# RightMed® Comprehensive Test Report

The RightMed Comprehensive Test is a pharmacogenomic test that identifies how a patient's DNA affects their response to hundreds of medications. This report can be used to help determine safer, more effective medications and doses tailored to a patient's genomic profile.

## Patient and report summary

Patient name: **Luis N**
Patient date of birth: 1992-06-111992-06-11
OneOme report date: 2020-07-022020-07-02

Ordering provider: **Eva Garcia**
Ordering facility: **Novagenic**
Product type: **Comprehensive**
Report type: **Original**

## Report legend

Based on this patient's genetic profile, medications are reported and classified according to the gene-drug interactions described below.

| | |
|---|---|
| Major gene-drug interaction | Major genotype-drug interaction identified that affects the metabolism of the medication and/or indicates an elevated risk of adverse reaction or loss of efficacy. |
| Moderate gene-drug interaction | Moderate genotype-drug interaction identified that affects the metabolism of the medication and/or indicates an elevated risk of adverse reaction or loss of efficacy. |
| Minimal gene-drug interaction | Minimal genotype-drug interaction identified that does not significantly affect medication metabolism nor indicate an elevated risk of adverse reaction or loss of efficacy. |
| Limited pharmacogenetic impact | No pharmacogenetic variants demonstrate a significant impact on medication response. Other types of genetic tests that may guide prescribing (e.g., tumor marker testing, diagnostic, or indication-establishing testing) are not taken into account. |

## Icon legend

Some medications are reported with icons to indicate that specific clinical annotations and/or dosing guidelines provided by FDA, CPIC, or other professional associations are available in the RightMed Advisor.

| | |
|---|---|
| Increased exposure | Total exposure to active compound(s) may be increased. Monitor for adverse effects. |
| Decreased exposure | Total exposure to active compound(s) may be decreased. Monitor for lack of therapeutic response. |
| Difficult to predict | Total exposure to active compound(s) is difficult to predict. Monitor patient response. |
| Reduced response | Response to medication may be lowered due to genetic changes impacting mechanisms other than exposure (e.g. receptor function). |
| Additional testing | According to FDA labeling, additional laboratory testing may be indicated. |
| Professional guideline | Medication has professional guidelines associated with this patient's genetic test results. Avoidance, dose adjustment, or heightened monitoring may be indicated. |

# Report and laboratory comments

## Interpretive guidance

Results and clinical annotations on this test report were derived from DNA that was submitted by Novagenic (Creston 335, Jardines del Pedregal, Mexico City, 01900 Mexico). Alternative sample types, such as externally extracted DNA, may be subject to additional test limitations that have not been independently assessed or validated by OneOme.

# Genotype-predicted interactions for medications

## Allergy/Pulmonology

### Major gene-drug interaction

- Dextromethorphan + 1 (Delsym®)

### Moderate gene-drug interaction

- Indacaterol + 1, 86 (Arcapta®)
- Loratadine + 245 (Claritin®)
- Salmeterol + 1 (Serevent®)
- Sildenafil + 1 (Revatio®, Viagra®)
- Tadalafil + 1 (Adcirca®, Cialis®)

### Minimal gene-drug interaction

### Limited pharmacogenetic impact

- Desloratadine (Clarinex®)
- Montelukast (Singulair®)

## Analgesic/Anesthesiology

### Major gene-drug interaction

- Codeine − 1, 2, 9, 21, 35, 36, 44, 199, 217
- Hydrocodone + 1, 35, 36 (Hysingla®, Zohydro®)
- Oxycodone + 1, 2, 35, 36, 44 (Oxycontin®, Roxicodone®)
- Tramadol − 1, 2, 35, 36, 44, 126, 203, 206, 222 (Ultram®)

### Moderate gene-drug interaction

- Alfentanil + 1, 53, 97, 107, 153, 167 (Alfenta®)
- Buprenorphine + 1 (Buprenex®, BuTrans®, Subutex®)
- Cyclobenzaprine + 1, 234 (Flexeril®)
- Fentanyl + 1, 47, 60, 78, 100, 111, 214, 240, 244, 250, 251, 252 (Duragesic®, Sublimaze®)
- Methadone + 1 (Dolophine®, Methadose®)

### Minimal gene-drug interaction

- Carisoprodol 1, 56 (Soma®)
- Ketamine 1, 120, 121, 173, 242 (Ketalar®)
- Midazolam 1, 221 (Versed®)
- Morphine 14, 21, 26, 27, 108, 118, 179, 197, 198, 213 (Kadian®, MS Contin®)

### Limited pharmacogenetic impact

- Dexmedetomidine (Precedex®)
- Naloxone (Evzio®, Narcan®)

## Anti-inflammatory

### Major gene-drug interaction

### Moderate gene-drug interaction

### Minimal gene-drug interaction

- Celecoxib 1 (Celebrex®)
- Diclofenac 1 (Voltaren®)
- Flurbiprofen 1, 207 (Ansaid®)
- Meloxicam 1 (Mobic®)
- Piroxicam 1 (Feldene®)

### Limited pharmacogenetic impact

## Anticoagulant/Antiplatelet

### Major gene-drug interaction

### Moderate gene-drug interaction

- Apixaban + 1 (Eliquis®)
- Cilostazol + 1, 221 (Pletal®)
- Ticagrelor + 1 (Brilinta®)
- Warfarin 1, 24, 83, 84 (Coumadin®, Jantoven®)

### Minimal gene-drug interaction

- Clopidogrel 1, 2, 44, 188, 189 (Plavix®)

### Limited pharmacogenetic impact

- Dalteparin (Fragmin®)
- Enoxaparin (Lovenox®)
- Prasugrel (Effient®)
- Tirofiban (Aggrastat®)

## Cardiovascular

### Major gene-drug interaction

- Carvedilol + 1 (Coreg®)
- Clonidine + 1 (Catapres®, Kapvay®)
- Flecainide + 1, 2 (Tambocor®)
- Metoprolol + 1, 2, 44 (Lopressor®, Toprol XL®)
- Propafenone + 1, 2, 44 (Rythmol®)
- Propranolol + 1 (Inderal®)
- Timolol + 228 (Blocadren®)

### Moderate gene-drug interaction

- Aliskiren + 1 (Tekturna®)
- Amiodarone + 1 (Cordarone®, Pacerone®)
- Amlodipine + 1 (Norvasc®)
- Atorvastatin + 1, 17, 44, 162 (Lipitor®)
- Diltiazem + 1, 221 (Cardizem®, Cartia®)
- Disopyramide + 1 (Norpace®)
- Dofetilide + 1 (Tikosyn®)
- Dronedarone + 1, 221 (Multaq®)
- Eplerenone + 1 (Inspra®)
- Felodipine + 1 (Plendil®)
- Guanabenz − 33 (Wytensin®)
- Lidocaine + 39, 156 (Xylocaine®)
- Lomitapide + 1 (Juxtapid®)
- Lovastatin + 1 (Mevacor®)
- Nifedipine + 1, 221 (Adalat®, Nifedical®, Procardia®)
- Nisoldipine + 1, 221 (Sular®)
- Pravastatin 1, 148 (Pravachol®)
- Quinidine + 1 (Quin-G®)
- Ranolazine + 1 (Ranexa®)
- Simvastatin + 1, 44, 105, 171, 190, 221, 236 (Zocor®)

### Minimal gene-drug interaction

- Azilsartan 1 (Edarbi®)
- Fluvastatin 1 (Lescol®)
- Irbesartan 1 (Avapro®)
- Labetalol 25 (Trandate®)
- Losartan 1 (Cozaar®)
- Verapamil 1, 221 (Calan®, Verelan®)

### Limited pharmacogenetic impact

- Alirocumab (Praluent®)
- Colesevelam (Welchol®)
- Digoxin (Digitek®, Digox®, Lanoxin®)
- Gemfibrozil (Lopid®)
- Lisinopril (Prinivil®, Zestril®)
- Sotalol (Betapace®, Sorine®)
- Spironolactone (Aldactone®)
- Telmisartan (Micardis®)

## Endocrinology

### Major gene-drug interaction

### Moderate gene-drug interaction

- Ethinyl estradiol + 1, 2

### Minimal gene-drug interaction

- Chlorpropamide 1, 196
- Glimepiride 1 (Amaryl®)

### Limited pharmacogenetic impact

- Exenatide (Bydureon®, Byetta®)
- Ibandronate (Boniva®)

## Endocrinology (cont.)

### Major gene-drug interaction

### Moderate gene-drug interaction

### Minimal gene-drug interaction

- Glipizide 1, 98, 103, 219 (Glucotrol®)
- Glyburide 1 (Diabeta®, Micronase®)
- Nateglinide 1 (Starlix®)
- Tolbutamide 2

### Limited pharmacogenetic impact

- Insulin aspart (Novolog®)
- Insulin aspart protamine/ Insulin aspart (Novolog mix®)
- Insulin aspart/Insulin degludec (Ryzodeg 70/30®)
- Insulin degludec (Tresiba®)
- Insulin detemir (Levemir®)
- Insulin glargine (Lantus®, Toujeo®)
- Insulin glulisine (Apidra®)
- Insulin lispro (Humalog®)
- Insulin lispro protamine/ Insulin lispro (Humalog mix®)
- Insulin NPH (Humulin N®, Novolin N®)
- Insulin NPH/Insulin regular (Humulin 70/30®, Novolin 70/30®)
- Insulin regular (Humulin R®, Novolin R®)
- Insulin regular (oral inhalation) (Afrezza®)
- Levothyroxine (Levoxyl®, Synthroid®)
- Metformin (Fortamet®, Glucophage®)
- Pamidronate (Aredia®)
- Risedronate (Actonel®, Atelvia®)
- Vasopressin (Vasostrict®)

## Gastroenterology

### Major gene-drug interaction

- Dolasetron 1 (Anzemet®)

### Moderate gene-drug interaction

- Aprepitant 1, 140 (Cinvanti®, Emend®)
- Fosaprepitant 1, 140 (Emend Injection®)
- Lansoprazole 1, 2, 44, 94, 109, 115, 124, 215 (Prevacid®)
- Omeprazole 1, 2, 44, 48, 50, 52, 186, 194, 209, 215, 216, 253 (Prilosec®)
- Ondansetron 1, 15, 87, 224 (Zofran®)
- Rabeprazole 1, 44, 49, 61, 75, 112, 116, 157, 209, 212 (Aciphex®)

### Minimal gene-drug interaction

- Dexlansoprazole 1 (Dexilant®)
- Dronabinol 1 (Marinol®, Syndros®)
- Esomeprazole 1, 2, 44 (Nexium®)
- Pantoprazole 1, 2, 44 (Protonix®)

### Limited pharmacogenetic impact

## Genetic disease

### Major gene-drug interaction

- Eliglustat + 1 (Cerdelga®)

### Moderate gene-drug interaction

- Ivacaftor + 1 (Kalydeco®)

### Minimal gene-drug interaction

### Limited pharmacogenetic impact

- Sapropterin (Kuvan®)
- Sodium phenylbutyrate (Buphenyl®)
- Velaglucerase alfa 1 (Vpriv®)

## Hematology/Oncology

### Major gene-drug interaction

- Tamoxifen − 1, 2, 55 (Soltamox®)

### Moderate gene-drug interaction

- Axitinib + 1 (Inlyta®)
- Bortezomib + 1 (Velcade®)
- Bosutinib + 1 (Bosulif®)
- Brentuximab vedotin + 1 (Adcetris®)
- Cabazitaxel + 1 (Jevtana®)
- Crizotinib + 1 (Xalkori®)
- Dasatinib + 1 (Sprycel®)
- Docetaxel + 1 (Docefrez®, Taxotere®)
- Enzalutamide + 1 (Xtandi®)
- Erlotinib + 1, 81 (Tarceva®)
- Etoposide + 1, 255 (Toposar®)
- Everolimus + 1, 221 (Afinitor®, Zortress®)
- Exemestane + 1 (Aromasin®)
- Gefitinib + 1 (Iressa®)
- Ifosfamide − 1, 28 (Ifex®)
- Imatinib + 1 (Gleevec®)
- Irinotecan + 1, 2, 44, 45, 54, 104 (Camptosar®)
- Ixabepilone + 1 (Ixempra®)
- Lapatinib + 1, 187 (Tykerb®)
- Nilotinib + 1, 4 (Tasigna®)
- Paclitaxel + 1 (Abraxane®)
- Pazopanib + 1 (Votrient®)
- Ponatinib + 1 (Iclusig®)
- Regorafenib + 1 (Stivarga®)
- Ruxolitinib + 1 (Jakafi®)
- Sorafenib + 1 (Nexavar®)
- Sunitinib + 1 (Sutent®)
- Temsirolimus + 1 (Torisel®)

### Minimal gene-drug interaction

- Belinostat 1, 233 (Beleodaq®)
- Capecitabine 1, 2, 23 (Xeloda®)
- Fluorouracil 1, 2, 23 (Adrucil®)
- Mercaptopurine 1, 2, 176, 177 (Purixan®)
- Methotrexate 1, 170, 172, 220, 249 (Rheumatrex®)
- Thioguanine 1, 2, 176, 177 (Tabloid®)
- Vincristine 1, 221 (Vincasar®)

### Limited pharmacogenetic impact

- Afatinib 1 (Gilotrif®)
- Alemtuzumab 1 (Campath®, Lemtrada®)
- Darbepoetin alfa (Aranesp®)
- Epoetin alfa (Epogen®, Procrit®)
- Ibritumomab 1 (Zevalin®)
- Obinutuzumab 1 (Gazyva®)
- Ofatumumab 1 (Arzerra®)
- Panitumumab 1 (Vectibix®)
- Pertuzumab 1 (Perjeta®)

## Hematology/Oncology (cont.)

### Major gene-drug interaction

### Moderate gene-drug interaction

- Teniposide + 106, 178 (Vumon®)
- Trabectedin + 1 (Yondelis®)
- Vemurafenib + 1 (Zelboraf®)
- Vinorelbine + 1 (Navelbine®)

### Minimal gene-drug interaction

### Limited pharmacogenetic impact

## Immunosuppression

### Major gene-drug interaction

### Moderate gene-drug interaction

- Cyclosporine + 1 (Gengraf®, Neoral®, Sandimmune®)
- Everolimus + 1, 221 (Afinitor®, Zortress®)
- Sirolimus + 1 (Rapamune®)

### Minimal gene-drug interaction

- Azathioprine 1, 2, 122, 176, 177 (Imuran®)
- Tacrolimus 1, 16 (Prograf®)

### Limited pharmacogenetic impact

- Mycophenolate sodium (Myfortic®)

## Infectious disease

### Major gene-drug interaction

### Moderate gene-drug interaction

- Clarithromycin + 1, 221 (Biaxin®)
- Darunavir + 1 (Prezista®)
- Delavirdine + 1 (Rescriptor®)
- Erythromycin + 221 (E.E.S.®, Ery-Tab®)
- Fosamprenavir + 1 (Lexiva®)
- Indinavir + 1, 221 (Crixivan®)
- Isavuconazole + 1 (Cresemba®)
- Itraconazole + 1 (Onmel®, Sporanox®)
- Ivermectin + 1, 248 (Stromectol®)
- Ketoconazole + 1
- Maraviroc + 1 (Selzentry®)
- Mefloquine + 1 (Lariam®)
- Quinidine + 1 (Quin-G®)
- Quinine + 1, 221 (Qualaquin®)
- Ritonavir + 1 (Norvir®)
- Saquinavir + 1, 221 (Invirase®)
- Simeprevir + 1 (Olysio®)
- Telithromycin + 1 (Ketek®)
- Tipranavir + 1 (Aptivus®)

### Minimal gene-drug interaction

- Abacavir 1, 2, 46, 128, 129, 133, 134, 182, 210 (Ziagen®)
- Atazanavir 51, 82 (Reyataz®)
- Atovaquone/Proguanil 1 (Malarone®)
- Efavirenz 1 (Sustiva®)
- Nelfinavir 1 (Viracept®)
- Nevirapine 1 (Viramune®)
- Peginterferon alfa-2a-containing regimens 1, 142 (Pegasys®)
- Peginterferon alfa-2b-containing regimens 1, 142 (Pegintron®)
- Terbinafine 1 (Lamisil®)
- Voriconazole 1, 2 (Vfend®)

### Limited pharmacogenetic impact

- Atovaquone (Mepron®)
- Cefdinir (Omnicef®)
- Ceftriaxone (Rocephin®)
- Fluconazole (Diflucan®)
- Flucytosine (Ancobon®)
- Levofloxacin (Levaquin®)
- Meropenem (Merrem®)
- Moxifloxacin (Avelox®)
- Nystatin (Bio-Statin®)
- Piperacillin (Pipracil®)
- Posaconazole (Noxafil®)
- Vancomycin (Vancocin®)
- Zanamivir (Relenza®)

## Neurology

### Major gene-drug interaction

- Tetrabenazine + 1 (Xenazine®)

### Moderate gene-drug interaction

- Caffeine − 1 (No Doz®, Vivarin®)
- Dextromethorphan/ Quinidine + 1 (Nuedexta®)
- Donepezil + 1 (Aricept®)
- Eletriptan + 1 (Relpax®)
- Ethosuximide + 10, 163 (Zarontin®)
- Frovatriptan − 1 (Frova®)
- Rasagiline − 1 (Azilect®)
- Zonisamide + 1 (Zonegran®)

### Minimal gene-drug interaction

- Brivaracetam 1 (Briviact®)
- Carbamazepine 1, 5, 6, 30, 31, 70, 117, 130, 138, 139, 149, 161, 166, 169, 191, 246 (Carbatrol®, Tegretol®)
- Clobazam 1 (Onfi®)
- Eslicarbazepine 1, 6, 89, 166 (Aptiom®)
- Fosphenytoin 1, 2, 6, 22, 29, 130, 150 (Cerebyx®)
- Lamotrigine 1, 6, 130, 166 (Lamictal®)
- Oxcarbazepine 1, 6, 166 (Trileptal®)
- Phenytoin 1, 2, 6, 22, 29, 130, 150 (Dilantin®)
- Selegiline 66, 88, 185 (Eldepryl®, Emsam®)

### Limited pharmacogenetic impact

- Gabapentin (Neurontin®)
- Levetiracetam (Keppra®)
- Memantine (Namenda®)
- Pramipexole (Mirapex®)
- Pregabalin (Lyrica®)
- Succimer (Chemet®)
- Vigabatrin (Sabril®)

## Psychiatry

### Major gene-drug interaction

- Amitriptyline + 1, 2, 44, 64, 65, 235 (Elavil®)
- Aripiprazole + 1, 2 (Abilify®)
- Atomoxetine + 1, 2 (Strattera®)
- Brexpiprazole + 1 (Rexulti®)
- Chlorpromazine + 1, 160, 204 (Thorazine®)
- Clomipramine + 1, 2, 65 (Anafranil®)
- Desipramine + 1, 2, 65 (Norpramin®)
- Doxepin + 1, 2, 65 (Silenor®)
- Fluoxetine + 1, 57, 74, 80, 123, 131, 164, 174, 202, 243 (Prozac®, Sarafem®)
- Fluvoxamine + 1, 63, 79, 90, 91, 192, 193, 200, 201, 202, 211, 247 (Luvox®)
- Haloperidol + 1, 2, 159, 195, 226 (Haldol®)
- Iloperidone + 1 (Fanapt®)
- Imipramine + 1, 2, 65, 232 (Tofranil®)
- Nortriptyline + 1, 2, 65, 155, 227 (Pamelor®)
- Paroxetine + 1, 2, 44, 63 (Paxil®)

### Moderate gene-drug interaction

- Alprazolam + 1, 221 (Xanax®)
- Asenapine − 1 (Saphris®)
- Buspirone + 1, 221, 254 (Buspar®)
- Cariprazine + 1, 3, 20, 32, 145 (Vraylar®)
- Citalopram 1, 2, 7, 42, 44, 63, 67, 68, 74, 92, 93, 110, 114, 119, 137, 141, 158, 165, 168, 183 (Celexa®)
- Diazepam + 1, 77 (Valium®)
- Duloxetine + 1 (Cymbalta®)
- Flibanserin + 1 (Addyi®)
- Guanfacine + 1, 135 (Intuniv®, Tenex®)
- Levomilnacipran + 1 (Fetzima®)
- Lurasidone + 1 (Latuda®)
- Mirtazapine + 1, 2, 101, 125, 205, 218 (Remeron®)
- Nefazodone + 1, 180, 229 (Serzone®)
- Nicotine 34, 38, 85, 143 (Nicoderm C-Q®, Nicorette®, Nicotrol®)
- Olanzapine − 1, 2, 113, 127 (Zydis®, Zyprexa®)

### Minimal gene-drug interaction

- Amphetamine/ Dextroamphetamine mixed salts 1, 59, 73, 136 (Adderall®)
- Bupropion 1 (Wellbutrin®)
- Clozapine 1, 8, 12, 208 (Clozaril®)
- Dextroamphetamine 1, 59, 73, 136 (Dexedrine®)
- Escitalopram 1, 2, 7, 19, 42, 63, 68, 69, 74, 110, 119, 132, 141, 147, 168, 239 (Lexapro®)
- Lisdexamfetamine 1, 59, 73, 136 (Vyvanse®)
- Selegiline 66, 88, 185 (Eldepryl®, Emsam®)
- Sertraline 1, 2, 41, 43, 63, 123, 144, 146, 151, 175, 181, 223, 231 (Zoloft®)

### Limited pharmacogenetic impact

- Desvenlafaxine (Pristiq®)
- Lithium (Lithobid®)
- Milnacipran (Savella®)
- Paliperidone (Invega®)
- Varenicline (Chantix®)

## Psychiatry (cont.)

### Major gene-drug interaction

- Perphenazine + 1, 154 (Etrafon®)
- Pimozide + 1, 226 (Orap®)
- Protriptyline + 1 (Vivactil®)
- Risperidone + 1, 2, 72, 241 (Risperdal®)
- Thioridazine + 1
- Trimipramine + 1, 2, 65, 102 (Surmontil®)
- Venlafaxine + 1, 2, 230 (Effexor®)
- Vortioxetine + 1 (Trintellix®)

### Moderate gene-drug interaction

- Quetiapine + 1, 11, 99, 221, 225 (Seroquel®)
- Trazodone + 1 (Desyrel®)
- Vilazodone + 1, 18 (Viibryd®)

### Minimal gene-drug interaction

### Limited pharmacogenetic impact

## Rheumatology

### Major gene-drug interaction

### Moderate gene-drug interaction

- Cevimeline + 1 (Evoxac®)
- Colchicine + 1 (Colcrys®)
- Tofacitinib + 1 (Xeljanz®)

### Minimal gene-drug interaction

- Allopurinol 40, 62, 71, 96, 184 (Aloprim®, Zyloprim®)
- Lesinurad 1 (Zurampic®)
- Methotrexate 1, 170, 172, 220, 249 (Rheumatrex®)

### Limited pharmacogenetic impact

- Belimumab (Benlysta®)

## Sleep medicine

### Major gene-drug interaction

### Moderate gene-drug interaction

- Armodafinil + 1 (Nuvigil®)
- Eszopiclone + 1 (Lunesta®)
- Modafinil + 1 (Provigil®)
- Ramelteon − 1 (Rozerem®)
- Triazolam + 1, 221 (Halcion®)
- Zolpidem + 1, 13, 229 (Ambien®)

### Minimal gene-drug interaction

### Limited pharmacogenetic impact

- Temazepam (Restoril®)

## Urology

### Major gene-drug interaction

- Tamsulosin + 1 (Flomax®)
- Tolterodine + 1 (Detrol®)

### Moderate gene-drug interaction

- Darifenacin + 37, 95 (Enablex®)
- Fesoterodine + 1 (Toviaz®)
- Finasteride + 1 (Propecia®, Proscar®)
- Oxybutynin + 1 (Ditropan®, Oxytrol®)
- Sildenafil + 1 (Revatio®, Viagra®)
- Tadalafil + 1 (Adcirca®, Cialis®)

### Minimal gene-drug interaction

### Limited pharmacogenetic impact

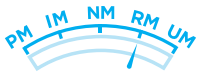
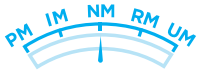
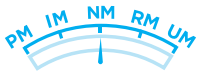
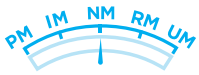
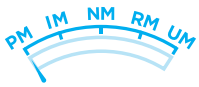
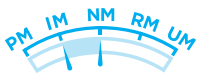
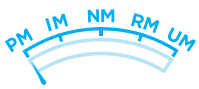
## Urology (cont.)

Major gene-drug interaction | Moderate gene-drug interaction | Minimal gene-drug interaction | Limited pharmacogenetic impact

- Vardenafil + 1 (Levitra®)

Genotype-derived classification of medications is provided as a service by OneOme and is intended solely for use by a medical professional who has reviewed and understands all sections within this report, including possible limitations of the services provided by OneOme. The relationships between the drugs and pharmacogenes annotated in this report are supported by scientific evidence that meets OneOme's critieria for inclusion. The order in which drugs are listed does not have any clinical or medical implications. Commonly used trade names for medications are listed for reference only. The list may not be inclusive of all trade names available and does not indicate preference or recommendation by OneOme of one medication product over another. For more information on these medications, for a list of additional medications curated but not annotated by OneOme, or to evaluate possible drug-to-drug interactions, please consult the RightMed Advisor, which is accessible through the provider portal at portal.oneome.com.

## Gene and phenotype summary

| Gene | Genotype | | Phenotype summary / Metabolic status |
|---|---|---|---|
| CYP1A2 | *1A/*1F |   | **Rapid**<br>Increased activity. Drugs converted to active metabolite(s) may cause side effects or toxicity. Active drugs converted to inactive metabolite(s) may lack efficacy. |
| CYP2B6 | *1/*1 |   | **Normal**<br>Normal level of activity. Drugs metabolized at a normal rate. |
| CYP2C9 | *1/*1 |   | **Normal**<br>Normal level of activity. Drugs metabolized at a normal rate. |
| CYP2C19 | *1/*1 |   | **Normal**<br>Normal level of activity. Drugs metabolized at a normal rate. |
| CYP2C Cluster | rs12777823 GG |  | **Normal**<br>Normal warfarin clearance associated with CYP2C rs12777823, independent of CYP2C9*2 and *3. CYP2C rs12777823, together with CYP4F2, CYP2C9, and VKORC1, influences response to warfarin therapy. |
| CYP2D6 | *4/*4 |   | **Poor**<br>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. |
| CYP3A4 | *1/*22 |   | **Intermediate to Normal**<br>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. |
| CYP3A5 | *3/*3 |   | **Poor**<br>Normal dosing may be required because original dosing guidelines for drugs have been established on patients with poor metabolizer phenotype. |
| CYP4F2 | *1/*3 |  | **Reduced activity**<br>Reduced activity of the CYP4F2 enzyme, which catalyzes the metabolism of vitamin K, in counterpoint to the activity of VKORC1. Impact of this variant on warfarin response has not been observed in individuals of West African ancestry. CYP4F2, together with CYP2C9, VKORC1, and a variant in CYP2C Cluster, influences response to warfarin therapy. |

## Gene and phenotype summary (cont.)

| | | | |
|---|---|---|---|
| COMT | rs4680 GA |  | **Intermediate activity**<br>COMT activity with GA (Val/Met) genotype is predicted to be lower than with GG (Val/Val) genotype, but higher than with AA (Met/Met) genotype at rs4680. |
| DPYD | *1/*1 |  | **Normal risk**<br>Normal metabolizer with a dihydropyrimidine dehydrogenase (DPD) activity score of 2. Fully functional DPD enzyme activity. Normal risk of toxicities related to the administration of fluoropyrimidines (5-fluorouracil, capecitabine, and tegafur). |
| DRD2 | rs1799978 AA |  | **Normal response**<br>Genotype is associated with a normal likelihood of improvement in schizophrenia symptoms with risperidone. Other clinical and/or genetic factors may influence the response. |
| F2 | rs1799963 GG |  | **Normal risk**<br>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**<br>Normal risk of thrombosis associated with Factor V. Other genetic and clinical factors contribute to the risk for thrombosis. |
| GRIK4 | rs1954787 TT |  | **Risk of reduced response**<br>Genotype predicts an 11% increase in the risk of not responding to citalopram in patients with major depressive disorder related to the GRIK4 genotype alone. Other clinical and genetic factors may influence response. |
| HLA-A | Negative |  | **Normal risk**<br>Negative for the presence of the HLA-A*31:01 allele. Normal risk of hypersensitivity induced by carbamazepine, and potentially by oxcarbazepine, eslicarbazepine, phenytoin, fosphenytoin, and lamotrigine. 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 has been associated with severe cutaneous reactions induced by certain antiepileptic agents. |

## Gene and phenotype summary (cont.)

| | | | |
|---|---|---|---|
| HLA-B | Negative |  | **Normal risk**<br>Negative for the presence of the HLA-B*15:02, HLA-B*57:01, and HLA-B*58:01 alleles. Normal risk of severe cutaneous reactions induced by carbamazepine, oxcarbazepine, eslicarbazepine, phenytoin, fosphenytoin, lamotrigine, and allopurinol. Normal risk of abacavir-induced hypersensitivity reaction. No increased risk of pazopanib-induced severe hepatotoxicity related to HLA-B*57:01 genotype. 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 has been associated with hypersensitivity reactions induced by carbamazepine and possibly other antiepileptic agents. |
| HTR2A | rs7997012 GG |  | **Intron 2 genotype GG**<br>Genotype predicts a 16-18% increased risk of non-response to citalopram related to the HTR2A genotype alone. Other clinical and genetic factors may influence response. |
| HTR2C | rs3813929 CC |  | **Normal risk**<br>Genotype predicts a normal risk of weight gain with clozapine or olanzapine treatment. Other clinical and/or genetic factors may influence response. The HTR2C gene is located on the X chromosome. In patients with only one X, result should read rs3813929 C;-. |
| IFNL4 | rs12979860 CC |  | **Normal response**<br>Genotype predicts a normal likelihood of sustained virologic response (SVR) with peginterferon-containing regimens. |
| NUDT15 | rs116855232 CC |  | **Normal risk**<br>No increased risk of severe toxicities with thiopurine administration related to the NUDT15 genotype. Toxicities with thiopurines can also occur due to impaired TPMT activity, regardless of the NUDT15 status. |
| OPRM1 | rs1799971 AA |  | **Asn/Asn isoform**<br>OPRM1 Asn/Asn (AA) genotype associated with normal to increased sensitivity to the analgesic effects of alfentanil, codeine, fentanyl, morphine, and tramadol compared to patients with the OPRM1 Asn/Asp (AG) or Asp/Asp (GG) genotypes at rs1799971. A class effect association of opioids and OPRM1 genotype has been suggested, however evidence for other opioids is limited. Additional studies are required for specific drug-gene pairs to confirm an association. |

## Gene and phenotype summary (cont.)

| | | | |
|---|---|---|---|
| SLC6A4 | L/S (La/Sa) |  | **Typical to reduced expression**<br>Genotype predicts typical to reduced expression of the SLC6A4 transporter compared to patients with the L/L (La/La) genotype. The L/S genotype has been associated with increased likelihood and potentially quicker response to the SSRI fluvoxamine and possibly citalopram and escitalopram compared with the S/S genotype. Genotype has been associated with reduced likelihood and potentially slower response to fluoxetine in Caucasian, Chinese, and South Indian populations. The opposite trend in response has been observed in East Asian populations, showing increased likelihood and potentially quicker response than in patients with the L/L (La/La) genotype. |
| SLCO1B1 | *1A/*21 |  | **Reduced response**<br>SLCO1B1 genotype consistent with decreased function of the OATP1B1 transporter. Unknown impact on risk of atorvastatin-induced myopathy. Impact on risk of simvastatin-induced myopathy is likely low but cannot be excluded. Increased pravastatin blood levels and reduced likelihood of response. Likely normal risk of methotrexate-induced toxicities when used at high dose. |
| TPMT | *1/*1 |  | **Normal risk**<br>Normal TPMT metabolizer. Normal risk of myelotoxicity associated with thiopurines (azathioprine, mercaptopurine, and thioguanine). Toxicities with thiopurines can also occur due to impaired NUDT15 activity independently from the TPMT status. |
| UGT1A1 | *1/*1 |  | **Normal risk**<br>Normal metabolizer with fully functional UGT1A1 enzyme activity. No increased risk for severe neutropenia while taking irinotecan or for toxicity and/or hyperbilirubinemia while taking atazanavir, nilotinib, pazopanib or belinostat. Consult drug labeling for dosing recommendations. |
| VKORC1 | rs9923231 GG |  | **Normal activity**<br>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, influences response to warfarin therapy. |

## CYP phenotype abbreviations

| | |
|---|---|
| **PM** | Poor metabolizer |
| **IM** | Intermediate metabolizer |
| **NM** | Normal metabolizer |
| **RM** | Rapid metabolizer |
| **UM** | Ultrarapid metabolizer |

# Test information

Specimen ID: **NA20200623006**
Specimen type: **DNA**
Collection date: **2020-06-20**
Receive date: **2020-06-23**

Clinical testing performed by:
**OneOme**
**807 Broadway St. NE Suite 100**
**Minneapolis, MN 55413**

Lab director: **Bronwyn R. Hartung, PhD**
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/*1F

| | | |
|---|---|---|
| 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 |
| rs762551 | NM_000761.4:c.-9-154C>A | CA |

## CYP2B6 *1/*1

| | | |
|---|---|---|
| rs3211371 | NM_000767.4:c.1459C>T | CC |
| rs3745274 | NM_000767.4:c.516G>T | GG |
| rs2279343 | NM_000767.4:c.785A>G | AA |
| rs28399499 | NM_000767.4:c.983T>C | TT |

## CYP2C9 *1/*1

| | | |
|---|---|---|
| rs28371685 | NM_000771.3:c.1003C>T | CC |
| rs1057910 | NM_000771.3:c.1075A>C | AA |
| rs56165452 | NM_000771.3:c.1076T>C | TT |
| rs28371686 | NM_000771.3:c.1080C>G | CC |
| rs1057911 | NM_000771.3:c.1425A>T | NO CALL |
| rs1799853 | NM_000771.3:c.430C>T | CC |
| rs7900194 | NM_000771.3:c.449G>A | GG |
| rs9332131 | NM_000771.3:c.817delA | AA |

## CYP2C19 *1/*1

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

## CYP2C Cluster rs12777823 GG

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

## CYP2D6 *4/*4

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

## CYP3A4 *1/*22

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

## CYP3A5 *3/*3

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

## CYP4F2 *1/*3

| | | |
|---|---|---|
| rs2108622 | NM_001082.4:c.1297G>A | GA |

## COMT rs4680 GA

| | | |
|---|---|---|
| rs4680 | NM_000754.3:c.472G>A | GA |

## DPYD *1/*1

| | | |
|---|---|---|
| rs55886062 | NM_000110.3:c.1679T>G | TT |
| rs3918290 | NM_000110.3:c.1905+1G>A | GG |
| rs67376798 | NM_000110.3:c.2846A>T | TT |

## 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

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

## HLA-A Negative

| | | |
|---|---|---|
| HLA00097 | NM_002116 (interrogated at exon 2) | Negative |

## Test results (cont.)

### HLA-B Negative

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

### HTR2A rs7997012 GG

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

### HTR2C rs3813929 CC

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

### IFNL4 rs12979860 CC

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

### NUDT15 rs116855232 CC

| | | |
|---|---|---|
| rs116855232 | NM_018283.3:c.415C>T | CC |

### OPRM1 rs1799971 AA

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

### SLC6A4 L/S (La/Sa)

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

### SLCO1B1 *1A/*21

| | | |
|---|---|---|
| rs4149015 | NM_006446.4:c.-910G>A | GA |
| rs2306283 | NM_006446.4:c.388A>G | GA |
| rs4149056 | NM_006446.4:c.521T>C | TT |

### TPMT *1/*1

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

### UGT1A1 *1/*1

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

### VKORC1 rs9923231 GG

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

## Methodology and limitations

Analytical results were produced using tests developed and validated 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. 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. Less frequent haplotypes or novel alleles may be reported when appropriate.

| | |
|---|---|
| CYP1A2 | *1C, *1D, *1E, *1F, *1J, *1K, *1L, *1V, *1W |
| CYP2B6 | *4, *5, *6, *7, *9, *16, *18 |
| 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, *20, *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, *13 |
| SLCO1B1 | *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.

The variant detection methods validated by OneOme provide >99.9% accuracy; however, 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 also 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.” Test results and clinical interpretation may be inaccurate for individuals 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.

Due to the complexity of interpreting some genetic test results, such as those 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 through the website or by calling 844-663-6635.

## OneOme liability disclaimer

The interpretations and clinical annotations provided by OneOme are intended solely for use by a medical professional 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, including information from and guidelines published by professional associations (e.g., CPIC, FDA, DPWG), and does not take into account other genetic variants and environmental or social factors that may affect a patient's response. 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, including the ones listed in the OneOme reports, requires careful therapeutic monitoring regardless of the phenotype or genotype-predicted interaction reported. As a matter of practice, OneOme will routinely update its pharmacogenomic database as new information becomes available to the scientific community. Genotype-predicted interactions and annotations found on the patient's RightMed Comprehensive Test Report, RightMed Advisor Reports, or RightMed specialty reports are therefore dependent on the date of generation and/or the database version used to generate that report. Providers may access these reports with updated annotations using OneOme's latest released version through the provider portal at portal.oneome.com.

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