

University of Pennsylvania Pharmacogenomic Program Epic Genomic Indicator language

Genomic Indicator Name	Description
CYP2B6 Intermediate Metabolizer	The CYP2B6 enzyme contributes to the metabolism of clinically relevant drugs including efavirenz and sertraline.
CYP2B6 Normal Metabolizer	The CYP2B6 enzyme contributes to the metabolism of clinically relevant drugs including efavirenz and sertraline.
CYP2B6 Poor Metabolizer	The CYP2B6 enzyme contributes to the metabolism of clinically relevant drugs including efavirenz and sertraline.
CYP2B6 Rapid Metabolizer	The CYP2B6 enzyme contributes to the metabolism of clinically relevant drugs including efavirenz and sertraline.
CYP2B6 Ultrarapid Metabolizer	The CYP2B6 enzyme contributes to the metabolism of clinically relevant drugs including efavirenz and sertraline.
CYP2C19 Intermediate Metabolizer	The CYP2C19 enzyme contributes to the metabolism of a large number of clinically relevant drugs and drug classes such as antidepressants, voriconazole, proton pump inhibitors (PPIs) and clopidogrel.
CYP2C19 Normal Metabolizer	The CYP2C19 enzyme contributes to the metabolism of a large number of clinically relevant drugs and drug classes such as antidepressants, voriconazole, proton pump inhibitors (PPIs) and clopidogrel.
CYP2C19 Poor Metabolizer	The CYP2C19 enzyme contributes to the metabolism of a large number of clinically relevant drugs and drug classes such as antidepressants, voriconazole, proton pump inhibitors (PPIs) and clopidogrel.
CYP2C19 Rapid Metabolizer	The CYP2C19 enzyme contributes to the metabolism of a large number of clinically relevant drugs and drug classes such as antidepressants, voriconazole, proton pump inhibitors (PPIs) and clopidogrel.
CYP2C19 Ultrarapid Metabolizer	The CYP2C19 enzyme contributes to the metabolism of a large number of clinically relevant drugs and drug classes such as antidepressants, voriconazole, proton pump inhibitors (PPIs) and clopidogrel.
CYP2C9 Intermediate Metabolizer	The CYP2C9 enzyme contributes to the metabolism of clinically relevant drugs and drug classes such as nonsteroidal anti-inflammatory drugs, phenytoin, warfarin and siponimod
CYP2C9 Normal Metabolizer	The CYP2C9 enzyme contributes to the metabolism of clinically relevant drugs and drug classes such as nonsteroidal anti-inflammatory drugs, phenytoin, warfarin and siponimod
CYP2C9 Poor Metabolizer	The CYP2C9 enzyme contributes to the metabolism of clinically relevant drugs and drug classes such as nonsteroidal anti-inflammatory drugs, phenytoin, warfarin and siponimod
CYP2D6 Intermediate Metabolizer	The CYP2D6 enzyme contributes to the metabolism of a large number of clinically relevant drugs and drug classes such as antidepressants, antiemetics and opioid analgesics.
CYP2D6 Needs Review	Please review CYP2D6 test results and manually apply the appropriate Genomic Indicator
CYP2D6 Normal Metabolizer	The CYP2D6 enzyme contributes to the metabolism of a large number of clinically relevant drugs and drug classes such as antidepressants, antiemetics and opioid analgesics.
CYP2D6 Poor Metabolizer	The CYP2D6 enzyme contributes to the metabolism of a large number of clinically relevant drugs and drug classes such as antidepressants, antiemetics and opioid analgesics.
CYP2D6 Ultrarapid Metabolizer	The CYP2D6 enzyme contributes to the metabolism of a large number of clinically relevant drugs and drug classes such as antidepressants, antiemetics and opioid analgesics.
CYP3A5 Intermediate Metabolizer	The CYP3A5 enzyme contributes to the metabolism of the immunosuppressant drug tacrolimus
CYP3A5 Normal Metabolizer	The CYP3A5 enzyme contributes to the metabolism of the immunosuppressant drug tacrolimus
CYP3A5 Poor Metabolizer	The CYP3A5 enzyme contributes to the metabolism of the immunosuppressant drug tacrolimus
DPYD Intermediate Metabolizer	The DPYD gene contributes to the metabolism of fluorouracil and capecitabine.
DPYD Normal Metabolizer	The DPYD gene contributes to the metabolism of fluorouracil and capecitabine.
DPYD Poor Metabolizer	The DPYD gene contributes to the metabolism of fluorouracil and capecitabine.
HLA-A*31:01 Negative	HLA-A*31:01 is associated with a severe cutaneous adverse reaction to carbamazepine
HLA-A*31:01 Positive	HLA-A*31:01 is associated with a severe cutaneous adverse reaction to carbamazepine
HLA-B*15:02 Negative	HLA-B*15:02 is associated with a severe cutaneous adverse reaction to carbamazepine, oxcarbazepine, phenytoin, and fosphenytoin
HLA-B*15:02 Positive	HLA-B*15:02 is associated with a severe cutaneous adverse reaction to carbamazepine, oxcarbazepine, phenytoin, and fosphenytoin
HLA-B*57:01 Negative	HLA-B*57:01 is associated with a hypersensitivity reaction to abacavir
HLA-B*57:01 Positive	HLA-B*57:01 is associated with a hypersensitivity reaction to abacavir

HLA-B*58:01 Negative	HLA-B*58:01 is associated with a severe cutaneous adverse reaction to allopurinol
HLA-B*58:01 Positive	HLA-B*58:01 is associated with a severe cutaneous adverse reaction to allopurinol
IFNL4 Favorable response genotype	The IFNL4 gene variation is the strongest baseline predictor of treatment response to peginterferon alpha containing regimens for hepatitis C treatment. (Some references refer to this gene as IFNL3)
IFNL4 Unfavorable response genotype	The IFNL4 gene variation is the strongest baseline predictor of treatment response to peginterferon alpha containing regimens for hepatitis C treatment. (Some references refer to this gene as IFNL3)
NUDT15 Intermediate Metabolizer	The NUDT15 gene encodes an enzyme that contributes to the metabolism of thiopurines (azathioprine, mercaptopurine, and thioguanine)
NUDT15 Normal Metabolizer	The NUDT15 gene encodes an enzyme that contributes to the metabolism of thiopurines (azathioprine, mercaptopurine, and thioguanine)
NUDT15 Poor Metabolizer	The NUDT15 gene encodes an enzyme that contributes to the metabolism of thiopurines (azathioprine, mercaptopurine, and thioguanine)
NUDT15 Possible Intermediate Metabolizer	The NUDT15 gene encodes an enzyme that contributes to the metabolism of thiopurines (azathioprine, mercaptopurine, and thioguanine)
SLCO1B1 Decreased Function	The SLCO1B1 gene encodes a transporter protein that is involved with the cellular influx of HMG-CoA reductase inhibitors (statins).
SLCO1B1 Increased Function	The SLCO1B1 gene encodes a transporter protein that is involved with the cellular influx of HMG-CoA reductase inhibitors (statins).
SLCO1B1 Normal Function	The SLCO1B1 gene encodes a transporter protein that is involved with the cellular influx of HMG-CoA reductase inhibitors (statins).
SLCO1B1 Poor Function	The SLCO1B1 gene encodes a transporter protein that is involved with the cellular influx of HMG-CoA reductase inhibitors (statins).
SLCO1B1 Possible Decreased Function	The SLCO1B1 gene encodes a transporter protein that is involved with the cellular influx of HMG-CoA reductase inhibitors (statins).
TPMT Intermediate Metabolizer	The TPMT gene encodes an enzyme that contributes to the metabolism of thiopurines (azathioprine, mercaptopurine, and thioguanine).
TPMT Normal Metabolizer	The TPMT gene encodes an enzyme that contributes to the metabolism of thiopurines (azathioprine, mercaptopurine, and thioguanine).
TPMT Poor Metabolizer	The TPMT gene encodes an enzyme that contributes to the metabolism of thiopurines (azathioprine, mercaptopurine, and thioguanine).
TPMT Possible Intermediate Metabolizer	The TPMT gene encodes an enzyme that contributes to the metabolism of thiopurines (azathioprine, mercaptopurine, and thioguanine).
TPMT Rapid Metabolizer	The TPMT gene encodes an enzyme that contributes to the metabolism of thiopurines (azathioprine, mercaptopurine, and thioguanine).
UGT1A1 Intermediate Metabolizer	The UGT1A1 enzyme contributes to the metabolism of irinotecan and atazanavir.
UGT1A1 Normal Metabolizer	The UGT1A1 enzyme contributes to the metabolism of irinotecan and atazanavir.
UGT1A1 Poor Metabolizer	The UGT1A1 enzyme contributes to the metabolism of irinotecan and atazanavir.