

Client: Example Client ABC123  
 123 Test Drive  
 Salt Lake City, UT 84108  
 UNITED STATES

Physician: Doctor, Example

**Patient: Patient, Example**

**DOB:** 2/2/1995  
**Gender:** Female  
**Patient Identifiers:** 01234567890ABCD, 012345  
**Visit Number (FIN):** 01234567890ABCD  
**Collection Date:**

**UDP Glucuronosyltransferase 1A1 (UGT1A1) Genotyping**

ARUP test code 0051332

UGT1A1 Genotyping Specimen	whole Blood
UGT1A1 Genotyping Allele 1	(TA)7 or *28 *
UGT1A1 Genotyping Allele 2	(TA)7 or *28 *
UGT1A1 Genotyping Interpretation	See Note

Indications for ordering:  
 - Determine sensitivity to irinotecan or related compounds.  
 - Confirm a diagnosis of Gilbert Syndrome.

Homozygous UGT1A1 (TA)7: Two copies of the UGT1A1 \*28 (TA)7 variant were detected. This is associated with decreased UGT1A1 enzyme and increased risk for irinotecan toxicity, namely, neutropenia and diarrhea. Dose reduction is recommended. This genotype has been reported to be associated with Gilbert's syndrome (benign familial hyperbilirubinemia).

This result has been reviewed and approved by Rong Mao, M.D.

H=High, L=Low, \*=Abnormal, C=Critical

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**BACKGROUND INFORMATION:** UDP Glucuronosyltransferase 1A1 (UGT1A1) Genotyping

**CHARACTERISTICS:** UGT1A1 is responsible for the clearance of drugs (e.g., irinotecan) and endobiotic compounds (e.g., bilirubin). Irinotecan's major active and toxic metabolite (SN-38) is inactivated by the UGT1A1 enzyme and then eliminated via the bile. UGT1A1 gene mutations cause accumulation of SN-38, which may lead to irinotecan-related toxicities (neutropenia, diarrhea).

**CAUSE:** Variations in TA repeat number in the TATAAA element of the 5'UGT1A1-promoter affects transcription efficiency. The common number of repeats is six [(TA)6, \*1 allele], while seven repeats [(TA)7, \*28 allele] is associated with reduced transcription activity. Homozygosity for the (TA)7 allele is also associated with Gilbert Syndrome (benign familial hyperbilirubinemia).

**ALLELES TESTED:** \*36 allele, (TA)5; \*1 allele, (TA)6; \*28 allele, (TA)7 and \*37 allele, (TA)8.

**CLINICAL SENSITIVITY/SPECIFICITY:** Risk of irinotecan toxicity by genotype (Br J Cancer (2004) 91:678-82).

6/6 (\*1/\*1): diarrhea 17 percent; neutropenia 15 percent

6/7 (\*1/\*28): diarrhea 33 percent; neutropenia 27 percent

7/7 (\*28/\*28): diarrhea 70 percent; neutropenia 40 percent

**ALLELIC FREQUENCY:**

\*1(TA)6: Caucasians 0.61, Asians 0.84, African Americans 0.47

\*28(TA)7: Caucasians 0.39, Asians 0.16, African Americans 0.43

**METHODOLOGY:** Polymerase chain reaction followed by size analysis using capillary electrophoresis.

**ANALYTICAL SENSITIVITY:** Greater than 99 percent.

**LIMITATIONS:** Variations in the UGT1A1 gene, other than those targeted, will not be detected. Clinical significance of the rare \*36, (TA)5 and \*37, (TA)8 alleles in predicting irinotecan toxicities is not well established. Genetic and non-genetic factors other than UGT1A1, may contribute to irinotecan toxicity and efficacy. Diagnostic errors can occur due to rare sequence variations.

Test developed and characteristics determined by ARUP Laboratories. See Compliance Statement C: aruplab.com/CS

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VERIFIED/REPORTED DATES

Procedure	Accession	Collected	Received	Verified/Reported
UGT1A1 Genotyping Specimen	18-178-108910	6/27/2018 12:02:00 PM	6/28/2018 11:01:41 AM	7/1/2018 5:52:00 PM
UGT1A1 Genotyping Allele 1	18-178-108910	6/27/2018 12:02:00 PM	6/28/2018 11:01:41 AM	7/1/2018 5:52:00 PM
UGT1A1 Genotyping Allele 2	18-178-108910	6/27/2018 12:02:00 PM	6/28/2018 11:01:41 AM	7/1/2018 5:52:00 PM
UGT1A1 Genotyping Interpretation	18-178-108910	6/27/2018 12:02:00 PM	6/28/2018 11:01:41 AM	7/1/2018 5:52:00 PM

END OF CHART

H=High, L=Low, \*=Abnormal, C=Critical