

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 \*2/\*2 \*

CYP2C8 Genotype \*1C/\*1C \*

CYP2C9 Genotype Neg/Neg

CYP2D6 Genotype \*2A/\*9

CYP3A4 Genotype Neg/Neg

CYP3A5 Genotype \*3/\*3 \*

CYP PANEL Interpretation See Note

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

Interpretation: Two no function CYP2C19 alleles were detected. This result predicts the poor metabolizer phenotype.

Interpretation: Two copies of the CYP2C8\*1C allele were detected. The functional status of this allele is not classified, but most likely this result predicts a phenotype between the normal and intermediate metabolizer phenotype. Impaired metabolic phenotypes may confer sensitivity to drug-drug interactions with CYP2C8 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 CYP2C9 variants were detected, which is consistent with functional \*1 alleles. This result predicts the normal 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

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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.

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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.

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:

[Redacted Link]  
 -Enter Username, Password: [Redacted]  
 Username: [Redacted]  
 Password: [Redacted]

VERIFIED/REPORTED DATES				
Procedure	Accession	Collected	Received	Verified/Reported
CYP PANEL Specimen	19-163-402129	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
CYP2C19 Genotype	19-163-402129	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
CYP2C8 Genotype	19-163-402129	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
CYP2C9 Genotype	19-163-402129	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
CYP2D6 Genotype	19-163-402129	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
CYP3A4 Genotype	19-163-402129	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
CYP3A5 Genotype	19-163-402129	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
CYP PANEL Interpretation	19-163-402129	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
EER Cytochrome P450 Genotyping Panel	19-163-402129	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