**Table S1.** Median (interquartile ranges), mean (standard deviation) of Gensini score defined by genotypes, in dominant, recessive and additive models, of the eight studied SNPs. Significance was determined by the Wilcoxon rank sum test.

| Single Nucleotide Polymorphisms | Genetic Models | N | Gensini Median ($Q_1$-$Q_3$) | Gensini Mean (SD) | *p* Value |
|---|---|---|---|---|---|
| *PON1* c.575A>G | A allele vs GG[D] | 1018 vs 73 | 40 (16-68) vs 50 (25-80) | 47.07(37.8) vs 57.3 (40.4) | **0.023**[B] |
| | G allele vs AA[R] | 517 vs 574 | 42 (19-71) vs 37 (14.25-68) | 49.74 (38.59) vs 45.97 (37.49) | ns |
| | AA vs AG vs GG[A] | 574 vs 444 vs 73 | 37 (14.25-68) vs 42 (16.75-68) vs 50 (25-80) | 45.97 (37.49) vs 48.5 (38.20) vs 57.30 (40.36) | **0.037**[k] |
| *MPO* c.-463A>G | G allele vs AA[D] | 1065 vs 26 | 40(16-69) vs 51 (37.75-81.25) | 47.45(37.98) vs 60.62 (40) | **0.048** |
| | A allele vs GG[R] | 331 vs 760 | 40 (16-66) vs 40 (16-70) | 48.03 (29.46) vs 47.64 (37.47) | ns |
| | GG vs GA vs AA[A] | 760 vs 305 vs 26 | 40 (16-70) vs 38 (14-66) vs 51 (37.75-81.25) | 47.64 (37.47) vs 46.96 (39.29) vs 60.62 (40) | ns[k] |
| *SOD2* c.47T>C | C allele vs TT[D] | 848 vs 243 | 38.5 (15-68) vs 44.0 (20-74) | 46.6(37.7) vs 51.8 (39.1) | **0.044** |
| | T allele vs CC[R] | 796 vs 295 | 40 (16-71) vs 38 (16-66) | 48.61 (38.38) vs 45.46 (37.11) | ns |
| | CC vs CT vs TT[A] | 295 vs 553 vs 243 | 38 (16-66) vs 39 (15-69) vs 44 (20-74) | 45.46 (37.11) vs 47.22 (38) vs 51.8 (39.1) | ns[k] |

| | | | | | |
|---|---|---|---|---|---|
| *GCLM* c.588C>T | C allele vs TT[D] | 1058 vs 33 | 40 (16-69) vs 37 (16-60) | 46.79 (38.96) vs 46.79 (38.96) | ns |
| | T allele vs CC[R] | 328 vs 763 | 40 (16-66.5) vs 40 (16-71.5) | 47.03 (37.3) vs 48.07 (38.39) | ns |
| | CC vs CT vs TT[A] | 763 vs 295 vs 33 | 40 (16-71.5) vs 40 (16-68) vs 37 (16-60) | 48.07 (38.39) vs 47.06 (37.18) vs 46.79 (38.96) | ns[k] |
| *eNOS* c.894G>T | G allele vs TT[D] | 1008 vs 84 | 40 (16-69.25) vs 41.5 (15.25-66.5) | 47.84 (38.21) vs 46.82 (37.05) | ns |
| | T allele vs GG[R] | 520 vs 572 | 42 (16-70.5) vs 38 (16-68.25) | 48.13 (37.29) vs 47.43 (38.86) | ns |
| | GG vs GT vs TT[A] | 572 vs 436 vs 84 | 38 (16-68.25) vs 42 (16-72) vs 41.5 (15.25-66.5) | 47.43 (38.86) vs 48.38 (37.37) vs 46.82 (37.05) | ns[k] |
| *eNOS* c.-786C>T | T allele vs CC[D] | 904 vs 151 | 39 (15-71.25) vs 42 (20-62) | 47.99 (39) vs 45.86 (32.55) | ns |
| | C allele vs TT[R] | 618 vs 437 | 40 (18-69) vs 38 (13-69) | 47.66 (36.05) vs 47.72 (40.95) | ns |
| | CC vs CT vs TT[A] | 151 vs 467 vs 437 | 42 (20-62) vs 40 (17-73.5) vs 38 (13-69) | 45.86 (32.55) vs 48.24 (37.13) vs 47.72 (40.95) | ns[k] |
| *CYBA* c.214T>C | C allele vs TT[D] | 944 vs 133 | 40 (16-68) vs 46 (16-80) | 47.47 (38.33) vs 50.56 (37.5) | ns |
| | T allele vs CC[R] | 613 vs 464 | 40 (14-71) vs 40 (16.75-68) | 47.14 (37.18) vs 48.8 (39.58) | ns |

| | | | | | |
|---|---|---|---|---|---|
| | CC vs CT vs TT[A] | 464 vs 480 vs 133 | 40 (16.75-68) vs 40 (13.75-68) vs 46 (16-80) | 48.8 (39.58) vs 46.2 (37.07) vs 50.56 (37.5) | ns[k] |
| *CYBA* c.-932G>A | G allele vs AA[D] | 893 vs 177 | 40 (16-71) vs 41 (17-172) | 48.39 (35.13) vs 46.36 (35.13) | ns |
| | A allele vs GG[R] | 687 vs 383 | 39 (16-67.5) vs 44 (19.5-74) | 46.27 (37.23) vs 51.25 (39.47) | ns |
| | GG vs AG vs AA[A] | 383 vs 510 vs 177 | 44 (19.5-74) vs 38 (14.25-68) vs 41 (17-172) | 51.25 (39.47) vs 46.24 (37.96) vs 46.36 (35.13) | ns[k] |
| GRS | 1~2 risk alleles vs 7~8 risk alleles | 66 vs 213 | 31.5 (13.5-53.75) vs 44 (22-68) | 38.24 (31.11) vs 49.81 (34.8) | **0.0181**[d] |
| | 1~2 risk alleles vs 9~12 risk alleles | 66 vs 55 | 31.5 (13.5-53.75) vs 52 (19-86) | 38.24 (31.11) vs 56.85 (42.1) | **0.0174**[d] |

ns: non significant; GRS: genetic risk score; [k] - Kruskal-Wallis rank sum test; [d] - Dunn's test; [B]-significant after Bonferroni correction; [D]-dominant model, [R]-recessive model, [A]-additive model; T allele = TT genotype + CT genotype; C allele = CC genotype + CT genotype; A allele = AA genotype + AG genotype; G allele = GG genotype + AG genotype.

**Table S2.** Genotyping conditions. Primers and probes sequences**.**

| **SNP** | **Probes, primers, other reagents** | | **Thermal profile** |
|---|---|---|---|
| **5′ Nuclease Real-Time PCR assay** | | | |
| rs1799983<br>NOS3 c.894T>G | T: FAM- CCAGATGATCCCCCAGAACTCTTCC -BHQ1 | 50 nM | 95 °C for 10 min |
| | G: HEX- CAGATGAGCCCCCAGAACTCTTCCT - BHQ1 | 50 nM | 95 °C for 15 s |
| | F: 5′-CATTCAGCACGGCTGGA –3′ | 0.5μM | 64 °C for 15 s |
| | R: 5′- ACCTCAAGGACCAGCTC -3′ | 0.5μM | repeat 60 times |
| rs2070744<br>NOS3 c.-786T>C | C: FAM- TCCCTGGCCGGCTGACCCTGCCTCA -BHQ1 | 50 nM | 95 °C for 10 min |
| | T: HEX- CTTCCCTGGCTGGCTGACCCTGCCTC - BHQ1 | 50 nM | 95 °C for 20 s |
| | F: 5′- TCCCACCAGGGCATCAA –3′ | 0.5μM | 68 °C for 20 s |
| | R: 5′- CCCTGTCATTCAGTGACG -3′ | 0.5μM | repeat 60 times |
| rs41303970<br>GCLM c.-590C>T | C: FAM- CTGAACGCCGGGAGACCTCACCA -BHQ1 | 50 nM | 95 °C for 10 min |
| | T: HEX- CCTGAACGCTGGGAGACCTCACCA - BHQ1 | 50 nM | 95 °C for 30 s |
| | F: 5′- CAGGCTGCCCTTTAAAGAG –3′ | 0.5μM | 64 °C for 30 s |
| | R: 5′- CCGCCTGGTGAGGTAGA -3′ | 0.5μM | repeat 60 times |
| rs2333227<br>MPO c.-463G>A | G: FAM- CTGAGGCGGGTGGATCACTTGA -BHQ1 | 50 nM | 95 °C for 10 min |
| | A: HEX- CTGAGGCAGGTGGATCACTTGAG - BHQ1 | 50 nM | 95 °C for 30 s |
| | F: 5′- CACACAATGGTGAGCTGAGA –3′ | 0.5μM | 64 °C for 30 s |
| | R: 5′- TTTGTATTTTTCCTTAGGCAAGAAGC -3′ | 0.5μM | repeat 60 times |
| rs4880<br>SOD2 c.47T>C | T: FAM- CTGGCTCCGGTTTTGGGGTATCT -BHQ1 | 50 nM | 95 °C for 10 min |
| | C: HEX- TGGCTCCGGCTTTGGGGTATC - BHQ1 | 50 nM | 95 °C for 30 s |
| | F: 5′- CTTTCTCGTCTTCAGCACCA –3′ | 0.5μM | 62 °C for 30 s |
| | R: 5′- CGCGTTGATGTGAGGTTC -3′ | 0.5μM | repeat 60 times |

| | | | |
|---|---|---|---|
| rs662<br>PON1 c.575A>G | A: FAM- CTACTTACAATCCTGGGAGATGT -BHQ1 | 50 nM | 95 °C for 10 min<br>95 °C for 30 s<br>55 °C for 30 s<br>repeat 60 times |
| | G: HEX- TACTTACGATCCTGGGAGATGTA - BHQ1 | 50 nM | |
| | F: 5′- GTTGCTGTGGGACCTGA –3′ | 0.5μM | |
| | R: 5′- AGACAACATACGACCACG -3′ | 0.5μM | |
| rs9932581<br>CYBA c.-932A>G | A: FAM-GGCAGTAATGCTGGT-BHQ1 | 50 nM | 95 °C for 10 min<br>95 °C for 30 s<br>56 °C for 1 min<br>repeat 60 times |
| | G: HEX-GGCAGCAATGCTGGT-BHQ1 | 50 nM | |
| | F: 5′-CTGGAATGGTGGCAGGAGT-3′ | 0.5μM | |
| | R: 5′- CGGGATGCTGGTTTACGAA-3′ | 0.5μM | |
| **PCR/RFLP assay** | | | |
| rs4673<br>CYBA c.214C>T | F: 5′-TGCTTGTGGGTAAACCAAGG-3′ | 0.5μM | 95°C for 5 min<br>95 °C for 30 s<br>55 °C for 30 s<br>72 °C for 30 s<br>repeat 60 times<br>72 °C for 10 min |
| | R: 5′-CACTTACCTCAGTGTTTTTCC-3′ | 0.5μM | |
| | dNTPs | 800 μM | |
| | 10x conc. PCR buffer (Thermo Scientific) | 2.0 μl | |
| | $MgCl_2$ | 1.5 μM | |
| | Taq DNA polymerase (Thermo Scientific) | 0.25 U | |
| | Genomic DNA | 2.0 μl | |
| | Total volume | 20 μl | |
| | PCR product of 353 bp digested with a restriction enzyme RsaI (Fermentas) which resulted in fragments: T allele: 160 bp and 193 bp and C allele: non-digested | | 37°C for 1 h |