ARUP LABORATORIES | www.aruplab.com
500 Chipeta Way, Salt Lake City, Utah 84108-1221
phone: (801) 583-2787, toll free: (800) 522-2787
Julio C. Delgado, MD, MS, Director of Laboratories

Client: Example Client ABC123
123 Test Drive
Salt Lake City, UT 84108
UNITED STATES

Physician: Doctor, Example

Patient: Patient, Example

DOB	[redacted]
Gender:	Male
Patient Identifiers:	01234567890ABCD, 012345
Visit Number (FIN):	01234567890ABCD
Collection Date:	00/00/0000 00:00

Cytochrome P450 Genotyping Panel

ARUP test code 3001524

CYP PANEL Specimen	Whole Blood	
CYP2C19 Genotype	Neg/Neg	
CYP2C8 Genotype	*3/*3	*
CYP2C9 Genotype	*2/*2	*
CYP2D6 Genotype	*9/Neg	
CYP3A4 Genotype	Neg/Neg	
CYP3A5 Genotype	*3/*3	*
CYP PANEL Interpretation	See Note	

H=High, L=Low, *=Abnormal, C=Critical

Interpretation: No impaired CYP2C19 variants were detected, consistent with functional alleles. This result predicts the normal metabolizer phenotype.

Interpretation: Two decreased function CYP2C8 alleles were detected. This result predicts the poor metabolizer phenotype.

Interpretation: Two impaired function CYP2C9 alleles were detected. This result predicts the poor metabolizer phenotype.

Interpretation: One copy of a decreased function CYP2D6 allele was detected. The resulting metabolizer phenotype is predicted to fall in the normal range with an activity score of 1.5. Impaired metabolic phenotypes may confer sensitivity to drug-drug interactions with CYP2D6 substrates. Depending on the metabolic pathway for the drug(s) of interest, the impact on dosing may depend on phenotype predictions for other genes.

Interpretation: No impaired CYP3A4 variants were detected, consistent with functional *1 alleles. This result predicts the normal metabolizer phenotype.

Interpretation: Two no function CYP3A5 alleles were detected. This result predicts the poor metabolizer phenotype.

This result has been reviewed and approved by Rong Mao, M.D.

BACKGROUND INFORMATION: Cytochrome P450 Genotyping Panel

CHARACTERISTICS: The cytochrome P450 (CYP) isozymes 2C19, 2C8, 2C9, 2D6 and the CYP3A subfamily are involved in the metabolism of many drugs. Variants in the genes that code for CYP2C19, CYP2C8, CYP2C9, CYP2D6, CYP3A4 and CYP3A5 will influence pharmacokinetics of respective substrates, and may predict or explain non-standard dose requirements, therapeutic failure or adverse reactions.
INHERITANCE: Autosomal co-dominant.
CAUSE: Gene variants affect enzyme expression or activity.
VARIANTS TESTED:
Variants are numbered according to the following transcripts: CYP2C19 (NM_000769), CYP2C8 (NM_000770), CYP2C9 (NM_000771), CYP2D6 (M33388 sequence), CYP3A4 (NM_017460) and CYP3A5 (NM_000777).
Negative: No variants detected is predictive of the *1 functional allele.

CYP2C19*2: rs4244285, c.681G>A
CYP2C19*3: rs4986893, c.636G>A
CYP2C19*4: rs28399504, c.1A>G
CYP2C19*5: rs56337013, c.1297C>T
CYP2C19*6: rs72552267, c.395G>A
CYP2C19*7: rs72558186, c.819+2T>A
CYP2C19*8: rs41291556, c.358T>C
CYP2C19*9: rs17884712, c.431G>A
CYP2C19*10: rs6413438, c.680C>T
CYP2C19*15: rs17882687, c.55A>C
CYP2C19*17: rs12248560, c.-806C>T
CYP2C19*35: rs12769205, c.12662A>G

CYP2C8*1C: rs17110453, c.-370T>G
CYP2C8*2: rs11572103, c.805A>T
CYP2C8*3: rs10509681, c.1196A>G
CYP2C8*4: rs1058930, c.792C>G

CYP2C9*2: rs1799853, c.430C>T
CYP2C9*3: rs1057910, c.1075A>C
CYP2C9*4: rs56165452, c.1076T>C
CYP2C9*5: rs28371686, c.1080C>G
CYP2C9*6: rs9332131, c.817delA
CYP2C9*8: rs7900194, c.449G>A
CYP2C9*11: rs28371685, c.1003C>T

CYP2D6*2: rs16947, c.2850C>T; rs1135840, c.4180G>C
CYP2D6*2A: rs1080985, c.-1584C>G; rs16947, c.2850C>T; rs1135840, c.4180G>C
CYP2D6*3: rs35743686, c.2549delA
CYP2D6*4: rs1065852, c.100C>T; rs3892097, c.1846G>A; rs1135840, c.4180G>C
CYP2D6*5: gene deletion
CYP2D6*6: rs5030655, c.1707delT; rs1135840, c.4180G>C
CYP2D6*7: rs5030867, c.2935A>C
CYP2D6*8: rs5030865, c.1758G>T; rs16947, c.2850C>T; rs1135840, c.4180G>C
CYP2D6*9: rs5030656, c.2615_2617delAAGA
CYP2D6*10: rs1065852, c.100C>T; rs1135840, c.4180G>C
CYP2D6*11: rs1080985, c.-1584C>G; rs201377835, c.883G>C; rs16947, c.2850C>T; rs1135840, c.4180G>C
CYP2D6*12: rs5030862, c.124G>A; rs16947, c.2850C>T; rs1135840, c.4180G>C
CYP2D6*13: a CYP2D7-derived exon 1 conversion
CYP2D6*14: rs5030865, c.1758G>A; rs16947, c.2850C>T; rs1135840, c.4180G>C
CYP2D6*15: rs774671100, c.137_138insT
CYP2D6*17: rs28371706, c.1023C>T; rs16947, c.2850C>T; rs1135840, c.4180G>C
CYP2D6*29: rs16947, c.2850C>T; rs59421388, c.3183G>A; rs1135840, c.4180G>C
CYP2D6*35: rs769258, c.31G>A; rs16947, c.2850C>T; rs1135840, c.4180G>C
CYP2D6*36: a CYP2D6*10 carrying a CYP2D7-derived exon 9 conversion
CYP2D6*36-*10: a CYP2D6*36 and a CYP2D6*10 in tandem
CYP2D6*41: rs16947, c.2850C>T; rs28371725, c.2988G>A; rs1135840, c.4180G>C
CYP2D6*45: rs28371710, c.1716G>A; rs16947, c.2850C>T; rs1135840, c.4180G>C
CYP2D6*46: rs28371696, c.77G>A; rs28371710, c.1716G>A; rs16947, c.2850C>T; rs1135840, c.4180G>C
CYP2D6*49: rs1065852, c.100C>T; rs1135822, c.1611T>A; rs1135840, c.4180G>C
CYP2D6*53: rs1135822, c.1611T>A
CYP2D6*69: rs1065852, c.100C>T; rs16947, c.2850C>T; rs28371725, c.2988G>A; rs1135840, c.4180G>C
CYP2D6*114: rs1065852, c.100C>T; rs5030865, c.1758G>A; rs16947, c.2850C>T; rs1135840, c.4180G>C
DUP: complete gene duplications

CYP3A4*1B: rs2740574, c.-392G>A
CYP3A4*15: rs4986907, c.485G>A
CYP3A4*22: rs35599367, c.522-191C>T

CYP3A5*3: rs776746, c.219-237A>G
CYP3A5*6: rs10264272, c.624G>A
CYP3A5*7: rs41303343, c.1035_1036insT

CLINICAL SENSITIVITY: Drug-dependent.
METHODOLOGY: Polymerase chain reaction (PCR) and fluorescence monitoring.
ANALYTICAL SENSITIVITY AND SPECIFICITY: Greater than 99 percent.
LIMITATIONS: Only the targeted variants will be detected by this panel, and assumptions about phase and content are made to assign alleles. Publically available sources such as the www.pharmvar.org or www.pharmgkb.org provide guidance on phenotype predictions and allele frequencies. A combination of the CYP2D6*5 (gene deletion) and a CYP2D6 gene duplication cannot be specifically identified; however, this combination is not expected to adversely affect the phenotype prediction. Diagnostic errors can occur due to rare sequence variations. Risk of therapeutic failure or adverse reactions with gene substrates may be affected by genetic and non-genetic factors that are not detected by this test. This result does not replace the need for therapeutic drug or clinical monitoring.

H=High, L=Low, *=Abnormal, C=Critical

Test developed and characteristics determined by ARUP Laboratories. See Compliance Statement C: aruplab.com/CS

EER Cytochrome P450 Genotyping Panel

See Note

Access ARUP Enhanced Report using either link below:

-Direct access: [redacted]

-Enter Username, Password: [redacted]
Username: [redacted]
Password: [redacted]

VERIFIED/REPORTED DATES

Procedure	Accession	Collected	Received	Verified/Reported
CYP PANEL Specimen	19-163-402131	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
CYP2C19 Genotype	19-163-402131	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
CYP2C8 Genotype	19-163-402131	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
CYP2C9 Genotype	19-163-402131	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
CYP2D6 Genotype	19-163-402131	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
CYP3A4 Genotype	19-163-402131	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
CYP3A5 Genotype	19-163-402131	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
CYP PANEL Interpretation	19-163-402131	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
EER Cytochrome P450 Genotyping Panel	19-163-402131	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00

END OF CHART

H=High, L=Low, *=Abnormal, C=Critical