**Table S4:** Frequencies of PGx haplotypes and predicted PGx phenotypes in the study population compared to literature

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Gene**  (number of individuals) a | **Haplotype / predicted phenotype** | **Frequency (%) in study population** | **Frequency (%) in (Dutch) Caucasian population** | **Reference** |
| ***CYP1A2*** | \*1A | 29.68 | 24.4 | 1 |
| (n = 155) | \*1C | 0 | 1 | 2,3,4 |
|  | \*1F | 69.03 | 67 | 2,3,4 |
|  | \*1L | 1.29 | 0.8 | 1 |
|  | Poor Metaboliser | 0 | - |  |
|  | Intermediate Metaboliser | 0 | - |  |
|  | Normal Metaboliser | 100 | - |  |
| ***CYP2B6*** | \*1 | 76.22 | 61.1 | 5 |
| (n = 164) | \*6 | 23.78 | 3.4 | 5 |
|  | Poor Metaboliser | 4.88 | 6–12 | 6 |
|  | Intermediate Metaboliser | 37.80 | 15–45 | 6 |
|  | Normal Metaboliser | 57.32 | 44–85 | 6 |
| ***CYP2C9*** | \*1 | 78.05 | 80.01 | 7 |
| (n = 164) | \*2 | 14.94 | 12.60 | 7 |
|  | \*3 | 7.01 | 7.08 | 7 |
|  | Poor Metaboliser | 3.05 | 4.00 | 7 |
|  | Intermediate Metaboliser | 37.80 | 31.99 | 7 |
|  | Normal Metaboliser | 59.15 | 64.01 | 7 |
| ***CYP2C19*** | \*1 | 62.04 | 62.4 | 8 |
| (n = 162) | \*2 | 17.59 | 14.6 | 8,9 |
|  | \*3 | 0.31 | 0.02 | 9 |
|  | \*4A | 0.31 | (\*4) 0.28 | 8 |
|  | \*4B | 0 | (\*4) 0.28 | 8 |
|  | \*17 | 19.75 | 21.3–21.7 | 8,9 |
|  | Poor Metaboliser | 4.94 | 2.5 | 8 |
|  | Intermediate Metaboliser | 26.54 | 26.8 | 8 |
|  | Normal Metaboliser | 64.20 | 66.1 | 8 |
|  | Ultra-rapid Metaboliser | 4.32 | 4.6–4.77 | 8,9 |
| ***CYP2D6*** | \*1 | 48.24 | 41.38 | 10 |
| (n = 142) | \*1x2 | 0.35 | 0.94 | 10 |
|  | \*3 | 2.46 | 1.36 | 10 |
|  | \*4 | 5.28 | 17.93 | 10 |
|  | \*4x2 | 0.35 | 0.28 | 10 |
|  | \*4M | 0.70 | - |  |
|  | \*5 | 3.52 | 2.65 | 10 |
|  | \*6 | 0 | 0.92 | 10 |
|  | \*7 | 0 | 0.07 | 10 |
|  | \*9 | 1.76 | 2.03 | 10 |
|  | \*10 b | 1.06 | 2.32 | 10 |
|  | \*12 | 0 | 0.01 | 10 |
|  | \*29 | 0 | 0.16 | 10 |
|  | \*36 | 0 | 0 | 10 |
|  | \*41 b | 0 | 8.88 | 10 |
|  | \*69 | 0 | - |  |
|  | \*109 | 0 | - |  |
|  | Not conclusive (\*1/\*4 or \*4M/\*10) c | 27.46 | - |  |
|  | Not conclusive (\*4/\*41 or \*4M/\*69) c | 2.11 | - |  |
|  | Not conclusive (\*1/\*10/\*36) d | 0.70 | - |  |
|  | Poor Metaboliser | 7.75 | 5.4–9 | 11 |
|  | Intermediate Metaboliser | 40.14 | 10–40 | 11 |
|  | Normal Metaboliser | 51.41 | 80 | 11 |
|  | Ultra-rapid Metaboliser | 0.70 | 1–2 | 11 |
| ***CYP3A4*** | \*1 | 92.38 | 91.5 | 5 |
| (n = 164) | \*22 | 7.62 | 5.0 | 5 |
|  | Poor Metaboliser | 0.61 | 0 | 12 |
|  | Intermediate Metaboliser | 14.02 | 6.40 | 12 |
|  | Normal Metaboliser | 85.37 | 93.60 | 12 |
| ***CYP3A5*** | \*1 | 8.54 | - |  |
| (n = 164) | \*3 | 91.46 | 91.7 | 13 |
|  | \*6 | 0 | - |  |
|  | Non-expressor | 84.15 | 81.4 | 13 |
|  | Heterozygous expressor | 14.63 | 18.4 | 13 |
|  | Homozygous expressor | 1.22 | 0.2 | 13 |
| ***Factor V*** | Wildtype allele | 94.82 | 95.6 | 14 |
| (n = 164) | Leiden mutation | 5.18 | 4.4 | 14 |
|  | Homozygous wildtype | 89.63 | 97.05 | 15 |
|  | Heterozygous Leiden mutation | 10.37 | 2.9 | 15 |
|  | Homozygous Leiden mutation | 0 | 0 | 15 |
| ***HLA-B*** | Wildtype allele | 97.53 | - |  |
| (n = 162) | \*5701 | 2.47 | 3.4 | 16 |
|  | No risk | 95.06 | - |  |
|  | Intermediate | 4.94 | - |  |
|  | High risk | 0 | - |  |
| ***MTHFR*** | 677C (wildtype) | 68.90 | 81.4 | 17 |
| (n = 164) | 677T (risk allele) | 31.10 | 18.6 | 17 |
|  | No risk | 45.73 | 51.70 | 18 |
|  | Intermediate risk | 46.34 | 40.25 | 18 |
|  | High risk | 7.93 | 8.05 | 18 |
| ***SLCO1B1*** | 521T (wildtype) | 83.94 | 81 | 19 |
| (n = 165) | 521C (risk allele) | 16.06 | 19 | 19 |
|  | No risk | 70.30 | 68.67 | 19 |
|  | Intermediate risk | 27.27 | 24.10 | 19 |
|  | High risk | 2.42 | 7.23 | 19 |
| ***TPMT*** *e* | \*1 | 95.12 | - |  |
| (n = 164) | \*2 | 0.30 | 0.4 | 20 |
|  | \*3A | 0 | 3.5 | 20 |
|  | \*3B | 0 | 0.4 | 20 |
|  | \*3C | 4.57 | 0.8 | 20 |
|  | Poor Metaboliser | 0 | 0.26 | 20 |
|  | Intermediate Metaboliser | 9.76 | 10 | 20 |
|  | Normal Metaboliser | 90.24 | 90 | 20 |
| ***UGT1A1*** | \*1 | 67.08 | 61.3 | 21 |
| (n = 161) | \*28 | 32.30 | 38.7 | 21 |
|  | \*36 | 0.62 | 0 | 21 |
|  | \*37 | 0 | 0 | 21 |
|  | Poor Metaboliser | 9.94 | 9 | 22 |
|  | Intermediate Metaboliser | 44.10 | 54 | 22 |
|  | Normal Metaboliser | 45.96 | 37 | 22 |
| ***VKORC1*** | \*1 (wildtype) | 60.98 | 58 | 23 |
| (n = 164) | \*2 (risk allele) | 39.02 | 37 | 23 |
|  | No risk | 40.24 | 36.3 | 24 |
|  | Intermediate risk | 41.46 | 48.7 | 24 |
|  | High risk | 18.29 | 15.0 | 24 |

a Number of genotyped individuals that passed QC thresholds.

b It was not possible to discriminate between \*10, \*14, \*37, \*47, \*49, \*52, \*54, \*56B, \*57, \*65, \*72, \*87, \*94, \*95, \*100 and \*101. The haplotype reported was \*10. It was not possible to discriminate between \*41 and \*91. The haplotype reported was \*41.

c It was not possible to discriminate between \*1/\*4 and \*4M/\*10, and \*4/\*41 and \*4M/\*69. For these diplotypes only, the predicted phenotypes were reported.

d It was not possible to discriminate which star alleles were located in tandem configuration. For this individual only, the predicted phenotype was reported.

e It was not possible to discriminate between \*1/\*3A and \*3B/\*3C. The diplotype reported was \*1/\*3A.

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