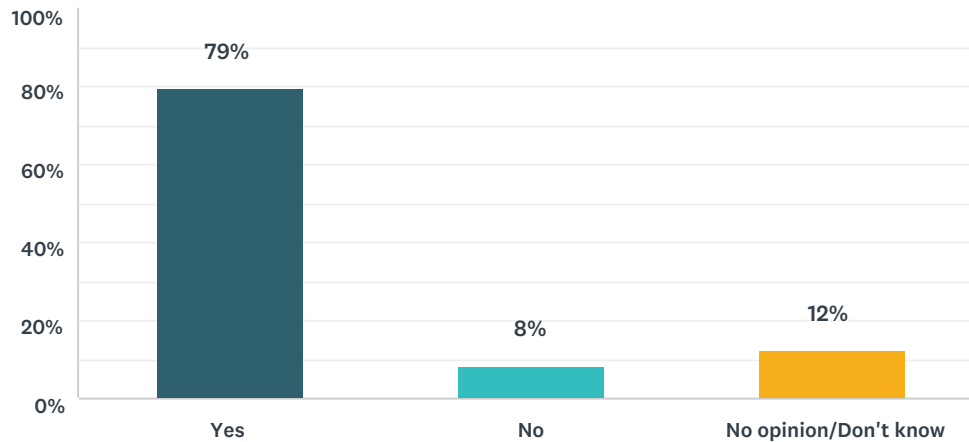


**Q1 We assume that 3 major categories of allele function are needed for TPMT and DPYD. Do you agree (yes or no)? If no, please indicate how many you think are needed and why:**

Answered: 73 Skipped: 4

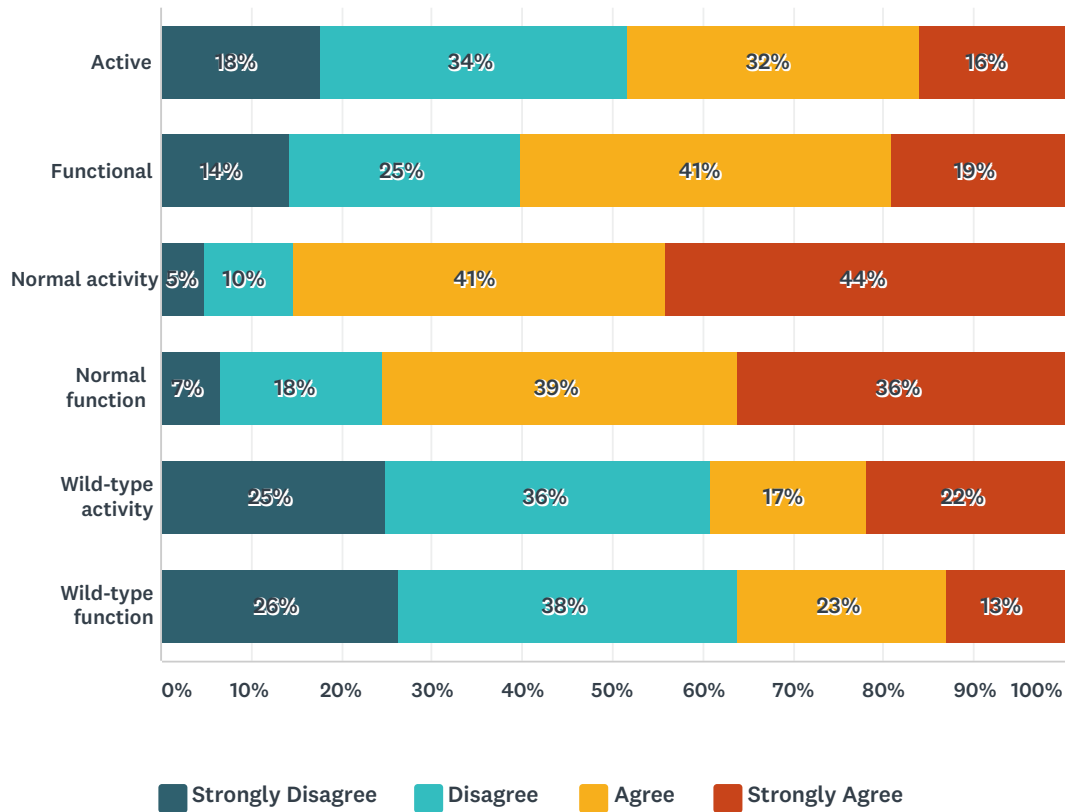


ANSWER CHOICES	RESPONSES	
Yes	79%	58
No	8%	6
No opinion/Don't know	12%	9
<b>TOTAL</b>		<b>73</b>

#	IF NO, PLEASE INDICATE HOW MANY YOU THINK ARE NEEDED AND WHY:	DATE
1	Need an unknown allele function	2/20/2015 5:33 PM
2	Possibly 4 to include UM due to some literature suggesting increased activity associated with methylated products leading to clinical presentation. Although rare, it may be pertinent with advancement of technology and new SNPs?	2/19/2015 3:41 PM
3	Though I wonder if having a placeholder for increased function would always be useful.	2/19/2015 3:32 PM
4	I do agree but one thought is to have all possible categories available for each pharmacogene, regardless of whether alleles have been described for all (to allow for future discoveries).	2/11/2015 1:29 PM
5	Four, should include "unknown".	2/3/2015 11:27 AM
6	need 4th, unknown at this time normal/moderate or some function/no function/unknown function also, from a physician use perspective there is likely a difference within the moderate/some function; "moderate or some" is one level but "little or no function" is another level of interpretation.	2/3/2015 11:26 AM
7	Unknown function alleles, particularly for novel variants identified by WGS/WES	2/3/2015 11:25 AM
8	4; need 'unknown'	2/2/2015 1:41 PM

## Q2 Describe your degree of acceptance of the following terms to describe the allele function for a TPMT or DPYD allele with high/normal function/activity (e.g., TPMT\*1 or DPYD\*1):

Answered: 73 Skipped: 4



	STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	TOTAL	WEIGHTED AVERAGE
Active	18% 11	34% 21	32% 20	16% 10	62	2.47
Functional	14% 9	25% 16	41% 26	19% 12	63	2.65
Normal activity	5% 3	10% 6	41% 25	44% 27	61	3.25
Normal function	7% 4	18% 11	39% 24	36% 22	61	3.05
Wild-type activity	25% 16	36% 23	17% 11	22% 14	64	2.36
Wild-type function	26% 16	38% 23	23% 14	13% 8	61	2.23

#	OTHER PLEASE SPECIFY	DATE
1	Reference activity	2/20/2015 5:33 PM
2	normal enzyme activity	2/16/2015 9:03 AM
3	don't know	2/11/2015 1:25 PM

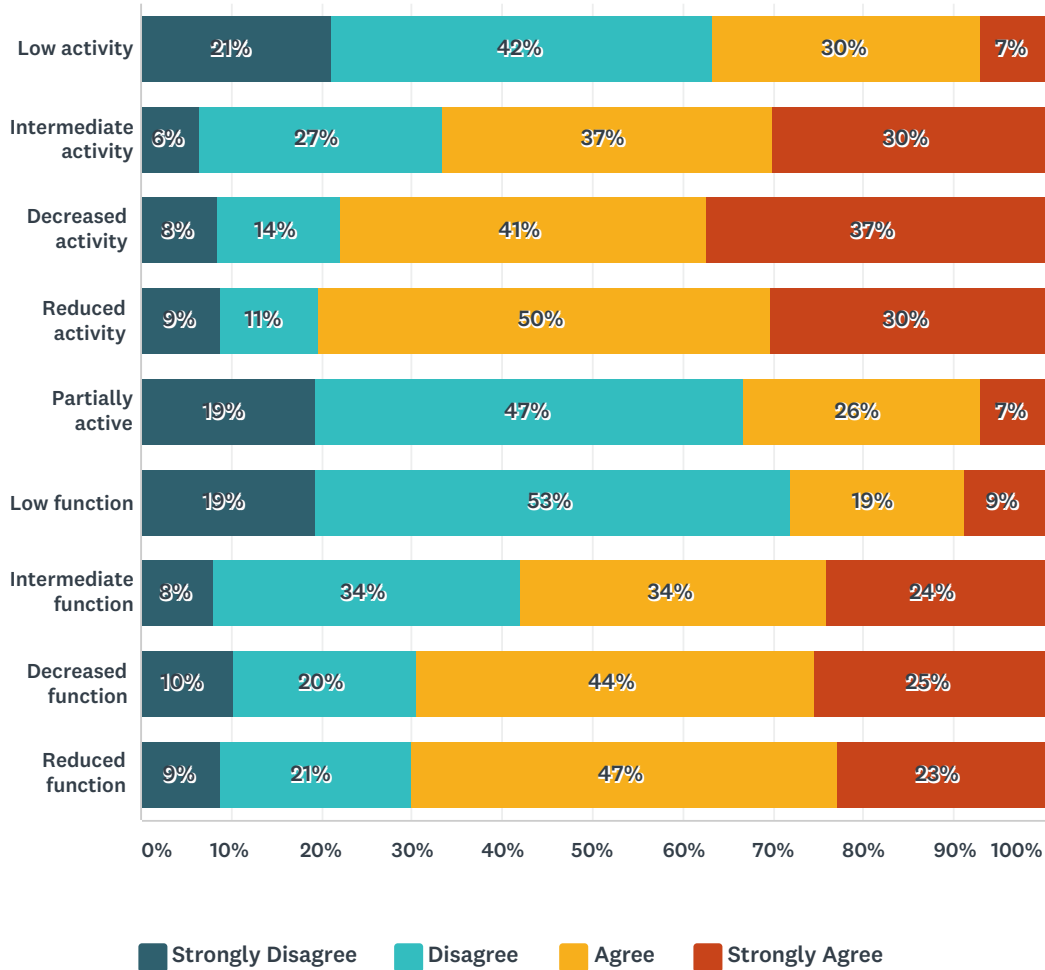
4 high does not mean normal to many physicians; so normal activity or normal function is a clearer interpretation. some physicians don't know what wild type means.

---

2/3/2015 11:26 AM

### Q3 Describe your degree of acceptance of the following terms to describe the allele function for a TPMT or DPYD allele with medium/some function/activity (e.g., TPMT\*8 or DPYD\*3):

Answered: 73 Skipped: 4



	STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	TOTAL	WEIGHTED AVERAGE
Low activity	21%	42%	30%	7%		
	12	24	17	4	57	2.23
Intermediate activity	6%	27%	37%	30%		
	4	17	23	19	63	2.90
Decreased activity	8%	14%	41%	37%		
	5	8	24	22	59	3.07
Reduced activity	9%	11%	50%	30%		
	5	6	28	17	56	3.02
Partially active	19%	47%	26%	7%		
	11	27	15	4	57	2.21
Low function	19%	53%	19%	9%		
	11	30	11	5	57	2.18
Intermediate function	8%	34%	34%	24%		
	5	21	21	15	62	2.74

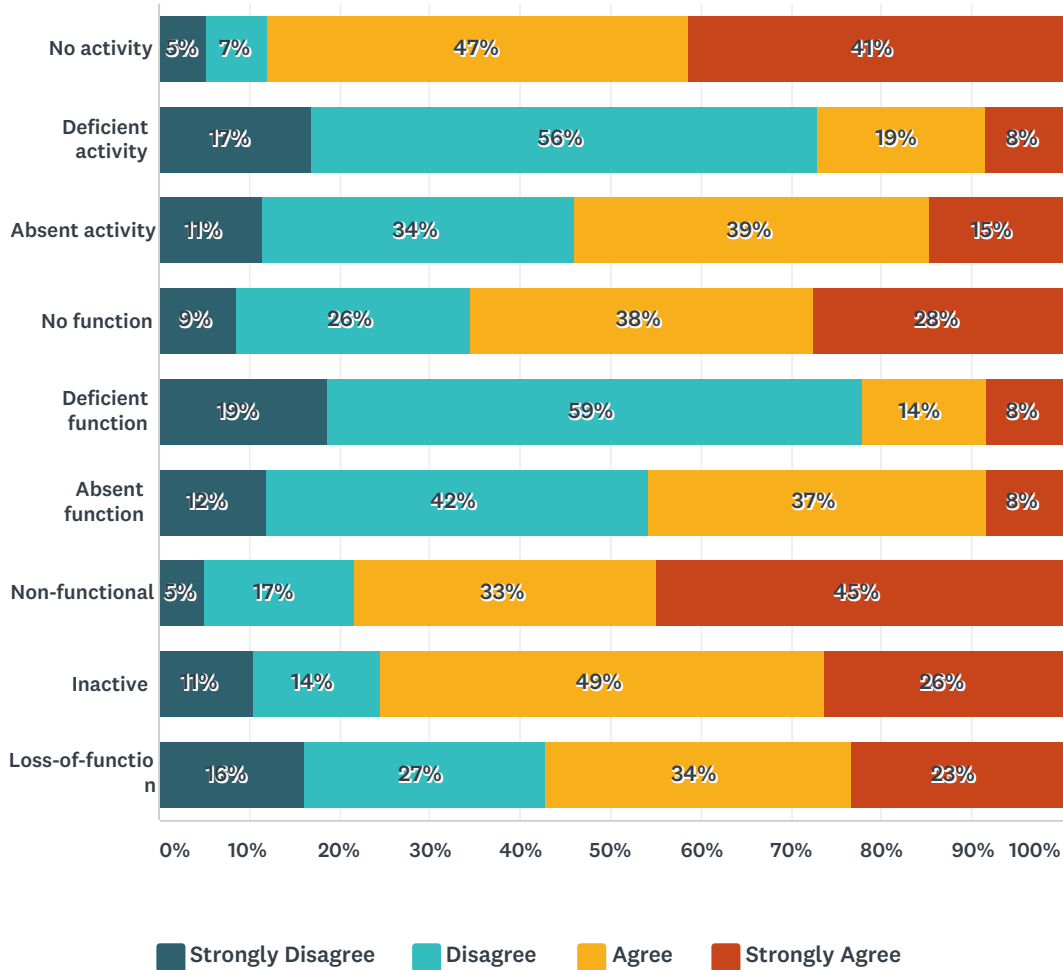
CPIC Term Standardization for Clinical Pharmacogenetic Test Results: alleles and phenotypes

Decreased function	10% 6	20% 12	44% 26	25% 15	59	2.85
Reduced function	9% 5	21% 12	47% 27	23% 13	57	2.84

#	OTHER (PLEASE SPECIFY)	DATE
1	intermediate/lower than normal enzyme activity	2/16/2015 9:03 AM
2	don't know	2/11/2015 1:25 PM

### Q4 Describe your degree of acceptance of the following terms to describe the allele function for a TPMT or DPYD allele with no function/activity (e.g., TPMT\*2 or DPYD\*2A):

Answered: 73 Skipped: 4



	STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	TOTAL	WEIGHTED AVERAGE
No activity	5% 3	7% 4	47% 27	41% 24	58	3.24
Deficient activity	17% 10	56% 33	19% 11	8% 5	59	2.19
Absent activity	11% 7	34% 21	39% 24	15% 9	61	2.57
No function	9% 5	26% 15	38% 22	28% 16	58	2.84
Deficient function	19% 11	59% 35	14% 8	8% 5	59	2.12
Absent function	12% 7	42% 25	37% 22	8% 5	59	2.42
Non-functional	5% 3	17% 10	33% 20	45% 27	60	3.18

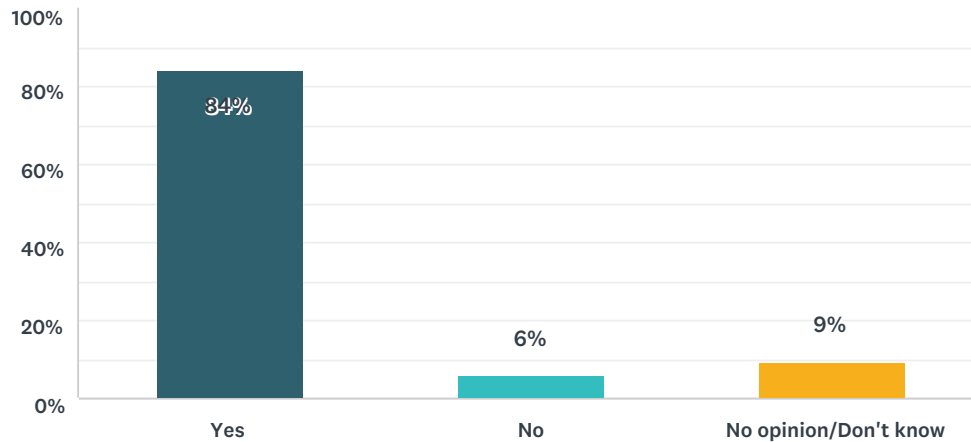
CPIC Term Standardization for Clinical Pharmacogenetic Test Results: alleles and phenotypes

Inactive	11% 6	14% 8	49% 28	26% 15	57	2.91
Loss-of-function	16% 9	27% 15	34% 19	23% 13	56	2.64

#	OTHER (PLEASE SPECIFY)	DATE
1	For this category, we need to differentiate between that caused by inactive protein and that caused by low protein level (but what is there has "normal" activity). The protein's phenotype is not necessarily the cellular/organismal phenotype.	2/20/2015 5:37 PM
2	undetectable activity	2/17/2015 6:33 PM
3	absent enzyme activity	2/16/2015 9:03 AM
4	don't know	2/11/2015 1:25 PM

**Q5 We assume that 3 major categories of phenotypes are needed for TPMT or DPYD. Do you agree (yes or no)? If no, please indicate how many you think are needed and why:**

Answered: 64 Skipped: 13

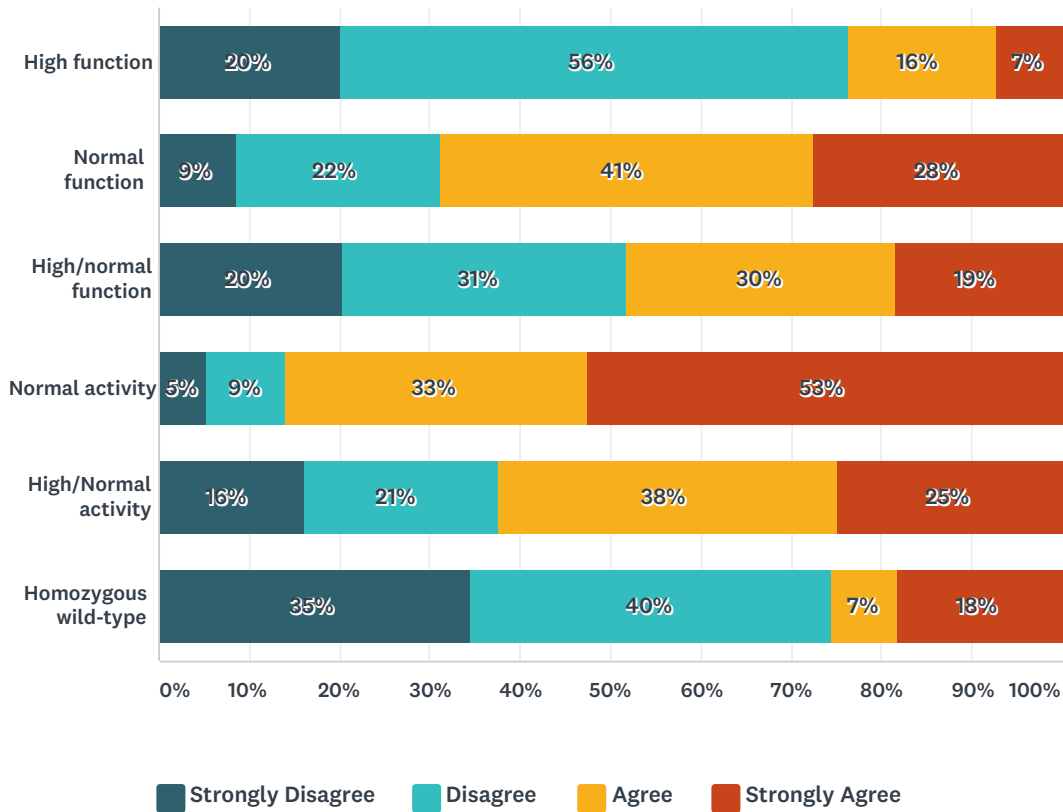


ANSWER CHOICES	RESPONSES	
Yes	84%	54
No	6%	4
No opinion/Don't know	9%	6
<b>TOTAL</b>		<b>64</b>

#	IF NO, PLEASE INDICATE HOW MANY YOU THINK ARE NEEDED AND WHY:	DATE
1	need an unknown phenotype	2/20/2015 5:37 PM
2	Possibly 4 to include UM due to some literature suggesting increased activity associated with methylated products leading to clinical presentation. Although rare, it may be pertinent with advancement of technology and new SNPs?	2/19/2015 3:44 PM
3	Should include Unknown.	2/3/2015 11:30 AM
4	you should indicate what the 3 major categories are in the question so everyone is on the same page.	2/3/2015 11:30 AM
5	category (ies) for diplotypes with alleles of unknown function	2/2/2015 1:41 PM

**Q6 Describe your degree of acceptance of the following terms to describe the presumed phenotype for TPMT in an individual with high/normal TPMT or DPYD function/activity (e.g., TPMT\*1/\*1 or DPYD\*1/\*1):**

Answered: 68 Skipped: 9

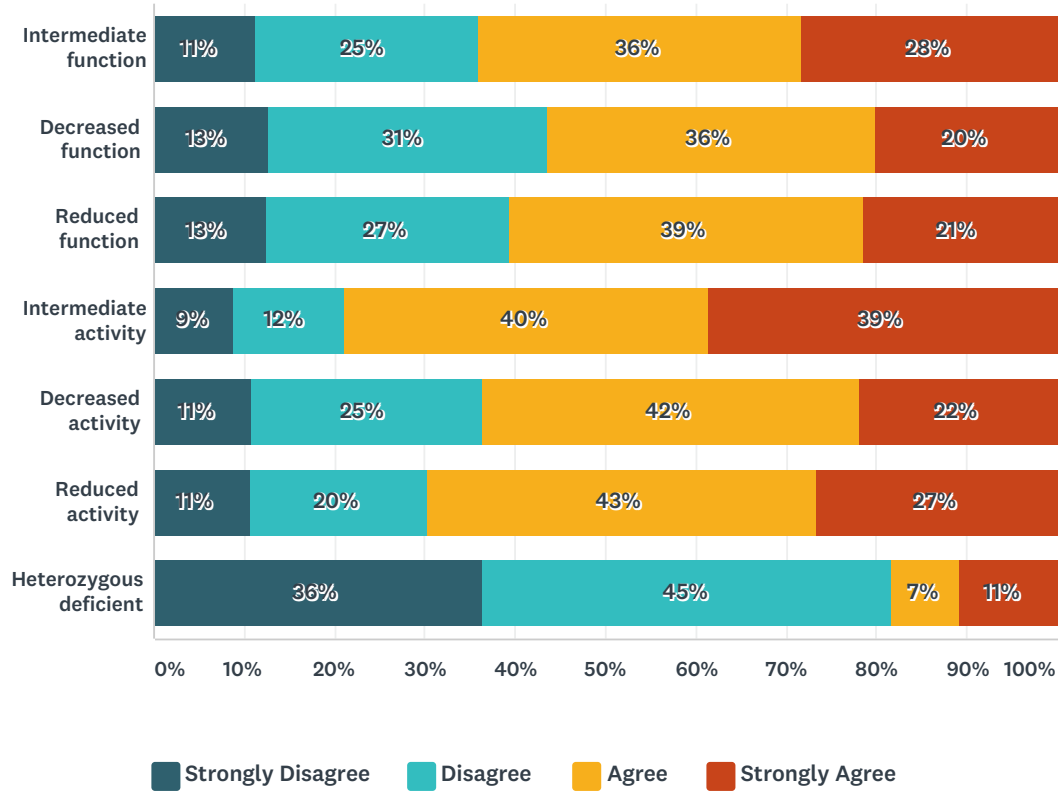


	STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	TOTAL	WEIGHTED AVERAGE
High function	20% 11	56% 31	16% 9	7% 4	55	2.11
Normal function	9% 5	22% 13	41% 24	28% 16	58	2.88
High/normal function	20% 11	31% 17	30% 16	19% 10	54	2.46
Normal activity	5% 3	9% 5	33% 19	53% 30	57	3.33
High/Normal activity	16% 9	21% 12	38% 21	25% 14	56	2.71
Homozygous wild-type	35% 19	40% 22	7% 4	18% 10	55	2.09

#	OTHER (PLEASE SPECIFY)	DATE
1	Reference function	2/20/2015 5:37 PM
2	normal metabolizer	2/16/2015 9:04 AM
3	don't know	2/11/2015 1:26 PM

**Q7 Describe your degree of acceptance of the following terms to describe the presumed phenotype for TPMT or DPYD in an individual with medium/some function/activity (e.g., TPMT\*1/\*3 or DPYD\*1/\*2A):**

Answered: 66 Skipped: 11



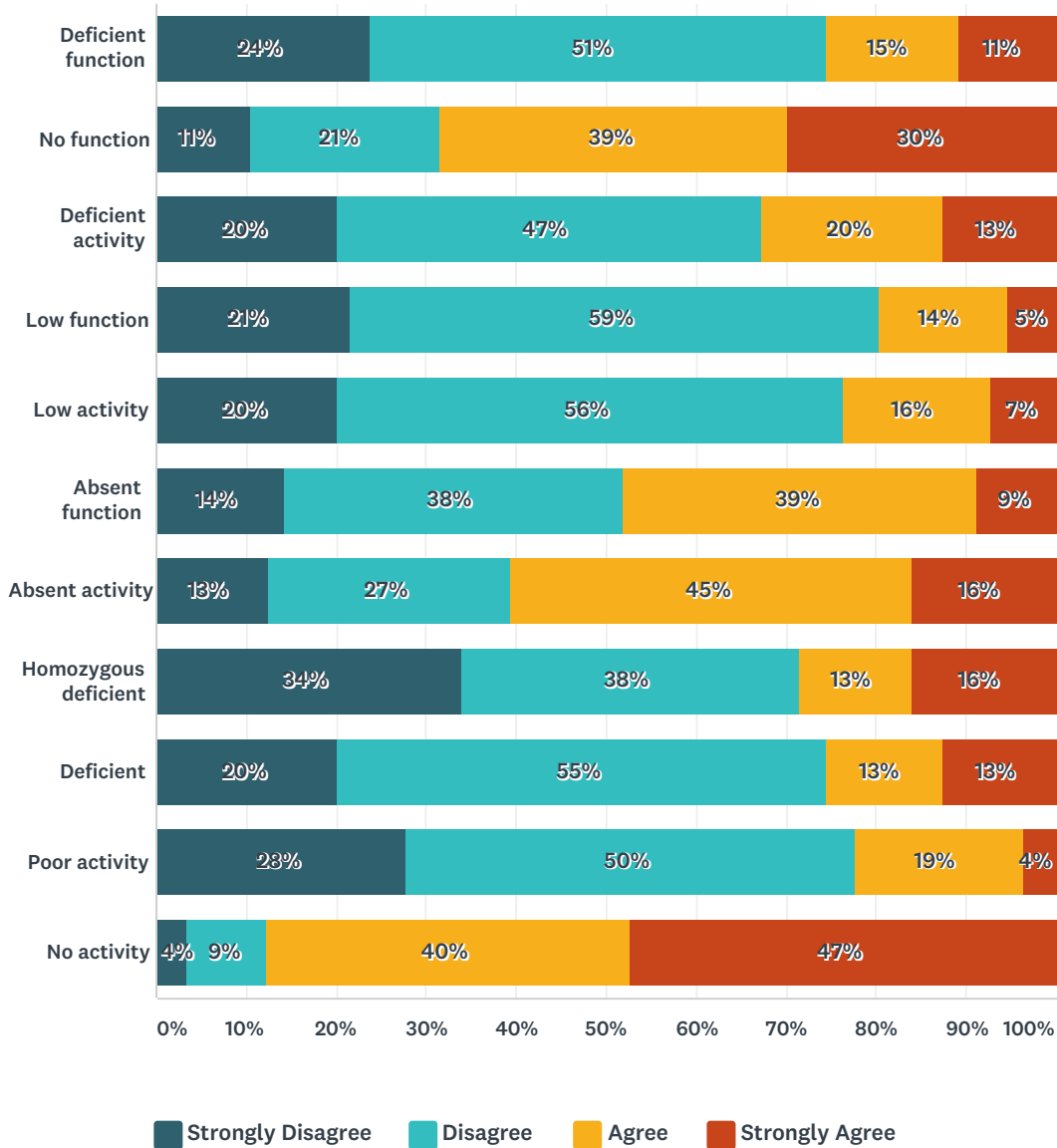
	STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	TOTAL	WEIGHTED AVERAGE
Intermediate function	11% 6	25% 13	36% 19	28% 15	53	2.81
Decreased function	13% 7	31% 17	36% 20	20% 11	55	2.64
Reduced function	13% 7	27% 15	39% 22	21% 12	56	2.70
Intermediate activity	9% 5	12% 7	40% 23	39% 22	57	3.09
Decreased activity	11% 6	25% 14	42% 23	22% 12	55	2.75
Reduced activity	11% 6	20% 11	43% 24	27% 15	56	2.86
Heterozygous deficient	36% 20	45% 25	7% 4	11% 6	55	1.93

#	OTHER (PLEASE SPECIFY)	DATE
1	intermediate metabolizer	2/16/2015 9:04 AM
2	don't know	2/11/2015 1:26 PM



**Q8 Describe your degree of acceptance of the following terms to describe the presumed phenotype for TPMT or DPYD in an individual with no function/activity (e.g., TPMT\*3/\*3 or DPYD\*2A/\*2A):**

Answered: 67 Skipped: 10



	STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	TOTAL	WEIGHTED AVERAGE
Deficient function	24% 13	51% 28	15% 8	11% 6	55	2.13
No function	11% 6	21% 12	39% 22	30% 17	57	2.88
Deficient activity	20% 11	47% 26	20% 11	13% 7	55	2.25
Low function	21% 12	59% 33	14% 8	5% 3	56	2.04

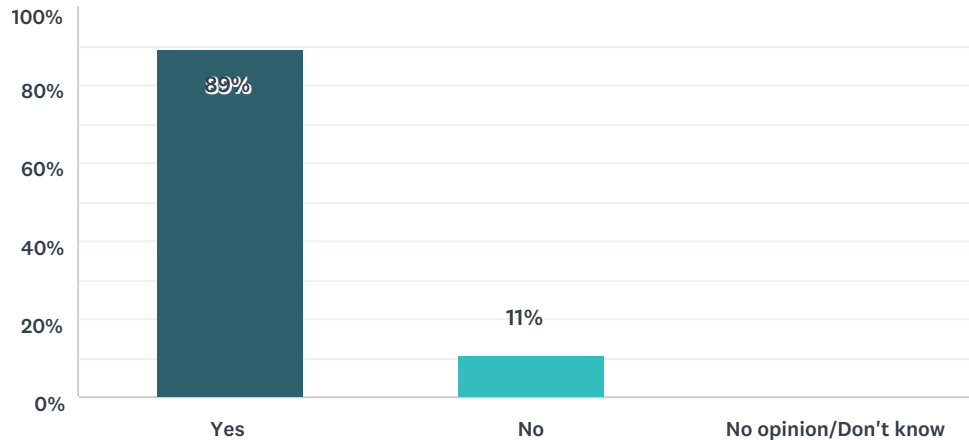
CPIC Term Standardization for Clinical Pharmacogenetic Test Results: alleles and phenotypes

Low activity	20% 11	56% 31	16% 9	7% 4	55	2.11
Absent function	14% 8	38% 21	39% 22	9% 5	56	2.43
Absent activity	13% 7	27% 15	45% 25	16% 9	56	2.64
Homozygous deficient	34% 19	38% 21	13% 7	16% 9	56	2.11
Deficient	20% 11	55% 30	13% 7	13% 7	55	2.18
Poor activity	28% 15	50% 27	19% 10	4% 2	54	1.98
No activity	4% 2	9% 5	40% 23	47% 27	57	3.32

#	OTHER (PLEASE SPECIFY)	DATE
1	For this category, we need to differentiate between that caused by inactive protein and that caused by low protein level (but what is there has "normal" activity). The protein's phenotype is not necessarily the cellular/organismal phenotype.	2/20/2015 5:38 PM
2	Poor function	2/20/2015 5:37 PM
3	poor metabolizer	2/16/2015 9:04 AM
4	don't know	2/11/2015 1:26 PM
5	homozygous nonfunctional	2/4/2015 3:11 PM

**Q9 We assume that 4 or 5 major categories of allele function (depending on enzyme) are needed for CYP2C19, CYP2D6, and CYP2C9. Do you agree (yes or no)? If no, please indicate how many you think are needed and why:**

Answered: 65 Skipped: 12

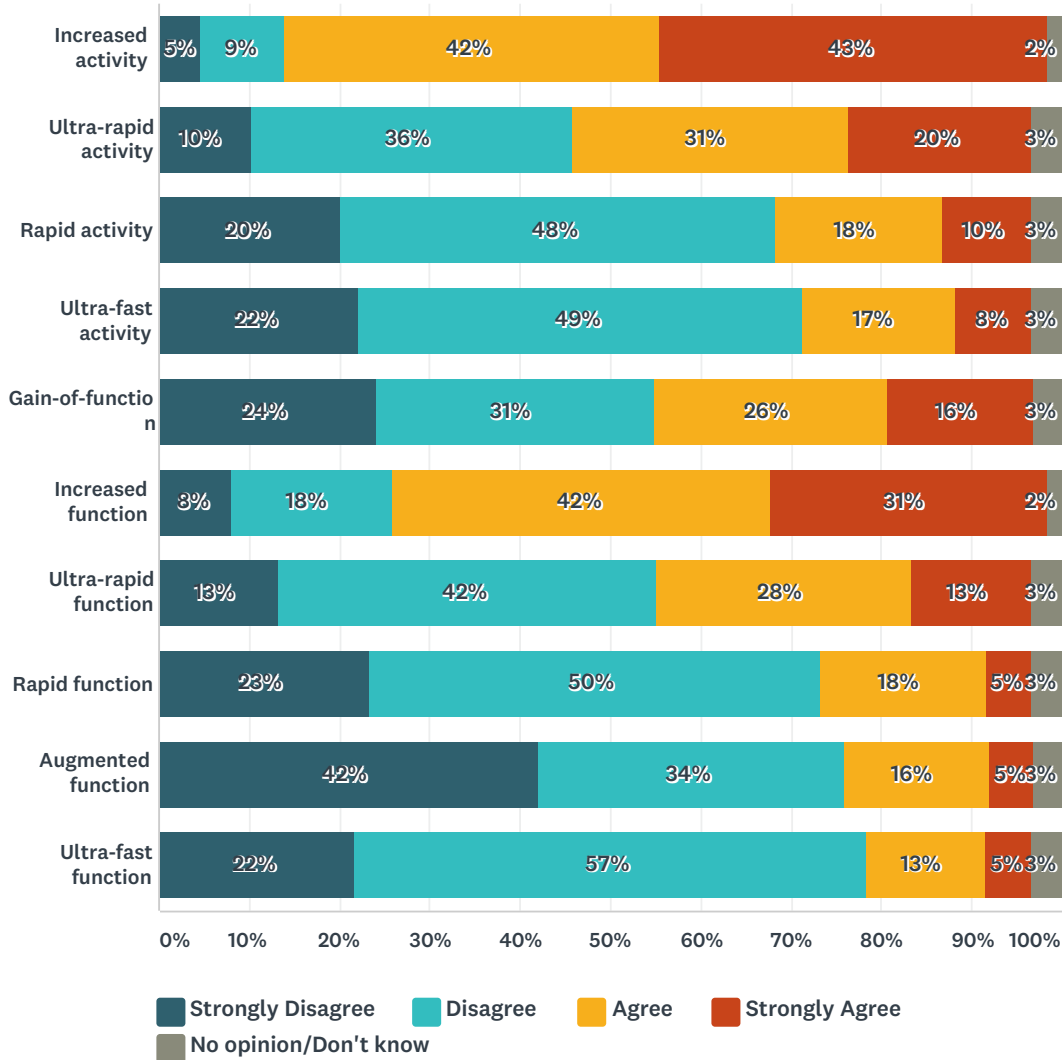


ANSWER CHOICES	RESPONSES	
Yes	89%	58
No	11%	7
No opinion/Don't know	0%	0
<b>TOTAL</b>		<b>65</b>

#	IF NO, PLEASE INDICATE HOW MANY YOU THINK ARE NEEDED AND WHY:	DATE
1	5 are needed because you need "unknown"	2/20/2015 5:44 PM
2	Again, I think this should be consistent across all PGx genes	2/19/2015 3:38 PM
3	4 for CYP2D6 and CYP2C19 (PM, IM, EM, UM) 3 for CYP2C9 (PM, IM, EM) Unless I missed the existence of CYP2C9 high activity alleles...?	2/13/2015 11:54 AM
4	For CYP2C9, only 3 categories are needed. There are no known alleles with increased or gain-of function.	2/9/2015 4:58 PM
5	i think the 50-80% activity should be different from the 10-30% activity. The former being decreased activity or function; the latter being greatly reduced activity (function).	2/4/2015 3:17 PM
6	I would favor 3 for 2C9. I don't think we should be cutting dosing recommendations for this CYP too finely. I would favor four for 2C19 and I am open to 4- 5 for 2D6 in view of all the activities described and since many of the substrates have CNS toxicity.	2/4/2015 1:53 PM
7	Stick with 4 categories here.	2/3/2015 1:58 PM
8	Unknown.	2/3/2015 11:34 AM
9	three to four and is dependent on which of the CYP genes listed above. For example, I would agree to three major categories of phenotypes for CYP2C9, but four categories for CYP2C19.	2/2/2015 2:45 PM
10	No convincing evidence of more than 3 phenotypes for CYP2C9	2/2/2015 1:46 PM
11	need categories for 'unknown'	2/2/2015 1:41 PM

## Q10 Describe your degree of acceptance of the following terms to describe the allele function for a CYP2C19, CYP2D6, or CYP2C9 allele with high function/activity (e.g., CYP2C19\*17):

Answered: 66 Skipped: 11



	STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	NO OPINION/DON'T KNOW	TOTAL	WEIGHTED AVERAGE
Increased activity	5% 3	9% 6	42% 27	43% 28	2% 1	65	3.25
Ultra-rapid activity	10% 6	36% 21	31% 18	20% 12	3% 2	59	2.63
Rapid activity	20% 12	48% 29	18% 11	10% 6	3% 2	60	2.19
Ultra-fast activity	22% 13	49% 29	17% 10	8% 5	3% 2	59	2.12
Gain-of-function	24% 15	31% 19	26% 16	16% 10	3% 2	62	2.35

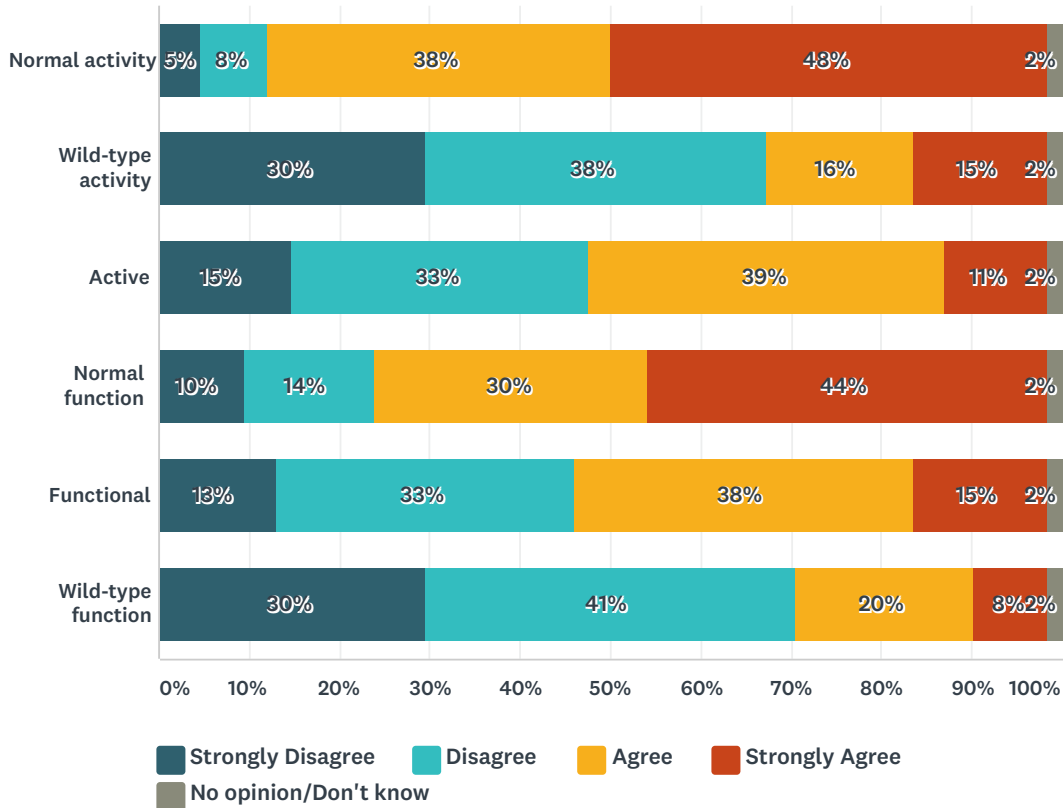
CPIC Term Standardization for Clinical Pharmacogenetic Test Results: alleles and phenotypes

Increased function	8% 5	18% 11	42% 26	31% 19	2% 1	62	2.97
Ultra-rapid function	13% 8	42% 25	28% 17	13% 8	3% 2	60	2.43
Rapid function	23% 14	50% 30	18% 11	5% 3	3% 2	60	2.05
Augmented function	42% 26	34% 21	16% 10	5% 3	3% 2	62	1.83
Ultra-fast function	22% 13	57% 34	13% 8	5% 3	3% 2	60	2.02

#	OTHER (PLEASE SPECIFY)	DATE
1	higher than normal enzyme activity	2/16/2015 9:04 AM
2	Hyperactive allele	2/13/2015 11:54 AM
3	don't know	2/11/2015 1:30 PM

### Q11 Describe your degree of acceptance of the following terms to describe the allele function for a CYP2C19, CYP2D6 or CYP2C9 allele with normal function/activity (e.g., CYP2C19\*1):

Answered: 66 Skipped: 11



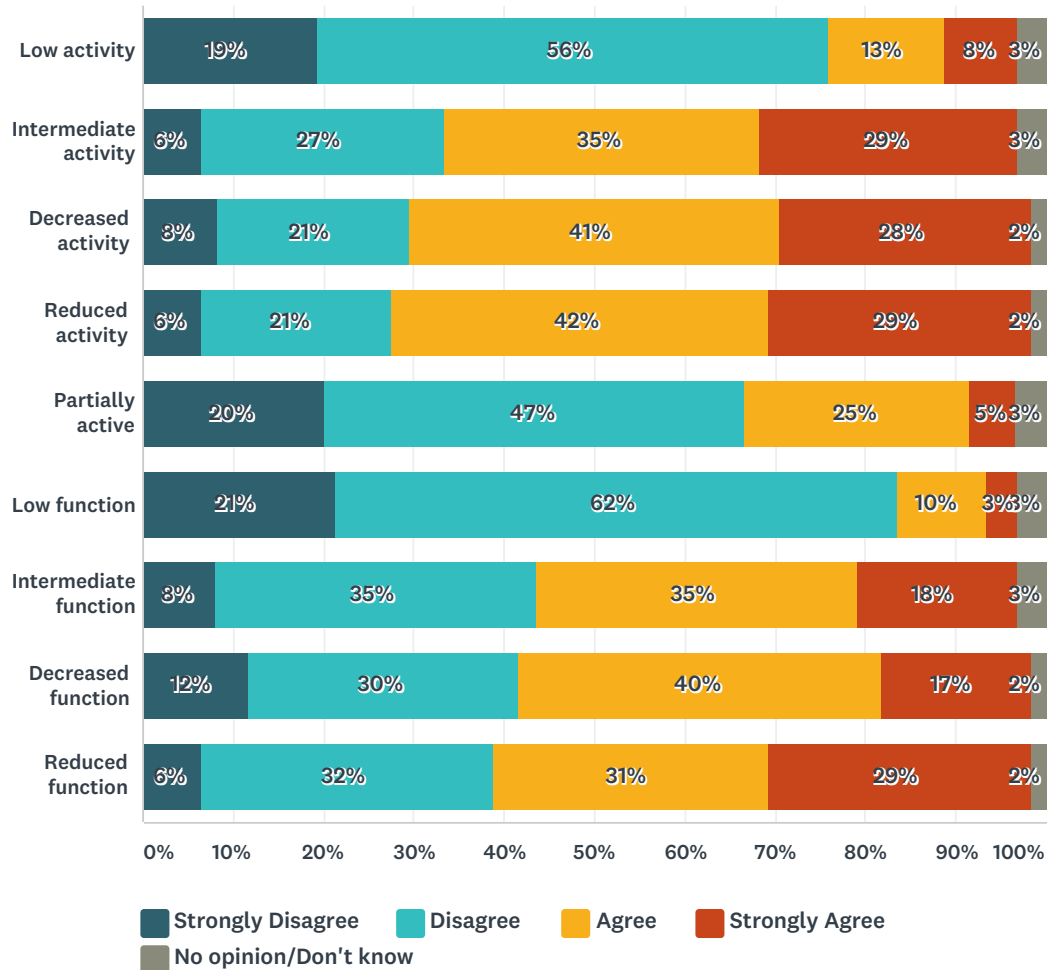
	STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	NO OPINION/DON'T KNOW	TOTAL	WEIGHTED AVERAGE
Normal activity	5% 3	8% 5	38% 25	48% 32	2% 1	66	3.32
Wild-type activity	30% 18	38% 23	16% 10	15% 9	2% 1	61	2.17
Active	15% 9	33% 20	39% 24	11% 7	2% 1	61	2.48
Normal function	10% 6	14% 9	30% 19	44% 28	2% 1	63	3.11
Functional	13% 8	33% 20	38% 23	15% 9	2% 1	61	2.55
Wild-type function	30% 18	41% 25	20% 12	8% 5	2% 1	61	2.07

#	OTHER PLEASE SPECIFY	DATE
1	Reference activity	2/20/2015 5:44 PM
2	fully functional?	2/18/2015 5:51 PM
3	normal enzyme activity	2/16/2015 9:04 AM



**Q12 Describe your degree of acceptance of the following terms to describe the allele function for a CYP2C19, CYP2D6 or CYP2C9 allele with medium/some function/activity (e.g., CYP2C19\*9 or CYP2D6\*17):**

Answered: 66 Skipped: 11



	STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	NO OPINION/DON'T KNOW	TOTAL	WEIGHTED AVERAGE
Low activity	19% 12	56% 35	13% 8	8% 5	3% 2	62	2.10
Intermediate activity	6% 4	27% 17	35% 22	29% 18	3% 2	63	2.89
Decreased activity	8% 5	21% 13	41% 25	28% 17	2% 1	61	2.90
Reduced activity	6% 4	21% 13	42% 26	29% 18	2% 1	62	2.95
Partially active	20% 12	47% 28	25% 15	5% 3	3% 2	60	2.16
Low function	21% 13	62% 38	10% 6	3% 2	3% 2	61	1.95

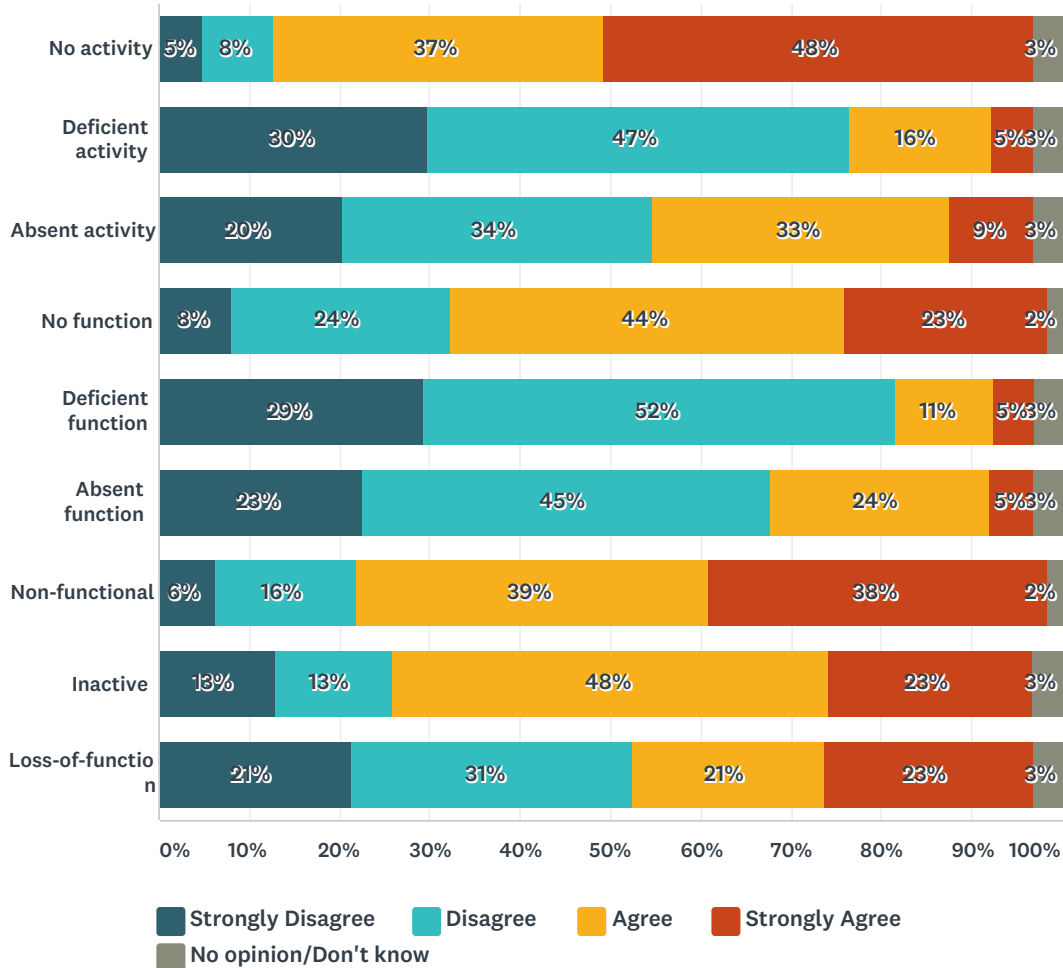
CPIC Term Standardization for Clinical Pharmacogenetic Test Results: alleles and phenotypes

Intermediate function	8% 5	35% 22	35% 22	18% 11	3% 2	62	2.65
Decreased function	12% 7	30% 18	40% 24	17% 10	2% 1	60	2.63
Reduced function	6% 4	32% 20	31% 19	29% 18	2% 1	62	2.84

#	OTHER (PLEASE SPECIFY)	DATE
1	intermediate/lower than normal enzyme activity	2/16/2015 9:04 AM
2	don't know	2/11/2015 1:30 PM

### Q13 Describe your degree of acceptance of the following terms to describe the allele function for a CYP2C19, CYP2D6 or CYP2C9 allele with no function/activity (e.g., CYP2C19\*2 or CYP2D6\*4 or CYP2C9\*6):

Answered: 69 Skipped: 8



	STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	NO OPINION/DON'T KNOW	TOTAL	WEIGHTED AVERAGE
No activity	5% 3	8% 5	37% 23	48% 30	3% 2	63	3.31
Deficient activity	30% 19	47% 30	16% 10	5% 3	3% 2	64	1.95
Absent activity	20% 13	34% 22	33% 21	9% 6	3% 2	64	2.32
No function	8% 5	24% 15	44% 27	23% 14	2% 1	62	2.82
Deficient function	29% 19	52% 34	11% 7	5% 3	3% 2	65	1.90
Absent function	23% 14	45% 28	24% 15	5% 3	3% 2	62	2.12

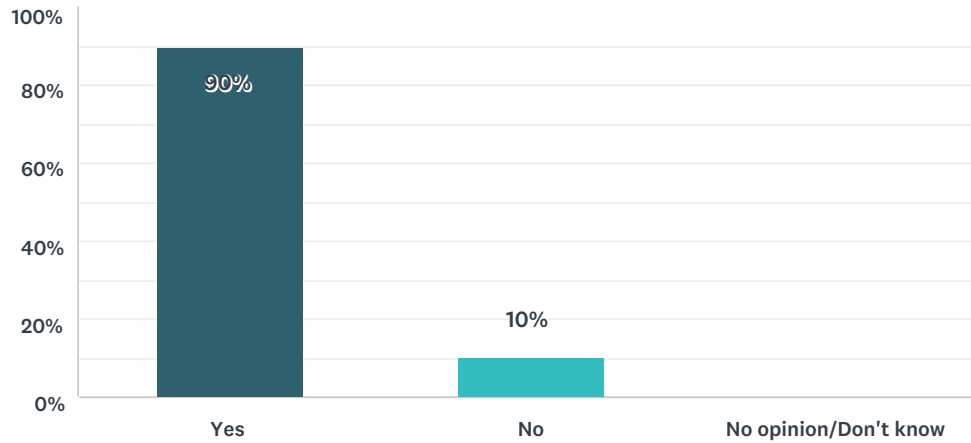
CPIC Term Standardization for Clinical Pharmacogenetic Test Results: alleles and phenotypes

Non-functional	6% 4	16% 10	39% 25	38% 24	2% 1	64	3.10
Inactive	13% 8	13% 8	48% 30	23% 14	3% 2	62	2.83
Loss-of-function	21% 13	31% 19	21% 13	23% 14	3% 2	61	2.47

#	OTHER (PLEASE SPECIFY)	DATE
1	For this category, we need to differentiate between that caused by inactive protein and that caused by low protein level (but what is there has "normal" activity). The protein's phenotype is not necessarily the cellular/organismal phenotype.	2/20/2015 5:42 PM
2	absent enzyme activity	2/16/2015 9:04 AM
3	Poor activity, poor metabolizer. This is the language consistent with current drug monographs and literature.	2/2/2015 2:45 PM

Q14 We assume that 4 or 5 major categories of phenotype (depending on enzyme) are needed for CYP2C19, CYP2D6 and CYP2C9. Do you agree (yes or no)? If no, please indicate how many you think are needed and why:

Answered: 58 Skipped: 19

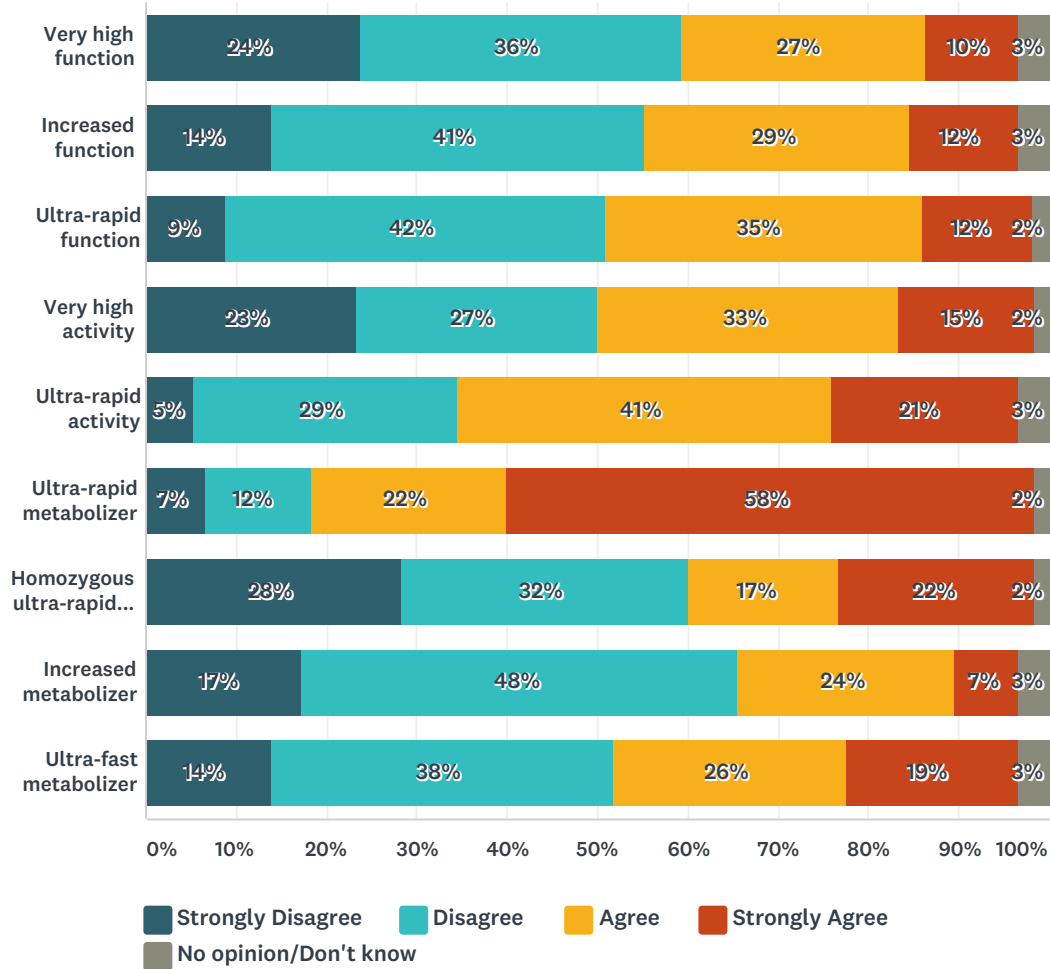


ANSWER CHOICES	RESPONSES	
Yes	90%	52
No	10%	6
No opinion/Don't know	0%	0
<b>TOTAL</b>		<b>58</b>

#	IF NO, PLEASE INDICATE HOW MANY YOU THINK ARE NEEDED AND WHY:	DATE
1	i just start pharmacogenetic project and I am still learning	2/11/2015 1:39 PM
2	4 categories. Difference between high and very high seems may not be clinically meaningful.	2/11/2015 1:36 PM
3	CYP2C9 does not have an ultrarapid metabolizer status, so would only have 3 major categories of phenotype (EM, IM, PM).	2/9/2015 5:01 PM
4	See my comments on the last screen.	2/4/2015 2:04 PM
5	I would stick with 4 categories (high/normal/low/none)	2/3/2015 1:58 PM
6	Should include unknown.	2/3/2015 11:37 AM
7	Agree that 3-4 categories exist, depending on gene. For example, CYP2C9 does not have characterized ultra-rapid or increased function alleles at this time, so a fourth phenotypic category for that gene may not be as applicable as for CYP2C19 or CYP2D6.	2/2/2015 2:53 PM
8	No convincing evidence for >3 phenotypes of clinical relevance for CYP2C9 or CYP2C19	2/2/2015 1:52 PM
9	need categories for genotypes with unknown alleles	2/2/2015 1:41 PM

### Q15 Describe your degree of acceptance of the following terms to describe the presumed phenotype for CYP2C19, CYP2D6 and CYP2C9 in an individual with very high function/activity (e.g., CYP2C19\*17/\*17):

Answered: 63 Skipped: 14



	STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	NO OPINION/DON'T KNOW	TOTAL	WEIGHTED AVERAGE
Very high function	24% 14	36% 21	27% 16	10% 6	3% 2	59	2.25
Increased function	14% 8	41% 24	29% 17	12% 7	3% 2	58	2.41
Ultra-rapid function	9% 5	42% 24	35% 20	12% 7	2% 1	57	2.52
Very high activity	23% 14	27% 16	33% 20	15% 9	2% 1	60	2.41
Ultra-rapid activity	5% 3	29% 17	41% 24	21% 12	3% 2	58	2.80

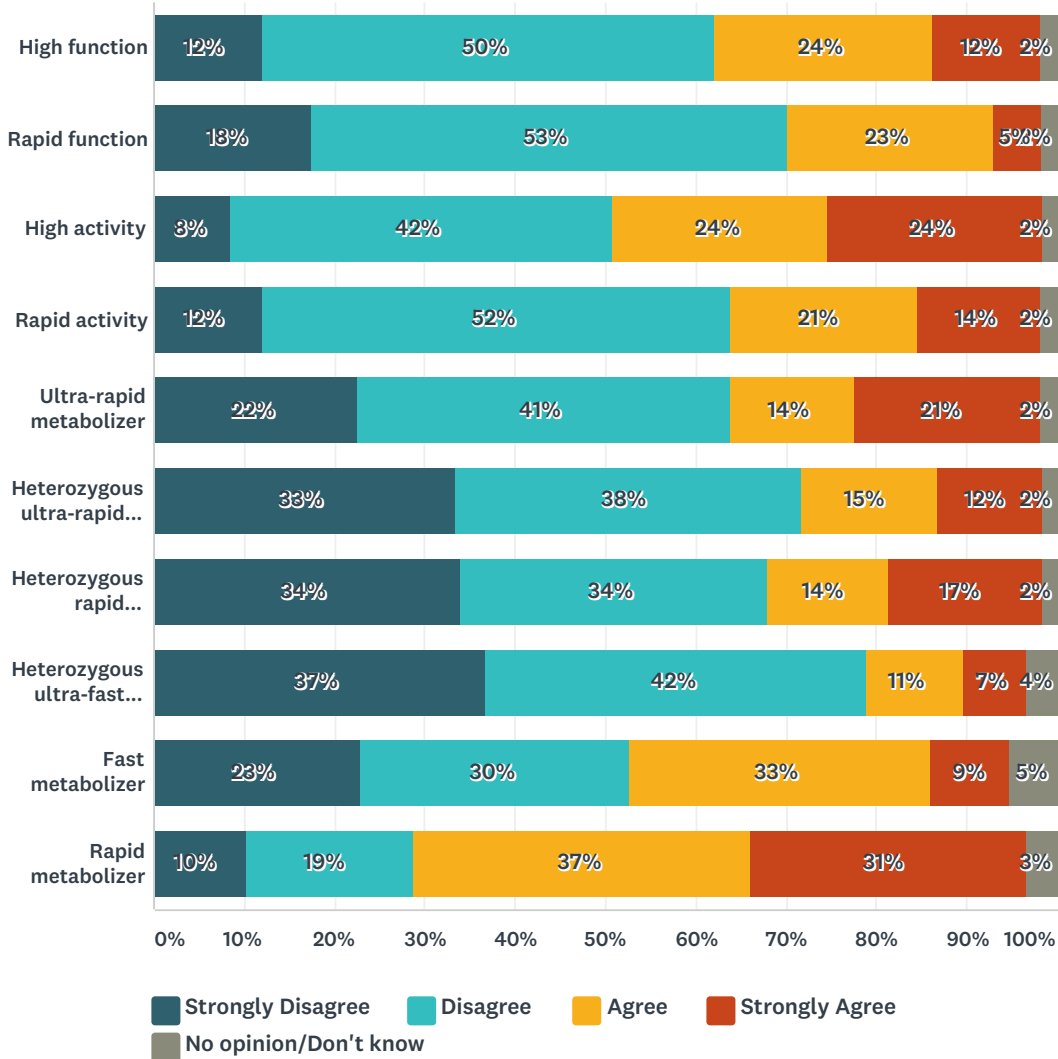
CPIC Term Standardization for Clinical Pharmacogenetic Test Results: alleles and phenotypes

Ultra-rapid metabolizer	7% 4	12% 7	22% 13	58% 35	2% 1	60	3.34
Homozygous ultra-rapid metabolizer	28% 17	32% 19	17% 10	22% 13	2% 1	60	2.32
Increased metabolizer	17% 10	48% 28	24% 14	7% 4	3% 2	58	2.21
Ultra-fast metabolizer	14% 8	38% 22	26% 15	19% 11	3% 2	58	2.52

#	OTHER (PLEASE SPECIFY)	DATE
1	Very increased function	2/20/2015 5:54 PM
2	Homozygous increased metabolizer	2/18/2015 10:41 AM
3	don't know	2/11/2015 1:39 PM
4	I'd prefer "greatly increased function" or "greatly increased activity" to contrast "increased activity" for high function	2/3/2015 2:20 PM
5	Increased activity	2/2/2015 1:52 PM

### Q16 Describe your degree of acceptance of the following terms to describe the presumed phenotype for CYP2C19, CYP2D6 and CYP2C9 in an individual with high function/activity (e.g., CYP2C19\*1/\*17):

Answered: 63 Skipped: 14



	STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	NO OPINION/DON'T KNOW	TOTAL	WEIGHTED AVERAGE
High function	12% 7	50% 29	24% 14	12% 7	2% 1	58	2.37
Rapid function	18% 10	53% 30	23% 13	5% 3	2% 1	57	2.16
High activity	8% 5	42% 25	24% 14	24% 14	2% 1	59	2.64
Rapid activity	12% 7	52% 30	21% 12	14% 8	2% 1	58	2.37

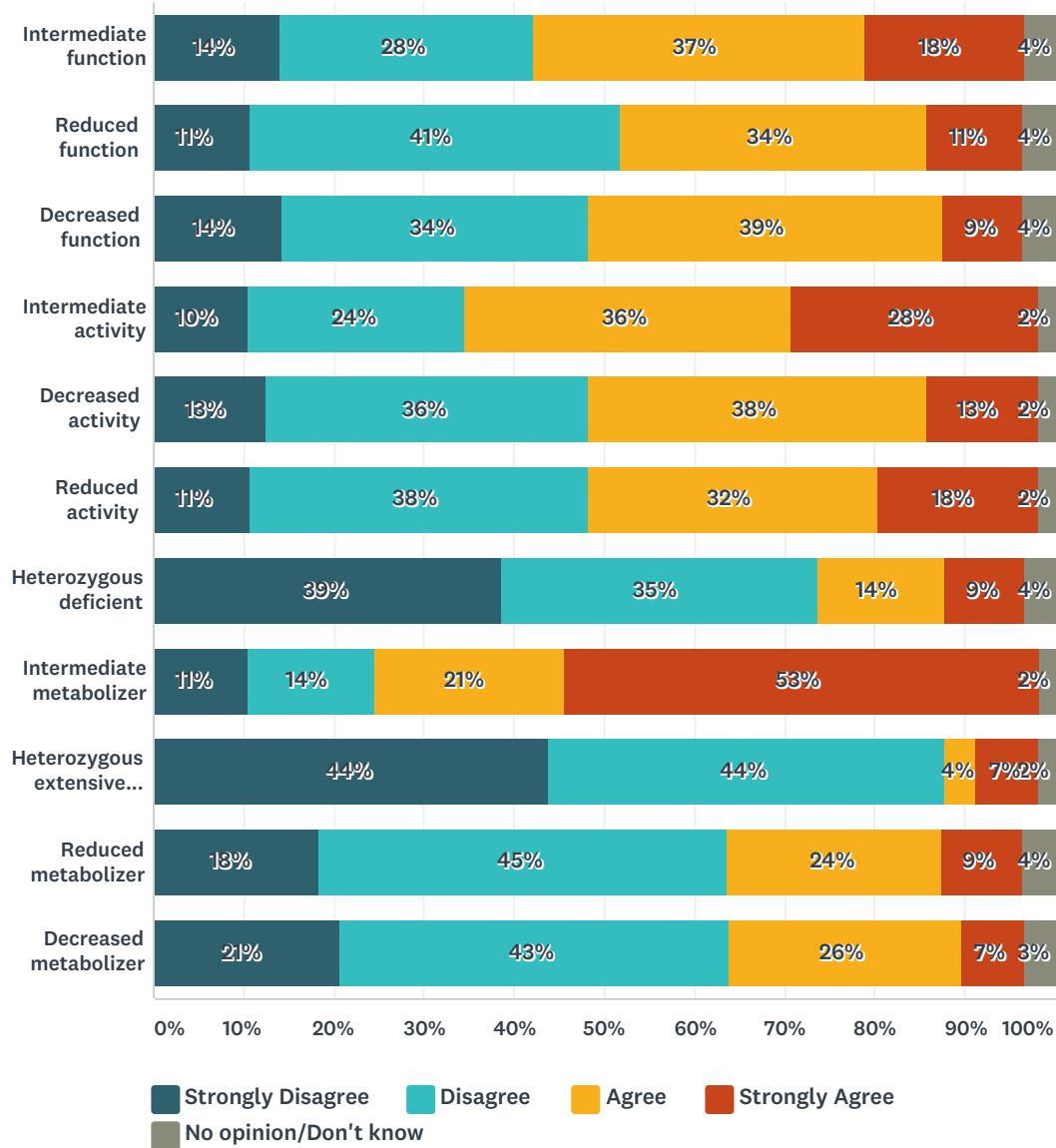
CPIC Term Standardization for Clinical Pharmacogenetic Test Results: alleles and phenotypes

Ultra-rapid metabolizer	22% 13	41% 24	14% 8	21% 12	2% 1	58	2.33
Heterozygous ultra-rapid metabolizer	33% 20	38% 23	15% 9	12% 7	2% 1	60	2.05
Heterozygous rapid metabolizer	34% 20	34% 20	14% 8	17% 10	2% 1	59	2.14
Heterozygous ultra-fast metabolizer	37% 21	42% 24	11% 6	7% 4	4% 2	57	1.87
Fast metabolizer	23% 13	30% 17	33% 19	9% 5	5% 3	57	2.30
Rapid metabolizer	10% 6	19% 11	37% 22	31% 18	3% 2	59	2.91

#	OTHER (PLEASE SPECIFY)	DATE
1	Increased function	2/20/2015 5:54 PM
2	Heterozygous increased metabolizer	2/18/2015 10:41 AM
3	I would not rate `CYP2C19*1/*17 as ultrarapid, but as normal. For CYP2C9 I am not aware of hypractivity alleles. So questions are answered fro CYP2D6 gene duplication positives.	2/13/2015 12:00 PM
4	"Increased function" or "increased activity" would differentiate from "normal" in a very clear way	2/3/2015 2:20 PM

Q17 Describe your degree of acceptance of the following terms to describe the presumed phenotype for CYP2C19, CYP2D6 and CYP2C9 in an individual with medium/some function/activity (e.g., CYP2C19\*1/\*2, CYP2D6\*4/\*17, CYP2C9\*1/\*3):

Answered: 62 Skipped: 15



	STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	NO OPINION/DON'T KNOW	TOTAL	WEIGHTED AVERAGE
Intermediate function	14% 8	28% 16	37% 21	18% 10	4% 2	57	2.60
Reduced function	11% 6	41% 23	34% 19	11% 6	4% 2	56	2.46
Decreased function	14% 8	34% 19	39% 22	9% 5	4% 2	56	2.44

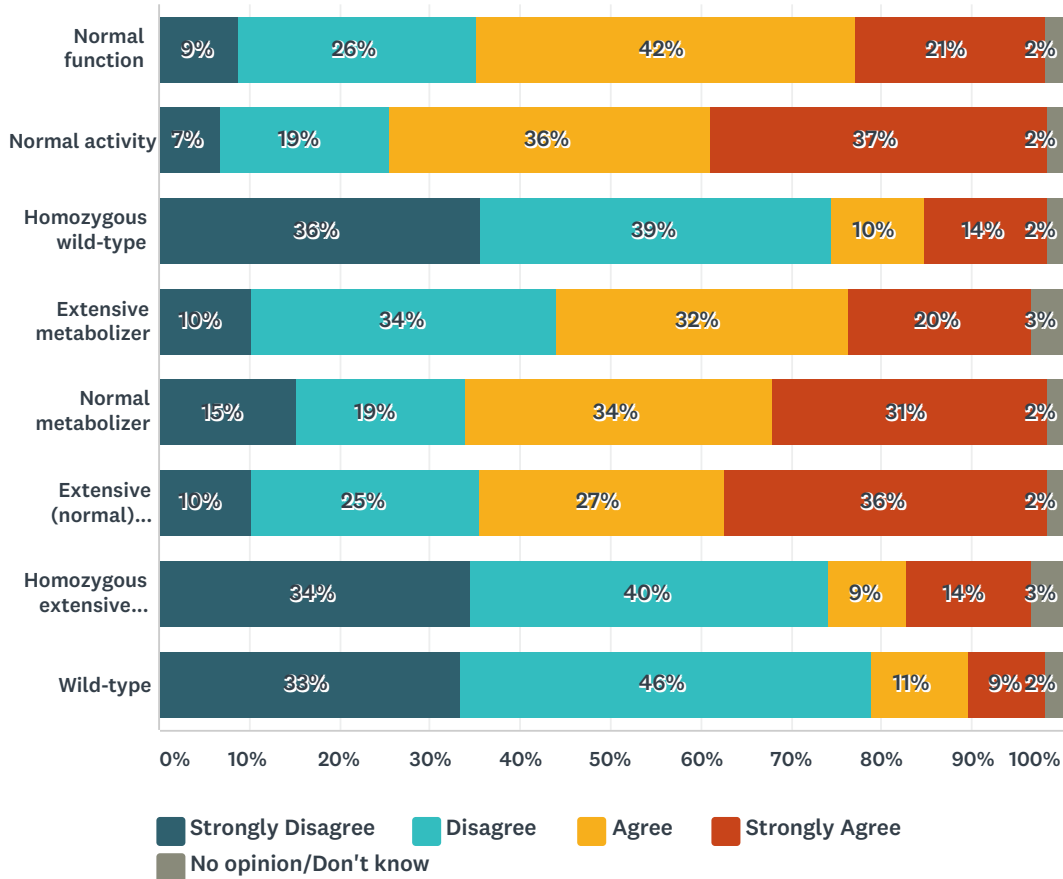
CPIC Term Standardization for Clinical Pharmacogenetic Test Results: alleles and phenotypes

Intermediate activity	10% 6	24% 14	36% 21	28% 16	2% 1	58	2.82
Decreased activity	13% 7	36% 20	38% 21	13% 7	2% 1	56	2.51
Reduced activity	11% 6	38% 21	32% 18	18% 10	2% 1	56	2.58
Heterozygous deficient	39% 22	35% 20	14% 8	9% 5	4% 2	57	1.93
Intermediate metabolizer	11% 6	14% 8	21% 12	53% 30	2% 1	57	3.18
Heterozygous extensive metabolizer	44% 25	44% 25	4% 2	7% 4	2% 1	57	1.73
Reduced metabolizer	18% 10	45% 25	24% 13	9% 5	4% 2	55	2.25
Decreased metabolizer	21% 12	43% 25	26% 15	7% 4	3% 2	58	2.20

#	OTHER (PLEASE SPECIFY)	DATE
1	heterozygous decreased metabolizer	2/18/2015 10:41 AM
2	don't know	2/11/2015 1:39 PM
3	Reduced metabolism; decreased metabolism	2/5/2015 8:07 AM

Q18 Describe your degree of acceptance of the following terms to describe the presumed phenotype for CYP2C19, CYP2D6 and CYP2C9 in an individual with normal function/activity (e.g., CYP2C19\*1/\*1, CYP2D6\*1/\*1, CYP2C9\*1/\*1):

Answered: 63 Skipped: 14



	STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	NO OPINION/DON'T KNOW	TOTAL	WEIGHTED AVERAGE
Normal function	9% 5	26% 15	42% 24	21% 12	2% 1	57	2.77
Normal activity	7% 4	19% 11	36% 21	37% 22	2% 1	59	3.05
Homozygous wild-type	36% 21	39% 23	10% 6	14% 8	2% 1	59	2.02
Extensive metabolizer	10% 6	34% 20	32% 19	20% 12	3% 2	59	2.65
Normal metabolizer	15% 9	19% 11	34% 20	31% 18	2% 1	59	2.81
Extensive (normal) metabolizer	10% 6	25% 15	27% 16	36% 21	2% 1	59	2.90
Homozygous extensive metabolizer	34% 20	40% 23	9% 5	14% 8	3% 2	58	2.02

CPIC Term Standardization for Clinical Pharmacogenetic Test Results: alleles and phenotypes

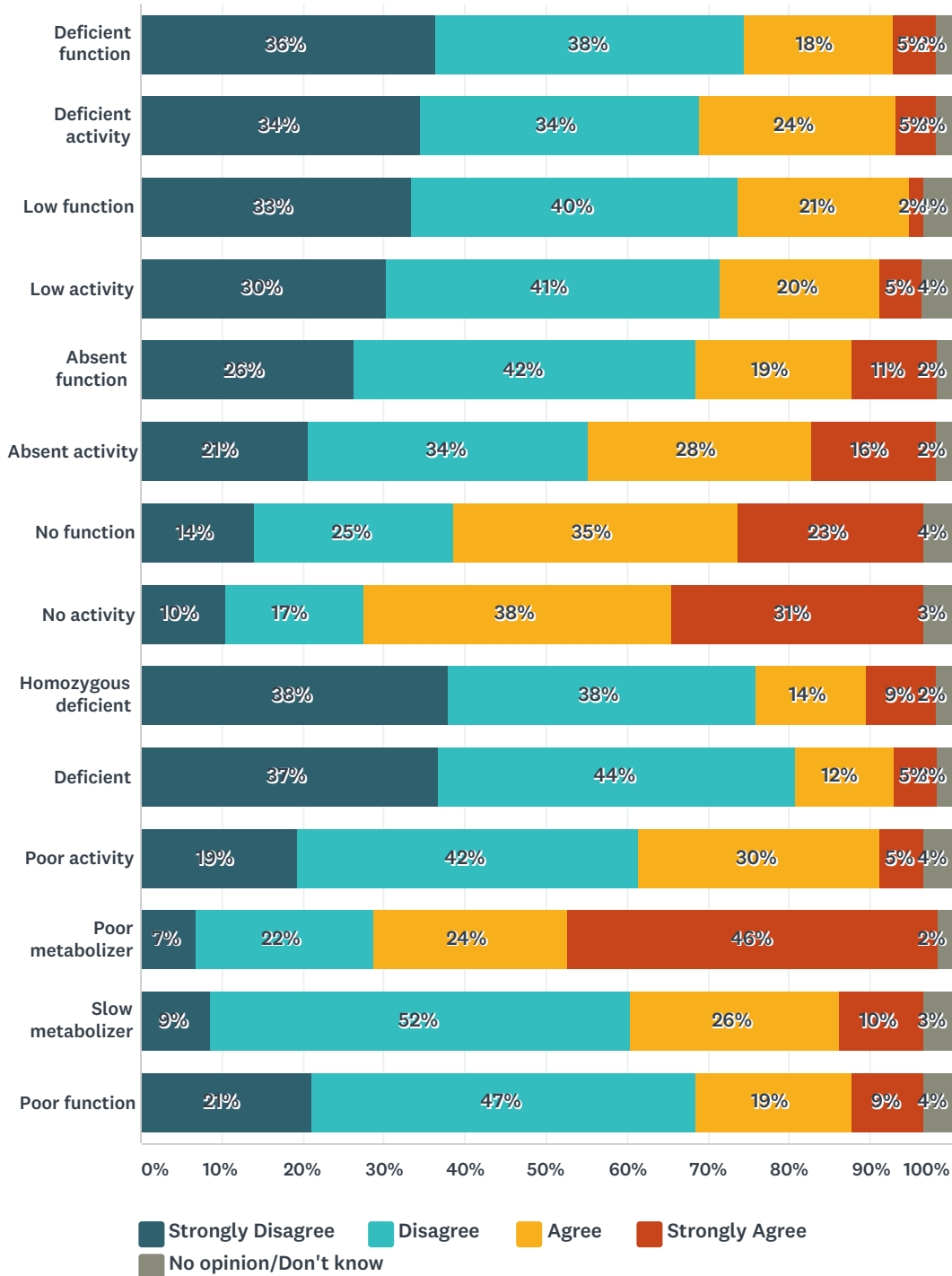
Wild-type	33%	46%	11%	9%	2%		
	19	26	6	5	1	57	1.95

#	OTHER (PLEASE SPECIFY)	DATE
1	Reference function	2/20/2015 5:54 PM
2	homozygous normal metabolizer	2/18/2015 10:41 AM

Q19 Describe your degree of acceptance of the following terms to describe the presumed phenotype for CYP2C19, CYP2D6 and CYP2C9 in an individual with no function/activity (e.g., CYP2C19\*2/\*2, CYP2D6\*4/\*4, CYP2C9\*6/\*6):

Answered: 64 Skipped: 13



STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	NO OPINION/DON'T KNOW	TOTAL	WEIGHTED AVERAGE
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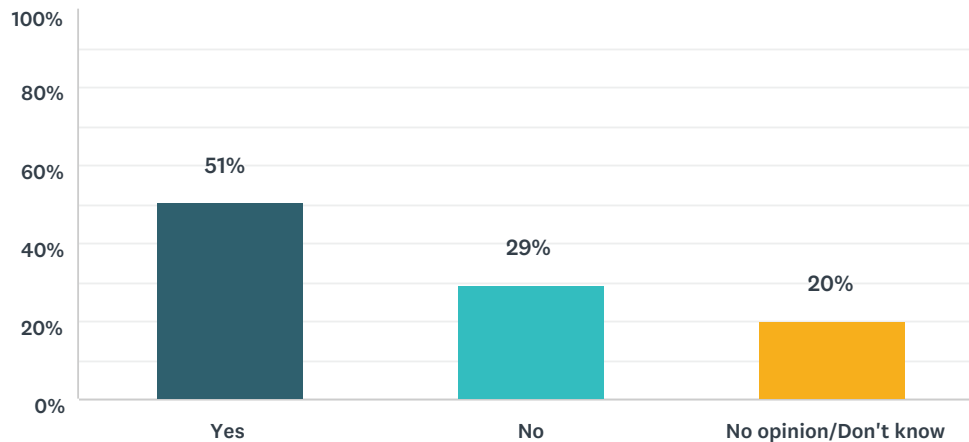
CPIC Term Standardization for Clinical Pharmacogenetic Test Results: alleles and phenotypes

Deficient function	36% 20	38% 21	18% 10	5% 3	2% 1	55	1.93
Deficient activity	34% 20	34% 20	24% 14	5% 3	2% 1	58	2.00
Low function	33% 19	40% 23	21% 12	2% 1	4% 2	57	1.91
Low activity	30% 17	41% 23	20% 11	5% 3	4% 2	56	2.00
Absent function	26% 15	42% 24	19% 11	11% 6	2% 1	57	2.14
Absent activity	21% 12	34% 20	28% 16	16% 9	2% 1	58	2.39
No function	14% 8	25% 14	35% 20	23% 13	4% 2	57	2.69
No activity	10% 6	17% 10	38% 22	31% 18	3% 2	58	2.93
Homozygous deficient	38% 22	38% 22	14% 8	9% 5	2% 1	58	1.93
Deficient	37% 21	44% 25	12% 7	5% 3	2% 1	57	1.86
Poor activity	19% 11	42% 24	30% 17	5% 3	4% 2	57	2.22
Poor metabolizer	7% 4	22% 13	24% 14	46% 27	2% 1	59	3.10
Slow metabolizer	9% 5	52% 30	26% 15	10% 6	3% 2	58	2.39
Poor function	21% 12	47% 27	19% 11	9% 5	4% 2	57	2.16

#	OTHER (PLEASE SPECIFY)	DATE
1	No metabolism	2/5/2015 8:07 AM

**Q20 Scoring systems have been developed in an attempt to provide a uniform approach to quantitate the predicted functional status of CYP2D6 alleles as follows: 1 for normal function, 0.5 for decreased function, and 0 for no function alleles. The sum of the activity values for each allele of the diplotype provides a CYP2D6 activity score. Do you think the CYP2D6 scoring system is adequate in determining CYP2D6 phenotype?**

Answered: 65 Skipped: 12



ANSWER CHOICES	RESPONSES	
Yes	51%	33
No	29%	19
No opinion/Don't know	20%	13
TOTAL		65

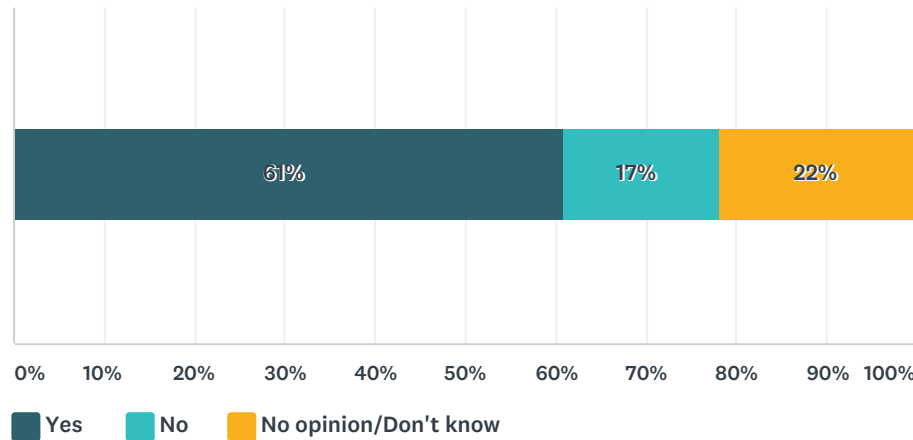
#	IF NO, PLEASE EXPLAIN WHY:	DATE
1	I'm admittedly not as educated as I need to be, but I suspect that intermediate alleles are not all equal in their degree of residual activity. I like a scoring system, but if there's sufficient data, perhaps it would be even more useful to assign a score that reflects the degree of allele activity on a scale from 0-1. Then the summary phenotype could be reflected as a quantitative score--raw data would be a scale from 0-2, but that could be transformed back to a % or 0-1 scale. Qualitative assessments of phenotype could then be assigned based on score ranges, and reported along with the associated score. Of course, if the evidence refutes this idea, then it should not be pursued. The sticky situation would be if the evidence fails to support but also fails to refute this idea (i.e. lack of evidence for a quantitative score is not the same as evidence against a quantitative score).	2/21/2015 8:42 PM
2	How to deal with increased function alleles that are due to duplications. For example, consider PersonA with CYP2D6*1 CYP2D6*1 = 1 + 1 = 2 and PersonB with 3 CYP2D6 alleles composed of CYP2D6*9 CYP2D6*1x2 (2 copies of *1 on 1 chromosome) = 0.5 + 2 = 2.5. However, both persons are categorized (based on literature today) as extensive metabolizers. Thus, two different scores are yielding the same phenotype and that is confusing.	2/20/2015 6:05 PM
3	I like the idea of quantifying function, but I don't have enough experience with the gene to know that this is the right system.	2/19/2015 3:44 PM
4	Clinical labs are not consistently reporting copy numbers which is critical for calculating the score, therefore until that happens it cannot be a reliably used metric.	2/19/2015 3:42 PM

## CPIC Term Standardization for Clinical Pharmacogenetic Test Results: alleles and phenotypes

5	probably the 1 - 0.5 - 0 classification is too rough and requires refinement. Also the assigned value may be substrate specific	2/18/2015 4:47 PM
6	Drug-drug interactions need to be included in the scoring system as well	2/17/2015 12:01 PM
7	My "yes" answer is the the question of whether the 2D6 scoring system inadequate in DESCRIBING the phenotype. I'm not sure what you mean by DETERMINING the phenotype.	2/11/2015 1:59 PM
8	The CYP2D6 scoring system does not distinguish between more functional 'decreased function' alleles (*10) and less functional 'decreased function' alleles (*41). In the CYP2D6 scoring system, a *17/*17 would be considered an EM, but perhaps IM would be more appropriate.	2/9/2015 5:10 PM
9	If a quantitative value is used it should reflect the actual quantitative activity of the allele as determined by testing.	2/9/2015 4:38 PM
10	I think it can be helpful for physicians, but not widely adopted, so not sure how well physicians understand.	2/9/2015 12:50 PM
11	The ultra rapid metabolizers will not be covered.	2/6/2015 8:36 AM
12	It may be useful for the time being but I would try to get information on the intrinsic clearance; also if you use the scoring system, need to include a score for the ultra-rapid metabolizers	2/4/2015 2:08 PM
13	For one thing it does not take into account the fact that for different drugs, the score could mean different things. Does not take into account location of the alleles relative to each other. Does not take into account whether having one functional allele actually confers normal function	2/3/2015 4:37 PM
14	This would seem to be an oversimplification. It may accurately predict a worthwhile course of action for a physician with the information we have now, but it doesn't take the extent of any decrease of activity into account, other than the drop to 0 for no activity. Also, some alleles may have substrate-dependent function. Practically, is it significantly easier for a physician to assign or use a function score of 1.5 than to simply think "one functional, one decreased allele?" However, once the activities of decreased-function alleles are better understood and assigned numbers other than 0.5, such a system could be very useful.	2/3/2015 2:20 PM
15	I would prefer a universal scoring system that includes HIGH function (that way it is not different for different genes). 0= no activity; 0.5 = reduced/low activity; 1 = normal activity (WT); 1.5 = high activity	2/3/2015 1:59 PM
16	Questionable utility, may lead to confusion (implies that activity is "exactly" 1/2 of the normal?)	2/3/2015 11:41 AM
17	You need to somehow score the multiple CYP2D6 copy alleles	2/3/2015 11:36 AM
18	The scoring system is a great concept and serves as a semi-quantitative way to distinguish challenging nuances of intermediate phenotypes. Additional data still needed to accurately predict the partially active alleles like *10 (eg, is it always a 0.25?), as well as differences across varying substrates.	2/2/2015 3:00 PM
19	Adequate on current knowledge, but ultimately needs to be fine-tuned	2/2/2015 1:41 PM
20	The gene-dose effect is not linear	2/2/2015 11:23 AM

## Q21 To date, a scoring system (e.g., CYP2D6 activity scores) for CYP2C19 has not been developed. Do you think a scoring system should be developed for CYP2C19 and possibly other enzymes?

Answered: 64 Skipped: 13

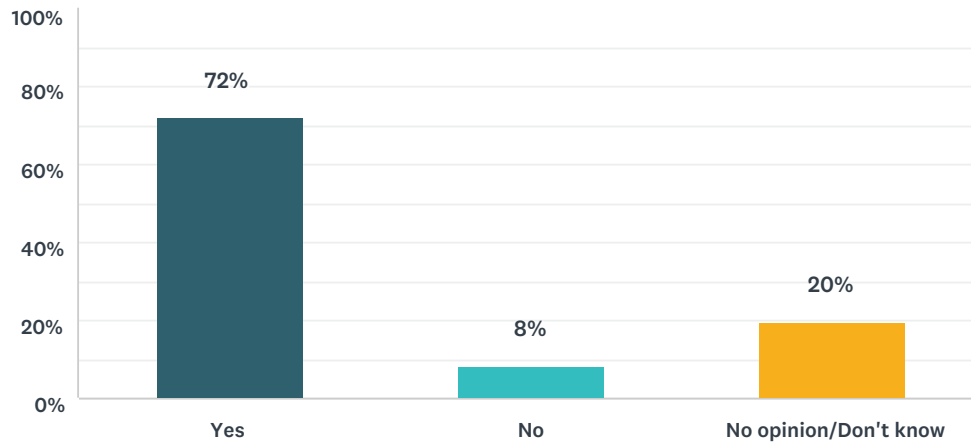


ANSWER CHOICES	RESPONSES	
Yes	61%	39
No	17%	11
No opinion/Don't know	22%	14
<b>TOTAL</b>		<b>64</b>

#	IF NO, PLEASE EXPLAIN WHY:	DATE
1	In reality, a quantitative scoring system would work if 1 lab produced all the cellular activity levels for each diplotype.	2/20/2015 6:05 PM
2	yes - qualitative system should be included	2/9/2015 4:38 PM
3	I would look to base it on the intrinsic clearance, because the drugs for these CYPs vary. It appears that you may need to involve Substrate effect with the enzyme activity.	2/4/2015 2:08 PM
4	For the same reasons listed above for 2D6 could be problematic	2/3/2015 4:37 PM
5	Questionable utility, may lead to confusion.	2/3/2015 11:41 AM
6	Given the lack of knowledge on the absolute function for many of the alleles, specifically in population outside of whites this would be difficult/ perhaps incorrect.	2/3/2015 11:40 AM
7	No evidence of clinical relevance for CYP2C19	2/2/2015 1:53 PM
8	The functional role of CYP2C19*17 requieres further anaylsis	2/2/2015 11:23 AM
9	CYP2C19 does not have nearly as many alleles/genotype classifications as CYP2D6	2/2/2015 11:12 AM

**Q22 We assume that 3 major categories of allele function are needed for CYP3A5. Do you agree (yes or no)? If no, please indicate how many you think are needed and why**

Answered: 61 Skipped: 16

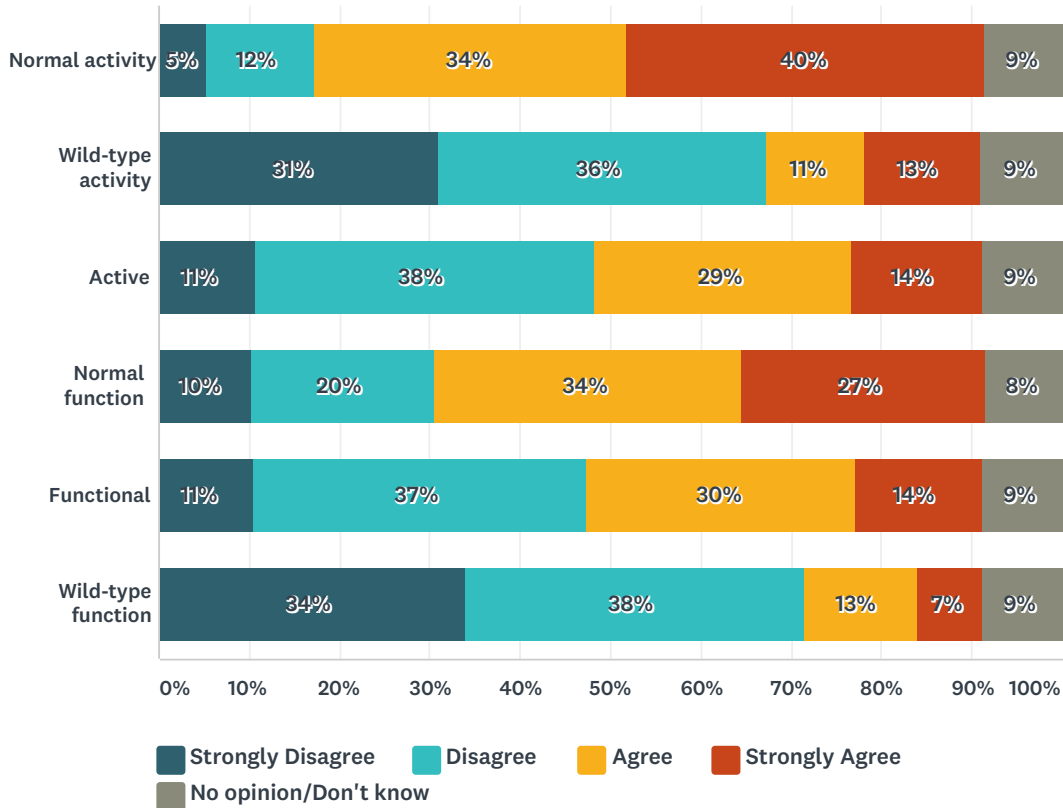


ANSWER CHOICES	RESPONSES	
Yes	72%	44
No	8%	5
No opinion/Don't know	20%	12
<b>TOTAL</b>		<b>61</b>

#	IF NO, PLEASE INDICATE HOW MANY YOU THINK ARE NEEDED AND WHY:	DATE
1	Need unknown	2/20/2015 6:09 PM
2	I don't have any experience with this gene, but now having heard the unique issues that some have raised for this gene I don't think I am in a position to give specific responses.	2/19/2015 3:46 PM
3	As before, all terms should be consistent for every gene	2/19/2015 3:44 PM
4	Given the overlap with CYP3A4, it appears that for high risk drugs CYP3A adds extended activity or plays a role when CYP3A4 alone is inhibited.	2/4/2015 2:14 PM
5	I think categories should be uniform (4 categories for ALL allelic function)	2/3/2015 2:01 PM
6	4; need 'unknown'	2/2/2015 1:41 PM

## Q23 Describe your degree of acceptance of the following terms to describe the allele function for a CYP3A5 allele with normal function/activity (e.g., CYP3A5\*1):

Answered: 61 Skipped: 16



	STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	NO OPINION/DON'T KNOW	TOTAL	WEIGHTED AVERAGE
Normal activity	5% 3	12% 7	34% 20	40% 23	9% 5	58	3.19
Wild-type activity	31% 17	36% 20	11% 6	13% 7	9% 5	55	2.06
Active	11% 6	38% 21	29% 16	14% 8	9% 5	56	2.51
Normal function	10% 6	20% 12	34% 20	27% 16	8% 5	59	2.85
Functional	11% 6	37% 21	30% 17	14% 8	9% 5	57	2.52
Wild-type function	34% 19	38% 21	13% 7	7% 4	9% 5	56	1.92

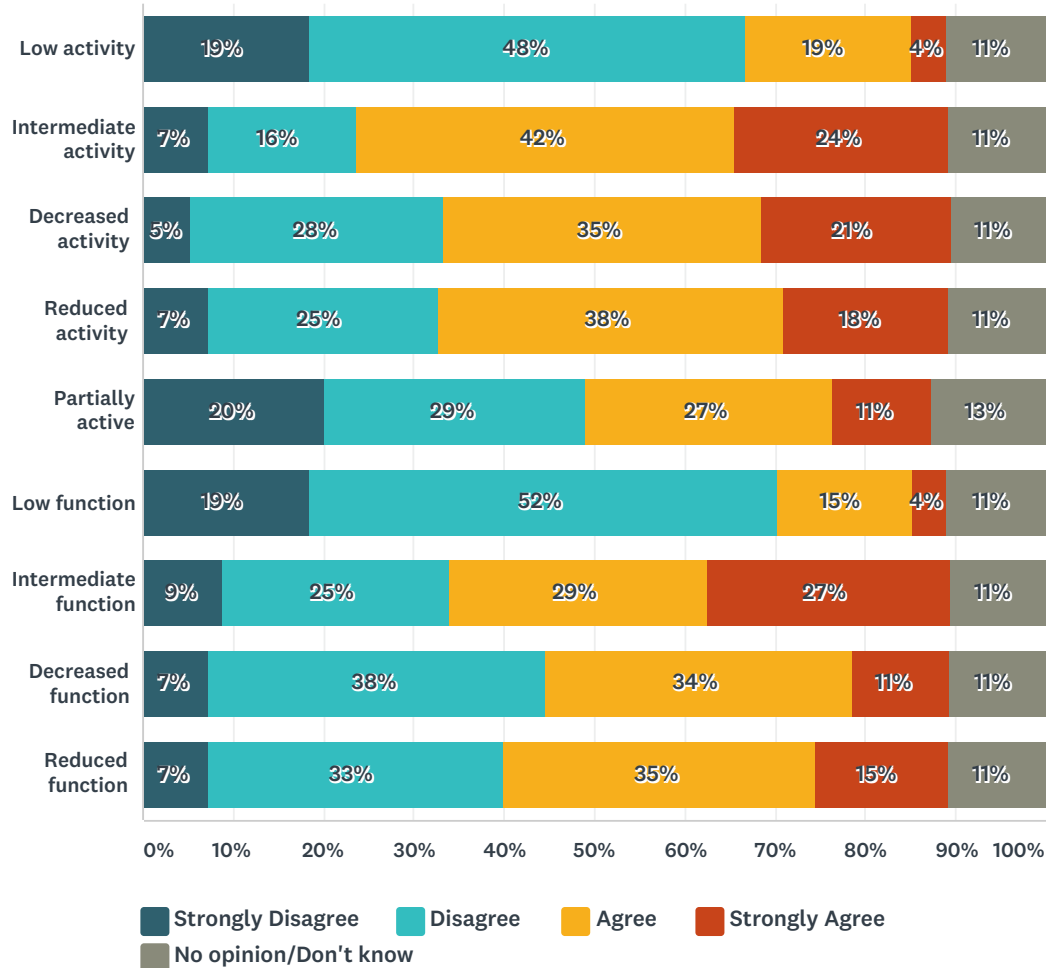
#	OTHER PLEASE SPECIFY	DATE
1	Reference activity	2/20/2015 6:09 PM
2	most prevalent allele is 3A5*3 -- that should actually be renamed *1	2/18/2015 4:49 PM
3	normal enzyme activity	2/16/2015 9:05 AM

## CPIC Term Standardization for Clinical Pharmacogenetic Test Results: alleles and phenotypes

4	Normal metabolism	2/5/2015 8:10 AM
5	AF for *3 is higher than that of *1 in many groups; calling fully-functional 3A5 "normal" or "wild-type" is inaccurate.	2/3/2015 2:23 PM
6	high expression	2/2/2015 11:54 AM

## Q24 Describe your degree of acceptance of the following terms to describe the allele function for a CYP3A5 allele with medium/some function/activity (e.g., CYP3A5\*8):

Answered: 60 Skipped: 17



	STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	NO OPINION/DON'T KNOW	TOTAL	WEIGHTED AVERAGE
Low activity	19% 10	48% 26	19% 10	4% 2	11% 6	54	2.08
Intermediate activity	7% 4	16% 9	42% 23	24% 13	11% 6	55	2.92
Decreased activity	5% 3	28% 16	35% 20	21% 12	11% 6	57	2.80
Reduced activity	7% 4	25% 14	38% 21	18% 10	11% 6	55	2.76
Partially active	20% 11	29% 16	27% 15	11% 6	13% 7	55	2.33
Low function	19% 10	52% 28	15% 8	4% 2	11% 6	54	2.04

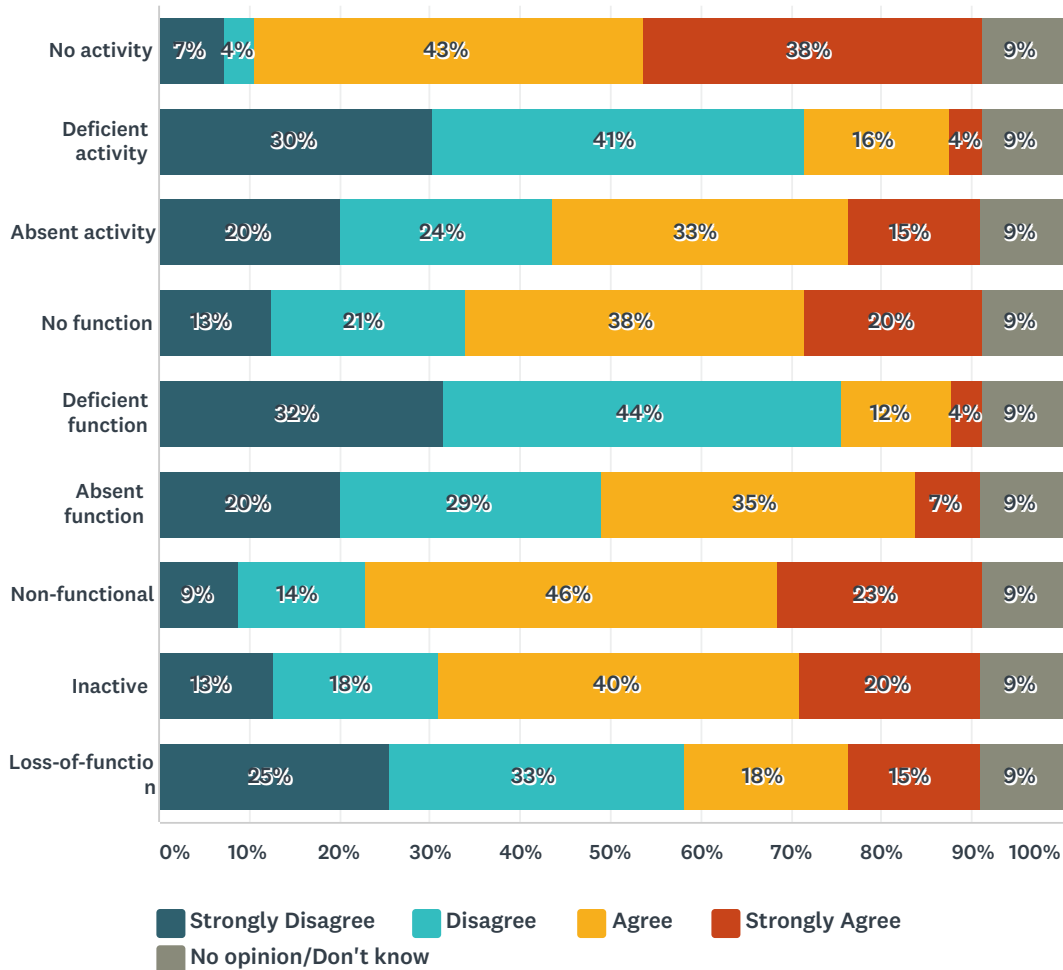
CPIC Term Standardization for Clinical Pharmacogenetic Test Results: alleles and phenotypes

Intermediate function	9% 5	25% 14	29% 16	27% 15	11% 6	56	2.82
Decreased function	7% 4	38% 21	34% 19	11% 6	11% 6	56	2.54
Reduced function	7% 4	33% 18	35% 19	15% 8	11% 6	55	2.63

#	OTHER (PLEASE SPECIFY)	DATE
1	intermediate (lower than normal) enzyme activity	2/16/2015 9:05 AM
2	decreased metabolism; reduced metabolism	2/5/2015 8:10 AM
3	Not sure that this is an important therapeutic/dosing distinction as of now	2/4/2015 2:14 PM
4	Expressor	2/2/2015 11:54 AM

## Q25 Describe your degree of acceptance of the following terms to describe the allele function for a CYP3A5 allele with no function/activity (e.g., CYP3A5\*3):

Answered: 62 Skipped: 15



	STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	NO OPINION/DON'T KNOW	TOTAL	WEIGHTED AVERAGE
No activity	7% 4	4% 2	43% 24	38% 21	9% 5	56	3.22
Deficient activity	30% 17	41% 23	16% 9	4% 2	9% 5	56	1.92
Absent activity	20% 11	24% 13	33% 18	15% 8	9% 5	55	2.46
No function	13% 7	21% 12	38% 21	20% 11	9% 5	56	2.71
Deficient function	32% 18	44% 25	12% 7	4% 2	9% 5	57	1.87
Absent function	20% 11	29% 16	35% 19	7% 4	9% 5	55	2.32

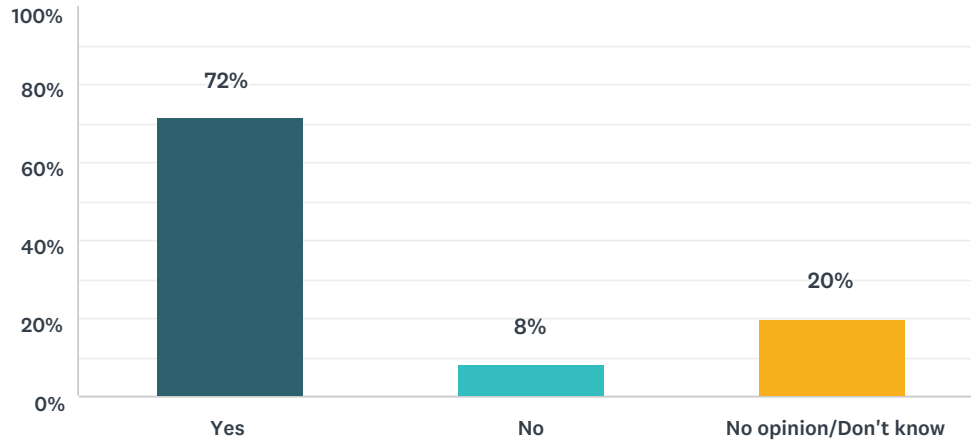
CPIC Term Standardization for Clinical Pharmacogenetic Test Results: alleles and phenotypes

Non-functional	9% 5	14% 8	46% 26	23% 13	9% 5	57	2.90
Inactive	13% 7	18% 10	40% 22	20% 11	9% 5	55	2.74
Loss-of-function	25% 14	33% 18	18% 10	15% 8	9% 5	55	2.24

#	OTHER (PLEASE SPECIFY)	DATE
1	absent enzyme activity	2/16/2015 9:05 AM
2	Non-expressor	2/2/2015 11:54 AM

**Q26 We assume that 3 major categories of phenotype are needed for CYP3A5. Do you agree (yes or no)? If no, please indicate how many you think are needed and why:**

Answered: 60 Skipped: 17

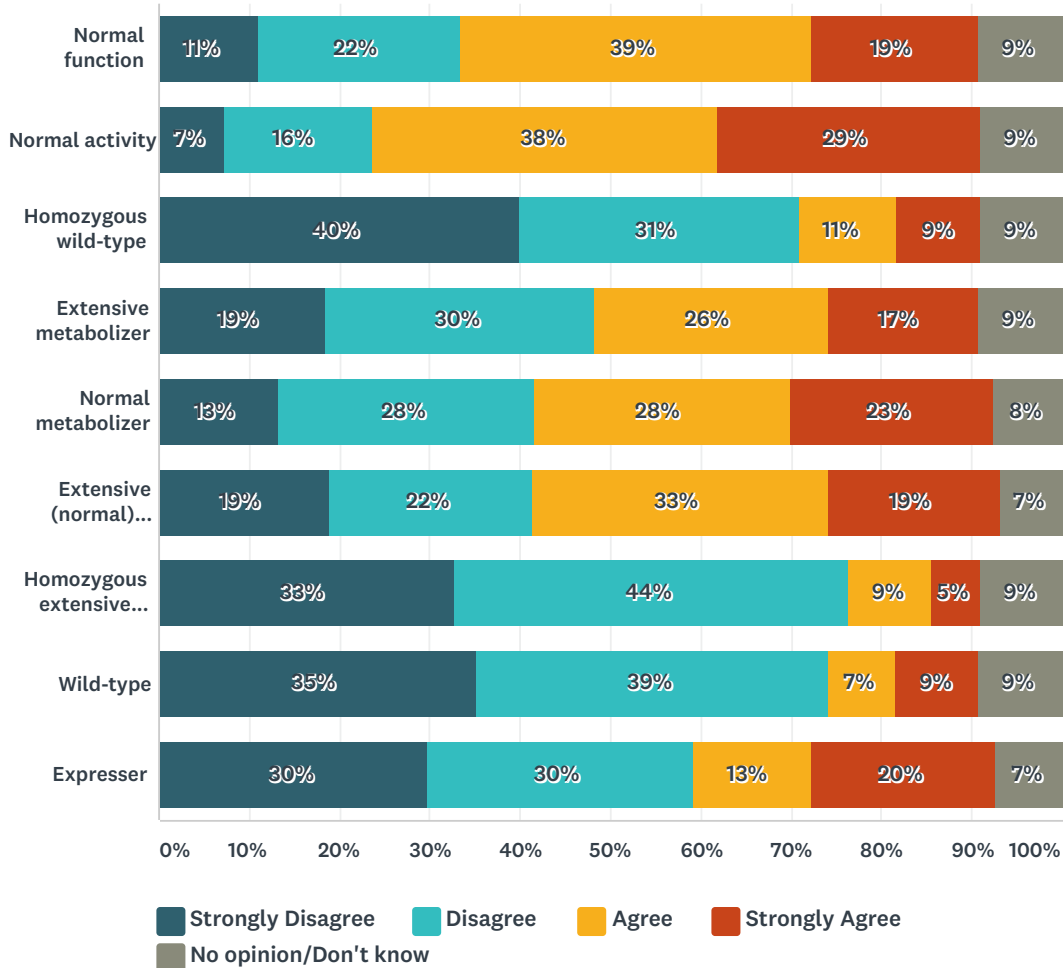


ANSWER CHOICES	RESPONSES	
Yes	72%	43
No	8%	5
No opinion/Don't know	20%	12
<b>TOTAL</b>		<b>60</b>

#	IF NO, PLEASE INDICATE HOW MANY YOU THINK ARE NEEDED AND WHY:	DATE
1	Need unknown	2/20/2015 6:11 PM
2	See last comment	2/19/2015 3:46 PM
3	I have not been convinced that more than 2 carries a dosing distinction at this point.	2/4/2015 2:20 PM
4	Keep the number of categories UNIVERSAL (4 - LOF; reduced; WT; high)	2/3/2015 2:03 PM
5	need categories for genotypes with unknown alleles	2/2/2015 1:43 PM

## Q27 Describe your degree of acceptance of the following terms to describe the presumed phenotype for CYP3A5 in an individual with normal CYP3A5 function/activity (e.g., CYP3A5\*1/\*1):

Answered: 60 Skipped: 17



	STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	NO OPINION/DON'T KNOW	TOTAL	WEIGHTED AVERAGE
Normal function	11% 6	22% 12	39% 21	19% 10	9% 5	54	2.71
Normal activity	7% 4	16% 9	38% 21	29% 16	9% 5	55	2.98
Homozygous wild-type	40% 22	31% 17	11% 6	9% 5	9% 5	55	1.88
Extensive metabolizer	19% 10	30% 16	26% 14	17% 9	9% 5	54	2.45
Normal metabolizer	13% 7	28% 15	28% 15	23% 12	8% 4	53	2.65
Extensive (normal) metabolizer	19% 11	22% 13	33% 19	19% 11	7% 4	58	2.56

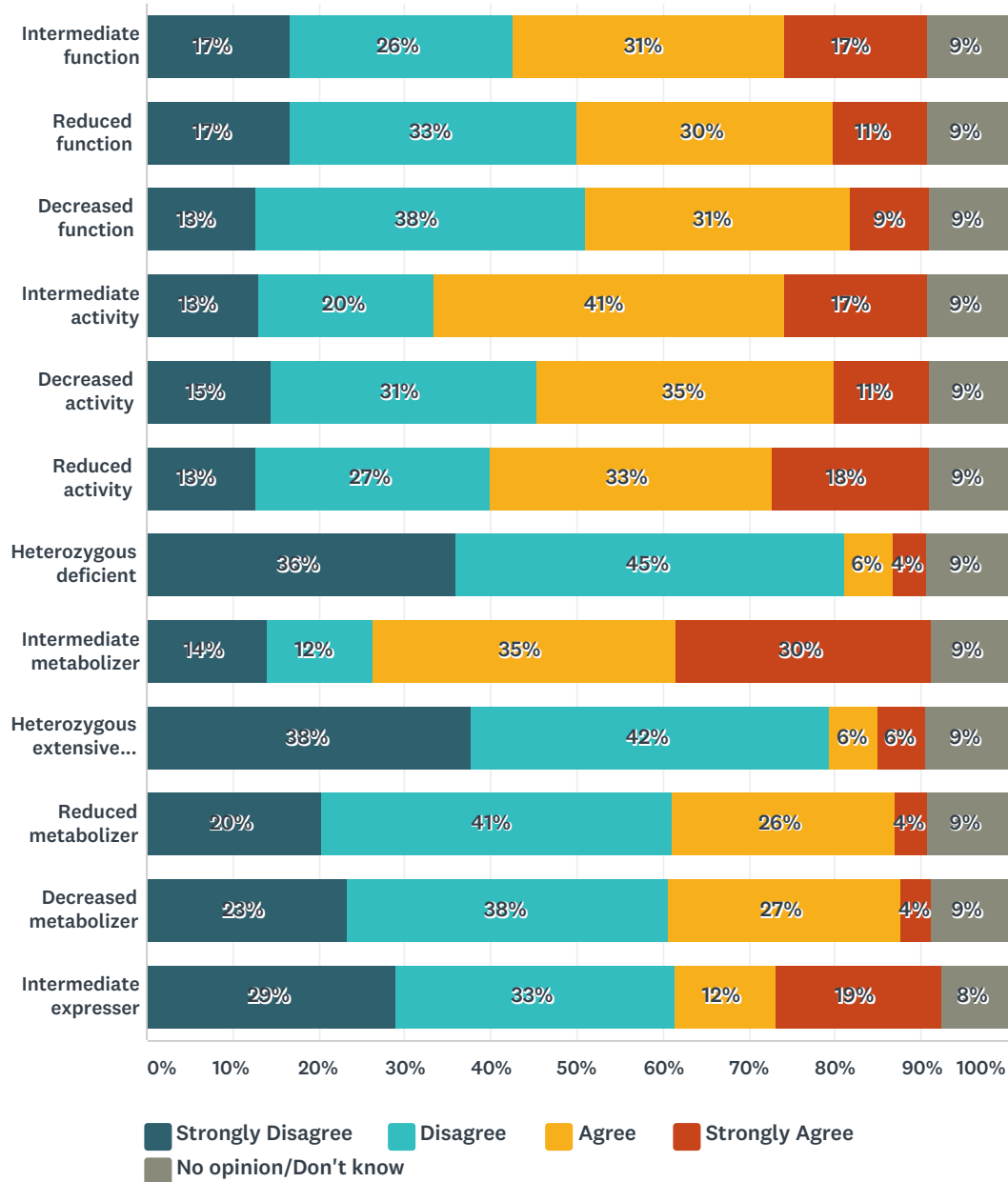
CPIC Term Standardization for Clinical Pharmacogenetic Test Results: alleles and phenotypes

Homozygous extensive metabolizer	33% 18	44% 24	9% 5	5% 3	9% 5	55	1.86
Wild-type	35% 19	39% 21	7% 4	9% 5	9% 5	54	1.90
Expresser	30% 16	30% 16	13% 7	20% 11	7% 4	54	2.26

#	OTHER (PLEASE SPECIFY)	DATE
1	Reference function	2/20/2015 6:11 PM
2	Homozygous normal metabolizer	2/18/2015 11:24 AM
3	"Full function" would also work. Just not "normal" or "wild-type."	2/3/2015 2:41 PM
4	there should be a caveat on this descriptor that states that this is low frequency (not common) in white and more frequent in blacks ect..	2/3/2015 11:48 AM

### Q28 Describe your degree of acceptance of the following terms to describe the presumed phenotype for CYP3A5 in an individual with medium/some CYP3A5 function/activity (e.g., CYP3A5\*1/\*3):

Answered: 60 Skipped: 17



	STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	NO OPINION/DON'T KNOW	TOTAL	WEIGHTED AVERAGE
Intermediate function	17% 9	26% 14	31% 17	17% 9	9% 5	54	2.53
Reduced function	17% 9	33% 18	30% 16	11% 6	9% 5	54	2.39

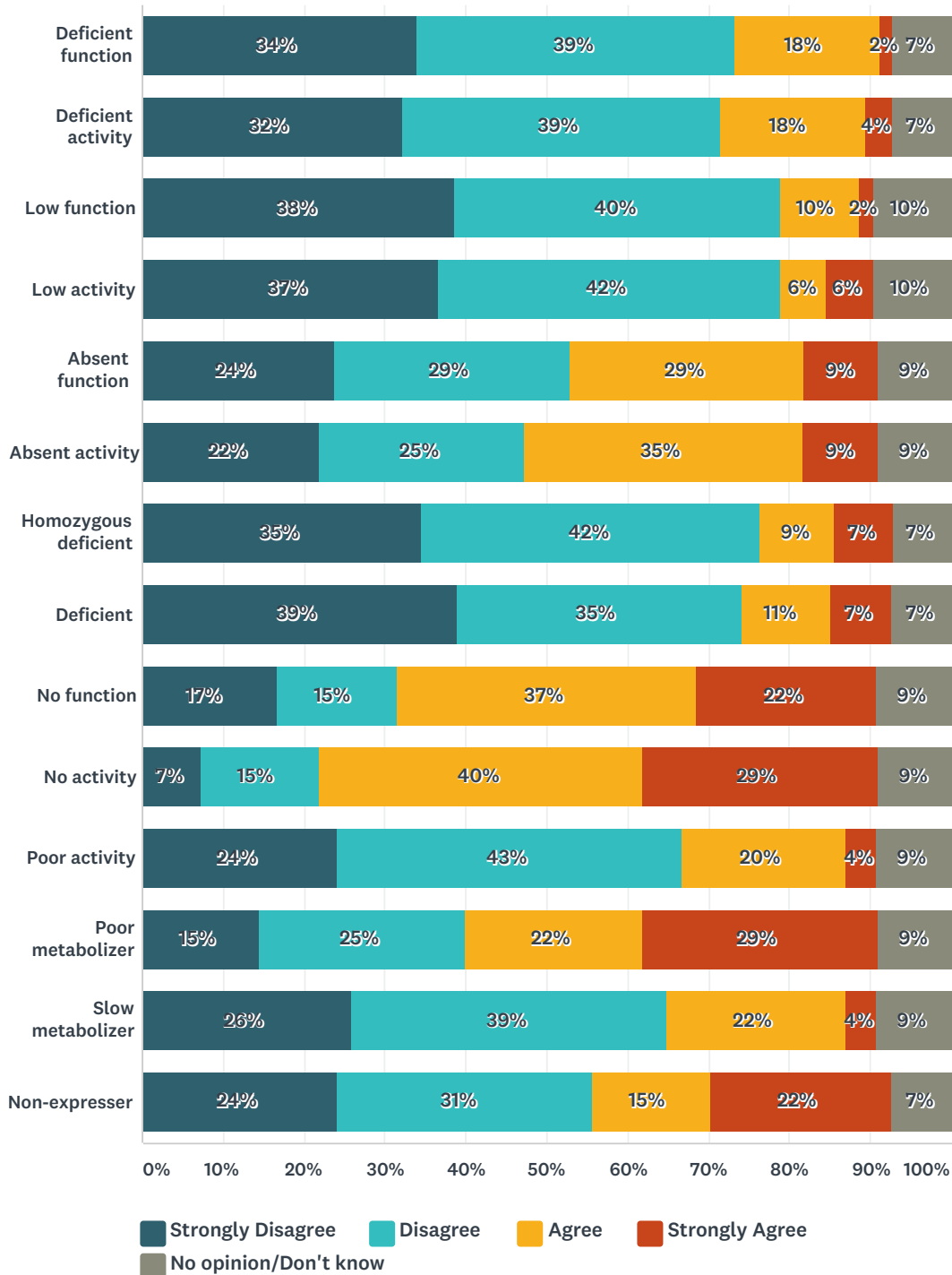
CPIC Term Standardization for Clinical Pharmacogenetic Test Results: alleles and phenotypes

Decreased function	13% 7	38% 21	31% 17	9% 5	9% 5	55	2.40
Intermediate activity	13% 7	20% 11	41% 22	17% 9	9% 5	54	2.67
Decreased activity	15% 8	31% 17	35% 19	11% 6	9% 5	55	2.46
Reduced activity	13% 7	27% 15	33% 18	18% 10	9% 5	55	2.62
Heterozygous deficient	36% 19	45% 24	6% 3	4% 2	9% 5	53	1.75
Intermediate metabolizer	14% 8	12% 7	35% 20	30% 17	9% 5	57	2.88
Heterozygous extensive metabolizer	38% 20	42% 22	6% 3	6% 3	9% 5	53	1.77
Reduced metabolizer	20% 11	41% 22	26% 14	4% 2	9% 5	54	2.14
Decreased metabolizer	23% 13	38% 21	27% 15	4% 2	9% 5	56	2.12
Intermediate expresser	29% 15	33% 17	12% 6	19% 10	8% 4	52	2.23

#	OTHER (PLEASE SPECIFY)	DATE
1	heterozygous expresser	2/18/2015 4:52 PM
2	Heterozygous decreased metabolizer	2/18/2015 11:24 AM
3	intermediate (less than normal) metabolizer	2/16/2015 9:05 AM
4	decreased metabolism; reduced metabolism	2/5/2015 8:12 AM
5	Partially Decreased Metabolizer	2/4/2015 3:22 PM
6	"reduced" or "decreased" make little sense here, when average activity is so low	2/3/2015 2:41 PM

### Q29 Describe your degree of acceptance of the following terms to describe the presumed phenotype for CYP3A5 in an individual with no CYP3A5 function/activity (e.g., CYP3A5\*3/\*3):

Answered: 60 Skipped: 17



STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	NO OPINION/DON'T KNOW	TOTAL	WEIGHTED AVERAGE
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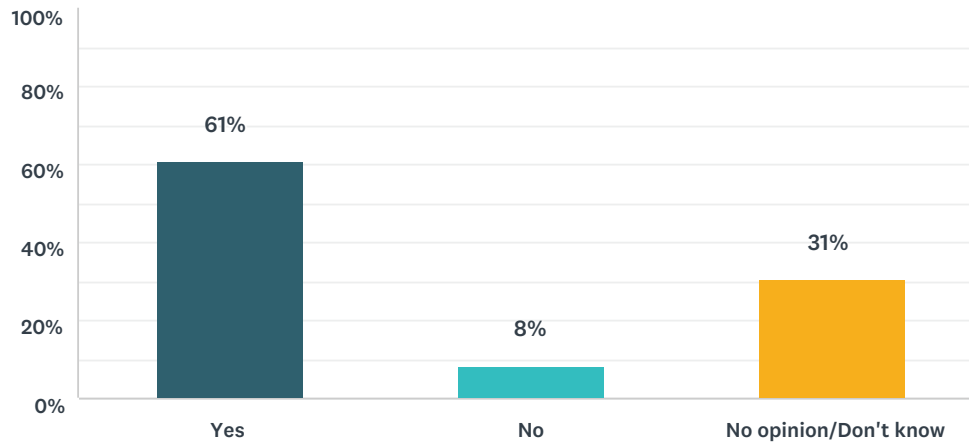
CPIC Term Standardization for Clinical Pharmacogenetic Test Results: alleles and phenotypes

Deficient function	34% 19	39% 22	18% 10	2% 1	7% 4	56	1.87
Deficient activity	32% 18	39% 22	18% 10	4% 2	7% 4	56	1.92
Low function	38% 20	40% 21	10% 5	2% 1	10% 5	52	1.72
Low activity	37% 19	42% 22	6% 3	6% 3	10% 5	52	1.79
Absent function	24% 13	29% 16	29% 16	9% 5	9% 5	55	2.26
Absent activity	22% 12	25% 14	35% 19	9% 5	9% 5	55	2.34
Homozygous deficient	35% 19	42% 23	9% 5	7% 4	7% 4	55	1.88
Deficient	39% 21	35% 19	11% 6	7% 4	7% 4	54	1.86
No function	17% 9	15% 8	37% 20	22% 12	9% 5	54	2.71
No activity	7% 4	15% 8	40% 22	29% 16	9% 5	55	3.00
Poor activity	24% 13	43% 23	20% 11	4% 2	9% 5	54	2.04
Poor metabolizer	15% 8	25% 14	22% 12	29% 16	9% 5	55	2.72
Slow metabolizer	26% 14	39% 21	22% 12	4% 2	9% 5	54	2.04
Non-expresser	24% 13	31% 17	15% 8	22% 12	7% 4	54	2.38

#	OTHER (PLEASE SPECIFY)	DATE
1	wild type	2/18/2015 4:52 PM
2	No metabolism; non-metabolizer	2/5/2015 8:12 AM
3	Decreased Metabolizer	2/4/2015 3:22 PM

Q30 We assume that 4 major categories of allele function are needed for UGT1A1. Do you agree (yes or no)? If no, please indicate how many you think are needed and why:

Answered: 59 Skipped: 18

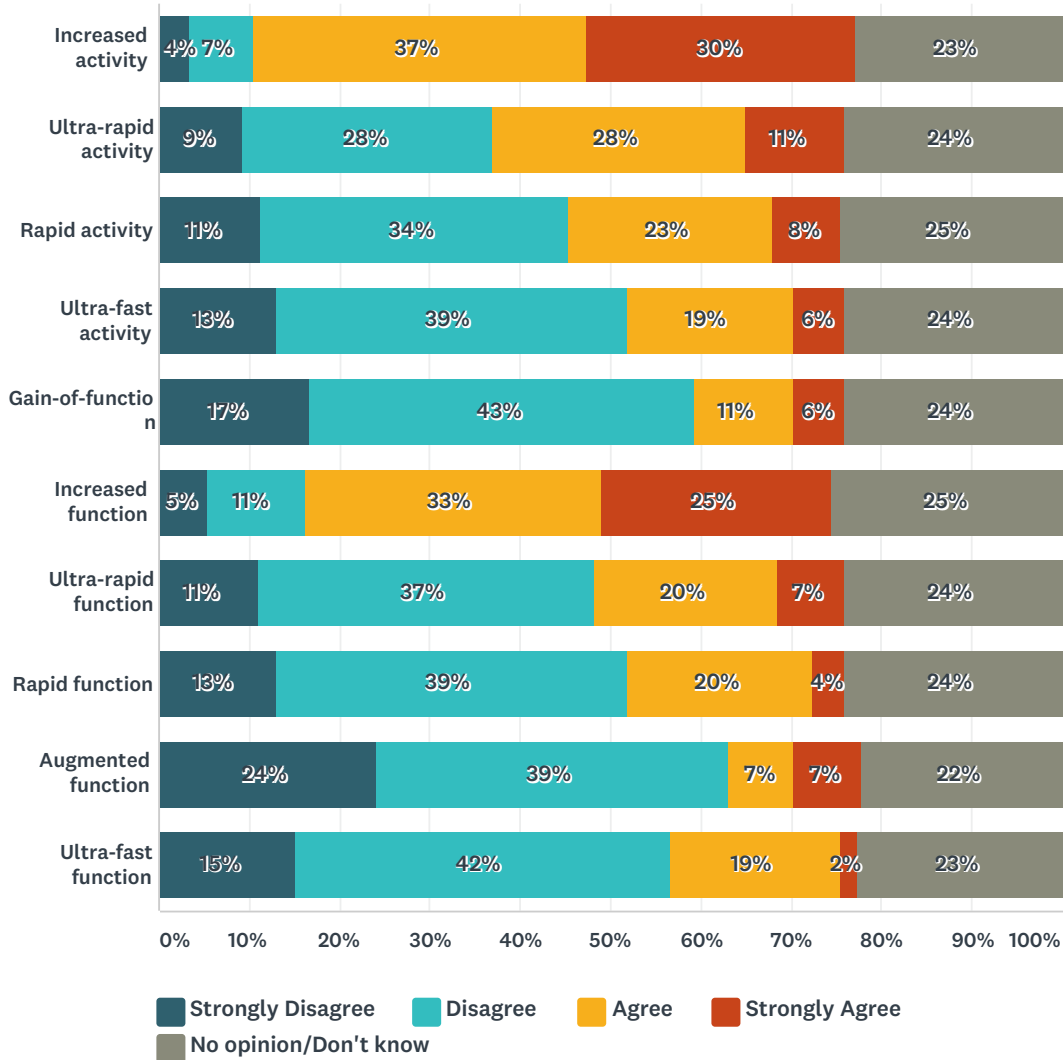


ANSWER CHOICES	RESPONSES	
Yes	61%	36
No	8%	5
No opinion/Don't know	31%	18
<b>TOTAL</b>		<b>59</b>

#	IF NO, PLEASE INDICATE HOW MANY YOU THINK ARE NEEDED AND WHY:	DATE
1	There is also UGT1A1 *37. We include it in the AGI assay.	2/3/2015 4:45 PM
2	This doesn't account for rare deleterious variants.	2/3/2015 2:36 AM
3	NO convinving evidence of clinical relevance of 4 categories	2/2/2015 1:58 PM
4	need category for unknown	2/2/2015 1:45 PM

### Q31 Describe your degree of acceptance of the following terms to describe the allele function for a UGT1A1 allele with high function/activity (e.g., UGT1A1\*36 (5 TA repeats)):

Answered: 58 Skipped: 19



	STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	NO OPINION/DON'T KNOW	TOTAL	WEIGHTED AVERAGE
Increased activity	4% 2	7% 4	37% 21	30% 17	23% 13	57	3.20
Ultra-rapid activity	9% 5	28% 15	28% 15	11% 6	24% 13	54	2.54
Rapid activity	11% 6	34% 18	23% 12	8% 4	25% 13	53	2.35
Ultra-fast activity	13% 7	39% 21	19% 10	6% 3	24% 13	54	2.22
Gain-of-function	17% 9	43% 23	11% 6	6% 3	24% 13	54	2.07

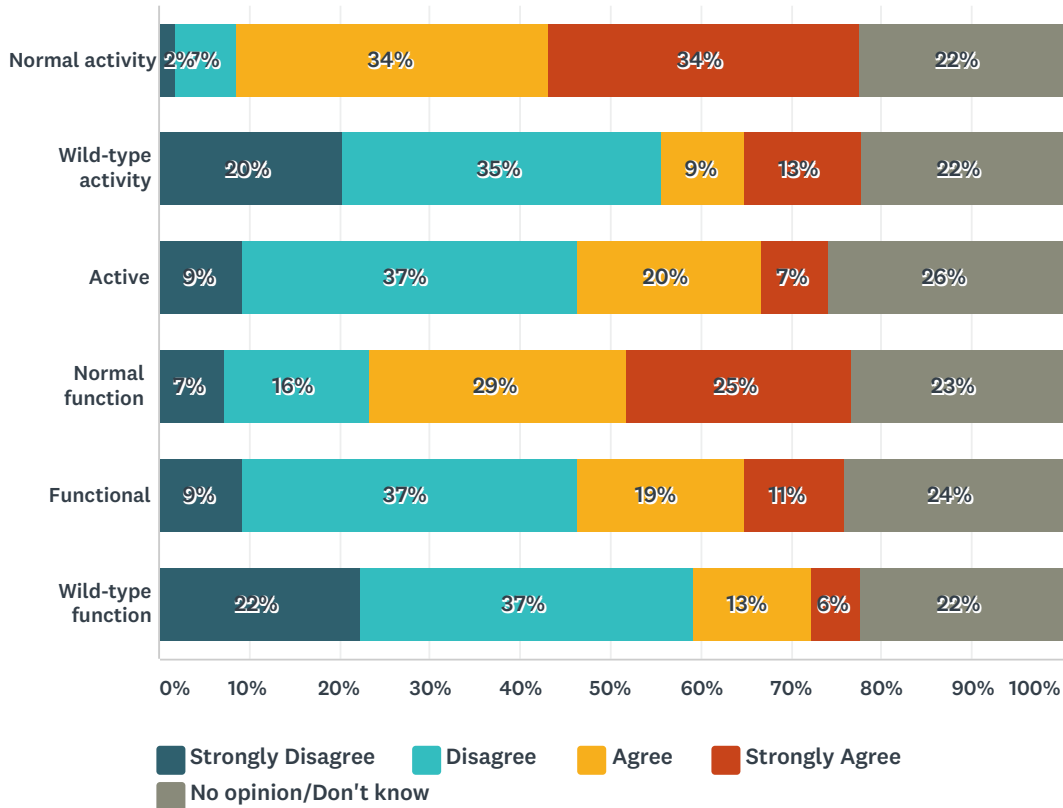
CPIC Term Standardization for Clinical Pharmacogenetic Test Results: alleles and phenotypes

Increased function	5% 3	11% 6	33% 18	25% 14	25% 14	55	3.05
Ultra-rapid function	11% 6	37% 20	20% 11	7% 4	24% 13	54	2.32
Rapid function	13% 7	39% 21	20% 11	4% 2	24% 13	54	2.20
Augmented function	24% 13	39% 21	7% 4	7% 4	22% 12	54	1.98
Ultra-fast function	15% 8	42% 22	19% 10	2% 1	23% 12	53	2.10

#	OTHER (PLEASE SPECIFY)	DATE
1	increased enzyme activity	2/16/2015 9:05 AM
2	High activity	2/3/2015 11:49 AM

### Q32 Describe your degree of acceptance of the following terms to describe the allele function for a UGT1A1 allele with normal function/activity (e.g., UGT1A1\*1 (6 TA repeats)):

Answered: 58 Skipped: 19

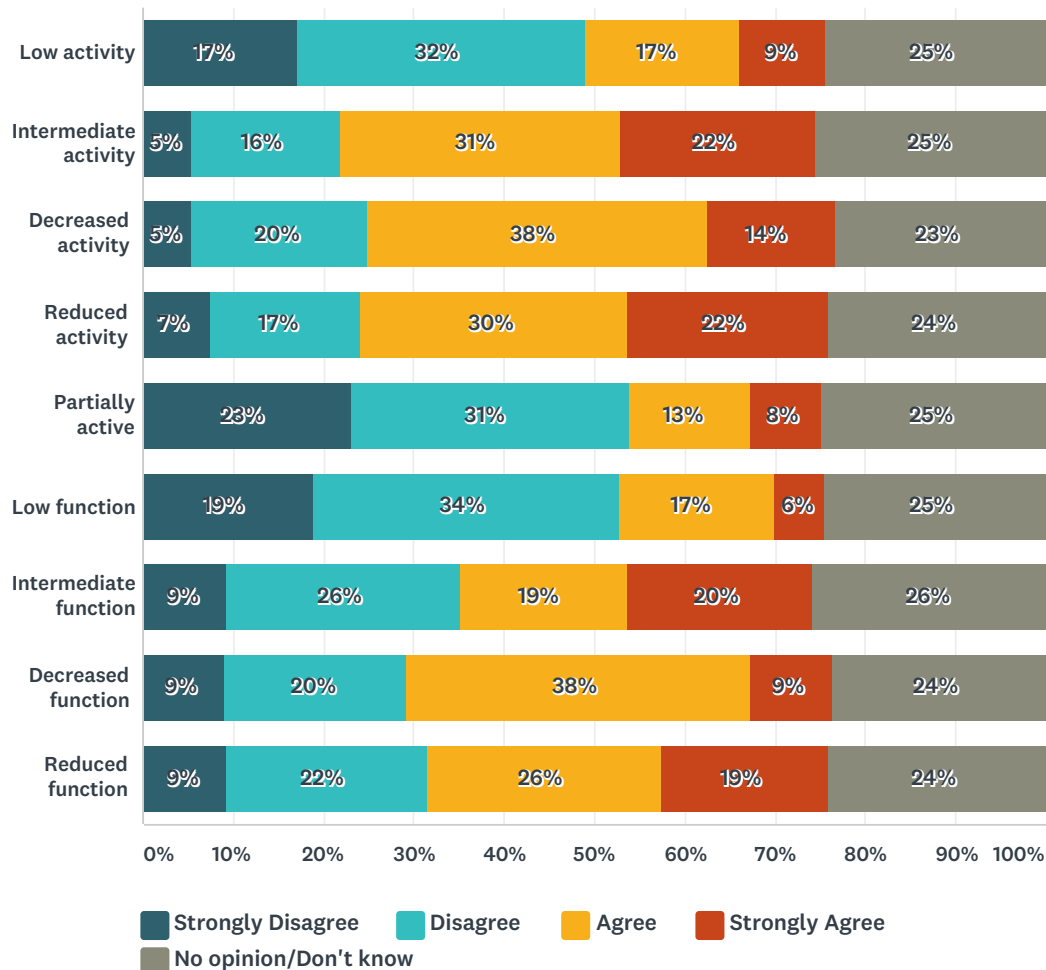


	STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	NO OPINION/DON'T KNOW	TOTAL	WEIGHTED AVERAGE
Normal activity	2% 1	7% 4	34% 20	34% 20	22% 13	58	3.31
Wild-type activity	20% 11	35% 19	9% 5	13% 7	22% 12	54	2.19
Active	9% 5	37% 20	20% 11	7% 4	26% 14	54	2.35
Normal function	7% 4	16% 9	29% 16	25% 14	23% 13	56	2.93
Functional	9% 5	37% 20	19% 10	11% 6	24% 13	54	2.41
Wild-type function	22% 12	37% 20	13% 7	6% 3	22% 12	54	2.02

#	OTHER PLEASE SPECIFY	DATE
1	Reference activity	2/20/2015 6:16 PM
2	normal enzyme activity	2/16/2015 9:05 AM

### Q33 Describe your degree of acceptance of the following terms to describe the allele function for a UGT1A1 allele with medium/some function/activity (e.g., UGT1A1\*28 (7 TA repeats)):

Answered: 58 Skipped: 19



	STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	NO OPINION/DON'T KNOW	TOTAL	WEIGHTED AVERAGE
Low activity	17% 9	32% 17	17% 9	9% 5	25% 13	53	2.25
Intermediate activity	5% 3	16% 9	31% 17	22% 12	25% 14	55	2.93
Decreased activity	5% 3	20% 11	38% 21	14% 8	23% 13	56	2.79
Reduced activity	7% 4	17% 9	30% 16	22% 12	24% 13	54	2.88
Partially active	23% 12	31% 16	13% 7	8% 4	25% 13	52	2.08
Low function	19% 10	34% 18	17% 9	6% 3	25% 13	53	2.13

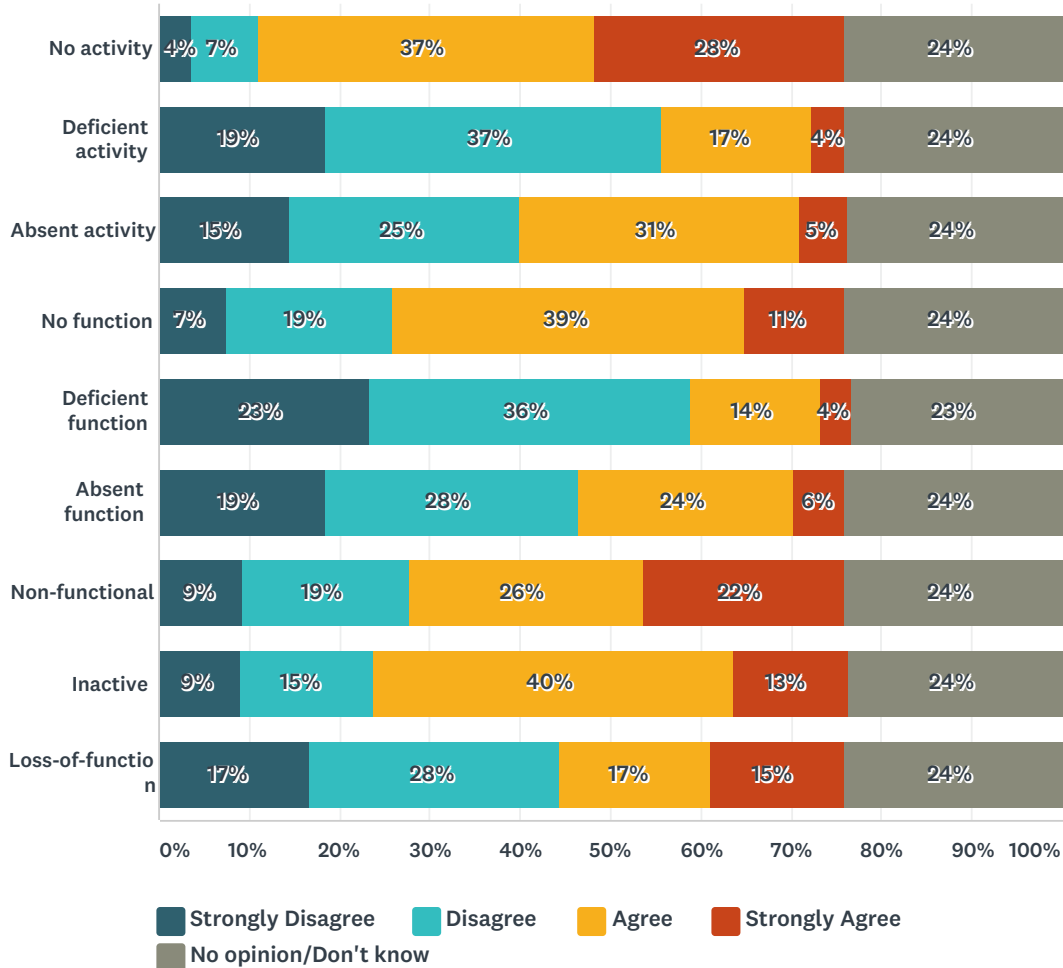
CPIC Term Standardization for Clinical Pharmacogenetic Test Results: alleles and phenotypes

Intermediate function	9% 5	26% 14	19% 10	20% 11	26% 14	54	2.67
Decreased function	9% 5	20% 11	38% 21	9% 5	24% 13	55	2.62
Reduced function	9% 5	22% 12	26% 14	19% 10	24% 13	54	2.71

#	OTHER (PLEASE SPECIFY)	DATE
1	intermediate (less than normal) enzyme activity	2/16/2015 9:05 AM

### Q34 Describe your degree of acceptance of the following terms to describe the allele function for a UGT1A1 allele with no function/activity (e.g., UGT1A1\*15):

Answered: 58 Skipped: 19



	STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	NO OPINION/DON'T KNOW	TOTAL	WEIGHTED AVERAGE
No activity	4% 2	7% 4	37% 20	28% 15	24% 13	54	3.17
Deficient activity	19% 10	37% 20	17% 9	4% 2	24% 13	54	2.07
Absent activity	15% 8	25% 14	31% 17	5% 3	24% 13	55	2.36
No function	7% 4	19% 10	39% 21	11% 6	24% 13	54	2.71
Deficient function	23% 13	36% 20	14% 8	4% 2	23% 13	56	1.98
Absent function	19% 10	28% 15	24% 13	6% 3	24% 13	54	2.22

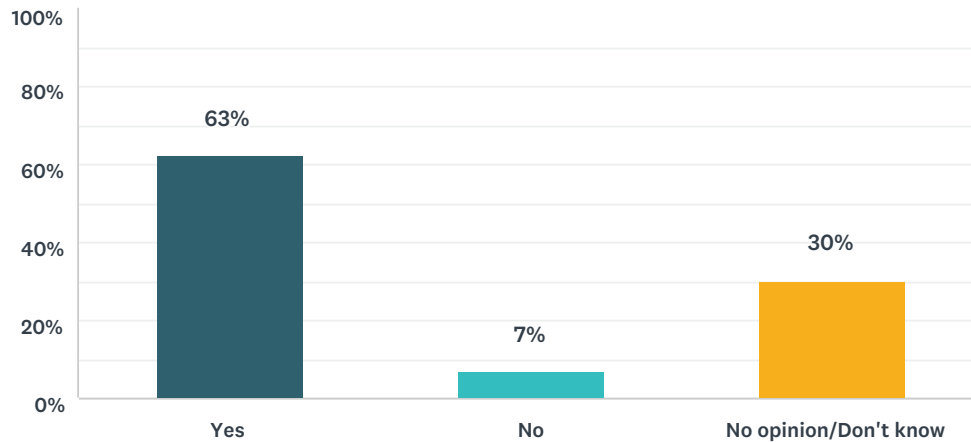
CPIC Term Standardization for Clinical Pharmacogenetic Test Results: alleles and phenotypes

Non-functional	9% 5	19% 10	26% 14	22% 12	24% 13	54	2.80
Inactive	9% 5	15% 8	40% 22	13% 7	24% 13	55	2.74
Loss-of-function	17% 9	28% 15	17% 9	15% 8	24% 13	54	2.39

#	OTHER (PLEASE SPECIFY)	DATE
1	absent enzyme activity	2/16/2015 9:05 AM

**Q35 We assume that 4 major categories of phenotype are needed for UGT1A1. Do you agree (yes or no)? If no, please indicate how many you think are needed and why:**

Answered: 56 Skipped: 21

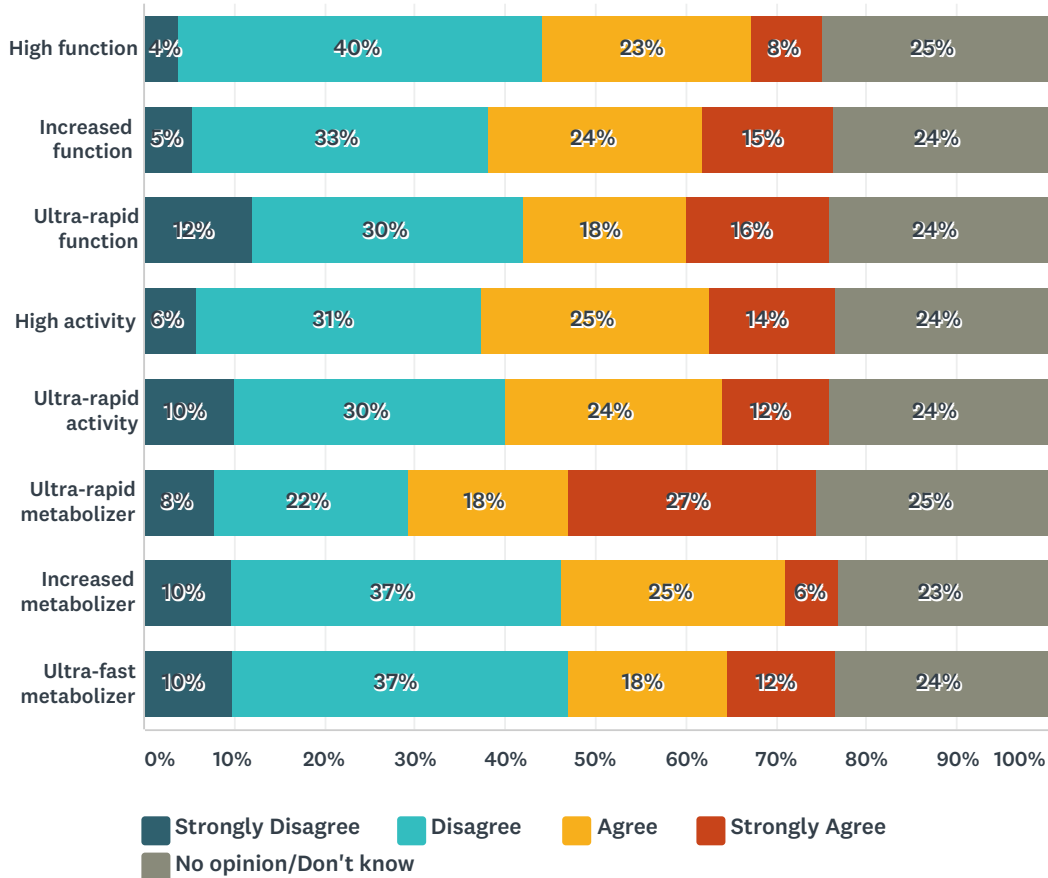


ANSWER CHOICES	RESPONSES	
Yes	63%	35
No	7%	4
No opinion/Don't know	30%	17
<b>TOTAL</b>		<b>56</b>

#	IF NO, PLEASE INDICATE HOW MANY YOU THINK ARE NEEDED AND WHY:	DATE
1	Need unknown	2/20/2015 6:16 PM
2	UGT1A1 genotyping assays also include 836 and *37	2/3/2015 4:49 PM
3	No evidence of clinical relevance of 4 phenotypes	2/2/2015 2:00 PM
4	need categories for genotypes with unknown alleles	2/2/2015 1:47 PM

### Q36 Describe your degree of acceptance of the following terms to describe the presumed phenotype for UGT1A1 in an individual with high UGT1A1 function/activity (e.g., UGT1A1\*36/\*36):

Answered: 55 Skipped: 22



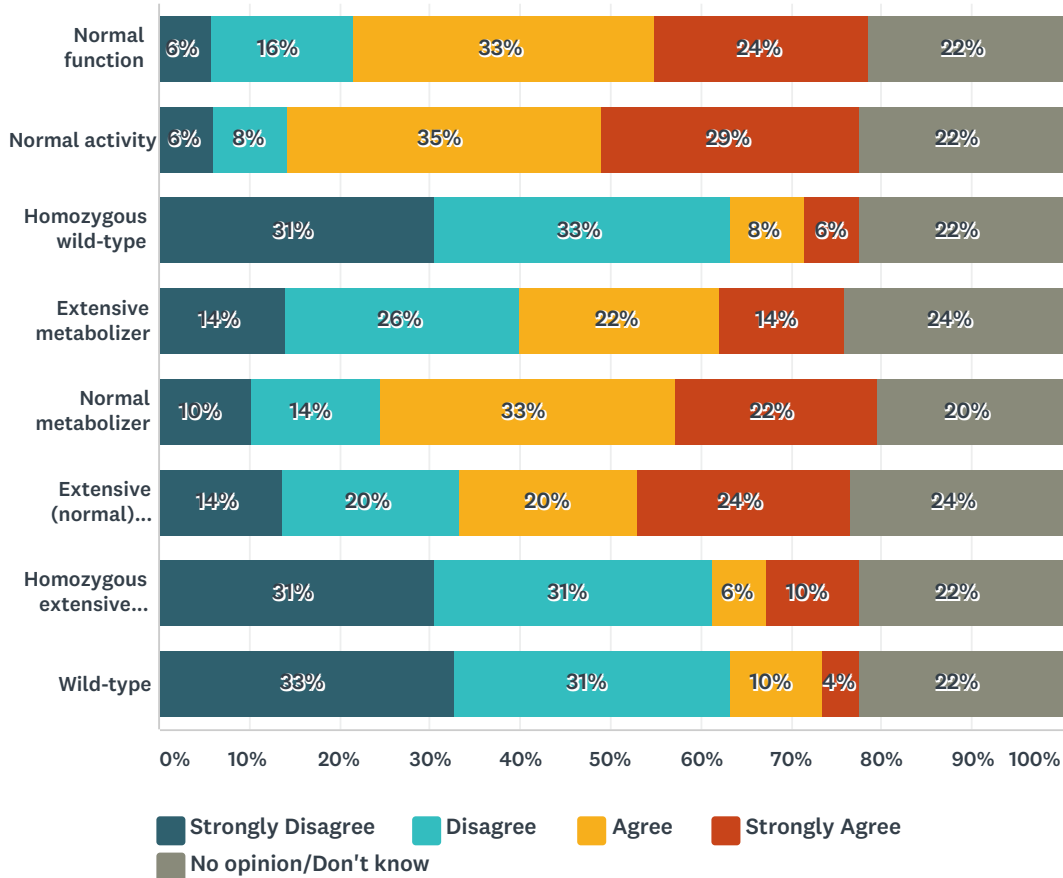
	STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	NO OPINION/DON'T KNOW	TOTAL	WEIGHTED AVERAGE
High function	4% 2	40% 21	23% 12	8% 4	25% 13	52	2.46
Increased function	5% 3	33% 18	24% 13	15% 8	24% 13	55	2.62
Ultra-rapid function	12% 6	30% 15	18% 9	16% 8	24% 12	50	2.50
High activity	6% 3	31% 16	25% 13	14% 7	24% 12	51	2.62
Ultra-rapid activity	10% 5	30% 15	24% 12	12% 6	24% 12	50	2.50
Ultra-rapid metabolizer	8% 4	22% 11	18% 9	27% 14	25% 13	51	2.87
Increased metabolizer	10% 5	37% 19	25% 13	6% 3	23% 12	52	2.35
Ultra-fast metabolizer	10% 5	37% 19	18% 9	12% 6	24% 12	51	2.41

## CPIC Term Standardization for Clinical Pharmacogenetic Test Results: alleles and phenotypes

#	OTHER (PLEASE SPECIFY)	DATE
1	Increased activity	2/21/2015 8:52 PM
2	Very increased function	2/20/2015 6:16 PM
3	Increased Activity	2/20/2015 5:13 PM
4	Homozygous increased metabolizer	2/18/2015 11:27 AM

### Q37 Describe your degree of acceptance of the following terms to describe the presumed phenotype for UGT1A1 in an individual with normal UGT1A1 function/activity (e.g., UGT1A1\*1/\*1):

Answered: 54 Skipped: 23



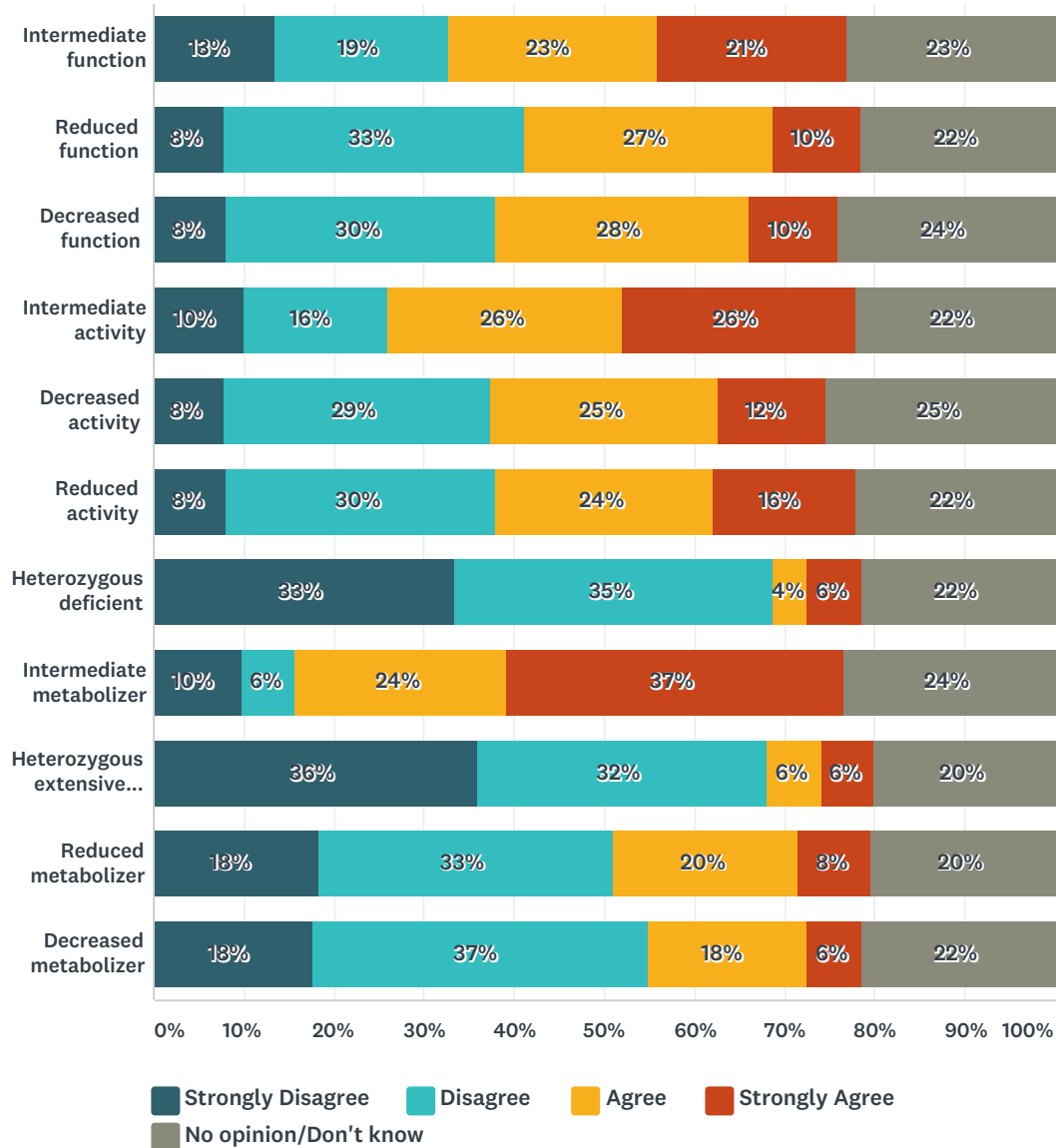
	STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	NO OPINION/DON'T KNOW	TOTAL	WEIGHTED AVERAGE
Normal function	6% 3	16% 8	33% 17	24% 12	22% 11	51	2.95
Normal activity	6% 3	8% 4	35% 17	29% 14	22% 11	49	3.11
Homozygous wild-type	31% 15	33% 16	8% 4	6% 3	22% 11	49	1.87
Extensive metabolizer	14% 7	26% 13	22% 11	14% 7	24% 12	50	2.47
Normal metabolizer	10% 5	14% 7	33% 16	22% 11	20% 10	49	2.85
Extensive (normal) metabolizer	14% 7	20% 10	20% 10	24% 12	24% 12	51	2.69
Homozygous extensive metabolizer	31% 15	31% 15	6% 3	10% 5	22% 11	49	1.95

CPIC Term Standardization for Clinical Pharmacogenetic Test Results: alleles and phenotypes

Wild-type	33%	31%	10%	4%	22%		
	16	15	5	2	11	49	1.82
#	OTHER (PLEASE SPECIFY)						DATE
1	Reference function						2/20/2015 6:16 PM
2	Homozygous normal metabolizer						2/18/2015 11:27 AM

### Q38 Describe your degree of acceptance of the following terms to describe the presumed phenotype for UGT1A1 in an individual with medium/some UGT1A1 function/activity (e.g., UGT1A1\*1/\*28):

Answered: 55 Skipped: 22



	STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	NO OPINION/DON'T KNOW	TOTAL	WEIGHTED AVERAGE
Intermediate function	13% 7	19% 10	23% 12	21% 11	23% 12	52	2.67
Reduced function	8% 4	33% 17	27% 14	10% 5	22% 11	51	2.50
Decreased function	8% 4	30% 15	28% 14	10% 5	24% 12	50	2.53
Intermediate activity	10% 5	16% 8	26% 13	26% 13	22% 11	50	2.87

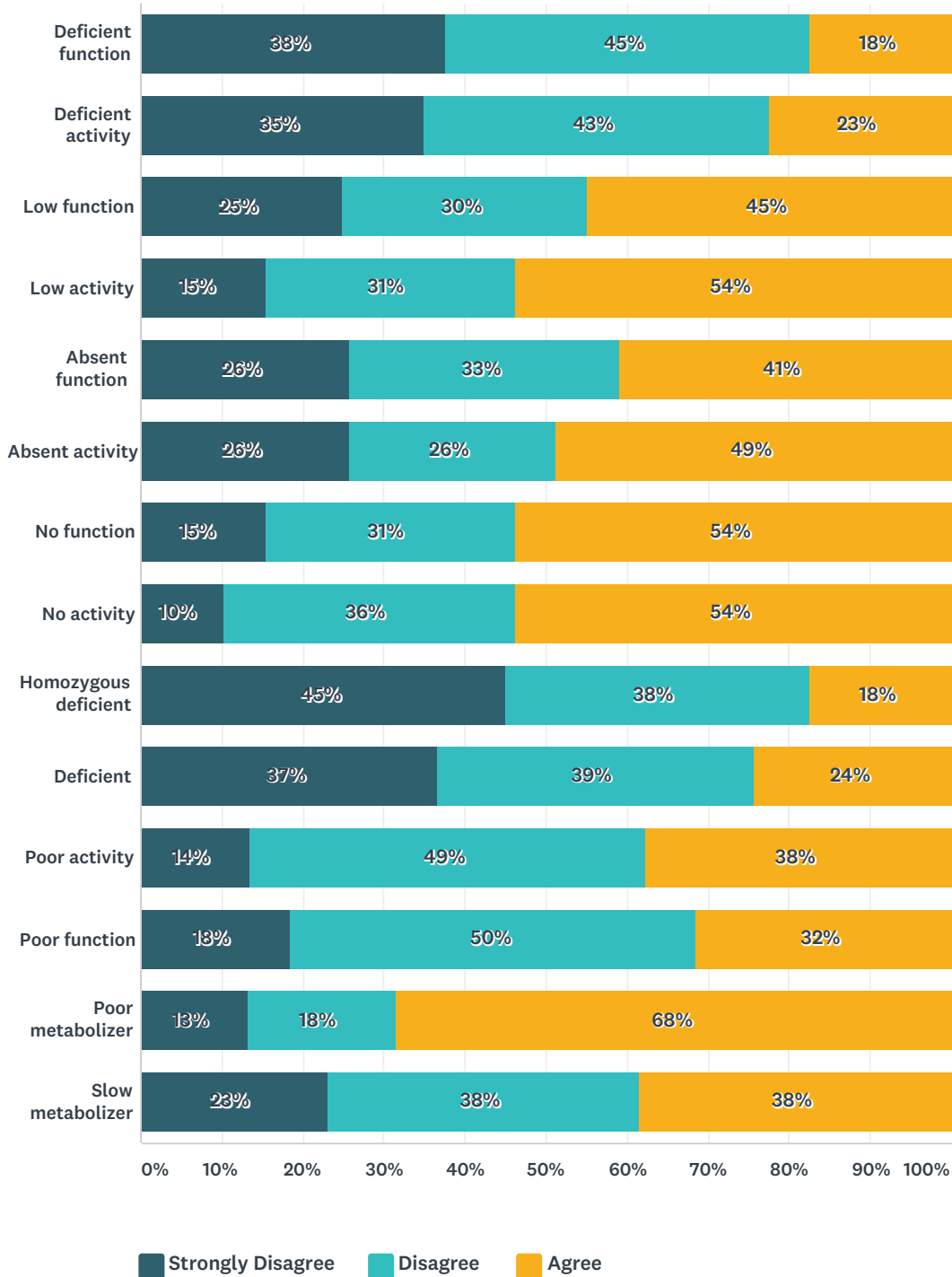
CPIC Term Standardization for Clinical Pharmacogenetic Test Results: alleles and phenotypes

Decreased activity	8% 4	29% 15	25% 13	12% 6	25% 13	51	2.55
Reduced activity	8% 4	30% 15	24% 12	16% 8	22% 11	50	2.62
Heterozygous deficient	33% 17	35% 18	4% 2	6% 3	22% 11	51	1.77
Intermediate metabolizer	10% 5	6% 3	24% 12	37% 19	24% 12	51	3.15
Heterozygous extensive metabolizer	36% 18	32% 16	6% 3	6% 3	20% 10	50	1.77
Reduced metabolizer	18% 9	33% 16	20% 10	8% 4	20% 10	49	2.23
Decreased metabolizer	18% 9	37% 19	18% 9	6% 3	22% 11	51	2.15

#	OTHER (PLEASE SPECIFY)	DATE
1	Heterozygous decreased metabolizer	2/18/2015 11:27 AM

### Q39 Describe your degree of acceptance of the following terms to describe the presumed phenotype for UGT1A1 in an individual with no or very little UGT1A1 function/activity (e.g., UGT1A1\*28/\*28):

Answered: 55 Skipped: 22



	STRONGLY DISAGREE	DISAGREE	AGREE	TOTAL	WEIGHTED AVERAGE
Deficient function	38%	45%	18%	40	1.80
	15	18	7		

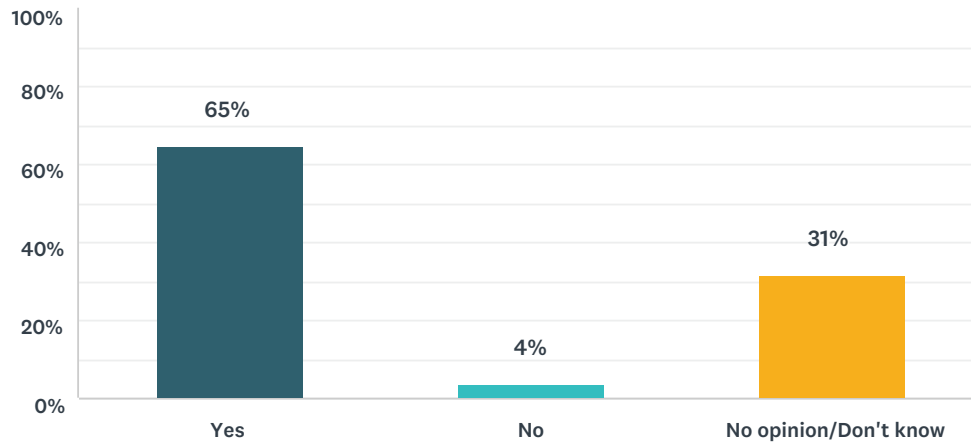
CPIC Term Standardization for Clinical Pharmacogenetic Test Results: alleles and phenotypes

Deficient activity	35% 14	43% 17	23% 9	40	1.88
Low function	25% 10	30% 12	45% 18	40	2.20
Low activity	15% 6	31% 12	54% 21	39	2.38
Absent function	26% 10	33% 13	41% 16	39	2.15
Absent activity	26% 10	26% 10	49% 19	39	2.23
No function	15% 6	31% 12	54% 21	39	2.38
No activity	10% 4	36% 14	54% 21	39	2.44
Homozygous deficient	45% 18	38% 15	18% 7	40	1.73
Deficient	37% 15	39% 16	24% 10	41	1.88
Poor activity	14% 5	49% 18	38% 14	37	2.24
Poor function	18% 7	50% 19	32% 12	38	2.13
Poor metabolizer	13% 5	18% 7	68% 26	38	2.55
Slow metabolizer	23% 9	38% 15	38% 15	39	2.15

#	OTHER (PLEASE SPECIFY)	DATE
1	Don't lump "no activity" and "very little activity" together	2/20/2015 5:59 PM
2	homozygous low activity	2/6/2015 12:54 PM
3	"Little or no activity" would seem to be appropriate	2/3/2015 2:49 PM

**Q40 We assume that 3 major categories of allele function are needed for SLCO1B1. Do you agree (yes or no)? If no, please indicate how many you think are needed and why:**

Answered: 54 Skipped: 23

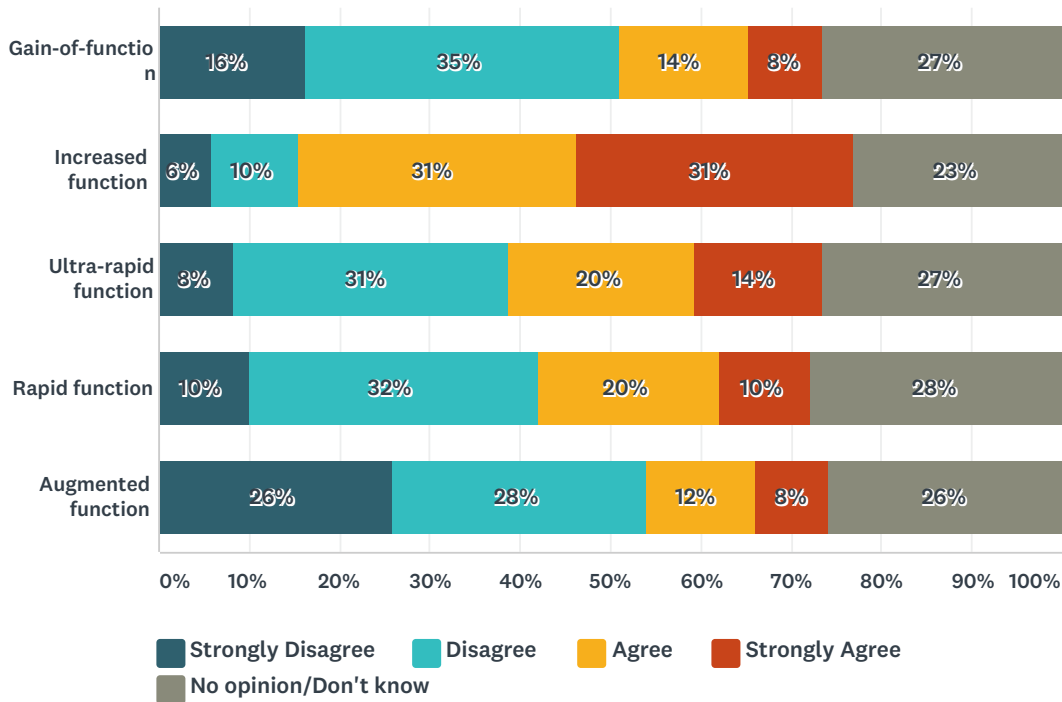


ANSWER CHOICES	RESPONSES	
Yes	65%	35
No	4%	2
No opinion/Don't know	31%	17
<b>TOTAL</b>		<b>54</b>

#	IF NO, PLEASE INDICATE HOW MANY YOU THINK ARE NEEDED AND WHY:	DATE
1	consistency across genes (keep 4 categories)	2/3/2015 2:07 PM
2	need category for unknown function	2/2/2015 1:49 PM

## Q41 Describe your degree of acceptance of the following terms to describe the allele function for a SLCO1B1 allele with high function (e.g., SLCO1B1\*14):

Answered: 54 Skipped: 23

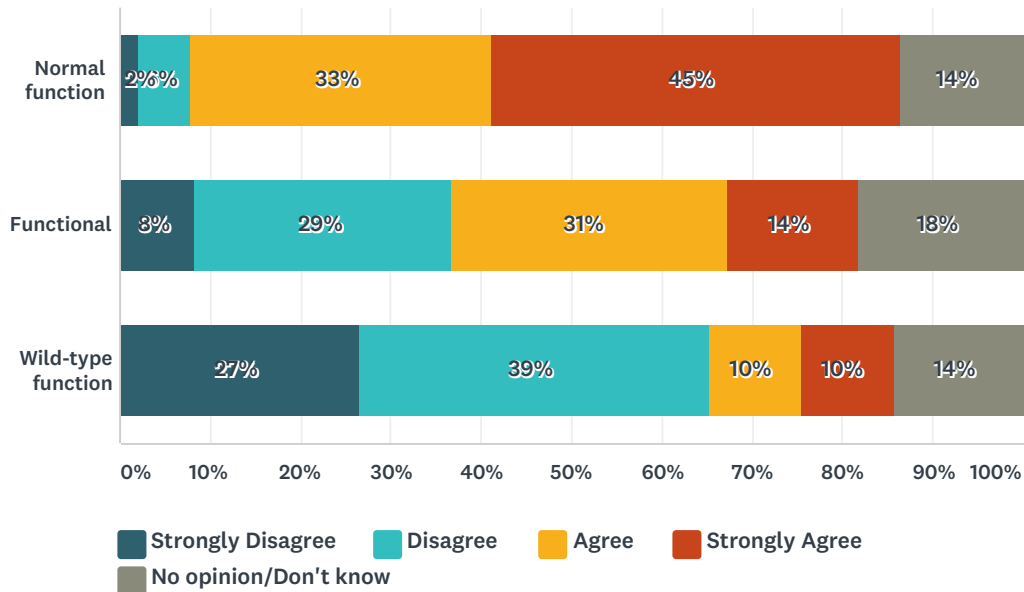


	STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	NO OPINION/DON'T KNOW	TOTAL	WEIGHTED AVERAGE
Gain-of-function	16% 8	35% 17	14% 7	8% 4	27% 13	49	2.19
Increased function	6% 3	10% 5	31% 16	31% 16	23% 12	52	3.13
Ultra-rapid function	8% 4	31% 15	20% 10	14% 7	27% 13	49	2.56
Rapid function	10% 5	32% 16	20% 10	10% 5	28% 14	50	2.42
Augmented function	26% 13	28% 14	12% 6	8% 4	26% 13	50	2.03

#	OTHER (PLEASE SPECIFY)	DATE
1	Increased activity	2/20/2015 6:18 PM
2	Increased Activity	2/20/2015 5:14 PM
3	Increased activity	2/20/2015 4:26 PM
4	higher than normal transport activity	2/16/2015 9:06 AM

### Q42 Describe your degree of acceptance of the following terms to describe the allele function for a SLCO1B1 allele with normal function (e.g., SLCO1B1\*1):

Answered: 53 Skipped: 24

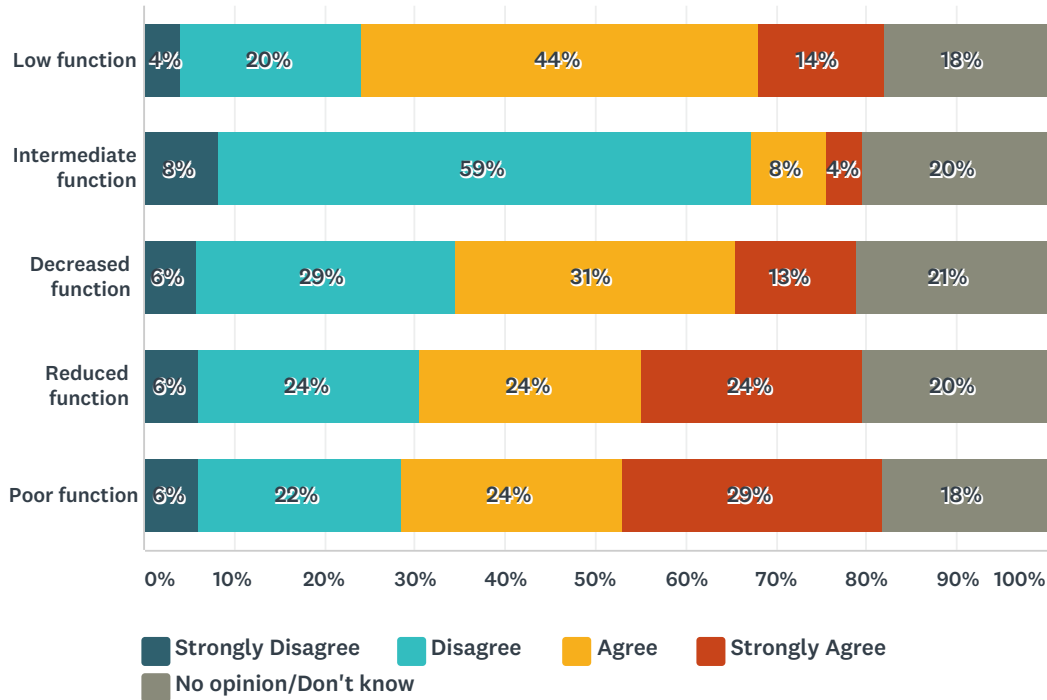


	STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	NO OPINION/DON'T KNOW	TOTAL	WEIGHTED AVERAGE
Normal function	2% 1	6% 3	33% 17	45% 23	14% 7	51	3.41
Functional	8% 4	29% 14	31% 15	14% 7	18% 9	49	2.63
Wild-type function	27% 13	39% 19	10% 5	10% 5	14% 7	49	2.05

#	OTHER PLEASE SPECIFY	DATE
1	Reference activity	2/20/2015 6:18 PM
2	Normal Activity or Wild-type activity	2/20/2015 5:14 PM
3	normal transport activity	2/16/2015 9:06 AM

## Q43 Describe your degree of acceptance of the following terms to describe the allele function for a SLCO1B1 allele very little function (e.g., SLCO1B1\*5):

Answered: 54 Skipped: 23

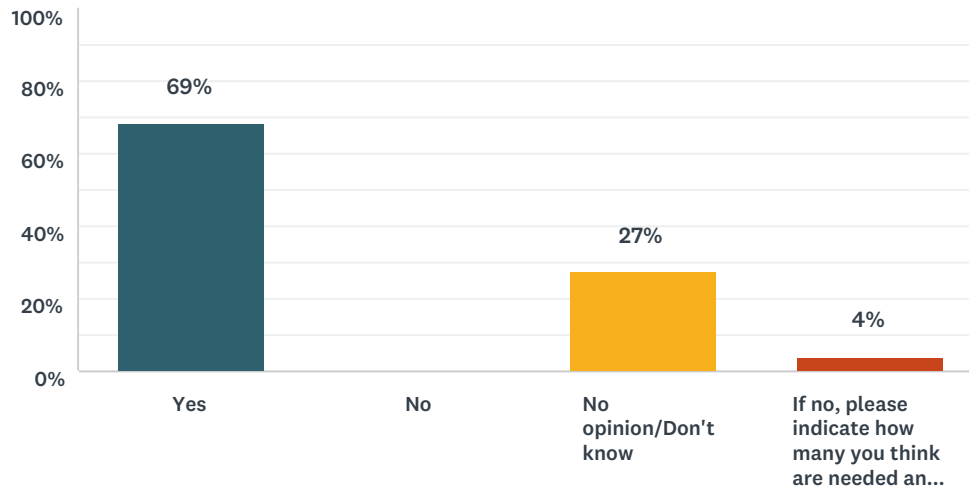


	STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	NO OPINION/DON'T KNOW	TOTAL	WEIGHTED AVERAGE
Low function	4% 2	20% 10	44% 22	14% 7	18% 9	50	2.83
Intermediate function	8% 4	59% 29	8% 4	4% 2	20% 10	49	2.10
Decreased function	6% 3	29% 15	31% 16	13% 7	21% 11	52	2.66
Reduced function	6% 3	24% 12	24% 12	24% 12	20% 10	49	2.85
Poor function	6% 3	22% 11	24% 12	29% 14	18% 9	49	2.92

#	OTHER (PLEASE SPECIFY)	DATE
1	Low activity	2/20/2015 6:18 PM
2	Reduced Activity or Decreased Activity	2/20/2015 5:14 PM
3	poor transport activity	2/16/2015 9:06 AM
4	Loss-of-function	2/11/2015 2:02 PM

**Q44 We assume that 4 major categories of allele function are needed for SLCO1B1. Do you agree (yes or no)? If no, please indicate how many you think are needed and why:**

Answered: 51 Skipped: 26

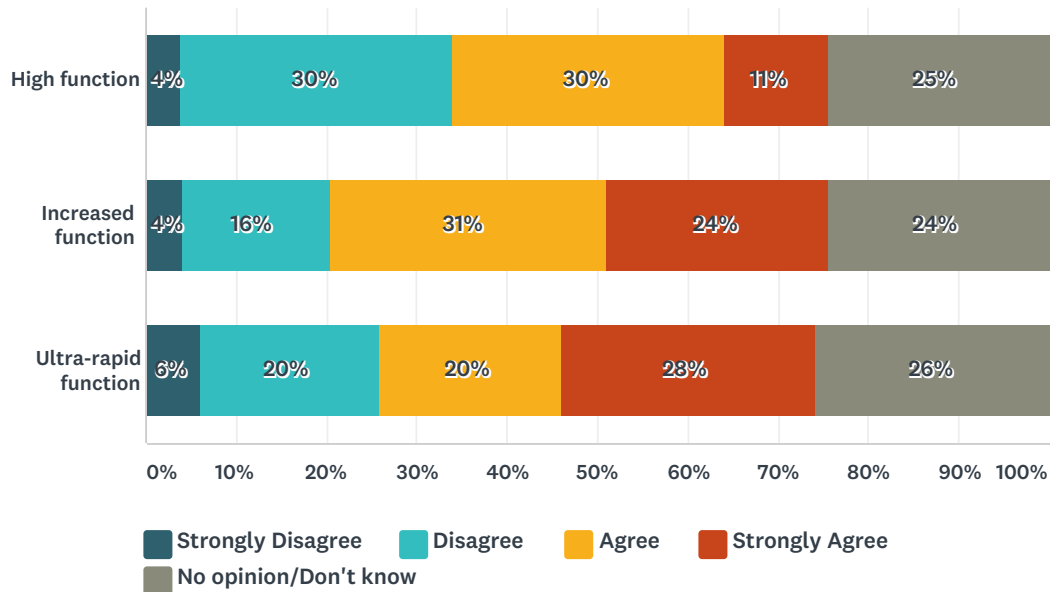


ANSWER CHOICES	RESPONSES	
Yes	69%	35
No	0%	0
No opinion/Don't know	27%	14
If no, please indicate how many you think are needed and why:	4%	2
<b>TOTAL</b>		<b>51</b>

#	IF NO, PLEASE INDICATE HOW MANY YOU THINK ARE NEEDED AND WHY:	DATE
1	I have no knowledge on this gene	2/11/2015 1:42 PM
2	need categories for unknown	2/2/2015 1:50 PM

### Q45 Describe your degree of acceptance of the following terms to describe the presumed phenotype for SLCO1B1 in an individual with very high SLCO1B1 function (e.g., SLCO1B1\*14/\*14):

Answered: 54 Skipped: 23

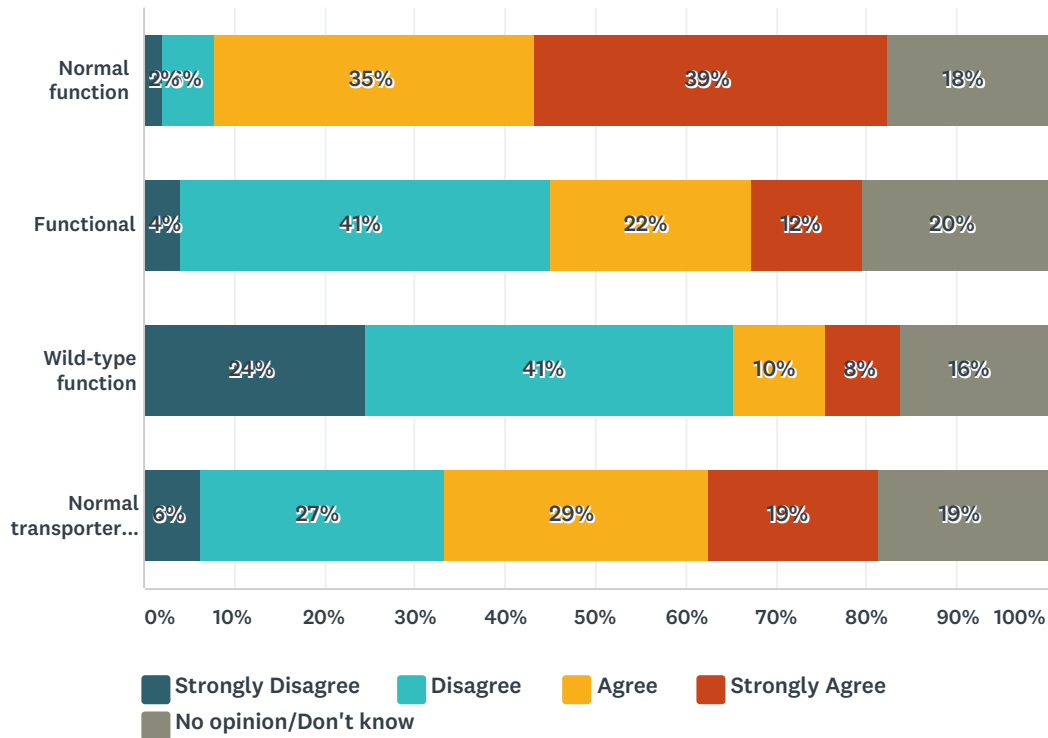


	STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	NO OPINION/DON'T KNOW	TOTAL	WEIGHTED AVERAGE
High function	4% 2	30% 16	30% 16	11% 6	25% 13	53	2.65
Increased function	4% 2	16% 8	31% 15	24% 12	24% 12	49	3.00
Ultra-rapid function	6% 3	20% 10	20% 10	28% 14	26% 13	50	2.95

#	OTHER (PLEASE SPECIFY)	DATE
1	Very increased function	2/20/2015 6:18 PM
2	High Activity	2/20/2015 5:16 PM
3	higher than normal transport activity	2/16/2015 9:06 AM
4	High transporter function	2/11/2015 2:04 PM

### Q46 Describe your degree of acceptance of the following terms to describe the presumed phenotype for SLCO1B1 in an individual with normal SLCO1B1 function (e.g., SLCO1B1\*1/\*1):

Answered: 53 Skipped: 24

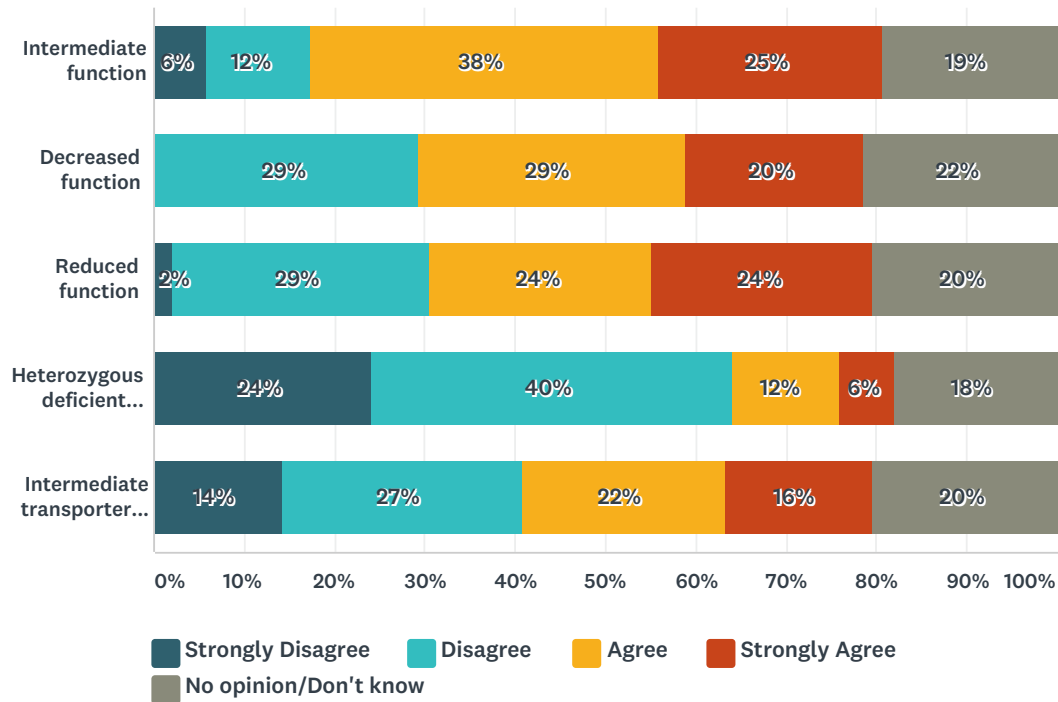


	STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	NO OPINION/DON'T KNOW	TOTAL	WEIGHTED AVERAGE
Normal function	2% 1	6% 3	35% 18	39% 20	18% 9	51	3.36
Functional	4% 2	41% 20	22% 11	12% 6	20% 10	49	2.54
Wild-type function	24% 12	41% 20	10% 5	8% 4	16% 8	49	2.02
Normal transporter function	6% 3	27% 13	29% 14	19% 9	19% 9	48	2.74

#	OTHER (PLEASE SPECIFY)	DATE
1	Reference function	2/20/2015 6:18 PM
2	Normal Activity or Wild-type activity	2/20/2015 5:16 PM
3	normal transport activity	2/16/2015 9:06 AM

### Q47 Describe your degree of acceptance of the following terms to describe the presumed phenotype for SLCO1B1 in an individual with medium/some SLCO1B1 function (e.g., SLCO1B1\*1/\*5):

Answered: 54 Skipped: 23

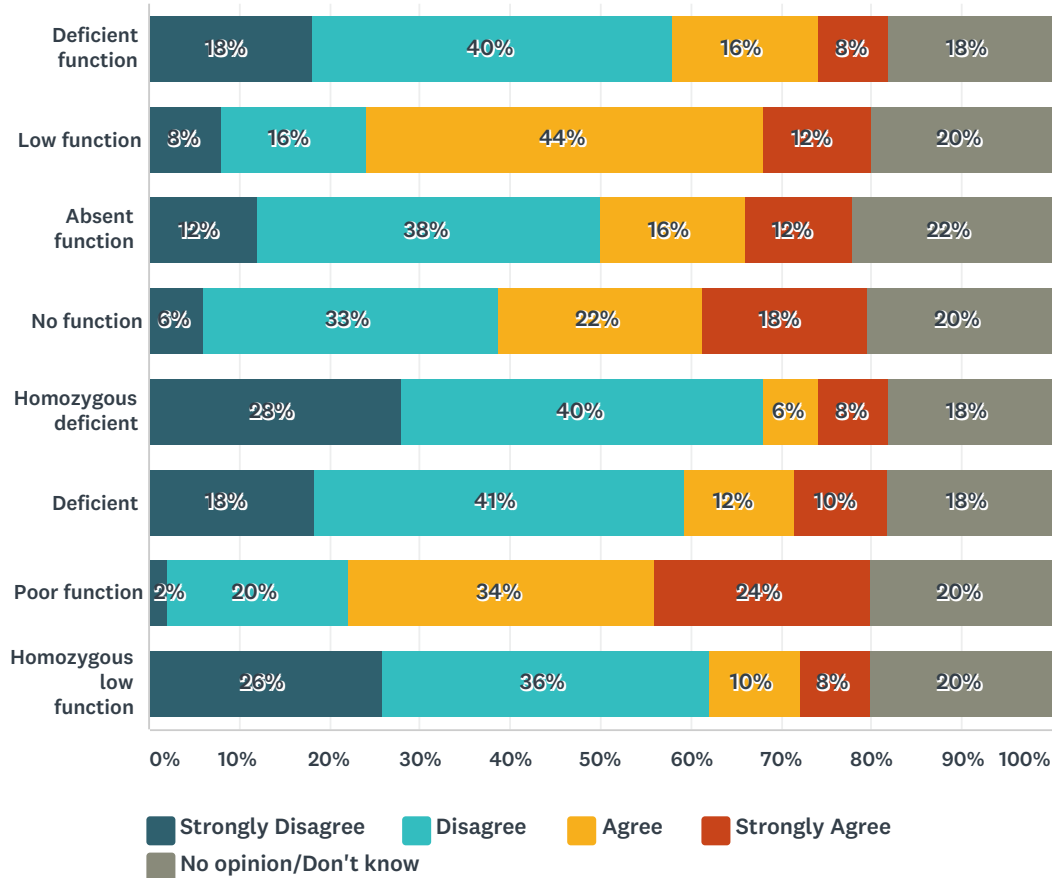


	STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	NO OPINION/DON'T KNOW	TOTAL	WEIGHTED AVERAGE
Intermediate function	6% 3	12% 6	38% 20	25% 13	19% 10	52	3.02
Decreased function	0% 0	29% 15	29% 15	20% 10	22% 11	51	2.88
Reduced function	2% 1	29% 14	24% 12	24% 12	20% 10	49	2.90
Heterozygous deficient function	24% 12	40% 20	12% 6	6% 3	18% 9	50	2.00
Intermediate transporter function	14% 7	27% 13	22% 11	16% 8	20% 10	49	2.51

#	OTHER (PLEASE SPECIFY)	DATE
1	Reduced Activity or Decreased Activity	2/20/2015 5:16 PM
2	Heterozygous decreased function	2/18/2015 11:50 AM
3	decreased transport activity	2/16/2015 9:06 AM

### Q48 Describe your degree of acceptance of the following terms to describe the presumed phenotype for SLCO1B1 in an individual with very little SLCO1B1 function (e.g., SLCO1B1\*5/\*5):

Answered: 54 Skipped: 23



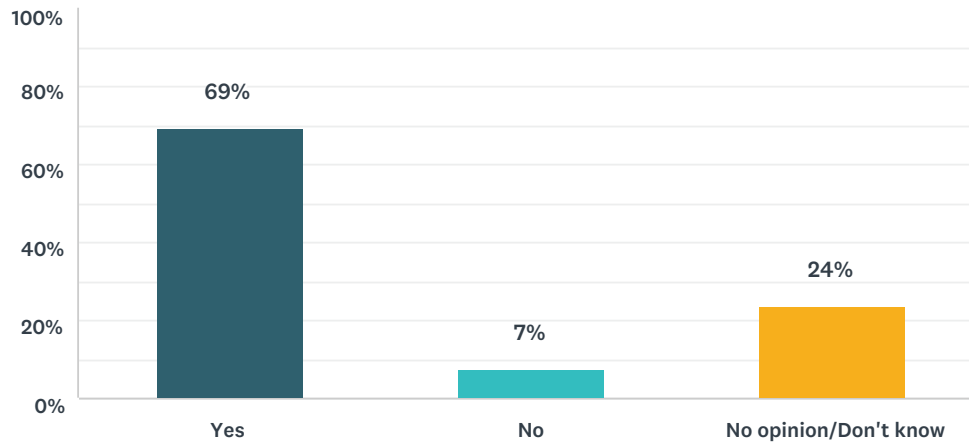
	STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	NO OPINION/DON'T KNOW	TOTAL	WEIGHTED AVERAGE
Deficient function	18% 9	40% 20	16% 8	8% 4	18% 9	50	2.17
Low function	8% 4	16% 8	44% 22	12% 6	20% 10	50	2.75
Absent function	12% 6	38% 19	16% 8	12% 6	22% 11	50	2.36
No function	6% 3	33% 16	22% 11	18% 9	20% 10	49	2.67
Homozygous deficient	28% 14	40% 20	6% 3	8% 4	18% 9	50	1.93
Deficient	18% 9	41% 20	12% 6	10% 5	18% 9	49	2.17
Poor function	2% 1	20% 10	34% 17	24% 12	20% 10	50	3.00

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Homozygous low function	26% 13	36% 18	10% 5	8% 4	20% 10	50	2.00
#	OTHER (PLEASE SPECIFY)						DATE
1	No activity						2/20/2015 5:16 PM
2	poor transport activity						2/16/2015 9:06 AM
3	Low transporter function						2/11/2015 2:04 PM

**Q49 We assume that 4 major categories of allele function are needed for VKORC1. Do you agree (yes or no)? If no, please indicate how many you think are needed and why:**

Answered: 55 Skipped: 22

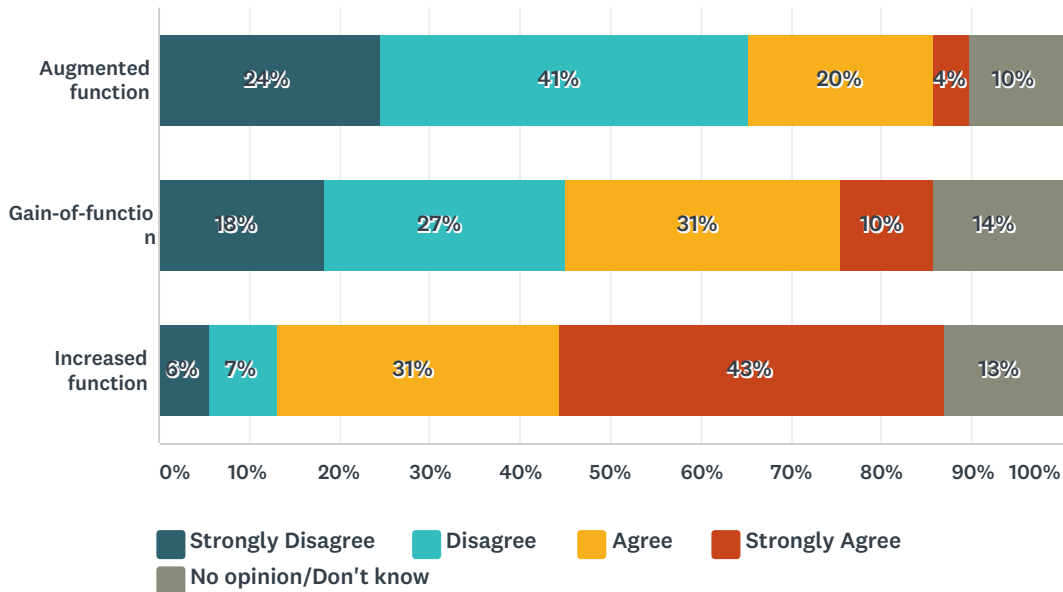


ANSWER CHOICES	RESPONSES	
Yes	69%	38
No	7%	4
No opinion/Don't know	24%	13
<b>TOTAL</b>		<b>55</b>

#	IF NO, PLEASE INDICATE HOW MANY YOU THINK ARE NEEDED AND WHY:	DATE
1	I am not sure if VKORC1 variants can be classified according to functional activities, I am not sure there is sufficient biochemical studies to classify the activity of the VKORC1 variants.	2/13/2015 11:34 PM
2	I think that I would describe this as a target: resistant to inhibitors, normal activity, and sensitive based on EC50s to warfarin.	2/4/2015 2:35 PM
3	Such a categorization strategy would be nice for consistency, but clinical use of VKORC1 genotyping only requires results at a few SNPs. We don't need to summarize allele function at the moment, although starting the project would be nice to support future research.	2/3/2015 2:54 PM
4	NO convincing evidence for 4 phenotypes	2/2/2015 2:04 PM
5	need categories for unknown alleles	2/2/2015 1:52 PM

## Q50 Describe your degree of acceptance of the following terms to describe the allele function for a VKORC1 allele with high function (e.g., VKORC1 D36Y):

Answered: 54 Skipped: 23

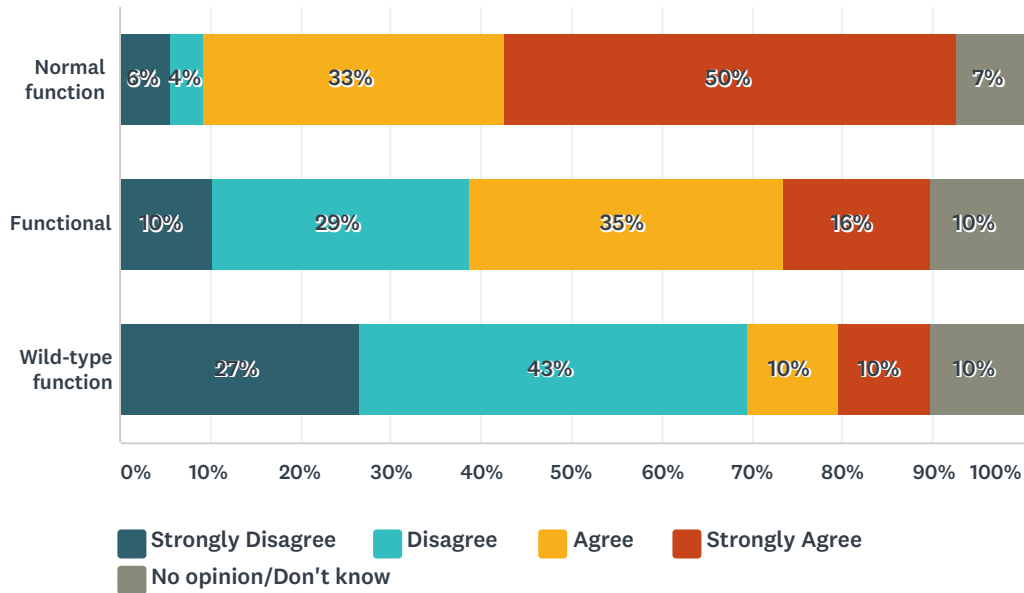


	STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	NO OPINION/DON'T KNOW	TOTAL	WEIGHTED AVERAGE
Augmented function	24% 12	41% 20	20% 10	4% 2	10% 5	49	2.05
Gain-of-function	18% 9	27% 13	31% 15	10% 5	14% 7	49	2.38
Increased function	6% 3	7% 4	31% 17	43% 23	13% 7	54	3.28

#	OTHER (PLEASE SPECIFY)	DATE
1	rather than function, might be more logical to categorize as degree of sensitivity to warfarin (or to inhibition)	2/21/2015 9:09 PM
2	Increased activity	2/20/2015 6:19 PM
3	Increased Activity	2/20/2015 5:17 PM
4	This allele is associated with higher doses. I wouldn't ascribe functional status to it.	2/20/2015 4:34 PM
5	higher than normal enzyme activity	2/16/2015 9:06 AM
6	Low warfarin sensitivity	2/4/2015 3:28 PM

## Q51 Describe your degree of acceptance of the following terms to describe the allele function for a VKORC1 allele with normal function:

Answered: 54 Skipped: 23

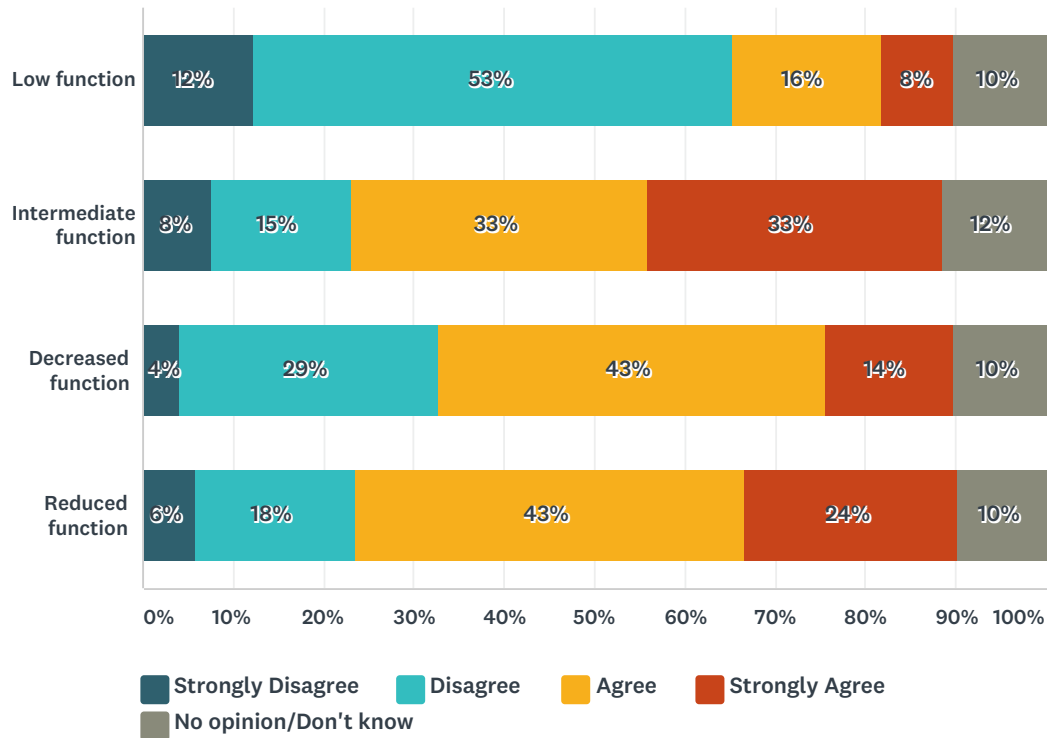


	STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	NO OPINION/DON'T KNOW	TOTAL	WEIGHTED AVERAGE
Normal function	6% 3	4% 2	33% 18	50% 27	7% 4	54	3.38
Functional	10% 5	29% 14	35% 17	16% 8	10% 5	49	2.64
Wild-type function	27% 13	43% 21	10% 5	10% 5	10% 5	49	2.05

#	OTHER PLEASE SPECIFY	DATE
1	rather than function, might be more logical to categorize as degree of sensitivity to warfarin (or to inhibition)	2/21/2015 9:09 PM
2	Reference activity	2/20/2015 6:19 PM
3	Normal Activity or Wild-type activity	2/20/2015 5:17 PM
4	normal enzyme activity	2/16/2015 9:06 AM
5	Normal warfarin sensitivity	2/4/2015 3:28 PM
6	Active	2/2/2015 2:04 PM

### Q52 Describe your degree of acceptance of the following terms to describe the allele function for a VKORC1 allele with medium/some function (e.g., VKORC1-1639G>A (rs9923231)):

Answered: 54 Skipped: 23

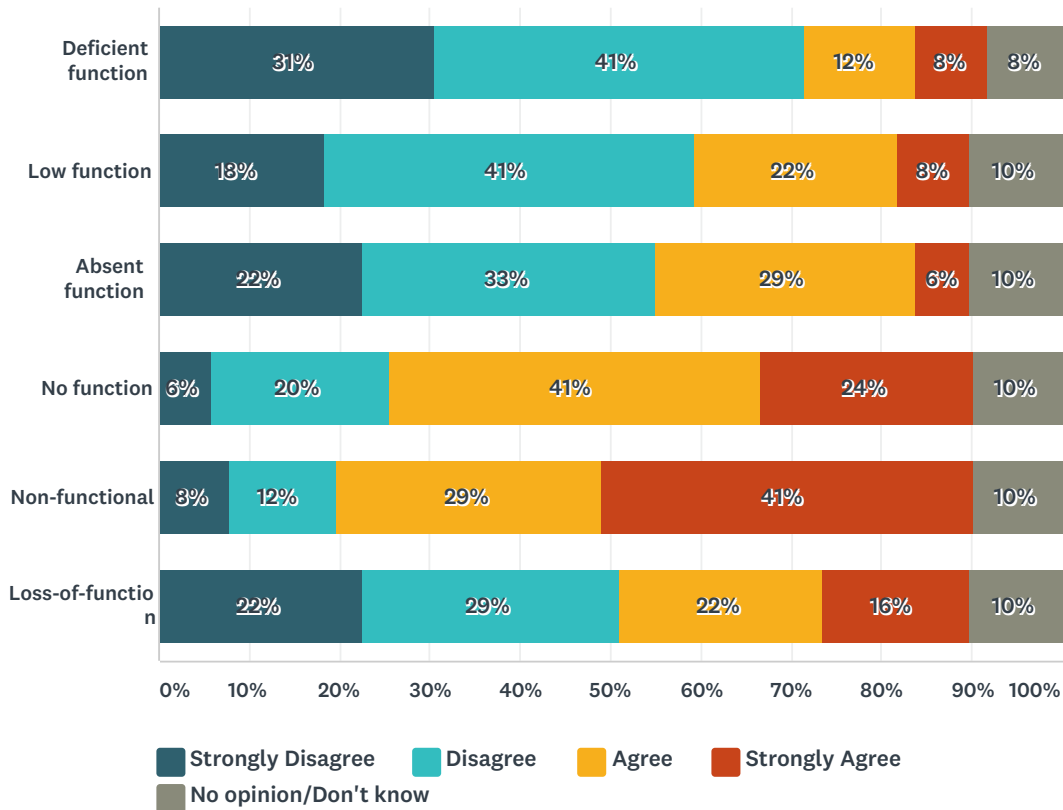


	STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	NO OPINION/DON'T KNOW	TOTAL	WEIGHTED AVERAGE
Low function	12% 6	53% 26	16% 8	8% 4	10% 5	49	2.23
Intermediate function	8% 4	15% 8	33% 17	33% 17	12% 6	52	3.02
Decreased function	4% 2	29% 14	43% 21	14% 7	10% 5	49	2.75
Reduced function	6% 3	18% 9	43% 22	24% 12	10% 5	51	2.93

#	OTHER (PLEASE SPECIFY)	DATE
1	rather than function, might be more logical to categorize as degree of sensitivity to warfarin (or to inhibition)	2/21/2015 9:09 PM
2	Decreased activity	2/20/2015 6:19 PM
3	Reduced activity or decreased activity	2/20/2015 5:17 PM
4	Reduced activity	2/20/2015 4:34 PM
5	lower than normal enzyme activity	2/16/2015 9:06 AM
6	Decreased activity or reduced activity	2/2/2015 2:04 PM

## Q53 Describe your degree of acceptance of the following terms to describe the allele function for a VKORC1 allele with no function (e.g., VKORC1 L128R):

Answered: 54 Skipped: 23



	STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	NO OPINION/DON'T KNOW	TOTAL	WEIGHTED AVERAGE
Deficient function	31% 15	41% 20	12% 6	8% 4	8% 4	49	1.98
Low function	18% 9	41% 20	22% 11	8% 4	10% 5	49	2.23
Absent function	22% 11	33% 16	29% 14	6% 3	10% 5	49	2.20
No function	6% 3	20% 10	41% 21	24% 12	10% 5	51	2.91
Non-functional	8% 4	12% 6	29% 15	41% 21	10% 5	51	3.15
Loss-of-function	22% 11	29% 14	22% 11	16% 8	10% 5	49	2.36

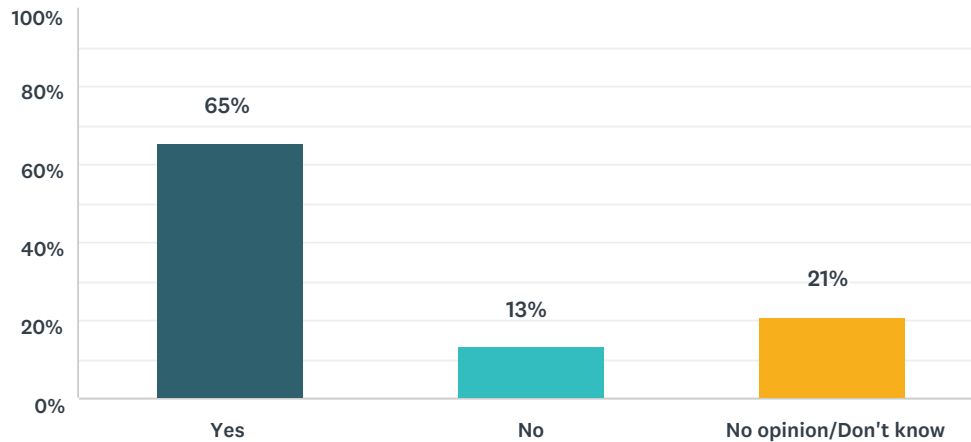
#	OTHER (PLEASE SPECIFY)	DATE
1	rather than function, might be more logical to categorize as degree of sensitivity to warfarin (or to inhibition)	2/21/2015 9:09 PM
2	No activity	2/20/2015 6:19 PM

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3	No Activity	2/20/2015 5:17 PM
4	absent enzyme activity	2/16/2015 9:06 AM
5	High warfarin sensitivity	2/4/2015 3:28 PM
6	No activity	2/2/2015 2:04 PM

### Q54 We assume that 4 major categories of phenotypes are needed for VKORC1. Do you agree (yes or no)? If no, please indicate how many you think are needed and why:

Answered: 52 Skipped: 25

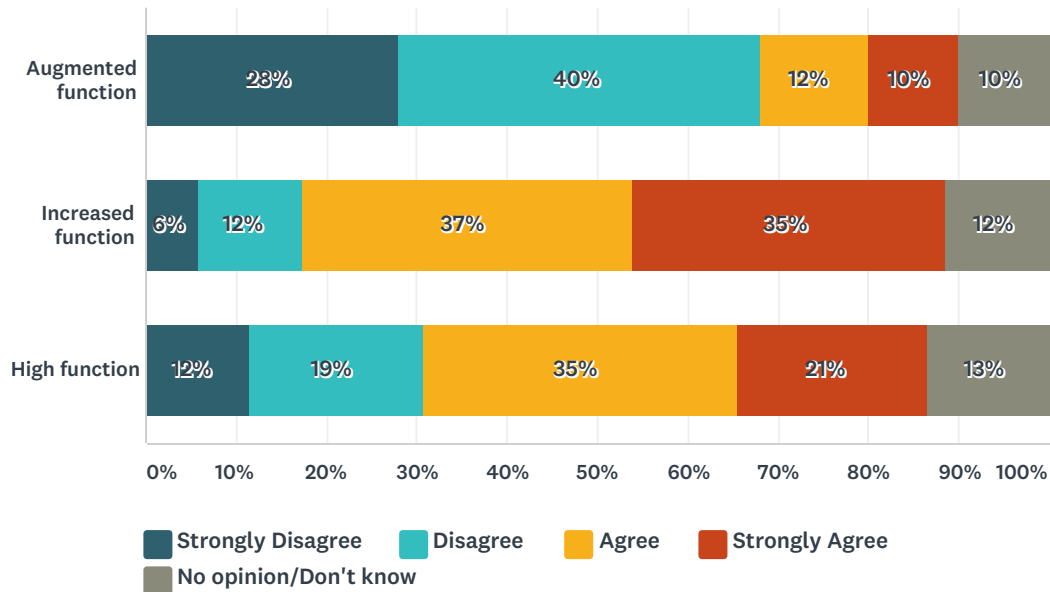


ANSWER CHOICES	RESPONSES	
Yes	65%	34
No	13%	7
No opinion/Don't know	21%	11
<b>TOTAL</b>		<b>52</b>

#	IF NO, PLEASE INDICATE HOW MANY YOU THINK ARE NEEDED AND WHY:	DATE
1	I am not sure if VKORC1 variants can be classified according to functional activities, I am not sure there is sufficient biochemical studies to classify the activity of the VKORC1 variants.	2/13/2015 11:35 PM
2	VKORC1 is reported with CYP2C9 for warfarin sensitivity. I don't know of any clinical scenario where VKORC1 would be needed separately from CYP2C9. Having a separate phenotype for VKORC1 seems unnecessarily complicated.	2/9/2015 5:19 PM
3	3. Low, Normal, High warfarin sensitivity	2/4/2015 3:29 PM
4	See my prior comment. The issue is whether VKOR resists inhibition or is more sensitive.	2/4/2015 2:37 PM
5	Again, summarization of VKORC1 results is not necessary in the current clinical landscape, but may be in the future. If it is, 4 categories would seem appropriate.	2/3/2015 3:28 PM
6	we need three 1. Low Warfarin Sensitivity 2. Intermediate Warfarin Sensitivity 3. High Warfarin Sensitivity	2/3/2015 12:29 PM
7	No clinical relevance of 4 phenotypes	2/2/2015 2:06 PM
8	need categories for genotypes with unknown alleles	2/2/2015 1:53 PM

### Q55 Describe your degree of acceptance of the following terms to describe the presumed phenotype for VKORC1 in an individual with high function (e.g., individual carrying VKORC1 D36Y):

Answered: 54 Skipped: 23

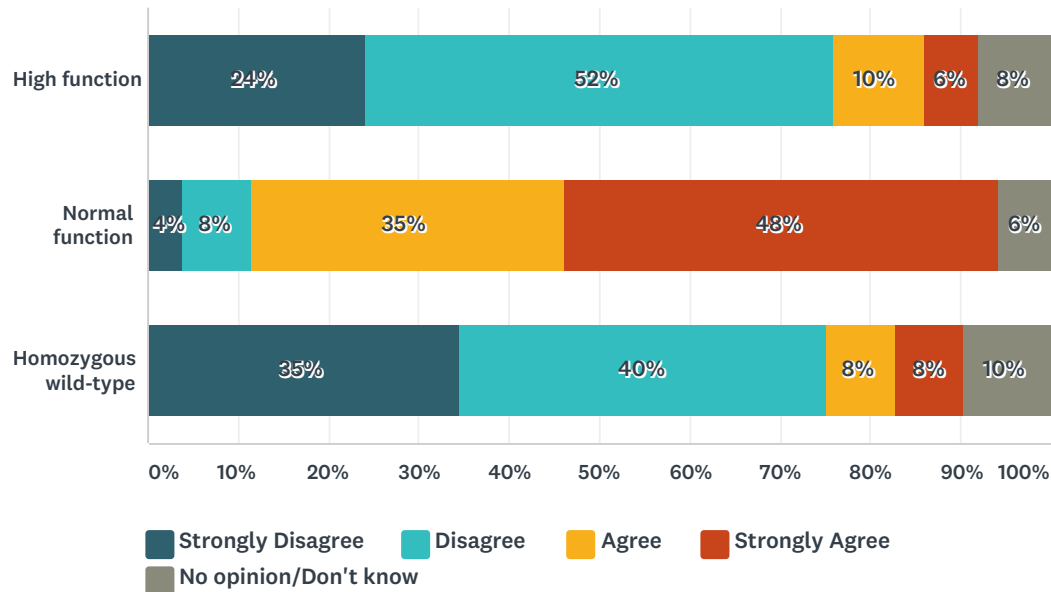


	STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	NO OPINION/DON'T KNOW	TOTAL	WEIGHTED AVERAGE
Augmented function	28% 14	40% 20	12% 6	10% 5	10% 5	50	2.04
Increased function	6% 3	12% 6	37% 19	35% 18	12% 6	52	3.13
High function	12% 6	19% 10	35% 18	21% 11	13% 7	52	2.76

#	OTHER (PLEASE SPECIFY)	DATE
1	Very increased function	2/20/2015 6:20 PM
2	Increased Activity	2/20/2015 5:18 PM
3	rapid metabolizer	2/16/2015 9:07 AM
4	Low warfarin sensitivity	2/4/2015 3:29 PM
5	see comment above	2/4/2015 2:37 PM

## Q56 Describe your degree of acceptance of the following terms to describe the presumed phenotype for VKORC1 in an individual with normal VKORC1 function:

Answered: 54 Skipped: 23

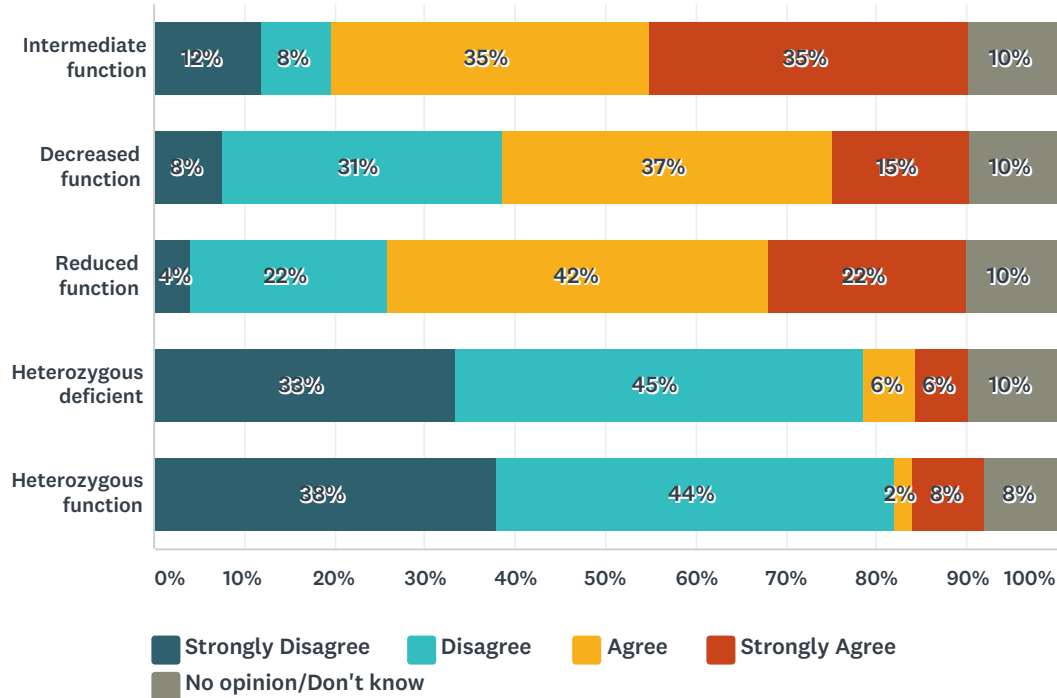


	STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	NO OPINION/DON'T KNOW	TOTAL	WEIGHTED AVERAGE
High function	24% 12	52% 26	10% 5	6% 3	8% 4	50	1.98
Normal function	4% 2	8% 4	35% 18	48% 25	6% 3	52	3.35
Homozygous wild-type	35% 18	40% 21	8% 4	8% 4	10% 5	52	1.87

#	OTHER (PLEASE SPECIFY)	DATE
1	Reference function	2/20/2015 6:20 PM
2	Normal activity or wild-type activity	2/20/2015 5:18 PM
3	normal metabolizer	2/16/2015 9:07 AM
4	Normal warfarin sensitivity	2/4/2015 3:29 PM
5	see comment above	2/4/2015 2:37 PM
6	"Full function" seems more appropriate for proteins with highly polymorphic function	2/3/2015 3:28 PM
7	Normal activity	2/2/2015 2:06 PM

**Q57 Describe your degree of acceptance of the following terms to describe the presumed phenotype for VKORC1 in an individual with medium/some function (e.g., VKORC1-1639G>A (rs9923231) heterozygous individual) :**

Answered: 54 Skipped: 23

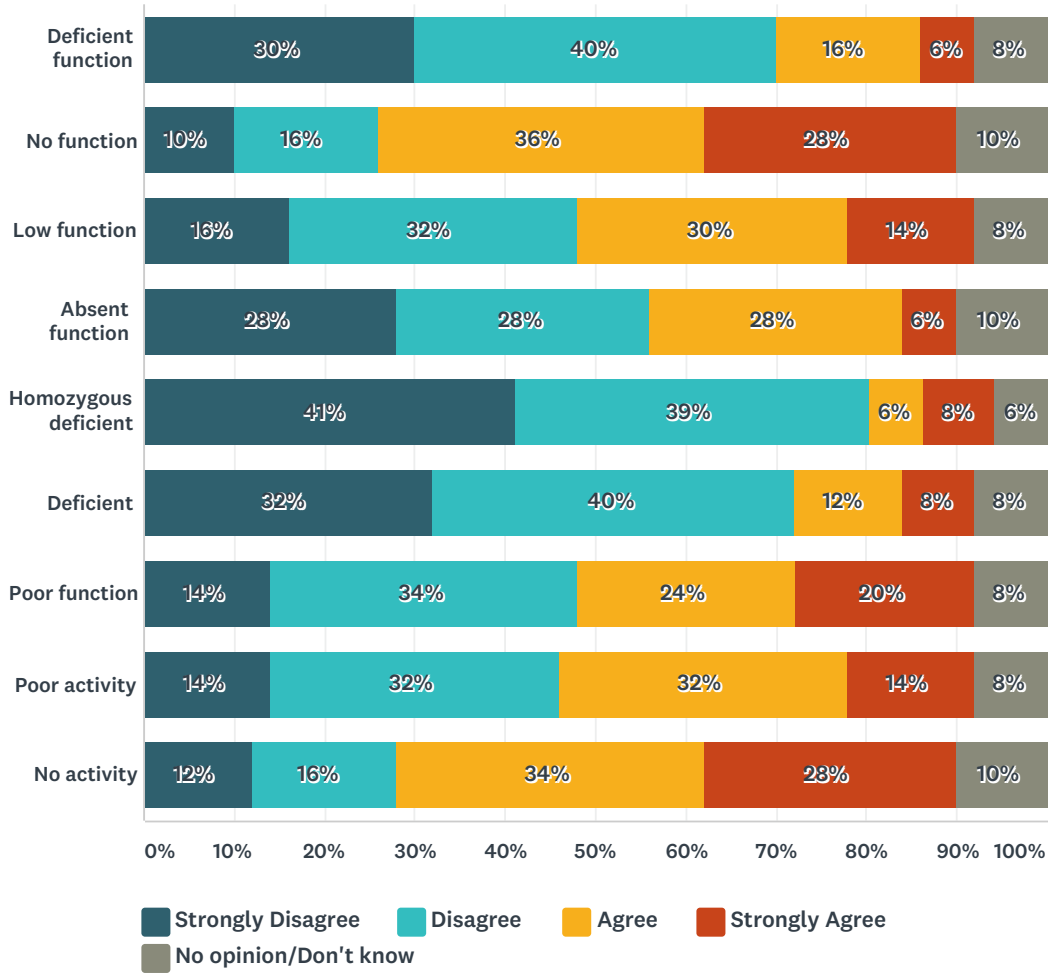


	STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	NO OPINION/DON'T KNOW	TOTAL	WEIGHTED AVERAGE
Intermediate function	12% 6	8% 4	35% 18	35% 18	10% 5	51	3.04
Decreased function	8% 4	31% 16	37% 19	15% 8	10% 5	52	2.66
Reduced function	4% 2	22% 11	42% 21	22% 11	10% 5	50	2.91
Heterozygous deficient	33% 17	45% 23	6% 3	6% 3	10% 5	51	1.83
Heterozygous function	38% 19	44% 22	2% 1	8% 4	8% 4	50	1.78

#	OTHER (PLEASE SPECIFY)	DATE
1	Decreased Activity or Reduced Activity	2/20/2015 5:18 PM
2	Heterozygous decreased function	2/18/2015 11:51 AM
3	intermediate metabolizer	2/16/2015 9:07 AM
4	see comment above	2/4/2015 2:37 PM
5	REduced activity	2/2/2015 2:06 PM

### Q58 Describe your degree of acceptance of the following terms to describe the presumed phenotype for VKORC1 in an individual with no/very little function (e.g., VKORC1-1639G>A (rs9923231) homozygous individual):

Answered: 53 Skipped: 24



	STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	NO OPINION/DON'T KNOW	TOTAL	WEIGHTED AVERAGE
Deficient function	30% 15	40% 20	16% 8	6% 3	8% 4	50	1.98
No function	10% 5	16% 8	36% 18	28% 14	10% 5	50	2.91
Low function	16% 8	32% 16	30% 15	14% 7	8% 4	50	2.46
Absent function	28% 14	28% 14	28% 14	6% 3	10% 5	50	2.13
Homozygous deficient	41% 21	39% 20	6% 3	8% 4	6% 3	51	1.79
Deficient	32% 16	40% 20	12% 6	8% 4	8% 4	50	1.96

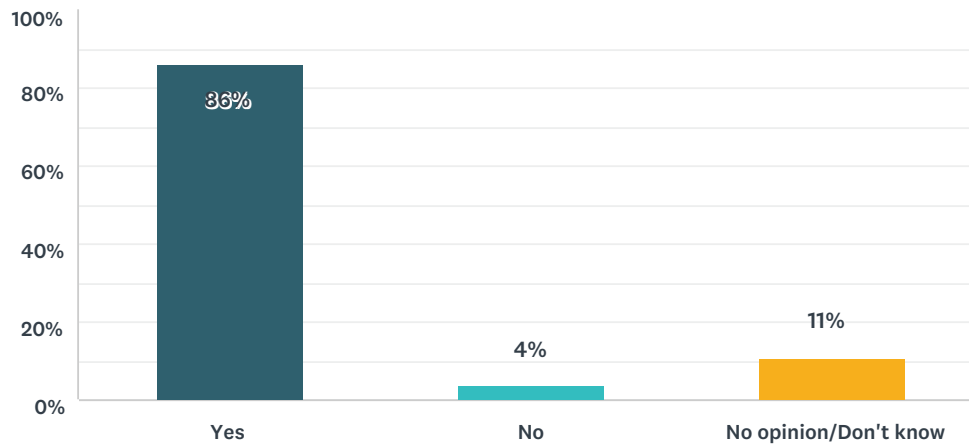
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Poor function	14% 7	34% 17	24% 12	20% 10	8% 4	50	2.54
Poor activity	14% 7	32% 16	32% 16	14% 7	8% 4	50	2.50
No activity	12% 6	16% 8	34% 17	28% 14	10% 5	50	2.87

#	OTHER (PLEASE SPECIFY)	DATE
1	Separate terms for "no function" and "very little function"	2/20/2015 6:04 PM
2	Homozygous no function	2/18/2015 11:51 AM
3	poor metabolizer	2/16/2015 9:07 AM
4	High warfarin sensitivity	2/4/2015 3:29 PM
5	see comment above	2/4/2015 2:37 PM
6	"Little or no activity" or "Little or no function"	2/3/2015 3:28 PM

**Q59** Currently, there are 3 HLA-B alleles that are subject to CPIC guidelines and strongly associated with specific adverse effects to drugs (HLA-B\*57:01 for abacavir hypersensitivity; HLA-B\*58:01 for allopurinol cutaneous reactions, and HLA-B\*15:02 for carbamazepine and phenytoin cutaneous reactions). We assume that the PRESENCE and ABSENCE of each high risk allele should be documented. Do you agree? Yes or No. If no, what do you recommend?

Answered: 57 Skipped: 20

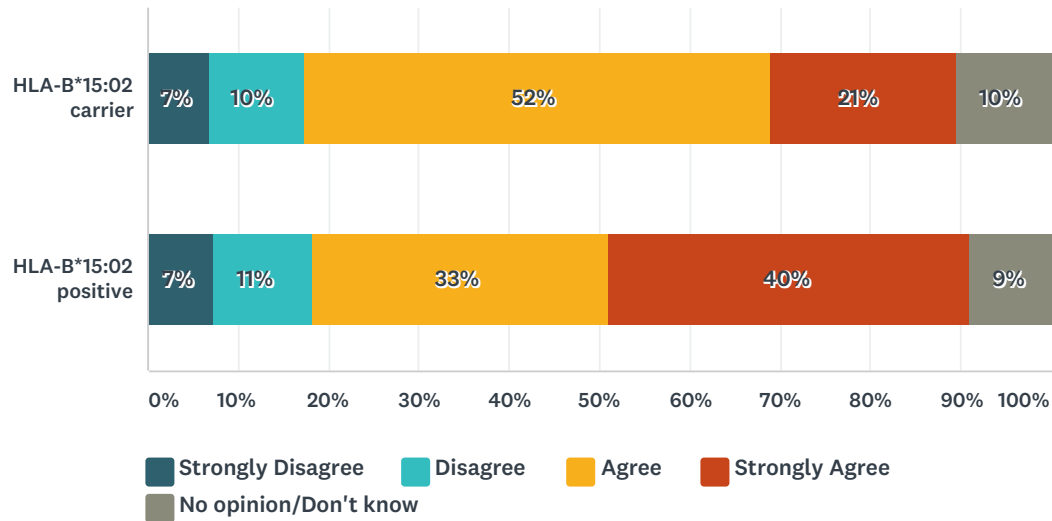


ANSWER CHOICES	RESPONSES
Yes	86% 49
No	4% 2
No opinion/Don't know	11% 6
TOTAL	57

#	IF NO, WHAT DO YOU RECOMMEND:	DATE
1	I have experienced the issues with a reference lab reporting the strands of DNA code and no interpretation - the physicians have NO idea what to do with that information. I completely agree with the presence or absence approach.	2/19/2015 4:00 PM
2	For *57:01, *58:01, *15:02 I agree. Just wanted to note that there have been case(s) in which HLA alleles show a gene-dose effect, see Zhang et al. NEJM 2013: <a href="http://www.nejm.org/doi/full/10.1056/NEJMoa1213096">http://www.nejm.org/doi/full/10.1056/NEJMoa1213096</a> , in case this becomes relevant in future CPIC guidelines.	2/3/2015 1:28 PM

## Q60 Describe your degree of acceptance of the following terms to describe the allele status for each high risk HLA-B allele tested (e.g., HLA-B\*15:02):

Answered: 59 Skipped: 18

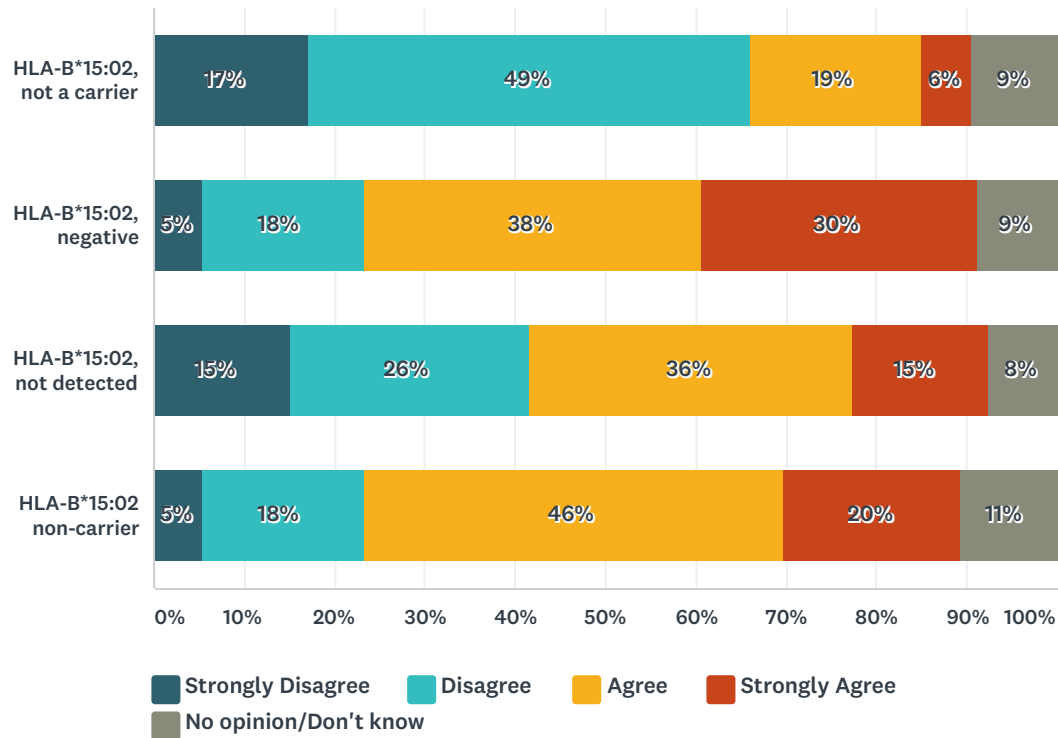


	STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	NO OPINION/DON'T KNOW	TOTAL	WEIGHTED AVERAGE
HLA-B*15:02 carrier	7% 4	10% 6	52% 30	21% 12	10% 6	58	2.96
HLA-B*15:02 positive	7% 4	11% 6	33% 18	40% 22	9% 5	55	3.16

#	OTHER (PLEASE SPECIFY)	DATE
1	I think this fits better with a disclaimer that the test for the allele was positive/negative	2/22/2015 10:57 AM
2	HLA-B*15:02 heterozygote and HLA-B*15:02 homozygote	2/20/2015 5:19 PM
3	HLA-B*15:02 present	2/16/2015 9:07 AM
4	the terms need to make sense genetically	2/3/2015 2:38 AM

**Q61 Describe your degree of acceptance of the following terms to describe the allele status for each high risk HLA-B allele tested for (e.g., HLA-B\*15:02) but found to be negative:**

Answered: 58 Skipped: 19

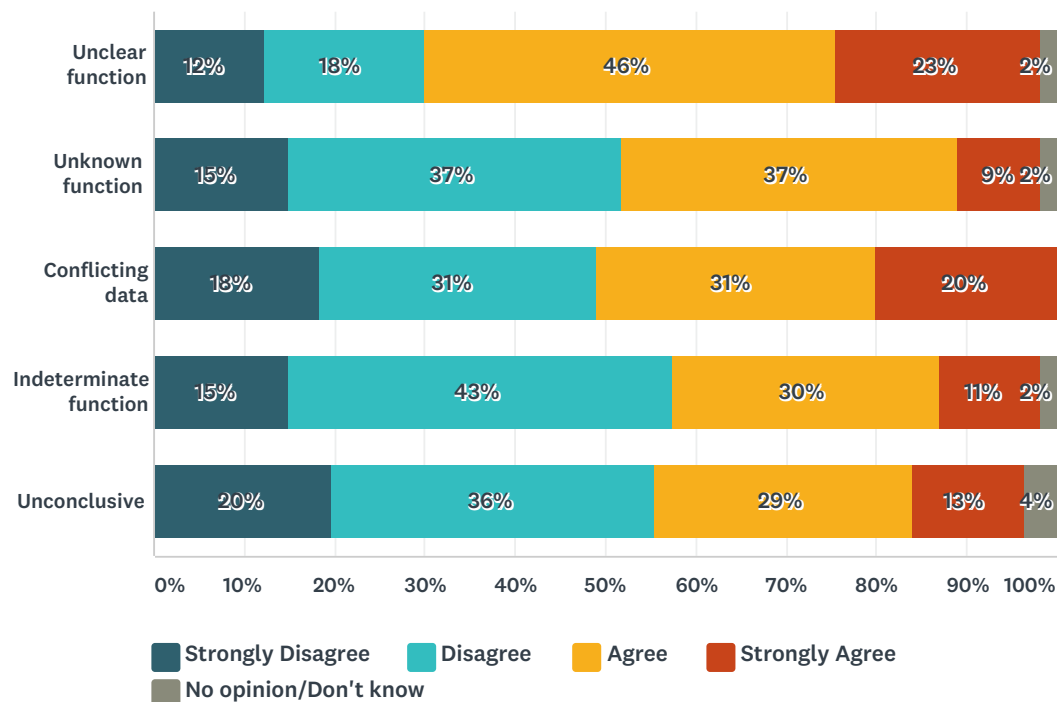


	STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	NO OPINION/DON'T KNOW	TOTAL	WEIGHTED AVERAGE
HLA-B*15:02, not a carrier	17% 9	49% 26	19% 10	6% 3	9% 5	53	2.15
HLA-B*15:02, negative	5% 3	18% 10	38% 21	30% 17	9% 5	56	3.02
HLA-B*15:02, not detected	15% 8	26% 14	36% 19	15% 8	8% 4	53	2.55
HLA-B*15:02 non-carrier	5% 3	18% 10	46% 26	20% 11	11% 6	56	2.90

#	OTHER PLEASE SPECIFY	DATE
1	HLA-B*15:02 absent	2/16/2015 9:07 AM

### Q62 For variants with unclear function (i.e. literature supporting function is conflicting), describe your degree of acceptance of the following terms to describe the allele functions:

Answered: 59 Skipped: 18



	STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	NO OPINION/DON'T KNOW	TOTAL	WEIGHTED AVERAGE
Unclear function	12% 7	18% 10	46% 26	23% 13	2% 1	57	2.80
Unknown function	15% 8	37% 20	37% 20	9% 5	2% 1	54	2.42
Conflicting data	18% 10	31% 17	31% 17	20% 11	0% 0	55	2.53
Indeterminate function	15% 8	43% 23	30% 16	11% 6	2% 1	54	2.38
Unconclusive	20% 11	36% 20	29% 16	13% 7	4% 2	56	2.35

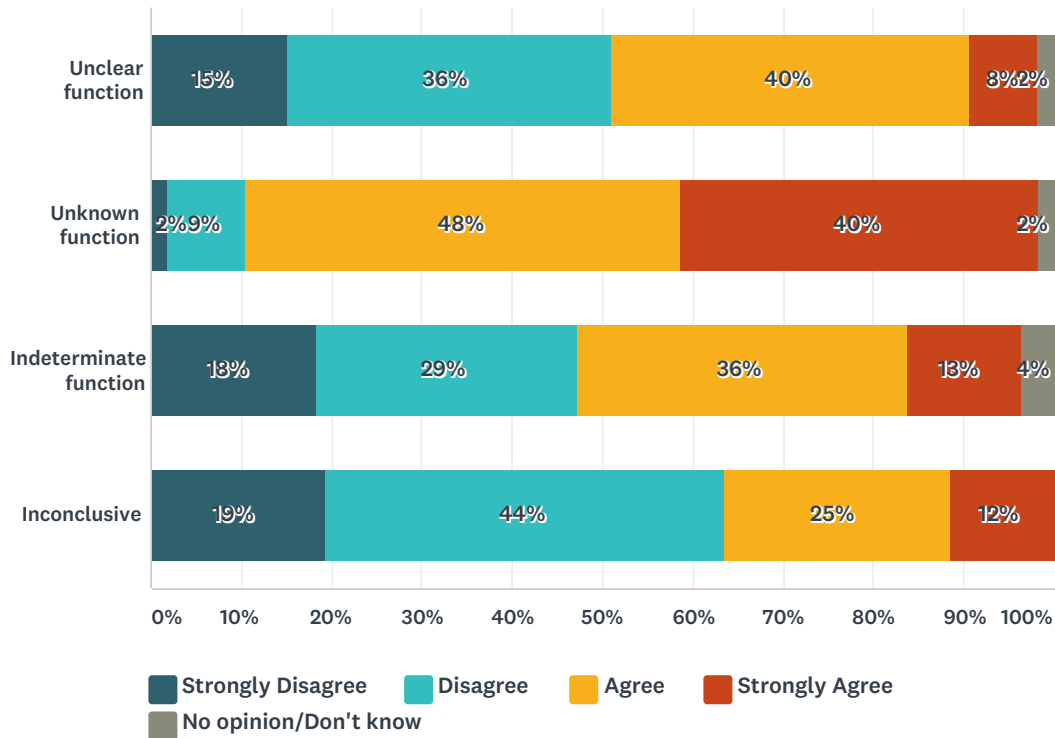
#	OTHER (PLEASE SPECIFY)	DATE
1	Inconclusive	2/22/2015 3:49 PM
2	"Unconclusive" should be "inconclusive function".	2/22/2015 10:54 AM
3	Uncertain function	2/21/2015 9:19 PM
4	Indeterminate activity	2/20/2015 6:22 PM
5	Prefer "inconclusive" to "unconclusive"	2/20/2015 6:08 PM
6	Uncertain significance	2/20/2015 5:24 PM
7	Uncertain	2/20/2015 4:39 PM

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8	A better terms would be "Uncertain function" which encompasses both Unknown (no data) and conflicting data and is also consistent with ACMG guidelines for Mendelian variants where we use "Uncertain significance" . Inconclusiev should be reserved for the overall result, not the individual variant.	2/19/2015 4:06 PM
9	I think you meant "Inconclusive"	2/19/2015 4:02 PM
10	unclear enzyme activity	2/16/2015 9:08 AM
11	Inconclusive	2/11/2015 1:51 PM
12	not known or not well understood	2/3/2015 4:54 PM
13	"Inconclusive" would be okay. "Unconclusive" is not standard English.	2/3/2015 3:33 PM
14	Inconclusive	2/3/2015 11:58 AM
15	Should use the term variant of uncertain significance to be compatible with ACMG terminology	2/3/2015 2:39 AM
16	Unclear activity	2/2/2015 2:08 PM

### Q63 For variants with unknown function (i.e. no literature describing function), describe your degree of acceptance of the following terms to describe allele functions:

Answered: 59 Skipped: 18



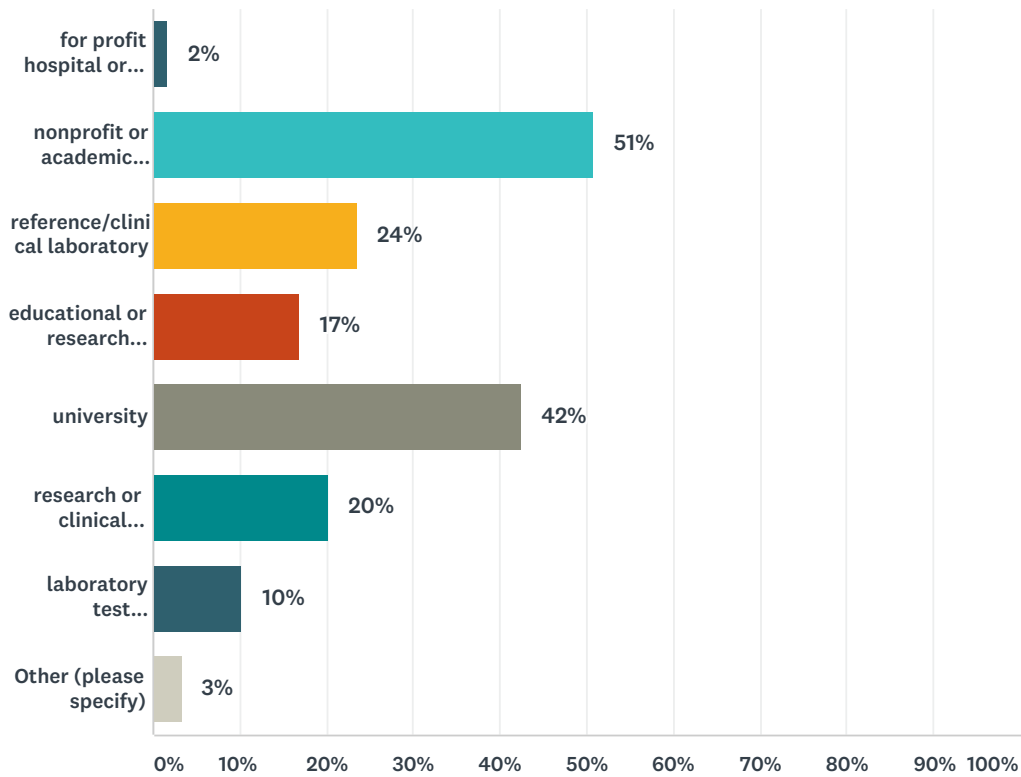
	STRONGLY DISAGREE	DISAGREE	AGREE	STRONGLY AGREE	NO OPINION/DON'T KNOW	TOTAL	WEIGHTED AVERAGE
Unclear function	15% 8	36% 19	40% 21	8% 4	2% 1	53	2.40
Unknown function	2% 1	9% 5	48% 28	40% 23	2% 1	58	3.28
Indeterminate function	18% 10	29% 16	36% 20	13% 7	4% 2	55	2.45
Inconclusive	19% 10	44% 23	25% 13	12% 6	0% 0	52	2.29

#	OTHER (PLEASE SPECIFY)	DATE
1	If there is no literature it is unknown.	2/22/2015 10:54 AM
2	Uncertain function	2/21/2015 9:19 PM
3	Unknown activity	2/20/2015 6:22 PM
4	Uncertain significance	2/20/2015 5:24 PM
5	Uncertain	2/20/2015 4:39 PM
6	see above	2/19/2015 4:06 PM
7	evidence unknown	2/18/2015 11:57 AM
8	unclear enzyme activity, unclear transport activity	2/16/2015 9:08 AM



### Q64 Which of the following describes your workplace setting (choose all that apply)?

Answered: 59 Skipped: 18

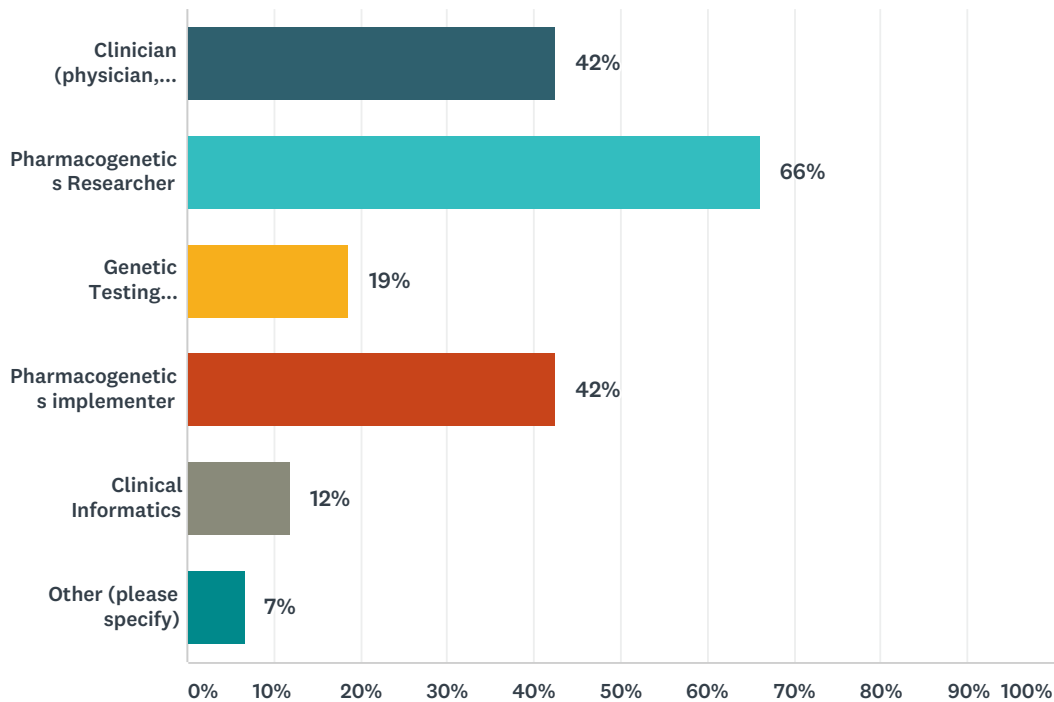


ANSWER CHOICES	RESPONSES
for profit hospital or clinic	2% 1
nonprofit or academic hospital or clinic	51% 30
reference/clinical laboratory	24% 14
educational or research resource	17% 10
university	42% 25
research or clinical institute	20% 12
laboratory test interpretation service	10% 6
Other (please specify)	3% 2
Total Respondents: 59	

#	OTHER (PLEASE SPECIFY)	DATE
1	Pharma	2/6/2015 1:00 PM
2	Manufacturer of genotyping and detection assays	2/3/2015 4:56 PM

## Q65 What capacity are you involved in clinical pharmacogenetics (choose all that apply)?

Answered: 59 Skipped: 18

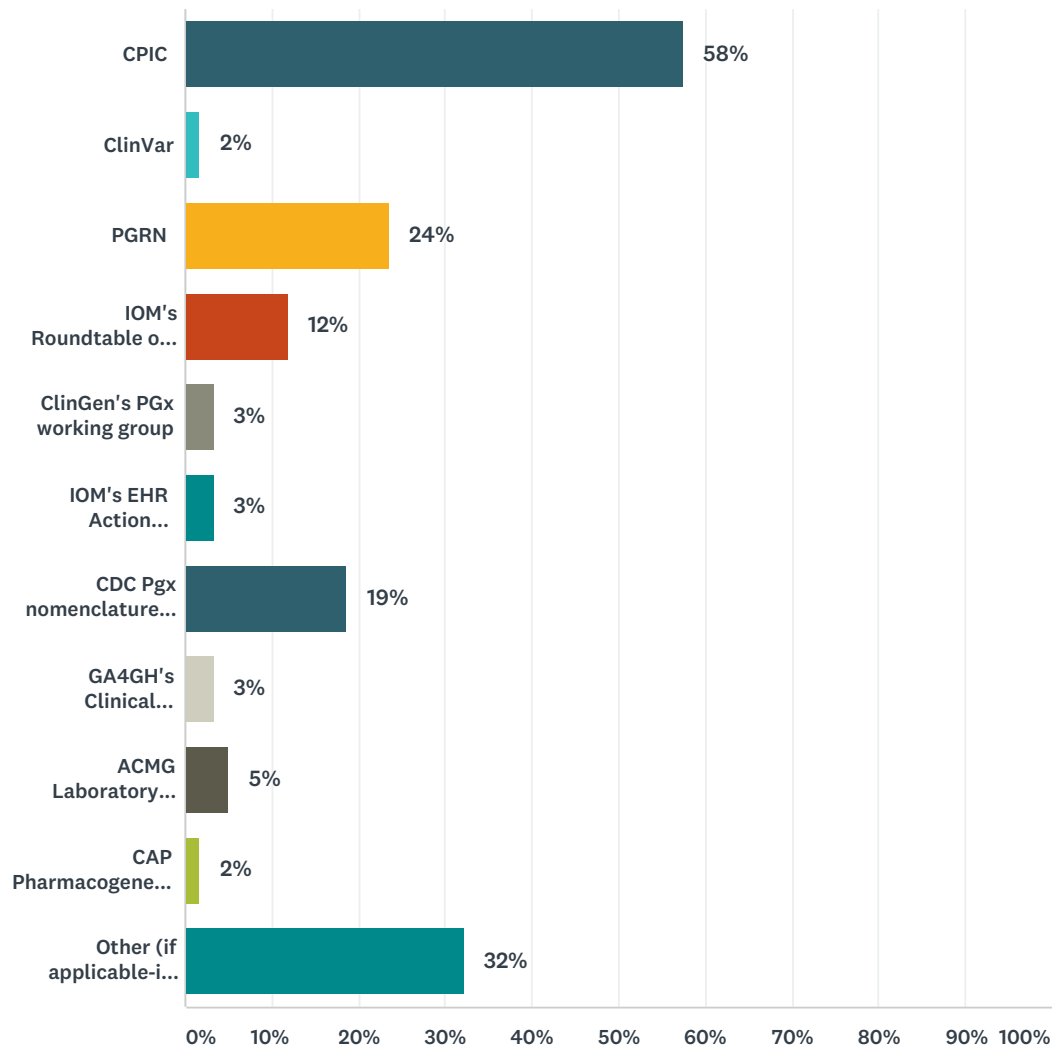


ANSWER CHOICES	RESPONSES	
Clinician (physician, pharmacist, nurse, etc.)	42%	25
Pharmacogenetics Researcher	66%	39
Genetic Testing Laboratory Staff	19%	11
Pharmacogenetics implementer	42%	25
Clinical Informatics	12%	7
Other (please specify)	7%	4
Total Respondents: 59		

#	OTHER (PLEASE SPECIFY)	DATE
1	Scientific curation	2/22/2015 10:54 AM
2	Developer of pg. educational materials for physicians	2/11/2015 2:28 PM
3	Scientific Curator	2/5/2015 2:19 PM
4	PGX Lab Director	2/4/2015 3:32 PM

### Q66 Which of the following groups are you associated/a member (choose all that apply)?

Answered: 59 Skipped: 18



ANSWER CHOICES	RESPONSES	
CPIC	58%	34
ClinVar	2%	1
PGRN	24%	14
IOM's Roundtable on Translating Genomic-Based Research for Health	12%	7
ClinGen's PGx working group	3%	2
IOM's EHR Action Collaborative	3%	2
CDC Pgx nomenclature working group	19%	11
GA4GH's Clinical Working Group	3%	2
ACMG Laboratory Standards and Guidelines Committee	5%	3

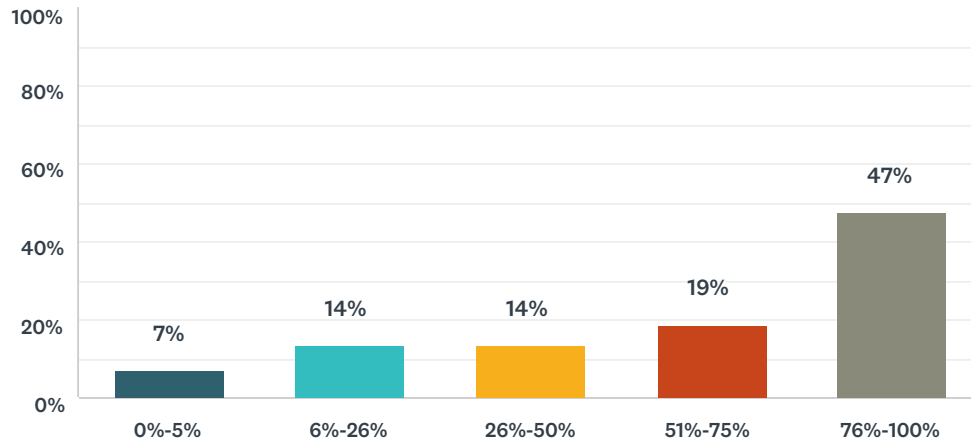
## CPIC Term Standardization for Clinical Pharmacogenetic Test Results: alleles and phenotypes

CAP Pharmacogenetics Working Group	2%	1
Other (if applicable-i.e. pharmacogenetics related):	32%	19
Total Respondents: 59		

#	OTHER (IF APPLICABLE-I.E. PHARMACOGENETICS RELATED):	DATE
1	Pharmacogenetics testing laboratory	2/22/2015 3:52 PM
2	none of the above	2/21/2015 9:21 PM
3	ClinGen Data Modeling working group, AMIA Genomics and Translational Bioinformatics working group, HL7 Clinical Genomics working group	2/20/2015 6:12 PM
4	N/A	2/19/2015 4:30 PM
5	eMERGE	2/19/2015 4:03 PM
6	DPWG	2/18/2015 4:59 PM
7	OBO foundry	2/18/2015 11:58 AM
8	PharmGKB	2/13/2015 11:37 PM
9	psychiatrists, other physicians	2/11/2015 1:46 PM
10	Children's Mercy Hospital Clinical Pharmacology	2/11/2015 1:44 PM
11	IPWG, ASCPT	2/6/2015 1:00 PM
12	TPMT nomenclature committee	2/6/2015 8:56 AM
13	PGRN TPP	2/5/2015 8:24 AM
14	AMP	2/4/2015 3:32 PM
15	AMP Member	2/3/2015 12:31 PM
16	IGNITE	2/3/2015 11:57 AM
17	European Medicines Agency, CHMP Pharmacogenomics Working Party; G2MC Pharmacogenomics Working Group leader	2/3/2015 11:46 AM
18	n/a	2/3/2015 11:15 AM
19	IUPHAR Pharmacogenomics and genetics section	2/2/2015 2:10 PM

### Q67 What percentage of time do you devote to pharmacogenetics (i.e. research time, clinic time, etc.)?

Answered: 59 Skipped: 18



ANSWER CHOICES	RESPONSES	
0%-5%	7%	4
6%-26%	14%	8
26%-50%	14%	8
51%-75%	19%	11
76%-100%	47%	28
<b>TOTAL</b>		<b>59</b>

**Q68 To reach consensus, there will be several future surveys, and it is important to complete each survey. In order to follow the progression of change in survey answers with each survey round, to make sure we are not getting duplicate responses, and to be able to follow up with questions about your responses, we are asking you to provide your name and contact information on each survey.**

Answered: 59 Skipped: 18

ANSWER CHOICES	RESPONSES
Your name:	100% 59
Your email:	100% 59
Your primary affiliation/place of work:	100% 59

#	YOUR NAME:	DATE
1	Colleen Campbell	2/22/2015 3:52 PM
2	Ellen McDonagh	2/22/2015 10:54 AM
3	Howard Levy	2/21/2015 9:21 PM
4	Michele Cargill	2/20/2015 6:24 PM
5	Robert Freimuth	2/20/2015 6:12 PM
6	Matthew Lebo	2/20/2015 5:26 PM
7	Stuart Scott	2/20/2015 4:40 PM
8	Katrin Sangkuhl	2/20/2015 1:37 PM
9	Laura Chadwick	2/19/2015 4:30 PM
10	Ben Kong	2/19/2015 4:22 PM
11	Heidi Rehm	2/19/2015 4:17 PM
12	Erica Woodahl	2/19/2015 4:07 PM
13	Shannon Manzi	2/19/2015 4:03 PM
14	Julio Duarte	2/19/2015 4:00 PM
15	Jesse Swen	2/18/2015 4:59 PM
16	Asiyah Yu Lin	2/18/2015 11:58 AM
17	Mary Relling	2/17/2015 6:59 PM
18	Gwen McMillin	2/17/2015 12:26 PM
19	Uli Zanger	2/16/2015 9:08 AM
20	Wafaa M Rashed	2/14/2015 4:13 PM
21	Li Gong	2/13/2015 11:37 PM
22	Otito Iwuchukwu	2/12/2015 5:02 PM
23	Katie Johansen Taber	2/11/2015 2:28 PM
24	Houda Hachad	2/11/2015 2:06 PM
25	Jeffrey Bishop	2/11/2015 1:52 PM

## CPIC Term Standardization for Clinical Pharmacogenetic Test Results: alleles and phenotypes

26	Chun Xu	2/11/2015 1:46 PM
27	Jean Dinh	2/11/2015 1:44 PM
28	Rika Yuliwulandari	2/10/2015 4:01 AM
29	Andria L. Del Tredici	2/9/2015 5:21 PM
30	vicky pratt	2/9/2015 1:11 PM
31	Rebecca Blanchard	2/6/2015 1:00 PM
32	Malin Lindqvist Appell	2/6/2015 8:56 AM
33	Maria Alvarellos	2/5/2015 2:19 PM
34	Laura Ramsey	2/5/2015 10:34 AM
35	Jasmine Luzum	2/5/2015 8:24 AM
36	Mark Borgman	2/4/2015 3:32 PM
37	Roseann Gammal	2/4/2015 3:09 PM
38	Callaghan	2/4/2015 2:40 PM
39	Ruth Epstein-Baak	2/3/2015 4:56 PM
40	Alex Schmidt	2/3/2015 3:35 PM
41	Emily K Pauli	2/3/2015 2:15 PM
42	Julia Barbarino	2/3/2015 1:29 PM
43	Ranjit Thirumaran	2/3/2015 12:31 PM
44	Aniwaa Owusu Obeng	2/3/2015 12:18 PM
45	Javier G Blanco	2/3/2015 12:04 PM
46	Linda Jeng	2/3/2015 12:00 PM
47	Minoli Perera	2/3/2015 11:57 AM
48	Larisa Cavallari	2/3/2015 11:57 AM
49	George P. Patrinos	2/3/2015 11:46 AM
50	Danxin Wang	2/3/2015 11:38 AM
51	Nisha Hull	2/3/2015 11:15 AM
52	Dylan Mordaunt	2/3/2015 2:40 AM
53	Dave Kisor	2/2/2015 5:14 PM
54	Sam Johnson	2/2/2015 4:36 PM
55	Andrea Gaedigk	2/2/2015 2:49 PM
56	Guilherme Suarez-Kurtz	2/2/2015 2:10 PM
57	Cristy Baldwin	2/2/2015 12:08 PM
58	José A. G. Agúndez	2/2/2015 11:31 AM
59	Claudia Kim	2/2/2015 11:19 AM
<b>#</b>	<b>YOUR EMAIL:</b>	<b>DATE</b>
1	colleen-campbell@uiowa.edu	2/22/2015 3:52 PM
2	elliemarymcdonagh@gmail.com	2/22/2015 10:54 AM
3	hlevy3@jhmi.edu	2/21/2015 9:21 PM
4	michele.cargill@invitae.com	2/20/2015 6:24 PM
5	freimuth.robert@mayo.edu	2/20/2015 6:12 PM
6	mlebo@partners.org	2/20/2015 5:26 PM

## CPIC Term Standardization for Clinical Pharmacogenetic Test Results: alleles and phenotypes

7	stuart.scott@mssm.edu	2/20/2015 4:40 PM
8	katrin@pharmgkb.org	2/20/2015 1:37 PM
9	laura.chadwick@childrens.harvard.edu	2/19/2015 4:30 PM
10	kongb.rx@gmail.com	2/19/2015 4:22 PM
11	hrehm@partners.org	2/19/2015 4:17 PM
12	erica.woodahl@umontana.edu	2/19/2015 4:07 PM
13	shannon.manzi@childrens.harvard.edu	2/19/2015 4:03 PM
14	juliod@uic.edu	2/19/2015 4:00 PM
15	j.j.swen@lumc.nl	2/18/2015 4:59 PM
16	linikujp@gmail.com	2/18/2015 11:58 AM
17	mary.relling@stjude.org	2/17/2015 6:59 PM
18	gwen.mcmillin@aruplab.com	2/17/2015 12:26 PM
19	uli.zanger@ikp-stuttgart.de	2/16/2015 9:08 AM
20	wafaaanor@gmail.com	2/14/2015 4:13 PM
21	lgong@stanford.edu	2/13/2015 11:37 PM
22	otito.f.iwuchukwu@vanderbilt.edu	2/12/2015 5:02 PM
23	katherine.johansen@ama-assn.org	2/11/2015 2:28 PM
24	houda.hachad@translationalsoftware.com	2/11/2015 2:06 PM
25	jrbishop@umn.edu	2/11/2015 1:52 PM
26	chun.xu@ttuhsc.edu	2/11/2015 1:46 PM
27	jdinh@cmh.edu	2/11/2015 1:44 PM
28	rika_yuliwulandari@yahoo.co.uk	2/10/2015 4:01 AM
29	andria.deltredici@millenniumhealth.com	2/9/2015 5:21 PM
30	vpratt@iu.edu	2/9/2015 1:11 PM
31	rebecca.blanchard@merck.com	2/6/2015 1:00 PM
32	malin.lindqvist.appell@liu.se	2/6/2015 8:56 AM
33	maria@pharmgkb.org	2/5/2015 2:19 PM
34	laura.ramsey@stjude.org	2/5/2015 10:34 AM
35	luzum.2@osu.edu	2/5/2015 8:24 AM
36	mark.borgman@pgxlab.com	2/4/2015 3:32 PM
37	roseann.gammal@stjude.org	2/4/2015 3:09 PM
38	Jcallagh@iu.edu	2/4/2015 2:40 PM
39	rbaak@autogenomics.com	2/3/2015 4:56 PM
40	aschmidt@castlemedical.com	2/3/2015 3:35 PM
41	emily.pauli@ccihsv.com	2/3/2015 2:15 PM
42	jmbabarino@pharmgkb.org	2/3/2015 1:29 PM
43	ranjit@genelex.com	2/3/2015 12:31 PM
44	aniwaa.owusu-obeng@mssm.edu	2/3/2015 12:18 PM
45	jgblanco@buffalo.edu	2/3/2015 12:04 PM
46	ljeng@som.umaryland.edu	2/3/2015 12:00 PM
47	mperera@bsd.uchicago.edu	2/3/2015 11:57 AM

## CPIC Term Standardization for Clinical Pharmacogenetic Test Results: alleles and phenotypes

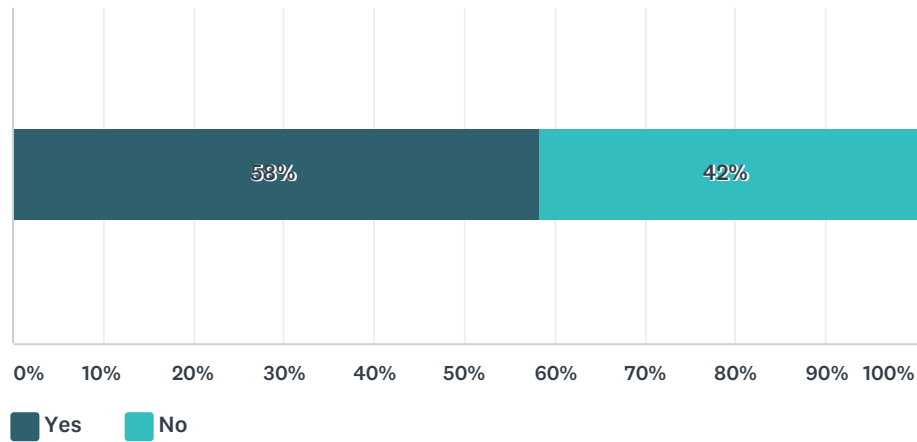
48	lcavallari@cop.ufl.edu	2/3/2015 11:57 AM
49	gpatrinos@upatras.gr	2/3/2015 11:46 AM
50	wang.808@osu.edu	2/3/2015 11:38 AM
51	nisha.hull@companiondxlab.com	2/3/2015 11:15 AM
52	d.a.mordaunt@gmail.com	2/3/2015 2:40 AM
53	dfkisor@manchester.edu	2/2/2015 5:14 PM
54	samuel.g.johnson@kp.org	2/2/2015 4:36 PM
55	agaedigk@cmh.edu	2/2/2015 2:49 PM
56	kurtz.guilherme@gmail.com	2/2/2015 2:10 PM
57	cbaldwin@cmh.edu	2/2/2015 12:08 PM
58	jagundez@unex.es	2/2/2015 11:31 AM
59	claudia.kim@companiondxlab.com	2/2/2015 11:19 AM
<b>#</b>	<b>YOUR PRIMARY AFFILIATION/PLACE OF WORK:</b>	<b>DATE</b>
1	University of Iowa, Iowa Institute of Human Genetics	2/22/2015 3:52 PM
2	Queen Mary University, Genomics England	2/22/2015 10:54 AM
3	Johns Hopkins University	2/21/2015 9:21 PM
4	Invitae Corporation	2/20/2015 6:24 PM
5	Mayo Clinic	2/20/2015 6:12 PM
6	Partners HealthCare Personalized Medicine	2/20/2015 5:26 PM
7	Icahn School of Medicine at Mount Sinai	2/20/2015 4:40 PM
8	Stanford	2/20/2015 1:37 PM
9	Boston Children's Hospital	2/19/2015 4:30 PM
10	Oregon Health and Science University	2/19/2015 4:22 PM
11	Harvard Medical School	2/19/2015 4:17 PM
12	University of Montana	2/19/2015 4:07 PM
13	Boston Children's Hospital	2/19/2015 4:03 PM
14	University of Illinois at Chicago	2/19/2015 4:00 PM
15	LUMC	2/18/2015 4:59 PM
16	University of Michigan	2/18/2015 11:58 AM
17	St. Jude Children's Research Hospital	2/17/2015 6:59 PM
18	ARUP Labs / University of Utah	2/17/2015 12:26 PM
19	Dr. Margarete Fischer-Bosch Institute of Clinical Pharmacology	2/16/2015 9:08 AM
20	Children's Cancer Hospital -Egypt 57357	2/14/2015 4:13 PM
21	Stanford University	2/13/2015 11:37 PM
22	Vanderbilt University Medical Center	2/12/2015 5:02 PM
23	American Medical Association	2/11/2015 2:28 PM
24	CSO	2/11/2015 2:06 PM
25	University of Minnesota	2/11/2015 1:52 PM
26	TTUHSC	2/11/2015 1:46 PM
27	Children's Mercy Hospital	2/11/2015 1:44 PM
28	Universitas YARSI, Jakarta	2/10/2015 4:01 AM

## CPIC Term Standardization for Clinical Pharmacogenetic Test Results: alleles and phenotypes

29	Millennium Health	2/9/2015 5:21 PM
30	indiana university	2/9/2015 1:11 PM
31	Merck	2/6/2015 1:00 PM
32	LInköping University	2/6/2015 8:56 AM
33	PharmGKB	2/5/2015 2:19 PM
34	SJCRH	2/5/2015 10:34 AM
35	Ohio State University	2/5/2015 8:24 AM
36	PGXL Laboratories	2/4/2015 3:32 PM
37	St. Jude Children's Research Hospital	2/4/2015 3:09 PM
38	RL Roudebush VAMC	2/4/2015 2:40 PM
39	AutoGenomics, Inc.	2/3/2015 4:56 PM
40	Castle Medical, LLC	2/3/2015 3:35 PM
41	Oncology Specialties, PC	2/3/2015 2:15 PM
42	PharmGKB, Stanford University	2/3/2015 1:29 PM
43	Genelex Corporation	2/3/2015 12:31 PM
44	Icahn School of Medicine at Mount Sinai	2/3/2015 12:18 PM
45	SUNY Buffalo. School of Pharmacy and Pharmaceutical Sciences	2/3/2015 12:04 PM
46	University of Maryland School of Medicine	2/3/2015 12:00 PM
47	University of Chicago	2/3/2015 11:57 AM
48	University of Florida	2/3/2015 11:57 AM
49	University of Patras, Department of Pharmacy, Patras, Greece	2/3/2015 11:46 AM
50	The Ohio State University	2/3/2015 11:38 AM
51	Companion Dx Lab	2/3/2015 11:15 AM
52	RCH, Melbourne	2/3/2015 2:40 AM
53	Manchester University College of Pharmacy	2/2/2015 5:14 PM
54	Kaiser Permanente Colorado	2/2/2015 4:36 PM
55	Children's Mercy Kansas City	2/2/2015 2:49 PM
56	Brazilian National Cancer Institute	2/2/2015 2:10 PM
57	Children's Mercy Hospitals and Clinics	2/2/2015 12:08 PM
58	University of Extremadura, Cáceres, Spain	2/2/2015 11:31 AM
59	Pharmacy Operations Manager	2/2/2015 11:19 AM

### Q69 Did you participate in the live webinar or listen to the recorded webinar before participating in this survey? (for documentation purposes only):

Answered: 55 Skipped: 22



ANSWER CHOICES	RESPONSES	
Yes	58%	32
No	42%	23
TOTAL		55

## Q70 Please use the space below to provide any additional comments:

Answered: 15 Skipped: 62

#	RESPONSES	DATE
1	Regardless of the gene, the same terms should be used to describe alleles and phenotypes so that it is easier for healthcare providers to understand the results. There were not terms for novel alleles. As next generation sequencing is beginning to be utilized for pharmacogenetics testing, novel alleles will be discovered (unlike when genotyping arrays are utilized) therefore it may be helpful to have a standard terminology for these alleles. It would also be helpful to have a standard system for reporting the discovery of these alleles to PharmGKB. After implementing these tests, we interviewed physicians who have said the current terms to describe alleles and phenotypes are not intuitive, i.e. it isn't intuitive that "extensive metabolizer" is a normal metabolizer. For physicians to adopt pharmacogenetics testing the terms should be intuitive so they can understand the results. There were no questions regarding terms for copy number variants. We are reporting copy number variants and it may be helpful as others start to report CNVs that there is a standard terminology. Star alleles do not mean anything to anyone outside of the pharmacogenetics community and we should move away from using these as it just requires another level of translation. If the pharmacogenetics community wants to be readily accepted they should use standard genetics HUGO nomenclature, especially as next generation sequencing is becoming utilized for pharmacogenetics testing. In interviews with physicians after implementing this testing, they have complained about star alleles and state they ignore these as it's not meaningful. In addition, star alleles are not amenable to longevity reporting in the EMR.	2/22/2015 6:43 PM
2	Great job, Kelly! I hope PHONT can continue to contribute to this effort as it progresses.	2/20/2015 6:13 PM
3	In general, I think we should provide standard nomenclature across all of PGx if possible to make the field more uniform and to allow for new genes to be included without needing committees. If we allow the nomenclature to describe what is happening, within the test interpretation is where we can detail what it means for this patient and certain drugs.	2/20/2015 5:28 PM
4	The webinar was very helpful in clarifying the goals of the survey. Thank you!	2/19/2015 4:31 PM
5	Thank you for doing this survey!	2/19/2015 4:18 PM
6	great idea!	2/18/2015 4:59 PM
7	Just a few commenst: great action plan, very important, I'm happy to participate. In my answers I consistently disagreed with the term "function" because I'm convinced that most gene products have several functions, but in most cases only one or few have been studied. TPMT, DPYD, UGT1A1, VKORC1, and many transporters have endogenous functions, and even CYP2D6 and others appear to have some. Additional unknown functions e.g. in membrane stabilization, complex formation etc. may exist. To designate a certain allele as "low function" would imply that this applies to all functions including the ones mentioned above, although this has in most cases not been investigated. I would therefore prefer the terms "enzyme activity" for alleles encoding enzymes and xxx metabolizer for corresponding phenotypes; accordingly, "xxx transport activity" might be used for transporter allele function. Unfortunately, there seems to be no good transporter correlate to the "metabolizer" phenotype. Generally we should be as precise as possible without compromising common understandability. If the nomenclature should also be understandable to patients, its important to realize that not every patient knows how a "heterozygote" differs from a "homozygote", and even experts don't know how to define the "wild-type". Technically, I worried about my work being lost when interrupting the work. Also, it would be helpful if one could not only interrupt but also print out the entire questionnaire in order to prepare and check for consistency. Time needed: about 2 hours	2/16/2015 9:08 AM
8	1-Are you considering cases where a "provisional" phenotype is assigned? Example CYP2C19*2/*17; intermediate metabolizer (provisional) 2-Are you considering terms for phenotype ranges?. Example: CYP2D6 extensive or rapid metabolizer 3-Are you considering terms to report results that cannot be assigned a specific phenotype?. Example: unknown phenotype; uncharacterized phenotype; indeterminate phenotype...	2/11/2015 2:11 PM
9	any grant opportunities for pharmacogenetics	2/11/2015 1:47 PM
10	Webinar very helpful - thank you!	2/11/2015 1:45 PM

## CPIC Term Standardization for Clinical Pharmacogenetic Test Results: alleles and phenotypes

11	This work will have major impact and is a service to the scientific community and to Researchers involved in Genetics.	2/3/2015 4:57 PM
12	I support the use of clear terms like "full function," "reduced function," and "unknown significance" over terms I consider somewhat euphemistic, like "extensive metabolizer" and "unclear significance" (this last in the context of a completely un-researched variant.) I'd prefer terms to be completely clear to laypeople, which are final consumers of these tests.	2/3/2015 3:41 PM
13	1. For CYP enzymes we report the phenotype as Normal/Intermediate/Poor Metabolizers. So why shouldn't the Transporters be reported as Normal/Intermediate/Poor Transporters and Acetylators as Normal/Intermediate/Slow Acetylators instead of Normal/Intermediate/Poor Function Phenotypes? 2. Just curious to know why is CPIC assigning CYP2D6*10/*10 as Extensive/Normal Metabolizers? Since *10 according to CPIC is a reduced functional allele. So for two reduced functional alleles shouldn't CPIC designate them as at least Intermediate Function? 3. What phenotype will you assign when you have a combination of Uncertain Functional Allele and Decreased Functional Allele. Would you treat the Uncertain Functional Allele as Wild Type just to take the conservative approach? Here by uncertain function, I mean not having enough evidence to even classify the allele function. If you feel any of these questions aren't tied to the survey please feel free to not answer. Thank you	2/3/2015 12:39 PM
14	Excellent initiative!	2/3/2015 11:46 AM
15	The premise I used was to start with "normal function" or "normal activity" and relate other choices relative to those terms.	2/2/2015 5:15 PM