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*****Example Report*****

Patient Age/Gender: Unknown Female
Printed: 24-Mar-20 10:52:14

Procedure	Result	Units	Ref Interval	Accession	Collected	Received	Reported/ Verified
CYP PANEL Specimen	Whole Blood			20-070-900320	10-Mar-20 15:37:00	10-Mar-20 15:37:00	11-Mar-20 13:24:02
CYP2C19 Genotype	Neg/Neg			20-070-900320	10-Mar-20 15:37:00	10-Mar-20 15:37:00	11-Mar-20 13:24:02
CYP2C8 Genotype	Neg/Neg			20-070-900320	10-Mar-20 15:37:00	10-Mar-20 15:37:00	11-Mar-20 13:24:02
CYP2C9 Genotype	Neg/Neg			20-070-900320	10-Mar-20 15:37:00	10-Mar-20 15:37:00	11-Mar-20 13:24:02
CYP2D6 Genotype	Neg/Neg			20-070-900320	10-Mar-20 15:37:00	10-Mar-20 15:37:00	11-Mar-20 13:24:02
CYP3A4 Genotype	Neg/Neg			20-070-900320	10-Mar-20 15:37:00	10-Mar-20 15:37:00	11-Mar-20 13:24:02
CYP3A5 Genotype	Neg/Neg			20-070-900320	10-Mar-20 15:37:00	10-Mar-20 15:37:00	11-Mar-20 13:24:02
CYP PANEL Interpretation	See Note f			20-070-900320	10-Mar-20 15:37:00	10-Mar-20 15:37:00	11-Mar-20 13:24:02
CYP PANEL, GeneDose Link	See Note			20-070-900320	10-Mar-20 15:37:00	10-Mar-20 15:37:00	11-Mar-20 13:24:02

10-Mar-20 15:37:00 CYP PANEL Interpretation:

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

10-Mar-20 15:37:00 CYP PANEL Interpretation:
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 codominant.
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; rs12769205, c.332-23A>G
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.332-23A>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.818del
CYP2C9*8: rs7900194, c.449G>A
CYP2C9*11: rs28371685, c.1003C>T

CYP2D6*2: rs16947, g.2850C>T; rs1135840, g.4180G>C
CYP2D6*2A: rs1080985, g.-1584C>G; rs16947, g.2850C>T; rs1135840, g.4180G>C
CYP2D6*3: rs35743686, g.2549del
CYP2D6*4: rs1065852, g.100C>T; rs3892097, g.1846G>A; rs1135840, g.4180G>C
CYP2D6*5: gene deletion
CYP2D6*6: rs5030655, g.1707del; rs1135840, g.4180G>C
CYP2D6*7: rs5030867, g.2935A>C
CYP2D6*8: rs5030865, g.1758G>T; rs16947, g.2850C>T; rs1135840, g.4180G>C
CYP2D6*9: rs5030656, g.2615_2617del
CYP2D6*10: rs1065852, g.100C>T; rs1135840, g.4180G>C
CYP2D6*11: rs1080985, g.-1584C>G; rs201377835, g.883G>C; rs16947, g.2850C>T; rs1135840, g.4180G>C
CYP2D6*12: rs5030862, g.124G>A; rs16947, g.2850C>T; rs1135840, g.4180G>C
CYP2D6*13: a CYP2D7-derived exon 1 conversion
CYP2D6*14: rs5030865, g.1758G>A; rs16947, g.2850C>T; rs1135840, g.4180G>C
CYP2D6*15: rs774671100, g.137_138insT
CYP2D6*17: rs28371706, g.1023C>T; rs16947, g.2850C>T; rs1135840, g.4180G>C
CYP2D6*29: rs16947, g.2850C>T; rs59421388, g.3183G>A; rs1135840, g.4180G>C
CYP2D6*35: rs769258, g.31G>A; rs16947, g.2850C>T; rs1135840, g.4180G>C; rs1080985, g.-1584C>G
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, g.2850C>T; rs28371725, g.2988G>A; rs1135840, g.4180G>C
CYP2D6*45: rs28371710, g.1716G>A; rs16947, g.2850C>T; rs1135840, g.4180G>C
CYP2D6*46: rs28371696, g.77G>A; rs28371710, g.1716G>A; rs16947, g.2850C>T; rs1135840, g.4180G>C
CYP2D6*49: rs1065852, g.100C>T; rs1135822, g.1611T>A; rs1135840, g.4180G>C
CYP2D6*53: rs1135822, g.1611T>A
CYP2D6*69: rs1065852, g.100C>T; rs16947, g.2850C>T; rs28371725, g.2988G>A; rs1135840, g.4180G>C
CYP2D6*114: rs1065852, g.100C>T; rs5030865, g.1758G>A; rs16947, g.2850C>T; rs1135840, g.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.1035dup

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.

Please note the information contained in this report does not contain medication recommendations, and should not be interpreted as recommending any specific medications. Any dosage adjustments or other changes to medications should be evaluated in consultation with a medical provider.

See Compliance Statement C: www.aruplab.com/CS