

Investigate and confirm pharmacogenetic biomarkers in *CYP2D6* associated with drug metabolism with high accuracy and rapid results.

The iPLEX® ADME CYP2D6 Panel v1.0, developed by Assays by Agena for use on the MassARRAY System, is a set of 35 pre-designed and pre-verified SNP assays for use in the screening of polymorphisms in *CYP2D6*. Screening for variants in *CYP2D6* allows clinical researchers to develop dosing protocols and surveillance techniques for model drugs and experimental biomarkers.

- Analyze 35 mutations in the pharmacogenetically relevant CYP2D6 gene.
- Perform high value CNV analysis using 5 CNV assays.
- Obtain biologically relevant data covering most of the known *CYP2D6* haplotypes.
- Use as little as 30 ng of DNA per sample.
- Use included AMELX/Y marker to assist in sample identification.
- Use included iPLEX WorkFlow Controls to assist in troubleshooting failed wells.

Agena Bioscience also offers the iPLEX ADME PGx Pro Panel, covering 36 key genes known to influence drug ADME/T, as well as panels for in-depth analysis of *CYP2C19* and *CYP2C9/VKORC1*. See *www.agenabio.com/pharmacogenomics* for more information.

# HAPLOTYPES<sup>1</sup> INCLUDED IN THE iPLEX ADME CYP2D6 PANEL v1.0

\*1, (\*2;\*28;\*32;\*55;\*59)<sup>2</sup>, (\*2A;\*31;\*51), \*2D, (\*2L;\*45B;\*46), \*2M, \*3, \*4, \*4B, \*4J, \*4K, \*4M, \*4N;P, \*5<sup>3</sup>,\*6, \*6C, \*7, \*8, \*9, (\*10A;\*37;\*54), (\*10B;\*47;\*49;\*52;\*72), \*11, \*12, \*14A, \*14B, \*15, \*17, \*18, \*19, \*20, \*21<sup>a</sup>, \*21B, \*27, \*29, \*30, \*34, \*35, \*36, \*38, \*39, \*40, \*41, \*42, \*44, \*45A, \*56A, \*56B, \*57, \*58, \*63, \*64, \*65, \*68, \*69, \*70, \*71, \*82, \*83, \*84

Disclaimer: CNV for different alleles (\*NxN) uses incorporated CNV assays and needs Excel file provided. Nomenclature is based on http://www.cypalleles.ki.se/cyp2d6.htm

<sup>1</sup>Rare haplotypes may only be validated for wild type allele.

<sup>2</sup>Haplotypes represented by mutations not present in the ADME CYP2D6 Panel are considered \*1. Also haplotypes that are indistinguishable are grouped with most likely haplotype in front.

<sup>3</sup> The ADME CYP2D6 Panel only detects the number of CYP2D6 copies present. It does not identify samples where a duplication of one allele AND a deletion of another allele is present (e.g., \*2x2/\*5 is called \*2/\*2).



vΑ



## CYP2D6 ALLELE NOMENCLATURE

ALLELE	NUCLEOTIDE CHANGES	AMINO ACID CHANGE	dbSNP IDs	CNV ASSAYS
*1	None	None		
*1XN	None	N active		CNV>2
*2;*28;*32;*59	1661G>C; 2850C>T; 4180G>C	R296C; S486T	rs1058164; rs16947; rs1135840	
*2A;*31;*51	-1584C>G; -1235A>G; 1661G>C; 2850C>T; 4180G>C	R296C; S486T	rs1080985; rs28735595; rs1058164; rs16947; rs1135840	
*2D	2850C>T; 4180G>C	R296C; S486T	rs16947; rs1135840	
*2L;*45B;*46	-1584C; -1235A>G; 1661G>C; 2850C>T; 3790C>T; 4180G>C	R296C; S486T	rs1080985; rs28735595; rs1058164; rs16947; rs28371731; rs1135840	
*2M;*31	-1584C; -1235A>G; 214G>C; 1661G>C; 2850C>T; 3790C>T; 4180G>C	R296C; S486T	rs1080985; rs28735595; rs1080995; rs1058164; rs16947; rs28371731; rs1135840	
*2XN (N=2, 3, 4, 5 or 13)	1661G>C; 2850C>T; 4180G>C	R296C; S486T	rs1058164; rs16947; rs1135840	CNV>2
*3	2549delA	259Frameshift	rs35742686	
*4	100C>T; 1661G>C; 1846G>A; 4180G>C	P34S; splicing defect; S486T	rs1065852; rs1058164; rs3892097; rs1135840	
*4B	100C>T; 1846G>A; 4180G>C	P34S; splicing defect; S486T	rs1065852; rs3892097; rs1135840	
*4J	100C>T; 1661G>C; 1846G>A	P34S; splicing defect	rs1065852; rs1058164; rs3892097	
*4К	100C>T; 1661G>C; 1846G>A; 2850C>T; 4180G>C	P34S; splicing defect; R296C; S486T	rs1065852; rs1058164; rs3892097; rs16947; rs1135840	
*4M	-1235A>G; 1661G>C; 1846G>A;	splicing defect	rs28735595; rs1058164; rs3892097	
*4N;*4P	-1416C>T; -1235A>G; 100C>T; 1661G>C; 1846G>A; 4180G>C; exon 9 conversion	P34S; splicing defect; S486T	Rs28588594; rs28735595; rs1065852; rs1058164; rs3892097; rs1135840	
*4XN	See CYP2D6*4			CNV>2
*5	CYP2D6 deleted	CYP2D6 deleted		CNV<2
*6	1707delT	118Frameshift	rs5030655	
*6C	1707delT; 4180G>C	118Frameshift; S486T	rs5030655; rs1135840	
*7	2935A>C	H324P	rs5030867	
*8	1661G>C; 1758G>T; 2850C>T; 4180G>C	G169X; R296C; S486T	rs1058164; rs5030865; rs16947; rs1135840	
*9	2615_2617deIAAG	K281del	rs5030656	
*9x2	2615_2617delAAG	K281del	rs5030656	CNV>2
*10;*37;*54	100C>T; 1661G>C; 4180G>C	P34S; S486T	rs1065852; rs1058164; rs1135840	
*10B; *47; *49; *52; *72	-1416C>T; -1235A>G; 100C>T; 1661G>C; 4180G>C	P34S; S486T	rs28588594; rs28735595; rs1065852; rs1058164; rs1135840	
*10X2	See CYP2D6*10A			CNV>2
*11	883G>C; 1661G>C; 2850C>T; 4180G>C	Splicing defect; R296C; S486T	rs5030863; rs1058164; rs16947; rs1135840	
*12	124G>A; 1661G>C; 2850C>T; 4180G>C	G42R; R296C; S486T	rs5030862; rs1058164; rs16947; rs1135840	
*14A	100C>T; 1758G>A; 2850C>T; 4180G>C	P34S; G169R; R296C; S486T	rs1065852; rs5030865; rs16947; rs1135840	
*14B	214G>C;1661G>C; 1758G>A; 2850C>T; 4180G>C	G169R; R296C; S486T	rs1080995;rs1058164; rs5030865; rs16947; rs1135840	
*15	137_138insT	46Frameshift	rs72549357	
*17	1023C>T; 1661G>C; 2850C>T; 4180G>C	T107I; R296C; S486T	rs28371706; rs1058164; rs16947; rs1135840	
*17XN	See CYP2D6*17			
*18	4125_4133dupGTGCCCACT	468_470dupVPT	G4125_4133T	
*19	1661G>C; 2539_2542delAACT; 2850C>T; 4180G>C	255Frameshift; R296C; S486T	rs1058164; rs72549353; rs16947; rs1135840	

ALLELE	NUCLEOTIDE CHANGES	AMINO ACID CHANGE	dbSNP IDs	CNV ASSAYS
*20	1661G>C; 1973_1974insG; 2850C>T; 4180G>C	211Frameshift; R296C; S486T	rs1058164; rs72549354; rs16947; rs1135840	
*21A	-1584C>G; -1416C>T; -1235A>G; 1661G>C; 2573_2574insC; 2850C>T; 4180G>C	267Frameshift; R296C; S486T	rs1080985; rs28588594; rs28735595; rs1058164; rs72549352; rs16947; rs1135840	
*21B	-1584C>G; -1235A>G; 214G>C; 1661G>C; 2573_2574insC; 2850C>T; 4180G>C	267Frameshift; R296C; S486T	rs1080985; rs28735595; rs1080995; rs1058164; rs72549352; rs16947; rs1135840	CNV>2
*29	1659G>A; 1661G>C; 2850C>T; 4180G>C	V136l; R296C; V338M; S486T	rs61736512; rs1058164; rs16947; rs1135840	
*30	1661G>C; 1863_1864insTTTCGCCCC; 2850C>T; 4180G>C	174_175insFRP; R296C; S486T	rs1058164; rs72549356; rs16947; rs1135840	
*34	2850C>T	R296C	rs16947	
*35	-1584C>G; 31G>A; 1661G>C; 2850C>T; 4180G>C	V11M; R296C; S486T	rs1080985; rs769258; rs1058164; rs16947; rs1135840	
*35X2	31G>A; 1661G>C; 2850C>T; 4180G>C	V11M; R296C; S486T	rs769258; rs1058164; rs16947; rs1135840	
*36	-1416C>T; 100C>T; 1661G>C; 4180G>C; exon 9 conversion	P34S; S486T	rs28588594; rs1065852; rs1058164; rs1135840	
*38	2587_2590delGACT	271Frameshift	rs72549351	CNV>2
*39	1661G>C; 4180G>C	S486T	rs1058164; rs1135840	CNV<2
*40	1023C>T; 1661G>C; 1863_1864insTTTCGCCCCx2; 2850C>T; 4180G>C	T107l; 174_175insFRPx2; R296C; S486T	rs28371706; rs1058164; rs72549356; rs16947; rs1135840	
*41	-1584C; -1235A>G; 214G>C; 1661G>C; 2850C>T; 2988G>A; 4180G>C	R296C; splicing defect; S486T	rs1080985; rs28735595;rs1080995; rs1058164; rs16947; rs28371725; rs1135840	
*42	-1584C; 1661G>C; 2850C>T; 3259_3260insGT; 4180G>C	R296C; 363Frameshift; S486T	rs1080985; rs1058164; rs16947; rs72549346; rs1135840	
*44	2950G>C	Splicing defect	rs72549349	
*45A	-1584C; 1661G>C; 2850C>T; 3790C>T; 4180G>C	R296C; S486T	rs1080985; rs1058164; rs16947; rs28371731; rs1135840	
*56A	-1584C>G; -1235A>G; 214G>C; 1661G>C; 2850C>T; 3201C>T; 3790C>T; 4180G>C	R296C; R344X; S486T	rs1080985; rs28735595; rs1080995; rs1058164; rs16947; rs72549347; rs28371731; rs1135840	CNV>2
*56B	-1235A>G; 100C>T; 1661G>C; 3201C>T; 4180G>C	P34S; R344X; S486T	rs28735595; rs1065852; rs1058164; rs72549347; rs1135840	
*57	-1416C>T; 100C>T; 1661G>C; 4180G>C; exon 9 conversion	P34S; S486T	rs28588594; rs1065852; rs1058164; rs1135840	
*58	-1416C>T; -1235A>G; 214G>C; 1023C>T; 1661G>T; 1863_1864insTTTCGCCCC; 2850C>T; 2850C>T; 3790C>T; 4180G>C	T107l; 174_175insFRP; R296C; S486T	rs28588594; rs28735595; rs1080995; rs28371706; rs1058164; rs72549356; rs16947; rs28371731; rs1135840	CNV>2
*63	-1584C>G; -1235A>G; 214G>C; 1661G>C; 2850C>T; 3790C>T	R296C; S486T	rs1080985; rs28735595; rs1080995; rs1058164; rs16947; rs28371731	
*64	-1416C>T; -1235A>G; 100C>T; 1023C>T; 1661G>C; 4180G>C;	P34S; T107I; S486T	rs28588594; rs28735595; rs1065852; rs28371706; rs1058164; rs1135840	
*65	100C>T; 1661G>C; 2850C>T; 3790C>T; 4180G>C	P34S; R296C; S486T	rs1065852; rs1058164; rs16947; rs28371731; rs1135840	
*68	-1416C>T; -1235A>G; 100C>T	P34S;	rs28588594; rs28735595; rs1065852	
*69	-1416C>T; -1235A>G; 100C>T; 1661G>C; 2850C>T; 2988G>A; 3790C>T; 4180G>C	P34S; R296C; splicing defect; S486T	rs28588594; rs28735595; rs1065852; rs1058164; rs16947; rs28371725; rs28371731; rs1135840	
*70	1659G>A; 1661G>C; 4180G>C	V136I; S486T	rs61736512; rs1058164; rs1135840	
*71	-1584C>G		rs1080985	
*82	1023C>T	T107Y	rs28371706	
*83	4180G>C; exon 9 conversion	S486T	rs1135840	
*84	-1235A>G; 214G>C; 1661G>C; 2850C>T; 3790C>T; 4180G>C	R296C; S486T	rs28735595; rs1080995; rs1058164; rs16947; rs28371731; rs1135840	

## THE MASSARRAY WORKFLOW

Each sample is subjected to PCR amplification and primer extension with the iPLEX ADME CYP2D6 reagents. The extension products are dispensed onto a SpectroCHIP® Array and detected via MassARRAY MALDI-TOF mass spectrometry. After the sample run, an automated software report provides the calls and mutation frequency for each sample as well as a confidence score.

#### THROUGHPUT

The iPLEX ADME CYP2D6 Panel v1.0 contains multiplexed assays in 3 wells, using 10 ng of input DNA per well. The panel can be run in 96-well format (32 samples per plate) or 384-format (128 samples per plate). Thirty-two to 1,024 samples can be processed per day, providing flexibility in sample throughput and batching requirements.

## **ORDERING INFORMATION**

Choose the best approach for you:

- Order the iPLEX ADME CYP2D6 Panel v1.0 components and run on your own MassARRAY System.
- Send your samples to our Assays by Agena Custom Services Laboratory and have our experienced scientists run the panel for you.

Please contact Agena Bioscience for more information.

#### COMPONENTS FOR RUNNING THE IPLEX ADME CYP2D6 PANEL v1.0





**Left:** Example of copy number plot for 48 samples run in quadruplicate. All repeats show up in same copy number group.

**Right:** Picture of the WorkFlow Controls showing adequate addition of PCR, SAP, and Extend cocktails to the sample reaction.

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Agena Bioscience's patented nucleic acid analysis by mass spectrometry methods and products are protected under United States patent rights including but not limited to 5,869,242; 6,024,925; 6,238,871; 6,258,538; 6,300,076; 6,440,705; 6,500,621; 6,558,623; 6,569,385; 6,979,425; 6,994,969; 7,019,288; 7,025,933; 7,285,422; 7,332,275; 7,390,672; 7,419,787; 7,501,251; 7,880,127; 8,003,317; 8,034,567; 8,315,805; and 8,349,566 and patents pending including but not limited to US20050272070 and US20130017960, and foreign counterparts including but not limited to, EP0815261B1, EP173622B1, EP1727911B1, EP1546385B1, EP1332000B1, EP1613723B1, EP1660680B1, and EP2107129B1.

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