase 14	DUSP14
0.000548	0.64	1.16	1.81	Lipin-1	LPIN1
0.0006327	0.11	0.18	1.64	basic, immunoglobulin-like variable motif containing	BIVM
0.0007365	0.5	0.94	1.88	Neuron-specific protein family member 1	NSG1_HUMAN
0.0009953	0.14	0.21	1.50	Integrin beta-7 precursor	ITGB7
0.0010413	0.1	0.16	1.60	Hexaprenyldihydroxybenzoate methyltransferase,	COQ3
0.0012408	1.45	2.04	1.41	SH2 domain-containing putative adapter SH2-B	SH2B1
0.0012447	0.38	0.59	1.55	Secretion-regulating guanine nucleotide exchange factor	SERGEF
0.0012634	0.22	0.31	1.41	WD repeat domain 70	WDR70
0.0013564	1.31	2.12	1.62	C16orf67 protein	Q96NS8_HUMAN
0.0014062	0.61	0.87	1.43	retinoic acid induced 16	RAI16
0.0015632	0.11	0.17	1.55	6-phosphofructokinase type C	PFKP
0.0016169	1.81	2.58	1.43	Linker for activation of T-cells family member 1	LAT
0.0017559	0.16	0.25	1.56	CD320 antigen precursor	CD320
0.0018419	0.91	1.29	1.42	coiled-coil domain containing 92	CCDC92
0.0019822	0.26	0.37	1.42	Mitochondrial deoxynucleotide carrier	SLC25A19
0.0022563	0.27	0.57	2.11	T-cell surface glycoprotein CD8 beta chain precursor	CD8B
0.0023055	0.83	1.17	1.41	Protein CBFA2T2	CBFA2T2
0.0026213	1.27	1.97	1.55	Leucine-rich repeat-containing protein 8C	LRRC8C

Negatively regulated genes of expression in ACS in the secondary non-fatal coronary event (NFE) group

Parametric p-value	Non-event	Event	Fold-change	Name	Symbol
0.0001886	4.65	2.43	0.52	NFAT activation molecule 1 precursor	NFAM1
0.0004891	1.94	1.19	0.61	DNA-binding protein RFX2	RFX2
0.0005549	1.92	1.18	0.61	**Death-associated protein kinase 1**	**DAPK1**
0.0008071	1.22	0.84	0.69	Tumor necrosis factor receptor superfamily member 16	NGFR
0.0008241	102.83	69.53	0.68	Leukocyte immunoglobulin-like receptor subfamily A member	LILRA2
0.0009186	4.63	2.46	0.53	Ninein	NIN
0.000995	8.51	5.48	0.64	Putative uncharacterized protein C9orf164.	C9orf164
0.0010128	4.99	2.82	0.57	Jun dimerization protein	NP_569736.1
0.0012464	6.26	3.94	0.63	Engulfment and cell motility protein 1	ELMO1
0.001476	4.64	3.22	0.69	Growth factor receptor-bound protein 2	GRB2
0.0014812	0.56	0.32	0.57	PH domain leucine-rich repeat-containing protein phosphatase	PHLPP
0.0015486	2.55	1.7	0.67	Wiskott-Aldrich syndrome protein	WAS
0.0018706	0.95	0.62	0.65	Ras-related GTP-binding protein D	RRAGD
0.0019416	1.21	0.77	0.64	Heme-binding protein 2	HEBP2
0.0020717	8.57	5.39	0.63	Trem-like transcript 2 protein precursor	TREML2
0.002299	1.27	0.83	0.65	Class B basic helix-loop-helix protein 8	BHLHB8
0.0024408	1.7	1.14	0.67	solute carrier family 35, member E3	SLC35E3
0.0024638	0.24	0.18	0.75	Tuftelin	TUFT1
0.0025682	1.94	1.38	0.71	Exostosin-like 3	EXTL3
0.002688	25.79	19.66	0.76	Neutrophil cytosol factor 4	NCF4

Univariate t test was done. The each of the first 20 genes that were the most significantly altered was listed, respectively.

Table S4-1. Pathways significantly altered in TLR group

	Pathway description	Number of genes	LS permutation P-value	KS permutation P-value	Efron-Tibshirani's GSA test P-value
Biocarta	Ras-Independent pathway in NK cell-mediated	12	0.02248	0.01501	* < 0.005 (+)
KEGG	Ribosome	77	* 0.00001	* 0.00001	0.285 (+)
	Primary immunodeficiency	20	* 0.00116	* 0.00273	0.65 (-)
	Prion diseases	12	* 0.00356	0.01682	0.315 (-)

1 out of 202 and 3 out of 203 investigated gene sets among the Biocarta pathways and the KEGG pathways respectively were passed the 0.005 significance threshold of LS/KS permutation test or Efron-Tibshirani's GSA maxmean test. * denotes significant p-value

Table S4-2. Pathways significantly altered in *de novo* PCI group

	Pathway description	Number of genes	LS permutation P-value	KS permutation P-value	Efron-Tibshirani's GSA test P-value
Biocarta	The Co-Stimulatory Signal During T-cell Activation	11	* 0.00001	* 0.00079	0.015 (+)
	Lck and Fyn tyrosine kinases in initiation of TCR Activation	9	* 0.00001	* 0.00008	0.335 (-)
	T Cell Receptor Signalling Pathway	26	* 0.00001	* 0.00001	0.525 (+)
	Role of Tob in T-cell activation	10	* 0.00025	0.01354	0.465 (+)
	Activation of Csk by cAMP-dependent Protein Kinase Inhibits	14	* 0.00048	0.00717	0.525 (-)
	Nerve growth factor pathway (NGF)	11	* 0.00084	0.03549	0.285 (+)
	HIV Induced T Cell Apoptosis	5	* 0.00085	0.01193	0.465 (+)
	Phosphoinositides and their downstream targets.	11	* 0.00088	0.00642	0.18 (-)
	Fc Epsilon Receptor I Signalling in Mast Cells	18	* 0.00133	0.0078	0.14 (+)
	BCR Signalling Pathway	15	* 0.0014	0.01407	0.16 (-)
	Granzyme A mediated Apoptosis Pathway	7	* 0.00157	* 0.00098	0.52 (-)
	T Helper Cell Surface Molecules	6	* 0.00311	0.04447	0.29 (+)
	CTL mediated immune response against target cells	8	* 0.00411	0.03833	0.385 (-)
	Erk1/Erk2 Mapk Signalling pathway	15	* 0.00496	0.03883	0.535 (+)
	HIV-I Nef: negative effector of Fas and TNF	35	0.00656	* 0.00475	0.615 (+)
	Ras-Independent pathway in NK cell-mediated cytotoxicity	12	0.02151	* 0.00318	0.15 (-)
KEGG	Systemic lupus erythematosus	48	* 0.00003	* 0.00028	0.21 (+)
	T cell receptor signalling pathway	57	* 0.00004	* 0.00317	0.53 (-)
	Pentose phosphate pathway	14	* 0.0004	0.02425	0.415 (+)
	Primary immunodeficiency	20	* 0.00075	0.01542	0.55 (-)
	B cell receptor signalling pathway	38	* 0.00373	0.02091	0.165 (-)
	Natural killer cell mediated cytotoxicity	54	* 0.00475	0.00967	0.33 (-)
	Ribosome biogenesis in eukaryotes	30	0.01553	* 0.00054	0.42 (-)
	RNA transport	63	0.05931	* 0.00101	0.065 (+)
	Melanoma	25	0.77271	0.86366	* < 0.005 (-)
	Ribosome	77	0.78477	* 0.00085	0.44 (+)

16 out of 202 and 10 out of 203 investigated gene sets among the Biocarta pathway and the KEGG pathway respectively were passed the 0.005 significance threshold of LS/KS permutation test or Efron-Tibshirani's GSA maxmean test. * denotes significant p-value

Table S5. Class prediction analyses using a supervised learning method

Class Prediction Results		**Number of genes in classifier**	**Compound covariate predictor correct?**
Non-fatal coronary event	P<0.01	182	60% No event = 12/19 Event = 6/11
	P<0.005	83	63% No event = 13/19 Event = 6/11
TLR	P<0.01	45	70% No event = 19/23 Event = 2/7
	P<0.005	23	77% No event = 22/23 Event = 1/7
***De novo* PCI**	P<0.01	263	70% No event = 17/23 Event = 4/7
	P<0.005	131	67% No event = 17/23 Event = 3/7

TLR: Target lesion revascularization, PCI: percutaneous coronary intervention