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

Patient Age/Gender: Unknown Female
Printed: 28-Mar-19 09:32:13

Procedure	Result	Units	Ref Interval	Accession	Collected	Received	Reported/ Verified
2C8/2C9 Specimen	Whole Blood			19-086-900180	27-Mar-19 15:50:00	27-Mar-19 15:50:00	28-Mar-19 09:30:33
CYP2C8 Genotype	***1C/*1C ***			19-086-900180	27-Mar-19 15:50:00	27-Mar-19 15:50:00	28-Mar-19 09:30:33
CYP2C9 Genotype	***2/*2 ***			19-086-900180	27-Mar-19 15:50:00	27-Mar-19 15:50:00	28-Mar-19 09:30:33
2C8/2C9 Interpretation	See Note f			19-086-900180	27-Mar-19 15:50:00	27-Mar-19 15:50:00	28-Mar-19 09:30:33

27-Mar-19 15:50:00 2C8/2C9 Interpretation:
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: Two copies of decreased or no function CYP2C9 alleles were detected. This result predicts the poor metabolizer phenotype. Dosing of CYP2C9 substrates is likely to be affected.

This result has been reviewed and approved by Pinar Bayrak-Toydemir, M.D., Ph.D.

27-Mar-19 15:50:00 2C8/2C9 Interpretation:
BACKGROUND INFORMATION: CYP2C8 and CYP2C9

CHARACTERISTICS: The cytochrome P450 (CYP) isozymes 2C8 and 2C9 are involved in the metabolism of many drugs. Variants in the genes that code for CYP2C8 and CYP2C9 may influence pharmacokinetics of substrates, and may predict or explain non-standard dose requirements, therapeutic failure or adverse reactions.
INHERITANCE: Autosomal co-dominant.
CAUSE: CYP2C8 and CYP2C9 gene variants affect enzyme expression or activity.
VARIANTS TESTED:
(Variants are numbered according to NM_000770 transcript for CYP2C8 and NM_000771 transcript for CYP2C9)
Negative: No variants detected is predictive of the *1 functional alleles (CYP2C8 or CYP2C9).

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

CLINICAL SENSITIVITY: Drug-dependent.
METHODOLOGY: Polymerase chain reaction (PCR) and fluorescence monitoring.
ANALYTICAL SENSITIVITY AND SPECIFICITY: Greater than 99 percent.
LIMITATIONS: Only the targeted CYP2C8 and CYP2C9 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. Diagnostic errors can occur due to rare sequence

variations. Risk of therapeutic failure or adverse reactions with CYP2C8 or CYP2C9 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