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PATIENT REPORT

Patient Age/Sex: Female

Specimen Collected: 5/9/2025 08:43 MDT

Pharmacogenetics Panel: Psychotropics | **Received: 5/9/2025 08:46 MDT** | **Report/Verified: 5/9/2025 09:07 MDT**

Procedure	Result	Units	Reference Interval
PGX PSYCH Specimen	Whole Blood		
CYP2C19 Genotype	*1/*2		
CYP2C19 Phenotype	**Intermediate** *		
CYP2C9 Genotype	*1/*5		
CYP2C9 Phenotype	**Intermediate** *		
CYP2D6 Genotype	*1/*4		
CYP2D6 Phenotype	**Intermediate** *		
CYP3A4 Genotype	*1/*22		
CYP3A5 Genotype	*1/*3		
CYP3A5 Phenotype	**Intermediate** *		
CYP2B6 Genotype	*1/*6		
CYP2B6 Phenotype	**Intermediate** *		
UGT2B15_1902023	T/G		
ANKK1 rs1800497	**G/A Hetero** *		
COMT rs4680	**G/A Hetero** *		
DRD2 rs1799978	**A/G Hetero** *		
GRIK4 rs1954787	**T/C Hetero** *		
HTR2A rs6311	**G/A Hetero** *		
HTR2A rs7997012	**T/C Hetero** *		
HTR2C rs3813929	**T/T Hemizygous** *		
MTHFR rs1801133	**C/T Hetero** *		
MTHFR rs1801131	**A/C Hetero** *		
OPRM1 Genotype,Interpretation	**AG** *		
OPRM1 Phenotype,Interpretation	See Note		
PGX PSYCH Interpretation	See Note f1 i1		
EER PGX Panel:Psych	See Note f2		

Result Footnote

f1: PGX PSYCH Interpretation
The following CYP2C19 allele(s) were detected: *1/*2. This result predicts the intermediate metabolizer phenotype.

The following CYP2C9 allele(s) were detected: *1/*5. This result predicts the intermediate metabolizer phenotype, with an activity score of 1.5 of 2.

The following CYP2D6 allele(s) were detected: *1/*4. This result predicts the intermediate metabolizer phenotype with an activity score estimated at 1 of 2.

The following CYP3A4 allele(s) were detected: *1/*22.

The following CYP3A5 allele(s) were detected: *1/*3. This result predicts the intermediate metabolizer phenotype.

The following CYP2B6 alleles were detected: *1/*6. This result predicts the intermediate metabolizer

*=Abnormal, #=Corrected, C=Critical, f=Result Footnote, H-High, i-Test Information, L-Low, t-Interpretive Text, @=Performing lab

Result Footnote

f1: PGX PSYCH Interpretation
phenotype.

Recommendation: Guidelines for gene-based dosing are published by the Clinical Pharmacogenetics Implementation Consortium (CPIC) and other organizations.

This test interrogates the UGT2B15 c.253T>G (rs1902023) variant, and the results are T/G. As such, the interpretation is heterozygous.

The UGT2B15 gene codes for the UDP glucuronosyltransferase family 2 member B15 (UGT2B15) that is involved in conjugative metabolism of many medications, such as the anxiolytics oxazepam and lorazepam.

The following ANKK1 c.2137G>A (rs1800497) alleles were detected: G/A. As such, the interpretation is heterozygous.

The ANKK1 gene codes for the TAQ1A polymorphism that affects the expression of binding sites for dopamine on the dopamine D2 receptor. Variants may influence the likelihood for toxicity and response to drugs that target the dopaminergic system. Variants are also associated with risk of substance use disorders.

The following COMT c.472G>A (rs4680) alleles were detected: G/A. As such, the interpretation is heterozygous.

The COMT gene codes for the catechol-O-methyltransferase (COMT) enzyme, which is involved in metabolism of catecholamines such as dopamine and norepinephrine. Variants are associated with variance in response to many drugs as well as tolerance to pain.

The following DRD2 c.-585A>G (rs1799978) alleles were detected A/G. As such, the interpretation is heterozygous.

The DRD2 gene codes for the dopamine D2 receptor. Variants may influence likelihood for toxicity and response to drugs that target the dopaminergic system.

The following GRIK4 c.83-10039T>C (rs1954787) alleles were detected: T/C. As such, the interpretation is heterozygous.

The GRIK4 gene codes for the subunit 4 of the kainite (glutamate) receptor. Variants are associated with variance in response to some antidepressants.

This test interrogates two variants. For HTR2A c.-998G>A (rs6311) the results are G/A. As such, the interpretation is heterozygous. For HTR2A c.614-2211T>C (rs7997012) the results are T/C. As such, the interpretation is heterozygous.

The HTR2A gene codes for the serotonin receptor 2A. Variants may influence response to some antipsychotics and antidepressants.
This test interrogates the HTR2C c.-850C>T (rs3813929) variant, and the result is T. As such, the interpretation is hemizygous.

The HTR2C gene codes for the serotonin 2C receptor that is involved in response to psychotropic medications, particularly antipsychotics.

This test interrogates two variants. For MTHFR c.665C>T (rs1801133, previously designated as C677T) the results are C/T. As such, the interpretation is heterozygous. For MTHFR c.1286A>C (rs1801131, previously designated A1298C) the results are A/G. As such, the interpretation is heterozygous.
The MTHFR gene codes for methylenetetrahydrofolate reductase (MTHFR), an enzyme that metabolizes folate. Variants are associated with variance in response to many drugs as well as symptoms of depression and

Result Footnote

f1: PGX PSYCH Interpretation
hyperhomocysteinemia.

Indication for testing: predict opioid sensitivity.

Interpretation: One copy of the OPRM1 A allele and one copy of the G allele (rs1799971) were detected in this sample. Further studies are needed to determine the clinical significance of this genotype; however, it is possible this patient may require higher or more frequent doses of opioid receptor agonists (e.g., morphine) to achieve adequate pain control. He/she may also be more likely to respond to opioid antagonists (e.g., naltrexone) in the treatment of alcohol and/or opioid dependency. This association of OPRM1 and drug sensitivity is not definitive and may be different for individual opioids.

Guidelines for genotype-based dosing for CYP2C19, CYP2C9, CYP2D6, CYP3A4, CYP3A5, CYP2B6 and COMT recommendations are published by the Clinical Pharmacogenetics Implementation Consortium (CPIC) and can be found at: https://cpicpgx.org/ and https://www.pharmgkb.org/.

The clinical evidence is limited for the drug associations described thus far, and gene - based dosing guidelines are not
currently published for the following Genes: ANKK1, CYP1A2, DRD2, EPHX1, HTR2A, HTR2c, MTHFR, SLC2A and UGT2B15.See PharmGKB.org for more information.

This result has been reviewed and approved by [redacted]

f2: EER PGX Panel: Psych
Authorized individuals can access the ARUP Enhanced Report
with an ARUP Connect account using the following link.

Your local lab can assist you in obtaining the patient
report if you don't have a Connect account.

[redacted]

Test Information

i1: PGX PSYCH Interpretation
Background Information for Pharmacogenetics Panel:
Psychotropics:

CHARACTERISTICS: Variation in genes affecting pharmacokinetics and/or pharmacodynamics (pharmacogenetics) may influence medication selection and dose planning. For example, variants in genes that code for metabolizing enzymes (CYP2B6, CYP2C19, CYP2C9, CYP2D6, CYP3A4, CYP3A5, and UGT2B15) may be associated with altered (slower or faster) metabolism which would affect the kinetics of medication activation, inactivation, and/or elimination. Other genes in this panel may predict risk of side effects and/or likelihood of response (ANKK1, COMT, DRD2, GRIK4, HTR2A, HTR2C, MTHFR, and OPRM1). This information may guide medication and dose selection for many prescription medications, including medications relevant to psychiatry such as psychostimulants (e.g., ADHD medication), antidepressants, antipsychotics, and anxiolytics.

Inheritance: Autosomal codominant.
Cause: Gene variants affect enzyme or protein function.

Test Information

i1: PGX PSYCH Interpretation

Genes Included: ANKK1, COMT, CYP2B6, CYP2C19, CYP2C9, CYP2D6, CYP3A4, CYP3A5, DRD2, GRIK4, HTR2A, HTR2C, MTHFR, OPRM1, and UGT2B15.

Variants Tested:
Variants are numbered according to the following transcripts:
ANKK1 NM_178510, COMT NM_000754, CYP2B6 NM_000767, CYP2C19 NM_000769, CYP2C9 NM_000771, CYP2D6 M33388 sequence, CYP3A4 NM_017460 and CYP3A5 NM_000777, DRD2 NM_000795, GRIK4 NM_014619, HTR2A NM_000621, HTR2C NM_001256760, MTHFR NM_005957, OPRM1 NM_000914, UGT2B15 NM_001076.

*1: Indicative of no detected targeted variants and an assumption of functional allele.

ANKK1: rs1800497, c.2137G>A

COMT: rs4680, c.472G>A

CYP2B6*4: rs2279343, c.785A>G
CYP2B6*6: rs3745274, c.516G>T; rs2279343, c.785A>G
CYP2B6*7: rs3745274, c.516G>T; rs2279343, c.785A>G; rs3211371, c.1459C>T
CYP2B6*9: rs3745274, c.516G>T
CYP2B6*18: rs28399499, c.983T>C
CYP2B6*22: rs34223104, c.-82T>C
CYP2B6*36: rs34223104, c.-82T>C; rs3745274, c.516G>T; rs2279343, c.785A>G

CYP2C19*2: rs4244285, c.681G>A; rs12769205, c.332-23A>G
CYP2C19*3: rs4986893, c.636G>A
CYP2C19*4A: rs28399504, c.1A>G
CYP2C19*4B: rs28399504, c.1A>G; rs12248560, c.-806C>T
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*17: rs12248560, c.-806C>T
CYP2C19*35: rs12769205, c.332-23A>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.818delA
CYP2C9*8: rs7900194, c.449G>A

Test Information

i1: PGX PSYCH Interpretation

CYP2C9*11: rs28371685, c.1003C>T
CYP2C9*12: rs9332239, c.1465C>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: rs35742686, g.2549delA
CYP2D6*4: rs1065852, g.100C>T; rs3892097, g.1846G>A; rs1135840, g.4180G>C
CYP2D6*5: gene deletion
CYP2D6*6: rs5030655, g.1707delT
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_2617delAAG
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*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: rs59421388, g.3183G>A; rs16947, g.2850C>T; rs1135840, g.4180G>C
CYP2D6*31: rs267608319, g.4042G>A; rs16947, g.2850C>T; rs1135840, g.4180G>C
CYP2D6*35: rs769258, g.31G>A; rs1080985, g.-1584C>G; rs16947, g.2850C>T; rs1135840, g.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*40: rs28371706, g.1023C>T; rs72549356, g.1863_1864insTTTCGCCCCTTTCGCCCC; rs16947, g.2850C>T; rs1135840, g.4180G>C
CYP2D6*41: rs28371725, g.2988G>A; rs16947, g.2850C>T; rs1135840, g.4180G>C
CYP2D6*42: rs72549346, g.3260_3261insTG; rs16947, g.2850C>T; rs1135840, g.4180G>C
CYP2D6*49: rs1135822, g.1611T>A; rs1065852, g.100C>T; rs1135840, g.4180G>C
CYP2D6*56: rs72549347, g.3201C>T; rs1135840, g.4180G>C
CYP2D6*59: rs79292917, g.2939G>A; rs16947, g.2850C>T; rs1135840, g.4180G>C
CYP2D6*69: rs28371725, g.2988G>A; rs1065852, g.100C>T; rs16947, g.2850C>T; rs1135840, g.4180G>C
CYP2D6*114: rs5030865, g.1758G>A; rs1065852, g.100C>T; rs16947, g.2850C>T; rs1135840, g.4180G>C
DUP: complete gene duplications

CYP3A4*22: rs35599367, c.522-191C>T

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

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DRD2: rs1799978, c.-585A>G

GRIK4: rs1954787, c.83-10039T>C

HTR2A: rs6311, c.-998G>A
HTR2A: rs7997012, c.614-2211T>C

HTR2C: rs3813929, c.-850C>T

MTHFR: rs1801131, c.1286A>C
MTHFR: rs1801133, c.665C>T

OPRM1: rs1799971, c.118A>G

UGT2B15: rs1902023, c.253T>G

Methodology: Polymerase chain reaction (PCR) and fluorescence monitoring. Long-range PCR and Sanger sequencing is only performed if needed to characterize a duplicated CYP2D6 gene.
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. Publicly 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. The assay used to detect CYP2D6*40 allele, cannot distinguish between insertions of 1 or 2 copies; it also cannot distinguish between heterozygous and homozygous mutant samples due to unavoidable cross-reactivity with the wild-type sequence. Additional assays will be used to help differentiate the CYP2D6*40 allele from other CYP2D6 star alleles. 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 nongenetic factors that are not detected by this test.

For ANKK1, DRD2, GRIK4, HTR2A, HTR2C, and UGT2B15, clinical evidence is limited for the drug associations described thus far, and gene-based dosing guidelines are not currently published.
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

Test Information

i1: PGX PSYCH Interpretation

medications. Any dosage adjustments or other changes to medications should be evaluated in consultation with a medical provider.

This test was developed and its performance characteristics determined by ARUP Laboratories. It has not been cleared or approved by the U.S. Food and Drug Administration. This test was performed in a CLIA-certified laboratory and is intended for clinical purposes.

Counseling and informed consent are recommended for genetic testing. Consent forms are available online.