

Appendix

Table A1. Gene, Seattle Program for Genomic Applications identifier and RS number for single nucleotide polymorphisms presented in appendix tables A2 to A26.

HUGO name	Seattle PGA #	RS #	HUGO name	Seattle PGA #	RS #
CPB2	2103	rs3742266	F13B	9706	rs2298883
CPB2	4947	rs17067700	F13B	17686	rs2990510
CPB2	7826	rs2181617	F13B	29759	rs5990
CPB2	10152	rs2404965	F2	2890	rs3136435
CPB2	18857	rs17844025	F2	3696	rs3136520
CPB2	31427	rs11620308	F2	4992	rs2070851
CPB2	32627	rs1326400	F2	5389	rs2070852
CPB2	35605	rs9562637	F2	5467	rs5896
CPB2	36326	rs17844078	F2	7530	rs3136460
CPB2	47956	rs17844129	F2	21239	rs3136516
CPB2	48100	rs11574991	F2	rs1799963	rs1799963
CPB2	51208	rs1926447	F3	599	rs958587
CPB2	54691	rs2274381	F3	5334	rs762484
F10	4544	rs556694	F3	7877	rs3917643
F10	8946	rs693335	F3	11185	rs610277
F10	9501	rs3211744	F3	13925	rs3354
F10	11962	rs3211752	F5	3578	rs3753305
F10	14881	rs2480945	F5	17557	rs2227245
F10	16893	rs3211764	F5	29565	rs9332570
F10	17396	rs2026160	F5	30539	rs9332575
F10	18352	rs3211770	F5	35788	rs6033
F10	22739	rs3211783	F5	38592	rs6025
F10	26242	rs5960	F5	42713	rs9332590
F11	3450	rs4253398	F5	45765	rs6018
F11	3543	rs3822057	F5	45888	rs4524
F11	4197	rs4253400	F5	46058	rs9332695
F11	6783	rs4253406	F5	66464	rs9332649
F11	10942	rs1593	F5	66872	rs9332653
F11	20423	rs4253423	F5	68717	rs3766103
F11	22771	rs2289252	F5	72877	rs9332701
F11	25455	rs4253430	F7	185	rs3093230
F11	26011	rs4253431	F7	2643	rs2774030
F12	6570	rs17876047	F7	15386	rs6046
F12	7532	rs17876032	F7	18311	rs3093261
F13A1	4377	rs5985	F8	25167	rs6655259
F13A1	72060	rs3024477	F8	55941	rs1936645
F13A1	148318	rs5982	F8	71159	rs5945258
F13A1	165306	rs3024455	F8	95826	rs1800291
F13A1	165399	rs2326707	F8	95910	rs1800292
F13A1	170779	rs3024457	F8	165293	rs1800297
F13A1	176866	rs3024460	F8	187661	rs17281377
F13A1	177424	rs3024462	F9	716	rs411017
F13A1	177778	rs3024486	F9	4135	rs371000
F13B	5995	rs5996	F9	6347	rs376165
F13B	7319	rs17514246	F9	10948	rs392959

HUGO name	Seattle PGA #	RS #	HUGO name	Seattle PGA #	RS #
F9	12806	rs4149755	PROC	3220	rs2069906
F9	16171	rs4149758	PROC	4515	rs2069910
F9	21554	rs422187	PROC	4732	rs2069912
F9	21975	rs6048	PROC	4919	rs2069915
F9	27226	rs110583	PROC	5867	rs2069918
F9	30893	rs4149762	PROC	10454	rs2069928
F9	35124	rs434144	PROC	11310	rs5937
FGA	251	rs2070006	PROCR	837	rs2069940
FGA	3807	rs2070016	PROCR	3600	rs2069946
FGA	5498	rs2070018	PROCR	6196	rs9574
FGA	6534	rs6050	PROCR	rs1415772	rs1415772
FGA	9205	rs2070022	PROS1	288	rs7650230
FGB	1038	rs1800791	PROS1	430	rs7644769
FGB	1643	rs1800788	PROS1	13154	rs8178591
FGB	9487	rs4220	PROS1	26890	rs7615840
FGB	11079	rs1044291	PROS1	66205	rs8178626
FGG	129	rs2066854	PROS1	66847	rs4857037
FGG	902	rs1800792	SERPINC1	1734	rs2227589
FGG	5836	rs2066860	SERPINC1	2415	rs2227593
FGG	9340	rs1049636	SERPINC1	5403	rs2227603
PLAT	2586	rs6980538	SERPINC1	7199	rs2227607
PLAT	6388	rs8178684	SERPINC1	9089	rs5877
PLAT	6971	rs8178687	SERPINE1	664	rs2227631
PLAT	9823	rs7837156	SERPINE1	4588	rs2227657
PLAT	9944	rs8178880	SERPINE1	5878	rs2227667
PLAT	12047	rs879293	SERPINE1	10381	rs2227692
PLAT	12264	rs8178712	SERPINE1	12219	rs11178
PLAT	16039	rs4736829	TFPI	1502	rs2192824
PLAT	17825	rs732612	TFPI	2418	rs2300412
PLAT	18289	rs8178733	TFPI	3437	rs8176597
PLAT	22323	rs8178750	TFPI	21164	rs8176612
PLAT	30619	rs1136159	TFPI	34214	rs3771059
PLAT	35171	rs4581040	THBD	4007	rs1042579
PLG	406	rs4252045	THBD	5110	rs1042580
PLG	1470	rs4252053	THBD	5318	rs3176123
PLG	1983	rs2314852	THBD	6235	rs1962
PLG	2967	rs4252065			
PLG	12881	rs4252093			
PLG	15255	rs4252105			
PLG	18114	rs3823055			
PLG	31439	rs4252125			
PLG	34158	rs1317026			
PLG	41108	rs4252166			
PLG	41494	rs1835346			
PLG	54925	rs4252200			
PROC	2583	rs1799810			

HUGO, Human Genome Organization  
PGA, Program for Genomic Applications

Table A2. Analysis of factor II haplotypes and single nucleotide polymorphisms and associations with incident venous thrombosis

Haplotype identifier	2890	3696	4992	5389	5467 (T165M)	7530	21239	rs1799963 (20210)	Haplotype frequency in cases N = 348	Haplotype frequency in controls N = 1677	Odds ratio (95% confidence interval)	P-value
1	G	C	T	C	C	C	A	G	45.4	48.8	1.00 (reference)	
2	G	C	T	C	C	C	G	G	14.6	14.3	1.15 (0.88-1.49)	0.31
3	G	C	C	G	T	G	G	G	15.3	13.7	1.23 (0.95-1.59)	0.12
4	G	C	C	G	C	C	G	G	7.7	8.5	0.97 (0.69-1.35)	0.84
5	A	C	T	G	C	C	G	G	6.7	7.0	1.01 (0.71-1.44)	0.95
other									3.7	3.8	1.28 (0.82-2.00)	0.28
6	G	T	T	C	C	C	G	G	3.9	2.3	<b>1.89 (1.16-3.09)</b>	<b>0.01</b>
7	G	C	T	C	C	C	A	A	2.6	1.5	<b>2.00 (1.13-3.54)</b>	<b>0.02</b>
Control MAF %	8.2	2.3	23.2	33.1	14.6	14.5	49.0	1.5			Global p-value Global p-value <sup>†</sup>	0.06 0.20
P-value	0.67	<b>0.009</b>	0.84	0.83	0.36	0.46	0.16	<b>0.03</b>				
Odds ratio and 95% confidence interval <sup>*</sup>	0.93 (0.68-1.28)	<b>1.82 (1.16-2.86)</b>	1.02 (0.84-1.24)	1.02 (0.85-1.22)	1.11 (0.89-1.40)	1.09 (0.87-1.37)	1.13 (0.95-1.34)	<b>1.86 (1.05-3.26)</b>				

MAF, minor allele frequency. Other, combined rare haplotypes. Bold entries have p-values <0.05. Shaded cells identify minor allele. \*Risk for each additional copy of the variant allele compared with risk associated with an additional copy of the wild-type allele. <sup>†</sup>Global p-value after removal of the carriers of the 20210A allele.

Table A3. Analysis of factor V (lower) haplotypes and single nucleotide polymorphisms and associations with incident venous thrombosis

Haplo- type identi- fier	3578	17557	29565	30539	35788 (M413T)	Haplotype frequency in cases N = 349	Haplotype frequency in controls N = 1680	Odds ratio (95% confidence interval)	P-value
1	G	G	G	A	T	41.6	37.7	1.00 (reference)	
2	C	G	C	A	T	14.2	18.3	<b>0.72 (0.56-0.92)</b>	<b>0.01</b>
3	C	A	G	A	T	14.0	14.5	0.89 (0.69-1.15)	0.37
other						9.3	9.9	0.86 (0.64-1.16)	0.34
4	C	A	G	G	T	9.8	9.2	0.90 (0.66-1.22)	0.48
5	C	G	G	A	T	7.6	7.4	0.94 (0.69-1.29)	0.71
6	G	G	G	A	C	3.5	2.9	1.17 (0.78-1.73)	0.45
Control MAF %	42.5	30.9	20.2	10.4	7.0			Global p-value	0.24
P- value	<b>0.04</b>	0.44	0.06	0.79	0.09				
Odd ratio and 95% confidence interval*	<b>1.20 (1.01-1.42)</b>	0.93 (0.77-1.12)	0.80 (0.64-1.01)	0.96 (0.73-1.27)	1.31 (0.96-1.78)				

MAF, minor allele frequency. Other, combined rare haplotypes. Bold entries have p-values <0.05. Shaded cells identify minor allele. \*Risk for each additional copy of the variant allele compared with risk associated with an additional copy of the wild-type allele.

Table A4. Analysis of factor V (upper) haplotypes and single nucleotide polymorphisms and associations with incident venous thrombosis

Haplo- type identi- fier	38592 (R534Q: FVL)	42713	45765 (N817T)	45888 (K858R: HR2)	46058 (T915S)	66464	66872	68717	72877 (M2148T)	Haplotype frequency in cases N = 349	Haplotype frequency in controls N = 1680	Odds ratio and 95% confidence interval	P-value
1	G	C	A	A	A	G	C	A	T	30.3	33.0	1.00 (reference)	-
2	G	T	A	G	A	G	C	G	T	19.0	24.4	0.86 (0.67-1.10)	0.22
3	G	T	A	A	A	G	T	A	T	11.1	13.6	0.95 (0.71-1.26)	0.72
4	G	T	C	A	A	G	C	G	T	7.3	5.9	1.40 (0.98-2.01)	0.06
5	G	T	A	A	A	T	T	G	T	6.7	5.5	1.34 (0.92-1.94)	0.12
6	G	C	A	A	A	G	C	A	C	6.3	4.7	1.39 (0.94-2.07)	0.10
7	G	T	A	A	A	G	C	G	T	4.0	4.7	0.91 (0.58-1.44)	0.70
other										5.1	4.6	1.29 (0.87-1.92)	0.20
8	A	T	A	A	A	G	C	G	T	7.6	2.3	<b>3.62 (2.42-5.40)</b>	<b>&lt;0.0001</b>
9	G	C	A	A	T	G	C	A	T	2.6	1.2	<b>2.22 (1.19-4.15)</b>	<b>0.01</b>
Control MAF %	2.3	40.9	6.3	27.0	1.3	5.7	19.6	46.0	4.7			Global p-value Global p-value <sup>†</sup>	<0.001 0.03
P- value	<b>&lt;0.001</b>	0.99	0.24	<b>0.003</b>	<b>0.02</b>	0.31	0.58	0.47	0.12				
Odds ratio and 95% confidence interval*	<b>3.75 (2.56-5.15)</b>	1.00 (0.84-1.19)	1.22 (0.88-1.69)	<b>0.74 (0.60-0.90)</b>	<b>2.01 (1.12-3.63)</b>	1.19 (0.85-1.68)	0.94 (0.75-1.17)	1.06 (0.90-1.26)	1.33 (0.93-1.92)				

MAF, minor allele frequency. Other, combined rare haplotypes. Bold entries have p-values <0.05. Shaded cells identify minor allele. \*Risk for each additional copy of the variant allele compared with risk associated with an additional copy of the wild-type allele. †Global p-value after removal of the allele of the Leiden variant.

Table A5. Analysis of factor VII haplotypes and single nucleotide polymorphisms and associations with incident venous thrombosis

Haplo- type identi- fier	185		2643		15386 (R413Q)		18311		Haplotype frequency in cases N = 349	Haplotype frequency in controls N = 1680	Odds ratio and 95% confidence interval	P-value
1	G	A	G	A	G	A	G	A	37.1	36.1	1.00 (reference)	
2	G	A	G	G	G	G	G	G	26.3	26.0	1.02 (0.82-1.27)	0.84
3	A	G	G	G	G	G	G	G	20.8	19.3	0.94 (0.74-1.18)	0.58
4	G	G	A	G	A	G	G	G	9.7	9.9	0.99 (0.74-1.34)	0.95
other									3.3	4.1	0.88 (0.54-1.44)	0.62
5	A	G	G	A	G	A	G	A	4.3	3.2	1.31 (0.87-1.96)	0.20
Control MAF %	24.2	36.8	10.4	41.2							Global p-value	0.64
P- value	0.86	0.78	0.85	0.75								
Odds ratio and 95% confidence interval*	0.98 (0.81-1.20)	0.98 (0.82-1.16)	0.97 (0.74-1.29)	1.03 (0.87-1.22)								

MAF, minor allele frequency. Other, combined rare haplotypes. Shaded cells identify minor allele. \* Risk for each additional copy of the variant allele compared with risk associated with an additional copy of the wild-type allele.

Table A6. Analysis of factor VIII haplotypes and single nucleotide polymorphisms and associations with incident venous thrombosis

Haplo- type identi- fier	25167	55941	71159	95910	95826 (D1260E)	187661	165293 (M2257V)	Haplotype frequency in cases N = 349	Haplotype frequency in controls N = 1680	Odds ratio and 95% confidence interval	P-value
1	G	C	G	A	C	G	A	59.0	62.7	1.00 (reference)	
2	G	G	A	A	G	G	A	16.3	13.6	1.25 (0.98-1.59)	0.07
3	G	C	G	A	C	A	A	10.9	9.3	1.24 (0.94-1.64)	0.13
4	G	G	G	C	C	G	A	8.2	8.9	0.94 (0.69-1.27)	0.68
other								3.0	3.8	0.90 (0.57-1.41)	0.65
5	A	G	G	A	G	G	A	2.6	1.7	1.38 (0.81-2.35)	0.23
Control MAF %	2.1	27.5	15.7	8.9	18.3	9.3	0.6			Global p-value	0.23
P- value	0.40	0.46	0.14	0.41	0.07	0.22	0.99				
Odds ratio and 95% confidence interval	1.24 (0.75-2.07)	1.07 (0.89-1.29)	1.18 (0.95-1.48)	0.88 (0.65-1.19)	1.21 (0.98-1.50)	1.19 (0.90-1.57)	0.99 (0.30-3.30)				

MAF, minor allele frequency. Other, combined rare haplotypes. Shaded cells identify minor allele. \*Risk for each additional copy of the variant allele compared with risk associated with an additional copy of the wild-type allele.



Table A8. Analysis of factor X haplotypes and single nucleotide polymorphisms and associations with incident venous thrombosis

Haplo- type identi- fier	4544	8946	9501	11962	14881	16893	17396	18352	22739 (G192R)	26242	Haplotype frequency in cases N = 349	Haplotype frequency in controls N = 1678	Odds ratio and 95% confidence interval	P-value
1	T	C	G	G	C	C	A	G	G	T	20.9	16.6	1.00 (reference)	
2	T	G	G	A	C	G	A	G	G	T	14.4	15.6	<b>0.76 (0.58-0.98)<sup>†</sup></b>	<b>0.04</b>
other											17.4	15.5	0.77 (0.59-1.02)	0.06
3	T	G	G	A	T	G	C	G	G	T	9.6	9.5	0.83 (0.62-1.10)	0.19
4	T	C	G	G	C	C	A	G	G	T	7.5	8.5	0.78 (0.57-1.07)	0.13
5	C	C	G	A	C	G	C	A	G	T	7.5	7.3	0.86 (0.62-1.21)	0.40
6	T	C	T	G	C	C	A	G	G	T	6.1	5.5	0.95 (0.66-1.36)	0.78
7	T	C	T	G	C	C	A	G	G	T	4.9	5.2	0.77 (0.53-1.12)	0.17
8	T	G	G	A	T	G	C	G	G	T	4.1	4.3	0.80 (0.52-1.21)	0.29
9	T	G	G	A	C	G	A	G	G	C	2.5	3.8	<b>0.56 (0.34-0.93)<sup>†</sup></b>	<b>0.02</b>
10	T	C	G	G	C	C	A	G	G	C	2.1	2.4	0.79 (0.46-1.34)	0.38
11	T	C	G	A	C	G	C	A	G	T	3.1	1.8	1.53 (0.89-2.63)	0.12
Control MAF %	10.9	40.4	13.3	47.6	16.5	46.9	28.0	11.1	0.3	16.2			Global p-value	0.15
P- value	0.74	<b>0.01</b>	0.96	0.54	0.84	0.50	0.70	0.46	0.78	0.27				
Odds ratio and 95% confidence interval*	1.05 (0.80-1.32)	<b>0.80 (0.68-0.96)</b>	0.99 (0.78-1.27)	1.05 (0.89-1.25)	0.98 (0.78-1.23)	1.06 (0.90-1.25)	1.04 (0.86-1.26)	1.11 (0.85-1.44)	0.75 (0.10-5.70)	0.87 (0.69-1.11)				

MAF, minor allele frequency. Other, combined rare haplotypes. Bold entries have p-values <0.05. Shaded cells identify minor allele. \*Risk for each additional copy of the variant allele compared with risk associated with an additional copy of the wild-type allele. <sup>†</sup>Haplotype p-value >0.5 when compared to all other haplotypes.



Table A10. Analysis of factor XII haplotypes and single nucleotide polymorphisms and associations with incident venous thrombosis

Haplotype identifier	6570	7532	Haplotype frequency in cases N = 349	Haplotype frequency in controls N = 1680	Odds ratio and 95% confidence interval	P-value
1	C	T	62.9	60.7	1.00 (reference)	
2	C	C	34.7	36.6	0.97 (0.81-1.16)	0.75
3	T	T	2.4	2.7	0.81 (0.46-1.40)	0.44
other			0.0	0.0	-	-
Control MAF %	2.7	36.6			Global p-value	0.73
P-value	0.47	0.83				
Odds ratio and 95% confidence interval*	0.81 (0.47-1.42)	0.98 (0.82-1.17)				

MAF, minor allele frequency. Other, combined rare haplotypes. Shaded cells identify minor allele. \* Risk for each additional copy of the variant allele compared with risk associated with an additional copy of the wild-type allele.

Table A11. Analysis of factor XIIIa1 haplotypes and single nucleotide polymorphisms and associations with incident venous thrombosis

Haplo- type identi- fier	4377 (V 35L)	72060 (Y205F)	148318 (P565L)	165306	165399	170779	176866	177424	177778	Haplotype frequency in cases N = 349	Haplotype frequency in controls N = 1680	Odds ratio and 95% confidence interval	P-value
1	G	A	C	C	C	G	G	A	A	29.4	30.6	1.00 (reference)	
2	T	A	C	C	C	G	G	A	A	11.5	10.4	1.14 (0.90-1.45)	0.28
3	G	A	C	A	T	T	A	A	A	8.2	10.2	0.86 (0.65-1.14)	0.29
4	G	A	C	C	T	G	G	A	A	9.4	9.2	1.12 (0.85-1.46)	0.42
other										9.8	8.1	1.29 (0.96-1.73)	0.10
5	G	A	T	C	C	G	G	A	A	7.8	8.0	1.03 (0.78-1.36)	0.84
6	G	A	C	A	T	G	G	A	A	4.6	3.8	1.29 (0.87-1.93)	0.21
7	G	A	T	C	T	G	G	A	A	3.3	3.4	1.06 (0.68-1.65)	0.81
8	T	A	C	A	T	T	A	A	A	2.9	3.4	0.92 (0.61-1.40)	0.71
9	G	A	C	C	T	G	G	A	G	3.4	3.3	1.09 (0.72-1.63)	0.70
10	T	A	C	C	T	G	G	A	A	1.9	3.1	0.74 (0.49-1.12)	0.15
11	G	A	C	A	T	G	G	A	A	2.9	2.5	1.20 (0.79-1.83)	0.40
12	T	A	C	C	T	G	G	A	G	2.4	2.0	1.33 (0.79-2.24)	0.29
13	G	A	T	A	T	T	A	A	A	2.5	1.9	1.31 (0.85-2.03)	0.22
of MAF %	24.3	2.6	20.1	22.8	45.8	16.7	17.6	0.3	6.1			Global p-value	0.27
P- value	0.69	0.62	0.42	0.78	0.88	0.51	0.37	0.05	0.21				
Odds ratio and 95% confidence interval <sup>†</sup>	1.04 (0.86-1.26)	1.13 (0.70-1.83)	1.09 (0.89-1.33)	0.97 (0.79-1.20)	1.01 (0.85-1.20)	0.92 (0.73-1.17)	0.90 (0.71-1.13)	3.69 (0.98-13.8)	1.23 (0.89-1.71)				

MAF, minor allele frequency. Other, combined rare haplotypes. Shaded cells identify minor allele. Non-synonymous substitution reported as V34L in the literature. <sup>†</sup>Risk for each additional copy of the variant allele compared with risk associated with an additional copy of the wild-type allele.

Table A12. Analysis of factor XIIIb haplotypes and single nucleotide polymorphisms and associations with incident venous thrombosis

Haplo- type identi- fier	5995	*7319 (H115R)	9706	17686	29759	Haplotype frequency in cases N = 349	Haplotype frequency in controls N = 1680	Odds ratio and 95% confidence interval	P-value
1	C	A	T	A	T	40.1	41.9	1.00 (reference)	
2	G	A	T	C	G	30.8	29.7	1.10 (0.90-1.35)	0.36
3	G	A	C	A	G	17.5	16.6	1.14 (0.89-1.46)	0.29
4	G	G	T	A	T	10.2	9.3	1.17 (0.87-1.56)	0.29
other						1.4	2.5	0.72 (0.36-1.43)	0.35
Control MAF %	42.0	10.2	17.4	29.9	47.4			Global p-value	0.52
P- value	0.31	0.73	0.56	0.61	0.35				
Odds ratio and 95% confidence interval †	0.91 (0.77-1.09)	1.05 (0.80-1.39)	1.07 (0.86-1.33)	1.05 (0.87-1.26)	1.09 (0.92-1.29)				

MAF, minor allele frequency. Other, combined rare haplotypes. Shaded cells identify minor allele. \*Non-synonymous substitution reported as H95R in the literature. †Risk for each additional copy of the variant allele compared with risk associated with an additional copy of the wild-type allele.

Table A13. Analysis of  $\alpha$ -fibrinogen haplotypes and single nucleotide polymorphisms and associations with incident venous thrombosis

Haplo- type identi- fier	251	3807	5498	6534 (T331A)	9205	Haplotype frequency in case N = 349	Haplotype frequency in controls N = 1680	Odds ratio and 95% confidence interval	P-value
1	G	T	T	A	C	27.9	29.2	1.00 (reference)	
2	A	T	T	G	C	29.9	26.0	<b>1.25 (1.00-1.57)</b>	<b>0.05</b>
3	G	T	T	A	T	15.5	17.6	0.91 (0.70-1.18)	0.49
4	G	C	T	A	C	13.3	14.5	0.96 (0.72-1.28)	0.78
5	A	T	C	A	C	13.1	12.0	1.13 (0.85-1.49)	0.40
other						0.4	0.8	0.76 (0.22-2.57)	0.66
Control MAF %	38.3	14.6	12.2	26.0	17.7			Global p-value	0.18
P- value	<b>0.01</b>	0.38	0.56	<b>0.02</b>	0.13				
Odds ratio and 95% confidence interval*	<b>1.25 (1.05-1.29)</b>	0.90 (0.70-1.14)	1.08 (0.84-1.38)	<b>1.24 (1.03-1.50)</b>	0.84 (0.66-1.06)				

MAF, minor allele frequency. Other, combined rare haplotypes. Bold entries have p-values <0.05. Shaded cells identify minor allele. \* Risk for each additional copy of the variant allele compared with risk associated with an additional copy of the wild-type allele.

Table A14. Analysis of  $\beta$ -fibrinogen haplotypes and single nucleotide polymorphisms and associations with incident venous thrombosis

Haplo- type identi- fier	1038		1643		Haplotype frequency in cases N = 349	Haplotype frequency in controls N = 1680	Odds ratio and 95% confidence interval	P-value
				9487 (R478K)				
1	G	C	G	T	30.2	32.9	1.00 (reference)	
2	G	T	G	C	25.4	21.3	<b>1.38 ( 1.09- 1.75)</b>	<b>0.007</b>
3	G	C	A	C	16.0	16.0	1.14 ( 0.88- 1.48)	0.33
4	A	C	G	C	13.5	15.2	0.98 ( 0.74- 1.29)	0.87
5	G	C	G	C	13.3	12.9	1.16 ( 0.88- 1.53)	0.30
other					1.6	1.6	1.02 ( 0.50- 2.08)	0.96
Control MAF %	15.2	21.3	17.6	32.9			Global p-value	0.11
P- value	0.23	<b>0.008</b>	0.95	0.09				
Odds ratio and 95% confidence interval*	0.86 (0.67-1.10)	<b>1.31 (1.08-1.60)</b>	1.01 (0.81-1.25)	0.85 (0.71-1.02)				

MAF, minor allele frequency. Other, combined rare haplotypes. Bold entries have p-values <0.05. Shaded cells identify minor allele. \* Risk for each additional copy of the variant allele compared with risk associated with an additional copy of the wild-type allele.

Table A15. Analysis of  $\gamma$ -fibrinogen haplotypes and single nucleotide polymorphisms and associations with incident venous thrombosis

Haplo- type identi- fier	129	902	5836	9340	Haplotype frequency in cases N = 349	Haplotype frequency in controls N = 1680	Odds ratio and 95% confidence interval	P-value
1	A	G	G	T	37.5	39.7	1.00 (reference)	
2	A	A	G	C	28.8	30.8	0.99 (0.81-1.22)	0.95
3	T	A	G	T	28.1	24.8	<b>1.25 (1.01-1.54)</b>	<b>0.04</b>
4	A	G	A	T	4.0	3.5	1.21 (0.77-1.88)	0.41
other					1.6	1.3	1.71 (0.87-3.35)	0.12
Control MAF %	24.8	43.2	3.5	30.9			Global p-value	0.10
P- value	<b>0.03</b>	0.31	0.57	0.22				
Odds ratio and 95% confidence interval*	<b>1.23 (1.02-1.49)</b>	0.92 (0.77-1.09)	1.14 (0.73-1.76)	0.89 (0.74-1.07)				

MAF, minor allele frequency. Other, combined rare haplotypes. Bold entries have p-values <0.05. Shaded cells identify minor allele. \* Risk for each additional copy of the variant allele compared with risk associated with an additional copy of the wild-type allele.

Table A16. Analysis of tissue factor (F3) haplotypes and single nucleotide polymorphisms and associations with incident venous thrombosis

Haplo- type identi- fier	599	5334	7877	11185	13925	Haplotype frequency in cases N = 349	Haplotype frequency in controls N = 1679	Odds ratio and 95% confidence interval	P-value	
1	T	A	A	T	G	43.5	41.1	1.00 (reference)		
2	C	A	A	T	A	17.1	20.5	0.79 (0.63-1.01)	0.06	
3	C	G	A	T	G	18.8	18.7	0.93 (0.74-1.16)	0.53	
4	C	A	A	T	G	6.7	6.4	0.95 (0.68-1.32)	0.74	
5	C	G	G	T	G	4.6	5.1	0.85 (0.57-1.29)	0.45	
6	C	A	A	C	A	4.1	4.2	0.86 (0.56-1.32)	0.50	
7	T	A	A	T	A	4.2	3.6	1.17 (0.77-1.76)	0.47	
other						1.0	0.4	<b>2.46 (1.11-5.44)</b>	<b>0.03</b>	
Control MAF %	44.9	24.2	5.1	4.2	28.4				Global p-value	0.17
P- value	0.10	0.94	0.79	0.76	0.23					
Odds ratio and 95% confidence interval*	1.16 (0.97-1.37)	1.01 (0.83-1.22)	0.95 (0.64-1.41)	0.94 (0.61-1.44)	0.89 (0.73-1.08)					

MAF, minor allele frequency. Other, combined rare haplotypes. Bold entries have p-values <0.05. Shaded cells identify minor allele. \* Risk for each additional copy of the variant allele compared with risk associated with an additional copy of the wild-type allele.

Table A17. Analysis of antithrombin (SERPINC1) haplotypes and single nucleotide polymorphisms and associations with incident venous thrombosis

Haplotype identifier	1734	2415	5403	7199	9089	Haplotype frequency in cases N = 349	Haplotypes frequency in controls N = 1680	Odds ratio and 95% confidence interval	P-value
1	G	C	T	G	A	66.5	64.6	1.00 (reference)	
2	G	A	T	G	G	10.5	11.2	0.91 (0.68-1.22)	0.53
3	A	C	T	G	G	10.0	10.1	1.01 (0.76-1.35)	0.94
4	G	C	T	T	G	7.5	7.6	0.95 (0.68-1.32)	0.76
5	G	C	G	T	G	3.8	3.3	1.11 (0.71-1.76)	0.65
other						1.7	3.2	0.76 (0.42-1.38)	0.37
Control MAF %	10.2	12.7	3.3	10.9	35.2	Global p-value			0.91
P-value	0.70	0.48	0.66	0.94	0.67				
Odds ratio and 95% confidence interval*	1.06 (0.80-1.40)	0.91 (0.69-1.19)	1.11 (0.70-1.75)	1.01 (0.77-1.32)	0.96 (0.80-1.15)				

MAF, minor allele frequency. Other, combined rare haplotypes. Shaded cells identify minor allele. \*Risk for each additional copy of the variant allele compared with risk associated with an additional copy of the wild-type allele.

Table A18. Analysis of protein C haplotypes and single nucleotide polymorphisms and associations with incident venous thrombosis

Haplo- type identi- fier	2583	3220	4515	4732	4919	5867	10454	11310	Haplotype frequency in cases N = 349	Haplotype frequency in controls N = 1680	Odds ratio and 95% confidence interval	P-value
1	A	G	T	T	A	G	G	T	29.1	34.2	1.00 (reference)	
2	T	G	C	T	G	G	G	C	39.2	31.2	<b>1.44 (1.17-1.77)</b>	<b>&lt;0.001</b>
3	A	G	C	C	G	A	T	T	17.3	19.2	1.07 (0.83-1.38)	0.61
4	T	G	T	T	A	G	G	T	4.0	5.2	0.97 (0.64-1.49)	0.90
other									3.6	3.8	1.39 (0.89-2.17)	0.15
5	T	A	T	C	G	G	G	T	4.0	3.8	1.31 (0.84-2.06)	0.23
6	A	G	C	C	G	A	G	T	2.7	2.6	1.08 (0.64-1.82)	0.78
Control MAF %	42.0	3.9	44.7	26.6	40.7	22.1	19.6	31.5			Global p-value	0.02
P- value	<b>0.001</b>	0.74	<b>0.03</b>	0.50	<b>0.005</b>	0.28	0.39	<b>&lt;0.001</b>				
Odds ratio and 95% confidence interval*	<b>1.33 (1.12-1.57)</b>	1.08 (0.70-1.67)	<b>0.82 (0.69-0.98)</b>	0.93 (0.77-1.14)	<b>0.78 (0.65-0.93)</b>	0.89 (0.72-1.10)	0.91 (0.73-1.13)	<b>1.37 (1.15-1.64)</b>				

MAF, minor allele frequency. Other, combined rare haplotypes. Bold entries have p-values <0.05. Shaded cells identify minor allele. \* Risk for each additional copy of the variant allele compared with risk associated with an additional copy of the wild-type allele.

Table A19. Analysis of endothelial protein C receptor (PROCR) haplotypes and single nucleotide polymorphisms and associations with incident venous thrombosis

Haplo- type identi- fier	837	3600	6196	rs1415772	Haplotype frequency in cases N = 349	Haplotype frequency in controls N = 1680	Odds ratio and 95% confidence interval	P-value
1	C	T	C	C	43.0	43.3	1.00 (reference)	
2	C	T	G	G	20.9	23.7	0.89 (0.71-1.10)	0.27
3	C	T	G	C	18.9	17.9	1.10 (0.88-1.38)	0.41
4	G	T	G	C	11.6	9.4	1.24 (0.93-1.66)	0.14
5	C	C	G	C	5.2	4.8	1.01 (0.67-1.51)	0.96
other					0.4	0.9	0.61 (0.20-1.83)	0.38
Control MAF %	9.4	4.9	43.3	23.8			Global p-value	0.29
P- value	0.09	0.90	0.86	0.09				
Odds ratio and 95% confidence interval*	1.27 (0.97-1.66)	1.02 (0.70-1.49)	0.99 (0.83-1.17)	0.84 (0.69-1.03)				

MAF, minor allele frequency. Other, combined rare haplotypes. Shaded cells identify minor allele. \* Risk for each additional copy of the variant allele compared with risk associated with an additional copy of the wild-type allele.

Table A20. Analysis of protein S haplotypes and single nucleotide polymorphisms and associations with incident venous thrombosis

Haplo- type identi- fier	288	430	13154	26890	66205	66847	Haplotype frequency in cases N = 349	Haplotypes frequency in controls N = 1680	Odds ratio and 95% confidence interval	P-value
1	C	G	G	T	A	T	41.1	44.7	1.00 (reference)	
2	C	A	A	T	T	T	24.5	22.1	1.23 (0.98-1.53)	0.08
3	C	A	G	C	A	T	9.6	10.3	0.98 (0.72-1.33)	0.90
4	T	A	G	T	T	C	10.0	8.7	1.20 (0.90-1.60)	0.22
5	T	A	G	T	T	T	7.1	8.2	0.94 (0.67-1.32)	0.72
6	C	A	G	T	T	T	3.9	3.9	1.23 (0.79-1.92)	0.36
other							3.7	2.0	<b>1.99 (1.19-3.31)</b>	<b>0.008</b>
Control MAF %	17.1	45.3	22.8	10.5	43.7	8.9			Global p-value	0.08
P- value	0.83	0.12	0.06	0.70	0.20	0.64				
Odds ratio and 95% confidence interval*	1.02 (0.82-1.28)	0.87 (0.74-1.03)	1.21 (0.99-1.47)	0.95 (0.72-1.24)	1.12 (0.94-1.32)	1.07 (0.81-1.41)				

MAF, minor allele frequency. Other, combined rare haplotypes. Bold entries have p-values <0.05. Shaded cells identify minor allele. \* Risk for each additional copy of the variant allele compared with risk associated with an additional copy of the wild-type allele.

Table A21. Analysis of thrombomodulin haplotypes and single nucleotide polymorphisms and associations with incident venous thrombosis

Haplo- type identi- fier	4007 (A473V)	5110	5318	6235	Haplotype frequency in cases N = 349	Haplotype frequency in controls N = 1680	Odds ratio and 95% confidence interval	P-value
1	C	G	A	A	40.5	34.8	1.00 (reference)	
2	C	A	A	G	21.7	22.6	0.87 (0.70-1.10)	0.25
3	C	A	A	A	18.9	22.0	<b>0.74 (0.58-0.94)</b>	<b>0.01</b>
4	T	A	C	A	16.7	18.1	<b>0.77 (0.60-0.99)</b>	<b>0.04</b>
other					2.2	2.4	0.84 (0.48-1.46)	0.53
Control MAF %	18.8	36.0	18.7	23.8			Global p-value	0.10
P- value	0.21	<b>0.02</b>	0.22	0.88				
Odds ratio and 95% confidence interval*	0.87 (0.70-1.09)	<b>1.24 (1.04-1.47)</b>	0.87 (0.70-1.09)	1.02 (0.83-1.24)				

MAF, minor allele frequency. Other, combined rare haplotypes. Bold entries have p-values <0.05. Shaded cells identify minor allele. \*Risk for each additional copy of the variant allele compared with risk associated with an additional copy of the wild-type allele.

Table A22. Analysis of tissue factor pathway inhibitor haplotypes and single nucleotide polymorphisms and associations with incident venous thrombosis

Haplotype identifier	1502	2418	3437	21164	34214	Haplotype frequency in cases N = 349	Haplotypes frequency in controls N = 1690	Odds ratio and 95% confidence interval	P-value
1	A	C	T	C	A	33.1	29.3	1.00 (reference)	
2	G	T	T	C	C	26.4	26.4	0.88 (0.71-1.10)	0.25
3	G	C	T	C	A	18.1	23.5	<b>0.69 (0.54-0.88)</b>	<b>0.003</b>
4	A	C	T	T	A	5.8	6.1	0.89 (0.60-1.30)	0.53
5	G	T	T	C	A	6.5	5.8	1.00 (0.70-1.44)	0.99
6	G	T	C	C	A	4.8	5.2	0.77 (0.52-1.15)	0.20
7	A	C	T	C	C	5.0	3.5	1.26 (0.84-1.87)	0.26
other						0.1	0.3	<b>0.37 (0.16-0.81)</b>	<b>0.01</b>
Control MAF %	38.8	37.5	5.2	6.2	30.1			Global p-value	0.005
P-value	<b>0.01</b>	0.94	0.45	0.93	0.49				
Odds ratio and 95% confidence interval*	<b>1.25 (1.05-1.48)</b>	1.01 (0.85-1.19)	0.86 (0.59-1.26)	0.98 (0.69-1.41)	1.07 (0.89-1.28)				

MAF, minor allele frequency. Other, combined rare haplotypes. Bold entries have p-values <0.05. Shaded cells identify minor allele. \*Risk for each additional copy of the variant allele compared with risk associated with an additional copy of the wild-type allele.

Table A23. Analysis of plasminogen haplotypes and single nucleotide polymorphisms and associations with incident venous thrombosis

Haplo- type identi- fier	406	1470	1983	2967	12881	15255	18114	31439 (D472N)	34158	41108	41494	54925	Haplotype frequency in cases N = 349	Haplotype frequency in controls N = 1679	Odds ratio and 95% confidence interval	P-value
1	A	A	A	C	A	A	G	G	C	G	A	A	13.2	13.2	1.00 (reference)	
2	A	A	A	C	G	T	G	A	C	C	A	A	12.7	13.1	0.91 ( 0.67- 1.24)	0.56
other													9.2	10.8	0.85 ( 0.62- 1.17)	0.32
3	A	A	A	C	G	T	G	A	C	G	A	A	9.3	9.2	0.98 ( 0.69- 1.38)	0.89
4	G	G	A	T	A	A	G	G	C	G	A	A	9.0	9.1	0.91 ( 0.65- 1.27)	0.58
5	G	A	G	T	A	T	A	G	C	G	A	A	8.3	8.4	0.91 ( 0.65- 1.28)	0.59
6	A	A	A	C	A	T	A	G	C	G	A	A	7.9	8.4	0.99 ( 0.69- 1.43)	0.96
7	G	A	G	T	A	A	G	G	C	G	A	A	7.1	7.8	0.84 ( 0.58- 1.19)	0.32
8	G	A	A	C	A	A	G	G	C	G	A	A	6.9	5.4	1.31 ( 0.89- 1.91)	0.17
9	G	A	A	T	A	T	A	G	C	G	A	A	6.6	4.8	1.24 ( 0.85- 1.83)	0.27
10	G	A	A	C	A	T	A	G	C	G	A	G	3.2	3.2	1.01 ( 0.61- 1.65)	0.98
11	G	A	G	T	G	T	G	A	C	G	A	A	2.7	3.0	0.84 ( 0.49- 1.43)	0.52
12	G	G	A	T	A	A	G	G	C	G	G	A	1.8	2.0	0.84 ( 0.43- 1.67)	0.63
13	G	G	A	T	A	T	A	G	C	G	A	A	2.0	1.6	1.18 ( 0.65- 2.13)	0.58
Control MAF %	46.0	16.3	20.1	43.6	29.7	40.0	29.0	29.2	3.0	16.4	2.3	4.7			Global p-value	0.66
P- value	0.74	0.35	0.27	0.45	0.42	0.93	0.23	0.40	0.40	0.26	0.89	0.76				
Odds ratio and 95% confidence interval	0.97 ( 0.83-1.15)	0.90 ( 0.71-1.13)	0.89 ( 0.71-1.10)	0.94 ( 0.79-1.11)	0.93 ( 0.77-1.12)	0.99 ( 0.84-1.18)	1.11 ( 0.93-1.33)	0.92 ( 0.76-1.12)	0.78 ( 0.44-1.37)	0.88 ( 0.69-1.11)	0.96 ( 0.54-1.70)	0.94 ( 0.62-1.42)				

MAF, minor allele frequency. Other, combined rare haplotypes. Shaded cells identify minor allele. \*Risk for each additional copy of the variant allele compared with risk associated with an additional copy of the wild-type allele.

Table A24. Analysis of tissue-type plasminogen activator (PLAT) haplotypes and single nucleotide polymorphisms and associations with incident venous thrombosis

Haplo- type identi- fier	2586	6388	6971	9823	9944	12047	12264	16039	17825	18289 (A34D)	22323	30619 (L285P)	35171	Haplotype frequency in cases N = 349	Haplotype frequency in controls N = 1678	Odds ratio and 95% confidence interval	P-value
1	G	C	T	A	A	A	T	G	A	C	C	T	T	34.9	35.7	1.00 (reference)	
2	G	C	T	<b>C</b>	A	G	T	<b>C</b>	<b>C</b>	C	C	T	<b>C</b>	23.4	21.8	1.06 (0.84-1.34)	0.63
other														8.7	10.8	0.82 (0.60-1.13)	0.23
3	G	C	T	A	A	G	T	G	A	C	<b>T</b>	T	T	6.3	7.9	0.79 (0.56-1.12)	0.19
4	G	<b>T</b>	T	A	A	G	T	G	A	C	<b>T</b>	T	T	8.6	7.5	1.10 (0.79-1.54)	0.57
5	<b>T</b>	C	<b>C</b>	<b>C</b>	A	G	<b>C</b>	<b>C</b>	<b>C</b>	C	C	<b>C</b>	T	4.4	4.3	0.99 (0.64-1.52)	0.95
6	G	C	T	<b>C</b>	<b>G</b>	G	T	<b>C</b>	<b>C</b>	C	C	T	<b>C</b>	3.0	3.3	0.88 (0.53-1.43)	0.60
7	G	C	T	A	A	G	T	G	<b>C</b>	C	C	<b>C</b>	T	3.4	2.9	1.36 (0.84-2.23)	0.22
8	G	C	T	<b>C</b>	A	G	<b>C</b>	<b>C</b>	<b>C</b>	C	C	<b>C</b>	T	3.0	2.2	1.54 (0.91-2.60)	0.11
9	G	C	T	A	A	G	T	G	A	C	C	T	T	2.0	2.2	0.90 (0.51-1.57)	0.70
10	G	C	<b>C</b>	<b>C</b>	A	G	<b>C</b>	<b>C</b>	<b>C</b>	C	C	<b>C</b>	T	2.2	1.4	1.60 (0.88-2.92)	0.12
Control MAF %	6.0	8.1	8.8	37.1	4.2	40.3	9.0	37.7	43.6	0.0	16.3	11.9	29.5			Global p-value	0.24
P- value	0.67	0.97	0.52	0.67	0.38	0.31	0.73	0.59	0.49	0.98	0.40	0.31	0.72				
Odds ratio and 95% confidence interval*	1.08 (0.76-1.54)	1.00 (0.74-1.36)	1.10 (0.82-1.48)	1.04 (0.87-1.23)	0.82 (0.53-1.28)	0.92 (0.77-1.09)	1.05 (0.79-1.41)	1.05 (0.88-1.24)	1.06 (0.90-1.26)	not estimable	0.91 (0.72-1.14)	1.14 (0.89-1.46)	0.97 (0.81-1.16)				

MAF, minor allele frequency. Other, combined rare haplotypes. Bold entries have p-values <0.05. Shaded cells identify minor allele. \*Risk for each additional copy of the variant allele compared with risk associated with an additional copy of the wild-type allele.

Table A25. Analysis of plasminogen activator inhibitor type-1 (SERPINE1) haplotypes and single nucleotide polymorphisms and associations with incident venous thrombosis

Haplo- type identi- fier	664	4588	5878	10381	12219	Haplotypes frequency in cases N = 349	Haplotype frequency in controls N = 1678	Odds ratio and 95% confidence interval	P-value
1	A	C	A	C	C	37.3	39.6	1.00 (reference)	
2	G	C	A	C	T	12.6	12.7	1.11 (0.86-1.45)	0.43
3	G	C	G	C	T	14.7	11.5	<b>1.44 (1.10-1.88)</b>	<b>0.007</b>
4	A	C	A	C	T	8.2	8.9	0.95 (0.70-1.29)	0.76
5	G	C	G	T	T	8.3	8.3	1.12 (0.81-1.57)	0.49
6	A	T	A	C	T	7.6	7.9	1.07 (0.78-1.46)	0.67
7	G	T	A	C	T	6.4	6.8	1.04 (0.73-1.47)	0.84
8	G	C	A	C	C	3.8	3.3	1.36 (0.87-2.14)	0.18
other						1.1	1.1	1.10 (0.50-2.41)	0.81
Control MAF %	42.7	14.7	20.8	8.5	43.2			Global p-value	0.32
P- value	<b>0.04</b>	0.82	<b>0.02</b>	0.86	0.17				
Odds ratio and 95% confidence interval*	<b>1.19 (1.01-1.41)</b>	0.97 (0.76-1.24)	<b>1.26 (1.03-1.55)</b>	1.03 (0.76-1.40)	0.89 (0.75-1.05)				

MAF, minor allele frequency. Other, combined rare haplotypes. Bold entries have p-values <0.05. Shaded cells identify minor allele. \* Risk for each additional copy of the variant allele compared with risk associated with an additional copy of the wild-type allele.

Table A26. Analysis of thrombin activatable fibrinolysis inhibitor (CPB2) haplotypes and single nucleotide polymorphisms and associations with incident venous thrombosis

Haplo- type identi- fier	2103	4947	7826	10152	18857	31427	32627	35605	36326	47956	48100	51208 (T 3471)	54691	Haplotype frequency in cases N = 349	Haplotype frequency in controls N = 1678	Odds ratio and 95% confidence interval	P-value
1	C	C	T	G	A	T	C	T	T	T	T	C	C	30.7	30.2	1.00 (reference)	
2	C	C	C	C	A	C	T	A	T	T	T	C	A	24.2	20.5	1.14 (0.90-1.45)	0.28
3	C	T	C	G	A	C	T	T	T	A	T	T	C	19.1	19.3	0.91 (0.71-1.17)	0.49
other														13.0	15.5	0.92 (0.71-1.20)	0.55
4	T	T	T	G	A	C	T	A	T	T	C	C	C	5.1	5.3	1.01 (0.69-1.49)	0.95
5	T	T	T	G	A	C	T	A	C	T	T	C	A	1.9	4.1	<b>0.48 (0.26-0.86)</b>	<b>0.01</b>
6	C	C	C	C	A	C	T	A	T	T	T	T	C	3.0	2.6	1.01 (0.62-1.63)	0.98
7	C	T	C	G	G	C	T	T	T	A	T	T	C	3.0	2.6	1.06 (0.63-1.79)	0.83
Control MAF %	14.9	39.4	49.9	25.7	3.2	32.8	32.8	42.2	4.4	24.8	7.2	27.6	28.8			Global p-value	0.18
P- value	0.10	0.06	0.32	0.06	0.97	0.75	0.83	0.61	<b>0.02</b>	0.40	0.30	0.44	0.42				
Odds ratio and 95% confidence interval*	0.80 (0.62-1.04)	0.84 (0.71-1.00)	0.92 (0.78-1.08)	1.20 (0.99-1.45)	0.99 (0.62-1.58)	1.03 (0.87-1.22)	1.02 (0.86-1.21)	1.05 (0.88-1.24)	<b>0.52 (0.30-0.88)</b>	0.92 (0.75-1.12)	0.82 (0.57-1.19)	0.93 (0.77-1.12)	1.08 (0.90-1.31)				

MAF, minor allele frequency. Other, combined rare haplotypes. Bold entries have p-values <0.05. Shaded cells identify minor allele. \*Risk for each additional copy of the variant allele compared with risk associated with an additional copy of the wild-type allele.