Table S2. Genotype results of *SERPINC1* polymorphism (rs2227589) among all recruited Chinese VTE subjects

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Author | Years | Ethnicity | Source | Case | Control | Methods |
| CC | CT | TT | CC | CT | TT |
| YUE,YY | 2019 | Asian | Chinese | 87(38.7%) | 111(49.3) | 27(12%) | 84(42.2%) | 100(50.3%) | 15(7.5%) | Sequenom |

Table S3. The results of pooled OR, 95% CIs and heterogeneity of all VTE subjects by meta-analysis

|  |  |  |  |
| --- | --- | --- | --- |
| Genetic models | Pooled effect | z | Heterogeneity |
| Models | Allele | OR(95%CIs) | Pz | I2(%) | PH |
| Additive | T vs C | 1.09(1.01-1.18) | 0.028 | 2.20 | 43.1 | 0.07 |
|  | Subgroups (Caucasian) | 1.10(1.01-1.20) | 0.023 | 2.27 | 44.9 | 0.08 |
| Dominant | TT+TC vs CC | 1.10(1.01-1.20) | 0.028 | 2.19 | 40.4 | 0.09 |
|  | Subgroups (Caucasian) | 1.12(1.02-1.22) | 0.017 | 2.39 | 45.1 | 0.08 |
| Recessive | TT vs TC+CC | 1.14(0.84-1.54) | 0.416 | 0.81 | 0.0 | 0.46 |
|  | Subgroups (Caucasian) | 1.06(0.74-1.52) | 0.741 | 0.33 | 0.0 | 0.54 |

Fig S1. Forest plots for the association between rs2227589 and risk of VTE among different populations (a, additive model; b, dominant model; c, recessive model).

Fig S2. Galbraith assay plots for the association between rs2227589 and risk of VTE (A, additive model; B, dominant model).

Fig S3. Trim-and-fill assay plots of genetic models (A, additive model; B, dominant model).