Supplemetnary Table S1, Characteristics of selected single nucleotide polymorphisms

SNP characteristics					Study characteristics			
Functional group	**Gene**	**Name**	**SNP**	**MAF**	**Endpoint**	**Sample size (% cases)**	**Effect**	**Ref**
Endothelial function/vascular remodeling	MMP1	Matrix metallopeptidase 1	rs11292517 (-1607 1G/2G)	?	AVF failure	596 (29%)	HR 2,32 for 1G/1G vs. 1G/2G or 2G/2G genotypes	(1)
	NOS3	Nitric oxide synthesis 3	rs1799983	0,34	Coronary restenosis	901 (10%)	HR 1.67 (95% CI 1.09–2.54)m p=0,018	(2)
	ELN	Elastin	rs2071307	0,37	Enzyme function	800 (NA)	SNP resulted in altered (decreased) enzyme function	(3)
	ANXA5	Annexin A5	rs4833229	0,43	Coronary restenosis	3104 (9,8%)	OR=1.294, P=0.011	(4)
	ANXA5	Annexin A5	rs6830321	0,48	Coronary restenosis	3104 (9,8%)	OR=1.347, p=0.003	(4)
	LRP1	low density lipoprotein receptor-related protein 1	rs1466535	0,33	Abdominal aortic aneurysm	55410 (11%)	OR 1.15 (1.10-1.21), p=4.52E-10	(5)
	QKI	Quaking	RS2759393 (34084C>A)	0,23	Coronary restenosis	3104 (9,8%)	HR 0.68 (0.52-0.88), P=0.0041	(6)
	QKI	Quaking	RS3763197 (2786A>G)	0,15	Coronary restenosis	3104 (9,8%)	HR 2.11 (1.23-3.62), P=0.007	(6)
	QKI	Quaking	RS3857504 (-2616C>T)	0,43	Coronary restenosis	3104 (9,8%)	HR 1.88 (1.10-3.24), P=0.022	(6)
	-	12q23.2	rs10861032 (T>C)		Coronary restenosis	866 (34,1%)	OR 1.75 (1.35-2.27), Pcombined=1.11E-07	(6)
	-	12q23.2	rs9804922 (C>T)		Coronary restenosis	866 (34,1%)	OR 2.48 (1.72-3.60), Pcombined=1.45E-06	(6)
Growth factors	CDKN1B ($p27^{kip1}$)	Cyclin-dependent kinase inhibitor 1B	rs36448499 (-838C>A)	0,45	Coronary restenosis (TVR)	685 (8,3%) (discovery)	HR 0.28 (95% CI 0.10-0.77), p=0,014	(7)
	CDKN1B ($p27^{kip1}$)	Cyclin-dependent kinase inhibitor 1B	rs36448499 (-838C>A)	0,45	Coronary restenosis (TVR)	2009 (9,0%) (replication)	HR 0.61 (95% CI 0.40-0.93), p-value not reported	(7)
	CTGF	connective tissue growth factor	rs6918698 (-945G>C)	0,41	CV mortality during HD	98 (12,2%)	OR 13 (95% CI 1.49–155), p=0.005	(8)
	FGFR4	Fibroblast Growth Factor receptor 4	rs351855 (Gly388Arg)	0,29	CAD	1419 (48,4%)	OR 0.77 (95% CI 0.66-0.90), p=0.001	(9)
	KLF5	Kruppel-like factor 5	rs3812852 (-1282A>G)	0,08	hypertension	472 (83,7%) (discovery)	OR 6,7 (95% 1,9-22,6) p=0.001	(10)
	KLF5	Kruppel-like factor 5	rs3812852 (-1282A>G)	0,08	hypertension	1261 (31,3%) (replication)	OR 2,8 (95% CI 1,1-7,3), p=0,007	(10)
	PDGFD	Platelet derived growth Factor D	rs974819 (T>C)	0,32	CAD	64881 (51,8%)	OR 1,07 (1,04-1,09) P=$2,4x10^{-9}$	(11)
	PDGFD	Platelet derived growth Factor D	rs974819 (T>C)	0,32	CAD	268 (58,6%)	OR 1,45 (95% CI 1,02-2,08). P=0,04	(12)
	PDGFD	Platelet derived growth Factor D	rs496339	0,12	Coronary restenosis	866 (34,1%)	OR 0,60 p=0,007	(6)
	TGFBR1	Transforming growth factor, beta receptor I	rs1626340	0,23	Abdominal aortic aneurysm	1760 (41,8%)	OR 1,32 (1,11-1,56), P=0,001	(13)
	TGFBR2	Transforming growth factor, beta receptor2	rs1036095	0,30	Abdominal aortic aneurysm	1760 (41,8%)	OR 1,32 (1,12-1,54), P=0,001	(13)
	TGFBR2	Transforming growth factor, beta receptor2	rs4522809	0,48	Abdominal aortic aneurysm	1760 (41,8%)	OR 1,28 (1,12-1,48), P=0,0004	(13)
	VEGF	Vascular endothelial growth factor	rs2010963	0,40	Death after CABG	62 (16,1%)	OR 6.7 (1.50-29.4), P=0,003	(14)
	VEGF	Vascular endothelial growth factor	rs3025039 (936C>T)	0,16	ESRD	290 (34,8%)	OR 2,02 (95% CI 1,27-3,53) p=0,013	(15)
	VEGF	Vascular endothelial growth factor	rs699947 (-2578C>A)	0,43	Mortality during Perit.dialysis	135 (14,8%)	HR 3.04 (95% CI 1.10-8.36), P=0,036	(16)
	VEGF	Vascular endothelial growth factor	rs699947 (-2578C>A)	0,43	CAD	418 (18,7%)	OR 2,97 (95% CI 1,45-6,09), p-value not reported	(17)
	VEGF	Vascular endothelial growth factor	rs699947 (-2578C>A)	0,43	Myocardial infarction	418 (11,0%)	OR 7,02 (95% CI 1,93-25,6), p-value not reported	(17)
Inflammation	IL6	Interleukin 6	rs1800795 (−174G>C)	0,48	index of coexistent disease (ICED) score	183 (NA)	OR of higher comorbidity score 4,87 (95%CI 1,35-17,58), P=0,02	(18)
	IL6	Interleukin 6	rs1800795 (−174G>C)	0,48	Karnofsky Index (functional status)	183 (NA)	OR of lower functional status 4,91 (95% CI 1,05-22,95), P=0,04	(18)
	IL10	Interleukin 10	rs1800896 (-1082G>A)	0,48	Coronary restenosis	3104 (9,8%)	RR 1.4 (95% CI 1.1-1.8), p-value not reported	(19)
	IL10	Interleukin 10	rs1800896 (-1082G>A)	0,48	CV events during HD	300 (7,7%)	RR 2,76 (131-4,17), p=0,004	(20)
	IL10	Interleukin 10	rs1800896 (-1082G>A)	0,48	mortality after acute renal failure	61 (42,6%)	HR 0,36 (95% Ci 0,15-0,89), P=0,03)	(21)
	IL10	Interleukin 10	rs3024498 (4559A>G)	0,23	Coronary restenosis	3104 (9,8%)	RR 2.0 (95% CI 1.4-2.8), p-value not reported	(19)
	LTA	lymphotoxin alpha (TNF superfamily, member 1)	rs1799964	0,21	Coronary restenosis	3104 (9,8%)	HR 0.75 (95% CI 0.57-0.98), P=0,04	(22)
	RP105	CD180	rs5744478	0,13	Coronary restenosis	3104 (9,8%)	OR 0.59(0.39-0.9) P=0.016	(23)
	TNF	Tumor necrosis factor alpha	rs361525	0,05	Coronary restenosis	3104 (9,8%)	HR 0.60 (95% CI 0.37-0.98), P=0,04	(22)
	TNF	Tumor necrosis factor alpha	rs1800629 (−308G>A)	0,17	index of coexistent disease (ICED) score	183 (NA)	OR of higher comorbidity score 2,00 (95%CI 1,03-3,88), P=0,04	(18)
	TNF	Tumor necrosis factor alpha	rs1800629 (−308G>A)	0,17	Karnofsky Index (functional status)	183 (NA)	OR of lower functional status 2,16 (95% CI 1,13-4,12), P=0,02	(18)
	TNF	Tumor necrosis factor alpha	rs1800629 (−308G>A)	0,17	mortality after acute renal failure	61 (42,6%)	HR 2,47 (95% CI 1,06-5,77), P=0,04	(21)
	TNF	Tumor necrosis factor alpha	rs1800629 (−308G>A)	0,17	Synthetic dialysis graft failure in 1yr	67 (40%)	OR 3,5 (95% CI 1,5-8,1), P=0,003	(24)
	TLR4	Toll-like receptor 4	rs4986790 (Asp299Gly)	0,06	carotid artery compliance	2201 (NA)	G allele increased carotid artery compliance, beta=0,099 (95% CI 0,029-0,169), p=0,006	(25)
Calcium/phosphate metabolism	AHSG	alpha-2-HS-glycoprotein (Fetuin-A)	rs4918 (Thr256Ser(C>G))	0,31	mortality and fetuin-A levels	215 (34%)	256Ser carriers had lower serum Fetuin-A levels, p<0,0001, and higher all-cause and cardiovascular mortality rate, p<0,05, if inflamed	(26)
	Klotho	Klotho	rs9527025 (Cys>Ser)	0,18	-	NA	likely functional variant	(27)
	Klotho	Klotho	rs564481 (C1818T)	0,36	LDL levels	219 (NA)	LDL in mg/dl in CC vs T carriers: 101,8±30,9 vs 92,8±	(28)
	Klotho	Klotho	rs577912 (A>C)	0,12	mortality during dialysis	1307 (16%)	HR 1,77 (1,20-2,62) p=0,004. In AA/AC subjects 16% higher Klotho mRNA expression, p=0,0045	(29)
	Klotho	Klotho	rs1207568 (-395G>A)	0,16	AVF failure	126 (27%)	A allele carriers increased risk of AVF failure, 46% vs 20%, p=0,003	(30)
	VDR	Vitamin D receptor	rs11574027	0,05	Coronary restenosis	866 (34,1%)	associated with restenosis (OR 4,2 p=0,0001)	(6)
	VDR	Vitamin D receptor	rs4516035	0,46	Coronary restenosis	3104 (9,8%)	HR 1,3 (1,1-1,5) p=0,006	(31)
	VDR	Vitamin D receptor	rs2238135	0,23	Coronary restenosis	3104 (9,8%)	HR 0,7 (0,6-0,9) p=0,004	(31)

Coagulation and platelet aggregation	FGB	fibrinogen-beta	rs1800790 (-455G>A)	0,20	AVF thrombosis	68 (49%)	No association	(32)
	FGB	fibrinogen-beta	rs1800790 (-455G>A)	0,20	Coronary restenosis	527 (5,3%)	OR 2.7 (1.2-6.2), p=0,016	(33)
	FGB	fibrinogen-beta	rs1800790 (-455G>A)	0,20	Coronary restenosis	2309 (10%)	No association	(34)
	FGB	fibrinogen-beta	rs1044291	0,33	Coronary restenosis	866 (34,1%)	OR 1,4, p=0,0028	(6)
	F5	Factor 5	rs6025 (1691G>A Leiden)	0,02	Dialysis graft survival	354 (86%)	HR 1.70 (1.32-2.19), p<0.0001	(35)
	F5	Factor 5	rs6025 (1691G>A Leiden)	0,02	AVF thrombosis	68 (49%)	No association	(32)
	ITGB3	integrin, beta 3 (platelet glycoprotein IIIa)	rs5918 (L33P)	0,15	AVF thrombosis	68 (49%)	No association	(32)
	ITGB3	integrin, beta 3 (platelet glycoprotein IIIa)	rs5918 (L33P)	0,15	Coronary thrombosis	139 (51%)	OR 2,8 (1,2-6,4), p-value not reported	(36)
	ITGB3	integrin, beta 3 (platelet glycoprotein IIIa)	rs5918 (L33P)	0,15	Myocardial infarction	604 (50%)	OR 2.11 (1.25–3.63), p-value not reported	(37)

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Supplementary Table S2, Quality control

SNP	Call rate	MAF	HW p-value
RS4833229	94,8%	0,43	0,52
RS6830321	95,6%	0,46	0,34
RS6918698	94,7%	0,46	0,11
RS36228499	95,1%	0,44	0,83
RS10861032	94,6%	0,18	0,06
RS9804922	94,8%	0,09	0,90
RS2071307	95,7%	0,38	0,65
RS6025	95,5%	0,03	0,22
RS4918	93,9%	0,31	0,64
RS1044291	94,7%	0,33	0,29
RS1800787 (Proxy voor rs1800790)	94,2%	0,21	0,49
RS351855	91,0%	0,32	0,03
RS1800896	94,5%	0,48	0,02
RS3024498	95,0%	0,27	0,14
RS1800795	95,7%	0,37	0,49
RS17218711 (Proxy voor rs5918)	94,9%	0,15	0,78
RS3812852	95,7%	0,07	0,39
RS397703 (Proxy voor 1207568)	95,0%	0,18	0,02
RS564481	93,0%	0,35	0,23
RS577912	94,4%	0,15	0,04
RS9527025	95,5%	0,12	0,77
RS1466535	95,7%	0,34	0,72
RS1799964	94,9%	0,23	0,53
RS11292517	93,0%	0,47	0,60
RS1799983	95,0%	0,30	0,94
RS496339	94,8%	0,10	0,79
RS974819	90,4%	0,32	0,40
RS2759393	94,5%	0,22	0,29
RS3763197	95,4%	0,16	0,20
RS3857504	93,3%	0,17	0,34
RS5744478	95,8%	0,08	0,24
RS1626340	91,5%	0,21	0,01
RS1036095	94,8%	0,25	0,97
RS4522809	94,7%	0,45	0,48
RS4986790	95,7%	0,07	0,82
RS1800629	95,0%	0,18	0,39
RS361525	95,0%	0,05	0,09
RS11574027	95,7%	0,02	0,26
RS2238135	94,2%	0,23	0,71
RS4516035	94,2%	0,43	0,01
RS2010963	94,8%	0,34	0,11
RS3025039	95,8%	0,13	0,60
RS699947	93,9%	0,48	0,15

MAF, minor allele frequency

HW p-value, Result of Hardy-Weinberg equilibrium analysis using chi-square analysis

Supplementary Table S3, Interaction analysis of clinical factors and genetic factors on AVF failure

Factor V Leiden		**HR with 95% CI**		**P**
-	Male	1	Reference	
-	Female	1.61	(1.21-2.15)	0,001
+	Male	5.00	(2.60-9.61)	<0,001
+	Female	1.06	(0.26-4.28)	0,94
-	Diabetes mellitus -	1	Reference	
-	Diabetes mellitus +	2.23	(1.59-3.13)	<0,001
+	Diabetes mellitus -	3.61	(1.95-6.68)	<0,001
+	Diabetes mellitus +	0.95	(0.13-6.82)	0,96
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GG/AG	Male	1	Reference	
GG/AG	Female	1.58	(1.17-2.15)	0,003
AA	Male	1.90	(1.15-3.15)	0,012
AA	Female	1.69	(0.94-3.01)	0,078
GG/AG	Diabetes mellitus -	1	Reference	
GG/AG	Diabetes mellitus +	2.11	(1.48-3.01)	<0,001
AA	Diabetes mellitus -	1.63	(1.07-2.47)	0,022
AA	Diabetes mellitus +	2.97	(1.10-8.05)	0,032

HR, hazard ratio; CI, confidence interval; P, p-value