Table 1 - Established VT-disease genes and their susceptibility variants

Locus	Polymorphism	Genomic location	Allele[1]	Risk Allele Frequency	Risk Estimate	Level of Certainty[2]
ABO[3]	rs579459	Intronic	T/**C**	0.22	1.50	★★★
	rs8176749	Leu310Leu	G/**A**	0.10	1.50	★★★
F2	rs1799963	3'UTR	G/**A**	0.008	2.29	★★★
	rs3136516	Intronic	G/**A**	0.40	1.12	★★
F5	rs6025	Arg506Gln	G/**A**	0.03	3.25	★★★
	rs4524	Lys858Arg	**A**/G	0.75	1.20	★★★
F8	rs114209171	Upstream	**T**/C	0.80	1.11	★★
F11	rs2289252	Intronic	C/**T**	0.41	1.35	★★
	rs2036914	Intronic	**C**/T	0.60	1.35	★★
FGG	rs2066865	3'UTR	C/**T**	0.25	1.25	★★★
	rs2227421	3'UTR	A/**C**	0.34	1.13[4]	★
KNG1	rs7100446	Ile581Thr	Ile/**Thr**	0.40	1.20	★★★
PROCR	rs6088735	Upstream	C/**T**	0.23	1.11	★★
	rs867186	Ser219Gly	Ser/**Gly**	0.10	1.22	★★★
PROS1	rs121918472	Ser501Pro	Ser/**Pro**	0.002	6.57	★★★
	rs121918474	Lys196Glu	Lys/**Glu**	0.009 [5]	5.00	★★★
SERPINC1	rs2227624	Val30Glu	Val/**Glu**	0.004	2.30	★★★
	rs2227589	Intronic	C/**T**	0.10	1.05	★★
SLC44A2	rs2288904	Arg154Gln	**Arg**/Gln	0.76	1.28	★★
STXBP5	rs1039084	Asn436Ser	**A**/G	0.55	1.11	★★
THBD	rs16984852	5'UTR	G/**T**	0.005 [6]	2.80	★★★
TSPAN15	rs78707713	Intronic	**T**/C	0.90	1.42	★
VWF	rs1063856	Thr789Ala	Thr/**Ala**	0.40	1.20	★★★

Private mutations in known VT genes (eg *F2*, *F9, PROC*, *PROS1*, *SERPINC1*) are not listed.

[1] Common/minor alleles. The allele associated with increased risk of VT is shown in bold.

[2] ★★★ variants achieving the three following criteria: definitive statistical evidence - established functionality - well-characterized associated pathophysiology; ★★ variants achieving two of the three above criteria; ★ variants achieving only one of the three above criteria

[3] The rs579459 and rs8176749 are tagging the ABO A1 and B blood groups, respectively.

[4] Information kindly provided by the INVENT consortium (Germain et al, 2015).

[5] variant identified so far only in the Japanese population

[6] variant identified so far only in the Chinese population