Pharmacogenetic Passport

Pharmacogenetic guidelines and clinical annotations connected to influential DNA changes

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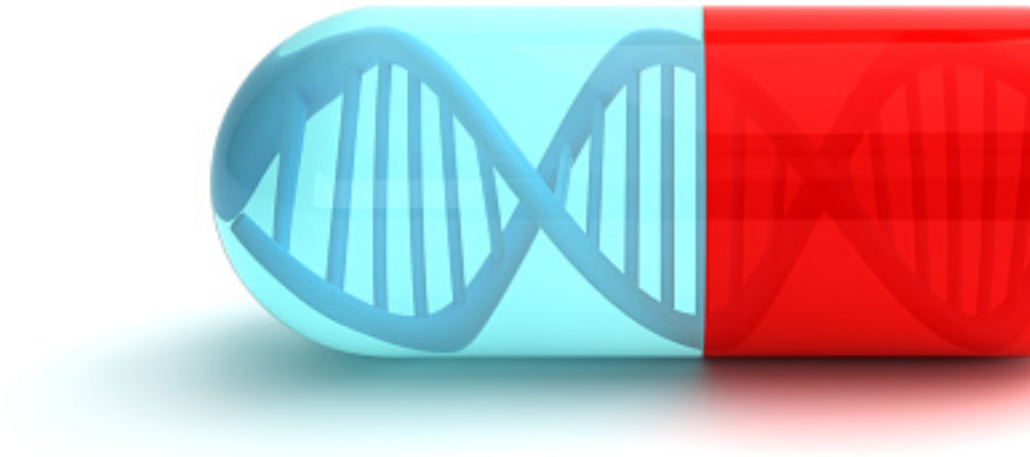

Contents

0.1 Patient haplotypes

Gene	Phylogenetic method[1]	Set method[2]
ABCB1	*1 / *2 (PMID: 12893986)	*2 (PMID: 12893986) / *2 (PMID: 12893986)
ABCC2	H1 / H2	H1 / H2
ADRB1	H1 / H1	H1 / H1
ADRB2	1 / 1	1 / 1
APOE	E3 / E2	E3 / E2
CDA	*1A / *1A	*1A / *1B
CFTR	Reference / Reference	Reference / Reference
CHRNA5	haplotype 1 / haplotype 1	haplotype 1 / haplotype 1
COMT	Haplotype low activity / Haplotype high activity	Haplotype low activity / Haplotype high activity
CYP1A1	*1 / *1	*1 / *1
CYP1A2	*1M / *1M	*1M / *1M
CYP1B1	*1 / *6	*1 / *6
CYP2A6	*1A / *2	*1A / *2
CYP2B6	*1 / *1	*1 / *1
CYP2C19	*1A / *3B	*1A / *3B
CYP2C8	*1A / *1A	*1A / *1A
CYP2C9	*1 / *18	*1 / *3
CYP2D6	*1 / *1E	*1 / *1E
CYP2E1	*1A / *1A	*1A / *1A
CYP3A4	*1 / *1	*1 / *1
CYP3A43	*1A / *1A	*1A / *1A
CYP3A5	*1A / *1A	*1A / *1A
CYP4B1	*1 / *1	*1 / *1
CYP4F2	*1 / *1	*1 / *1
DDC	#1 / #1	#1 / #1
DPYD	*1 / *1	*1 / *1
G6PD	B (wildtype) / B (wildtype)	B (wildtype) / B (wildtype)
HMGCR	H2 / H2	H7 / H7
HNF4A	TATTT / TGCGC	TATTT / TGCGC
HTR2C	1–2–1 / 1–2–1	1–2–1 / 1–2–1
IFNL3	rs12979860C / rs12979860T	rs12979860C / rs12979860T
IGFBP3	1 / 1	1 / 1
LDLR	L5 / L1	L5 / L1
NAT1	*4 / *4	*4 / *4
NAT2	*6A / *6A	*6A / *6A
NUDT15	*1 / *1	*1 / *1
P2RY12	B / B	B / B
PIK3CA	H1 / H2	H1 / H2
RXRA	AG / AG	AG / AG
RYR1	571I;3366R;3933Y / 571I;3366R;3933Y	571I;3366R;3933Y / 571I;3366R;3933Y
SCN1A	#1 / #1	#1 / #2
SCNN1B	1-1 / 1-1	1-1 / 1-1
SLC22A1	*1 / *1	*1 / *1
SLCO1B1	*1A / *20	*1A / *20
STAT3	TTG / CCG	TTG / CCG
SULT1A1	*1 / *2	*1 / *2
SULT1A2	*1 / *2	*1 / *2
TPMT	*1 / *1	*1 / *3E
UGT1A1	*1 / *60	*1 / *60
UGT1A10	*1a / *1a	*1a / *1a
UGT1A3	*1 / *2a	*1 / *2a
UGT1A4	*1a / *1a	*1a / *1a
UGT1A5	*1 / *1	*1 / *1
UGT1A6	*1a / *2e	*1a / *2e
UGT1A7	*1a / *3	*1a / *3
UGT1A8	*1a / *1a	*1a / *1a
UGT2B15	*1 / *4	*1 / *4
VEGFA	H1 / H1	H1 / H1
VKORC1	H1 / H2	H1 / *2

[1]Method using phylogenetic trees to find closest 'relative' to patient alleles. Trees can be seen in Appendix A.

[2]Method looking for overlap of haplotype non-reference variants and patient non-reference variants. Reference variants are filtered out of both sets prior to comparison. Top 5 hits can be seen in Appendix 2.