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RightMed® Gene Report

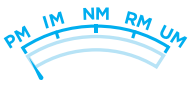
Patient and report summary

Patient name: **Sample Patient**
Patient date of birth: **1977-09-02**
OneOme report date: **2023-11-29**

Ordering provider: **Sample Doctor**
Ordering facility: **Sample Clinic (US)**
Report type: **Specialty**

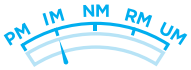
Phenotype icon legend for CYP genes

CYP phenotype, or metabolizer status, is determined by the total predicted activity of the gene based on the genotype, and is represented by a gauge icon. Total predicted activity which falls between phenotypes will be reported as a range phenotype.



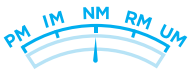
Poor metabolizer

No to very low activity. Drugs converted to active metabolite(s) may have reduced efficacy. Active drugs converted to inactive metabolite(s) may cause side effects or toxicity.



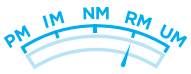
Intermediate metabolizer

Decreased activity. Drugs converted to active metabolite(s) may have reduced efficacy. Active drugs converted to inactive metabolite(s) may cause side effects or toxicity.



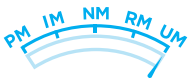
Normal metabolizer

Normal level of activity. Drugs metabolized at a normal rate.



Rapid metabolizer

Increased activity. Drugs converted to active metabolite(s) may cause side effects or toxicity. Active drugs converted to inactive metabolite(s) may lack efficacy.



Ultrarapid metabolizer

Increased activity. Drugs converted to active metabolite(s) may cause side effects or toxicity. Active drugs converted to inactive metabolite(s) may lack efficacy.

Phenotype icon legend for other genes

Phenotype icons for other genes represent the extent of impact of the genotype on protein activity, expression, or function, and/or observed clinical impact (e.g., adverse event risk).

Atypical

Genotype indicates an absence of or major increase in protein activity, expression, or function.

Atypical

Genotype indicates a moderate loss of or increase in protein activity, expression, or function.

Typical

Genotype indicates normal or typical protein activity, expression, or function.

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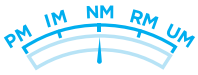
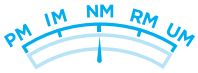
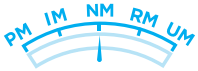
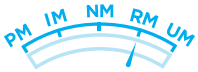
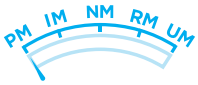
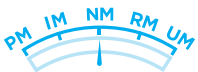
Report and laboratory comments

Interpretive guidance

Hemizygous males and homozygous females are reported as HTR2C CC.

The reported NUDT15 genotype was inferred based on available variant data. The *2 and *3 alleles are detected by the rs116855232 variant; however, both alleles have no function and *2 is defaulted as *3. Please contact OneOme with any additional questions.

Gene and phenotype summary

Gene	Genotype		Phenotype summary / Metabolic status
CYP1A2	*1A/*1A		**Normal metabolizer** Fully functional enzyme activity is likely based on the genotype results. Normal metabolism of the medication affected by this gene is predicted.
CYP2B6	*1/*1		**Normal metabolizer** Fully functional enzyme activity is likely based on the genotype results. Normal metabolism of the medication affected by this gene is predicted.
CYP2C9	*1/*1		**Normal metabolizer** Fully functional enzyme activity is likely based on the genotype results. Normal metabolism of the medication affected by this gene is predicted.
CYP2C19	*1/*1*17		**Rapid metabolizer** Increased enzyme activity is likely based on the genotype results. This activity is more than a normal metabolizer, but less than an ultrarapid metabolizer. The metabolism of the medication affected by this gene is predicted to be increased.
CYP2C Cluster	rs12777823 GG		**Normal** CYP2C rs12777823 homozygous wild-type genotype consistent with normal clearance of a certain medication, independent of the impact of CYP2C9*2 and *3. CYP2C rs12777823, together with CYP4F2, CYP2C9, and VKORC1, may affect treatment management of a certain medication.
CYP2D6	*3/*3		**Poor metabolizer** Little to no enzyme activity is likely based on the genotype results. Little to no metabolism of the medication affected by this gene is predicted.
CYP3A4	*1/*1		**Normal metabolizer** Fully functional enzyme activity is likely based on the genotype results. Normal metabolism of the medication affected by this gene is predicted.

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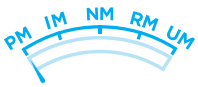
Gene and phenotype summary (cont.)

CYP3A5	*3/*3		**Poor metabolizer** This CYP3A5 genotype is associated with the phenotype most prevalent in studies used to define standard dosing guidelines.
CYP4F2	*1/*1		**Normal activity** Genotype consistent with normal activity of the CYP4F2 enzyme, which catalyzes the metabolism of vitamin K, in counterpoint to the activity of VKORC1. CYP4F2, together with CYP2C9, VKORC1, and a variant in CYP2C Cluster, may affect treatment management of a certain medication.
COMT	rs4680 AA		**Low activity** The AA (Met/Met) genotype is associated with lower COMT activity than the GG (Val/Val) or GA (Val/Met) genotypes.
DPYD	*1/*1		**Normal metabolizer** DPD activity score= 2. This genotype and activity score is consistent with a normal metabolizer phenotype.
DRD2	rs1799978 AA		**Normal receptor expression** Homozygous wild-type dopamine receptor D2 (DRD2) rs1799978 AA genotype is consistent with normal receptor expression.
F2	rs1799963 GG		**Normal risk** Normal risk of thrombosis associated with Factor II (prothrombin). Other genetic and clinical factors contribute to the risk for thrombosis.
F5	rs6025 GG		**Normal risk** Normal risk of thrombosis associated with Factor V. Other genetic and clinical factors contribute to the risk for thrombosis.
GRIK4	rs1954787 TT		**Altered receptor function** Homozygous variant glutamate ionotropic receptor kainate type subunit 4 (GRIK4) genotype is consistent with altered receptor function.
HLA-A	Negative		**Normal risk** Negative for the presence of the HLA-A*31:01 allele. Normal risk of hypersensitivity induced by certain medications, and possibly others of structural similarity. Hypersensitivity and severe cutaneous reactions may occur regardless of the presence of the HLA-A*31:01 allele, in particular the presence of the HLA-B*15:02 allele is associated with severe cutaneous reactions induced by certain medications.

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Gene and phenotype summary (cont.)

HLA-B	Negative		**Normal risk** Negative for presence of the HLA-B*15:02, HLA-B*57:01, and HLA-B*58:01 alleles. Normal risk of hypersensitivity, severe cutaneous reactions, and severe hepatotoxicity induced by certain medications. Hypersensitivity, severe cutaneous reactions, and severe hepatotoxicity may occur regardless of the presence of HLA-B*15:02, HLA-B*57:01, or HLA-B*58:01 alleles. In particular, the presence of the HLA-A*31:01 allele is associated with hypersensitivity reactions induced by a certain medication, and possibly other medications of structural similarity.
HTR2A	rs7997012 AA		**Intron 2 genotype AA** Homozygous wild-type HTR2A (5-hydroxytryptamine receptor 2A) genotype is consistent with normal HTR2A receptor function.
HTR2C	rs3813929 CC		**Normal receptor expression** This genotype is associated with normal transcriptional activity of the HTR2C gene.
IFNL4	rs12979860 CC		**Normal** Genotype consistent with a normal likelihood of hepatitis C sustained virologic response (SVR) with certain treatment options.
NUDT15	*1/*3		**Intermediate metabolizer** NUDT15 genotype is consistent with impaired enzyme activity and is associated with an increased risk of thiopurine-induced toxicities.
OPRM1	rs1799971 AA		**Variant absent** The AA genotype (or Asn/Asn isoform) is the wildtype genotype associated with the mu-1 opioid receptor.
SLC6A4	L/L (La/La)		**Typical to increased expression** Genotype consistent with a typical to increased expression of the SLC6A4 transporter compared to other genotypes. This genotype was shown to exhibit different phenotypes in East Asian populations, as opposite outcomes were observed for this genotype in East Asian populations when compared to Caucasian populations.
SLCO1B1	*5/*5		**Poor function** SLCO1B1 genotype consistent with poor function of the OATP1B1 transporter.
TPMT	*1/*1		**Normal metabolizer** TPMT genotype is consistent with a normal metabolizer phenotype and is not associated with an increased risk of thiopurine-induced toxicities. Toxicities with thiopurines can occur due to impaired NUDT15 activity independently from the TPMT activity.

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Gene and phenotype summary (cont.)

UGT1A1	*1/*28		**Intermediate metabolizer (Heterozygous *28)** Genotype consistent with decreased UGT1A1 enzyme activity, or an intermediate metabolizer phenotype, and is associated with an increased risk of certain drug-induced toxicities.
VKORC1	rs9923231 GG		**Normal activity** Genotype consistent with normal activity of the vitamin K epoxide reductase enzyme, associated with c.-1639GG (rs9923231). VKORC1, together with CYP2C9, CYP4F2, and a variant in CYP2C Cluster, may affect treatment management of a certain medication.

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Test information

Specimen ID: **2350706821927**
Specimen type: **Buccal swab**
Collection date: **2023-11-27**
Receive date: **2023-11-29**

Clinical testing performed by:
OneOme
807 Broadway St. NE Suite 100
Minneapolis, MN 55412, United States

Reported by: **Cathryn Jennissen in None**
CLIA: **24D2109855**
CAP: **9432670**
NY PFI: **9226**

Test results

The following analytical results were interpreted by OneOme to produce the pharmacogenomic interpretations and annotations described in the *Gene and phenotype summary*. Method-specific analytical limitations or inferred haplotypes may limit the ability to produce a definitive phenotype interpretation. See *Methodology and limitations* and/or the *Report and laboratory comments* sections for additional information.

CYP1A2 *1A/*1A

rs762551	NM_000761.4:c.-9-154C>A	CC
rs2069514	NG_008431.2:g.28338G>A	GG
rs2069526	NM_000761.4:c.-10+103T>G	TT
rs12720461	NM_000761.4:c.-10+113C>T	CC
rs35694136	NM_000761.4:c.-1635delT	TT

CYP2B6 *1/*1

rs3745274	NM_000767.4:c.516G>T	GG
rs2279343	NM_000767.4:c.785A>G	AA
rs34223104	NM_000767.5:c.-82T>C	TT
rs3211371	NM_000767.4:c.1459C>T	CC
rs36079186	NM_000767.5:c.593T>C	TT
rs28399499	NM_000767.4:c.983T>C	TT

CYP2C9 *1/*1

rs7900194	NM_000771.3:c.449G>A	GG
rs1799853	NM_000771.3:c.430C>T	CC
rs1057910	NM_000771.3:c.1075A>C	AA
rs28371686	NM_000771.3:c.1080C>G	CC
rs56165452	NM_000771.3:c.1076T>C	TT
rs28371685	NM_000771.3:c.1003C>T	CC
rs9332131	NM_000771.3:c.817delA	AA

CYP2C19 *1/*17

rs12248560	NM_000769.2:c.-806C>T	CT
rs4244285	NM_000769.2:c.681G>A	GG
rs4986893	NM_000769.2:c.636G>A	GG
rs6413438	NM_000769.2:c.680C>T	CC
rs28399504	NM_000769.2:c.1A>G	AA

CYP2C Cluster rs12777823 GG

rs12777823	NC_000010.10:g.96405502G>A	GG

CYP2D6 *3/*3

rs28371706	NM_000106.5:c.320C>T	CC
rs267608319	NM_000106.5:c.1319G>A	GG
rs16947	NM_000106.5:c.886C>T	CC
rs79292917	NM_000106.5:c.975G>A	GG
rs1065852	NM_000106.5:c.100C>T	CC
rs1135840	NM_000106.5:c.1457G>C	GG
rs3892097	NM_000106.5:c.506-1G>A	GG
rs769258	NM_000106.5:c.31G>A	GG
rs5030862	NM_000106.5:c.124G>A	GG
rs201377835	NM_000106.5:c.181-1G>C	GG
rs5030867	NM_000106.5:c.971A>C	AA
rs765776661	NM_000106.5:c.1411_1412insTGCCCACTG	GTGCCCACGTGCCCAC
rs5030656	NM_000106.5:c.841_843delAAG	AAGAAG
rs35742686	NM_000106.5:c.775delA	--
rs72549353	NM_000106.5:c.765_768delAACT	AACTAACT
rs5030655	NM_000106.5:c.454delT	TT
rs774671100	NM_000106.5:c.137_138insT	--
rs1080985	NM_000106.5:c.-1584C>G	CC
rs59421388	NM_000106.5:c.1012G>A	GG
rs28371725	NM_000106.5:c.985+39G>A	GG
rs72549346	NM_000106.5:c.1088_1089insGT	--
rs5030865	NM_000106.5:c.505G>[A,T]	GG

CYP3A4 *1/*1

rs2740574	NM_017460.5:c.-392G>A	AA
rs35599367	NM_017460.5:c.522-191C>T	CC

CYP3A5 *3/*3

rs776746	NM_000777.4:c.219-237G>A	GG
rs10264272	NM_000777.4:c.624G>A	GG
rs41303343	NM_000777.4:c.1035_1036insT	--

CYP4F2 *1/*1

rs2108622	NM_001082.4:c.1297G>A	GG

COMT rs4680 AA

rs4680	NM_000754.3:c.472G>A	AA

DPYD *1/*1

rs75017182	NM_000110.4:c.1129-5923C>G	CC
rs55886062	NM_000110.3:c.1679T>G	TT
rs67376798	NM_000110.3:c.2846A>T	TT
rs3918290	NM_000110.3:c.1905+1G>A	GG
rs115232898	NM_000110.4:c.557A>G	AA

DRD2 rs1799978 AA

rs1799978	NM_000795.3:c.-585A>G	AA

F2 rs1799963 GG

rs1799963	NM_000506.4:c.*97G>A	GG

F5 rs6025 GG

rs6025	NM_000130.4:c.1601G>A	GG

GRIK4 rs1954787 TT

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Test results (cont.)

rs1954787	NM_001282470.2:c.83-10039T>C	TT

HLA-A Negative

HLA00097	NM_002116 (interrogated at exon 2)	Negative

HLA-B Negative

rs144012689	NM_005514.7:c.1012+104A>T	TT
HLA00386	NM_005514 (interrogated at exon 2 and intron 2)	Negative
HLA00381	NM_005514 (interrogated at exon 3)	Negative

HTR2A rs7997012 AA

rs7997012	NM_000621.4:c.614-2211T>C	TT

HTR2C rs3813929 CC

rs3813929	NM_000868.3:c.-759C>T	CC

IFNL4 rs12979860 CC

rs12979860	NM_001276254.2:c.151-152G>A	CC

NUDT15 *1/*3

rs116855232	NM_018283.3:c.415C>T	CT

OPRM1 rs1799971 AA

rs1799971	NM_000914.4:c.118A>G	AA

Electronically signed by:
Cathryn Jennissen in None
2023-11-29

SLC6A4 L/L (La/La)

rs25531	NM_001045.5:c.-1936A>G	AA
rs774676466	NM_001045.5:c.-1917_-1875del43	LL

SLCO1B1 *5/*5

rs2306283	NM_006446.4:c.388A>G	AA
rs4149056	NM_006446.4:c.521T>C	CC
rs4149015	NM_006446.4:c.-910G>A	GG

TPMT *1/*1

rs1142345	NM_000367.3:c.719A>G	AA
rs1800584	NM_000367.3:c.626-1G>A	CC
rs1800462	NM_000367.3:c.238G>C	GG
rs1800460	NM_000367.3:c.460G>A	GG

UGT1A1 *1/*28

rs4148323	NM_001072.3:c.862-6536G>A	GG
rs1976391	NM_001072.3:c.862-9697A>G	AG

VKORC1 rs9923231 GG

rs7200749	NM_024006.5:c.358C>T	GG
rs9923231	NM_001311311.1:c.-1639G>A	GG

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Methodology and limitations

This test was developed and its performance characteristics determined by OneOme, LLC, a clinical laboratory located at 807 Broadway Street NE Suite 100, Minneapolis, MN 55413. These tests have not been cleared or approved by the U.S. Food and Drug Administration. The FDA does not require this test to go through premarket FDA review. OneOme is certified under CLIA-88 and accredited by the College of American Pathologists as qualified to perform high-complexity testing. This test is used for clinical purposes and should not be regarded as investigational or for research.

Genomic DNA was analyzed by PCR using Thermo Fisher TaqMan® and/or LGC Biosearch BHQ® probe-based methods to interrogate the variant locations listed in the *Test results* table above. In addition, CYP2D6 copy number status was assessed at sites within the promoter, intron 2, intron 6, and exon 9. The test detects CYP2D6 deletions, duplications/multiplications, and hybrid alleles, but cannot differentiate duplications in the presence of a deletion.

Haplotypes, or combinations of inherited variants on a chromosome, are annotated according to legacy nomenclature for the genes and alleles in the table below.

CYP1A2	*1C, *1D, *1E, *1F, *1J, *1K, *1L, *1V, *1W
CYP2B6	*4, *5, *6, *7, *9, *18, *22, *35, *36
CYP2C9	*2, *3, *4, *5, *6, *8, *11
CYP2C19	*2, *3, *4, *4B, *10, *17
CYP2D6	*2, *2A, *3, *4, *4M, *4N, *5, *6, *6C, *7, *8, *9, *10, *11, *12, *13, *14, *15, *17, *18, *19, *29, *31, *34, *35, *36, *39, *41, *42, *59, *63, *64, *68, *69, *70, *91, *109, *114
CYP3A4	*1B, *22
CYP3A5	*3, *6, *7
CYP4F2	*3
DPYD	*2A, Asp949Val, *13, HapB3, Tyr186Cys
SLCO1B1	*1B, *5, *15, *17, *21
TPMT	*2, *3A, *3B, *3C, *4
UGT1A1	*6, *28

The test does not detect all known and unknown variations in the gene(s) tested, nor does absence of a detectable variant (designated as *1 for genes encoding drug metabolizing enzymes) rule out the presence of other, non-detected variants.

As with other common SNP genotyping techniques, these assays cannot differentiate between the maternal and paternal chromosomes. In cases where observed variants are associated with more than one haplotype, OneOme infers and reports the most likely diplotype based on published allele frequency and/or ethnicity data. Inferences with potential clinical impact are reported in the *Report and laboratory comments* section.

PCR may be subject to general interference by factors such as reaction inhibitors and low quality or quantity of extracted DNA. When present, these interferents typically yield no result rather than an inaccurate one. Very infrequent variants or polymorphisms occurring in primer- or probe-binding regions may affect testing and could produce an erroneous result or assay failure. Variant locations tested by the assay but not assigned a genotype call are reported as “No Call.”

The variant detection methods validated by OneOme provide >99.9% accuracy for the adult population; however, clinical interpretation may be inaccurate for patients who have undergone or are receiving non-autologous blood transfusions, tissue, and/or organ transplant therapies. Although extremely rare, results could also be impacted by other factors not addressed above, such as laboratory error.

Pharmacogenetic correlation is largely based on studies of adult populations. Gene-drug guidance may not be informative in pediatric patients. For patients that may carry a probabilistic risk of disease, patients and providers should consider the benefits of consulting with a trained genetic counseling professional, physician, or pharmacogenomic specialist. For additional support, contact OneOme

Methodology and limitations (cont.)

through the website or by calling 844-663-6635.

OneOme liability disclaimer

The clinical annotations provided by OneOme are intended solely for use by a medical professional in the treatment of adult patients and do not constitute medical advice by OneOme. The treating provider remains ultimately responsible for all diagnosis and treatment decisions for the patient. OneOme disclaims liability for any errors, omissions or ambiguities in any translation or interpretation of a report by a third party, including without limitation direct, indirect, incidental, special, consequential or exemplary damages, whether such damages arise in contract, negligence, tort, under statute, in equity, at law or otherwise. Information included in this report is based upon scientific literature and does not take into account other genetic variants and environmental or social factors that may impact each patient. Other factors not included in this report include, but are not limited to, environmental factors (e.g., smoking), health factors (e.g., diet), social and familial factors, various medical conditions, and drug-to-drug interactions. Administration of any medication requires careful therapeutic monitoring regardless of the phenotype or genotype-derived interaction reported. As a matter of practice, OneOme will routinely update its pharmacogenomic database as new information becomes available to the scientific community. Clinical annotations, including phenotype summaries, are therefore dependent on the date of generation and/or the database version used to generate that report.