Supplemental Material

Clinical Pharmacogenetics Implementation Consortium (CPIC) Guidelines for Dihydropyrimidine Dehydrogenase Genotype and Fluoropyrimidine Dosing: 2017 update

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Guideline Updates

The Clinical Pharmacogenetics Implementation Consortium (CPIC) guideline for *DPYD* genotypes and the dosing of fluoropyrimidines is published in full on https://cpicpgx.org/guidelines/guideline-for-fluoropyrimidines-and-dpyd/(1) and at pharmgkb.org. Relevant information will be reviewed periodically and updated guidelines published online.

Literature Review

2013 guideline

A literature search of the PubMed® database (1966 to March 2013) using the keywords ((DPD OR DPYD OR Dihydropyrimidine Dehydrogenase) AND (fluorouracil OR 5-FU OR fluoropyrimidines OR capecitabine OR tegafur) AND genotype) was performed and results were limited to those available in English. Further articles were found via the reference sections of reviews. Using these search terms, 104 publications were identified. Study inclusion criteria included publications that included analyses for the association between *DPYD* genotypes (c.1905+1G>A, c.1679T>G, and c.2846A>T) and metabolism of dihydropyrimidines and adverse drug events or clinical outcomes. Non-English manuscripts were excluded. Following application of these inclusion criteria, 30 publications were reviewed and included in the evidence tables

2017 guideline

We searched PubMed® database as described above between 1966 and March 2017. The 2013 literature review was repeated to include all known *DPYD* genotypes. Using these search terms, 150 publications were identified. Following application of the inclusion criteria, 49 publications were reviewed and included in the evidence tables. An additional 43 studies were identified from the reference sections of reviews and other published paper, and included in the evidence tables, bringing the total included studies to 92 (Supplemental Table S1).

Genetic Test Interpretation

While some *DPYD* variants have been assigned a (*) allele, this nomenclature has not been updated to include more recently identified decreased function variants. As a consequence, only a minority of DPYD variants has a (*) allele designation. Furthermore, the (*) allele nomenclature is used for other drug metabolizing enzymes to designate haplotypes. Due to the size of *DPYD*, the gene encompasses several haplotype blocks (2, 3) with low linkage disequilibrium between variants located in different haplotype blocks. As a consequence, it is not possible to reliably determine full haplotypes that incorporate genotypes for common polymorphisms (e.g. c.85T>C, c.2194G>A) across the entire gene. Therefore, any (*) alleles used for *DPYD* generally do not refer to haplotypes but only to a genotype at one specific SNP locus. To avoid confusion with (*) allele nomenclature used for haplotypes of other drug metabolizing enzymes, the preferred nomenclature for *DPYD* variants is therefore the use of rs# or HGVS nomenclature.

Test results for *DPYD* do not report a diplotype for the entire gene, but genotypes for individual SNP loci. Importantly, however, all currently established toxicity-associated decreased/no function DPYD variants have a low population frequency (<5%) and are observed most frequently in individuals without a second decreased/no function variant. Therefore, in patients who carry two different decreased/no function variants, for the test interpretation, it is assumed that the two variants with an impact on DPD activity are located on different gene copies. For patients, in whom novel DPYD variants with suspected deleterious impact are detected in combination with known decreased/no function variants, this assumption may not be correct. In such a case, a phenotyping test may be helpful to determine enzyme activity, or genotyping of relatives (parents, siblings, and offspring) to determine segregation patterns. In addition, a genetic test may also include genotyping of other, common DPYD variants (e.g. c.85T>C, c.1627A>G, c.2194G>A). If this is case, a patient may be heterozygous for multiple of these variants and it cannot be determined which alleles are located on the same gene copy. However, based on current data, none of these common variants have a clinically relevant impact in the context of 5-fluorouracil related toxicity. The exact haplotype configuration of these

normal function variants is thus not required for the test interpretation. Therefore, to calculate the *DPYD* gene activity score, only the variant activity scores for the two variants with the lowest activity score is considered. For example, if a patient is a heterozygous carrier of a decreased function variant (e.g. c.1129–5923C>G) and two normal function variants (e.g. c.85T>C and c.1627A>G), the variant activity score of 0.5 for c.1129–5923C>G would be considered for one gene copy, and an activity score of 1 for the second gene copy, resulting in a total gene activity score of 1.5.

The dosing recommendations in this guideline are specific for variant alleles in which there are clear data linking the *DPYD* genotype to fluoropyrimidine toxicity (c.1905+1G>A, c.1679T>G, c.2846A>T, c.1129–5923C>G) (**Supplementary Table S1**). Several other variants have been reported to be associated with reduced enzyme activity and/or linked to fluoropyrimidine toxicity, albeit with somewhat weaker evidence (see *DPYD* Allele Functionality Table (4), "moderate evidence supporting function"). While most of these variants are rare (see *DPYD* Allele Frequency Table (4)), the decreased function variant rs115232898 (c.557T>C, p.Y186C) is relatively common in individuals of African ancestry and has been observed in case reports of patients with severe 5-fluorouracil related toxicity (5, 6).

On the other hand, several *DPYD* variants that are relatively common in the population have strong or moderate evidence that they do not impact DPD function in a clinically relevant manner in the context of 5-fluorouracil related toxicity. For rs1801159 (*5, c.1627A>G, p.I543V) and rs1801265 (*9A, c.85T>C, p.C29R) none of the large cohort and case-control studies observed a significant association with toxicity or reduced DPD activity (see **Supplemental Table S1**). For other variants, associations with toxicity have been observed in single studies, but could not be reproduced in a majority of studies (rs1801160, *6, c.2194G>A, p.V732I; rs2297595, c.496T>C, p.M166V) or by meta-analysis (rs1801158, *4, c.1601G>A, p.S534N) (see **Supplemental Table S1**). Based on current knowledge, a fluorouracil dose adaptation in carriers of these variants is thus not warranted.

Many of the variants listed in the "in vitro data only and/or limited clinical/ex vivo data" category (see *DPYD* Allele Functionality Table (4)) as decreased or no function variants have a very low (<0.5%) allele frequency in the populations studied (see *DPYD* Allele Frequency Table (4)) and to date, there are no studies linking these variant alleles directly to toxicity related to fluoropyrimidines. Their functional effect was evaluated by comparison of their in vitro activity to the *in vitro* activity of known toxicity-associated *DPYD* variants: All variants with *in vitro* activity similar to c.1905+1G>A and c.1679T>G were categorized as "no function" variants; variants with *in vitro* activity greater than that of known "no function" variants but equal to or lower than the *in vitro* activity of c.2846A>T were classified as "decreased function" variants.

Several variants listed in the "unclear or conflicting data supporting function" category had *in vitro* DPD activity (i.e. homozygous expression of the variant) that was significantly lower than wildtype activity, but the magnitude of the decrease was smaller than for any established toxicity-associated variant. For these variants, it is currently not known if the decrease in DPD activity observed *in vitro* has a clinically relevant impact on 5-fluorouracil toxicity. At the time of writing, these variants would thus not be actionable for a reduction of the starting dose in fluoropyrimidine-based therapies.

Other considerations

Several other genes may influence responses to 5-fluorouracil (7, 8), in particular genes of the folate pathway. The most well-studied of these are *MTHFR* and *TYMS*, although to date for *TYMS* the underlying causal variants of associations (9) and their clinical utility (10) are unclear, and associations have been inconsistent for *MTHFR* (10). Therefore, predictive dosing strategies for these genes have yet to be successfully applied. Similarly, a recently identified association of a variant (rs17822471) in *ABCC11*, a transporter of 5-fluorouracil metabolites, with fluoropyrimidine-related leukopenia requires further investigation (11, 12). In the context of capecitabine-based therapies, genes in the capecitabine activation pathway have also been studied, most notably *CDA*, *CES1* and *CES2* (13, 14). While some associations have been reported, these results have not been sufficiently replicated to determine potential genotype-based therapeutic strategies.

Furthermore, Fernandez-Rozadilla *et al* performed a genome-wide association study on 221 colorectal cancer patients (including a validation set of 791 patients) that had been treated with a 5-fluorouracil-based regimen (15). Seven SNPs (rs16857540 (*NLGN1*), rs2465403 (*COLEC10*), rs10876844 (*OR10AE3P*, *PSMB2P*), rs10784749, rs17626122 (*PARD3B*), rs7325568 and rs4243761) showed evidence of association with adverse drug reactions. They also evaluated the association signals for seven SNPs that had been linked to 5-fluorouracil-related toxicity in the literature (rs1801159 and rs1801265 (*DPYD*), rs18010919 (*UMPS*), rs1801133 (*MTHFR*), rs34743033, rs34489327 (*TYMS*), rs1695 (*GSTP1*)). Four of these variants had good proxy SNPs in the study, but none of them showed a statistically significant association. Some of the identified associations underscore the potential importance of other genes that may contribute increased risk of toxicity of 5-fluorouracil, although further studies are needed to determine their clinical utility.

Level of Evidence

The evidence summarized in **Supplemental Table S1** is graded using a scaled modified slightly from Valdes *et al* (16).

High: Evidence includes consistent results from well-designed, well-conducted studies.

Moderate: Evidence is sufficient to determine effects, but the strength of the evidence is limited by the number, quality, or consistency of the individual studies; generalizability to routine practice; or indirect nature of the evidence.

Weak: Evidence is insufficient to assess the effects on health outcomes because of limited number or power of studies, important flaws in their design or conduct, gaps in the chain of evidence, or lack of information

Strength of Recommendation

CPIC's dosing recommendations (**Table 2, main manuscript**) are based on weighting the evidence from a combination of preclinical functional and clinical data, as well as on some existing disease-specific consensus guidelines. Some of the factors that are taken

into account include *in vivo* clinical outcome for reference drug, in vivo PK/PD for reference drug, and *in vitro* enzyme activity with probe substrate only.

Overall, the dosing recommendations are simplified to allow rapid interpretation by clinicians. We chose to use a slight modification of a transparent and simple system for just three categories for recommendations adopted from the rating scale for evidence-based recommendations on the use of retroviral agents

(http://aidsinfo.nih.gov/contentfiles/AdultandAdolescentGL.pdf):

Strong recommendation for the statement: "The evidence is high quality and the desirable effects clearly outweigh the undesirable effects."

Moderate recommendation for the statement: "There is a close or uncertain balance" as to whether the evidence is high quality and the desirable clearly outweigh the undesirable effects.

Optional recommendation for the statement: The desirable effects are closely balanced with undesirable effects, or the evidence is weak or based on extrapolations. There is room for differences in opinion as to the need for the recommended course of action. **No recommendation**: There is insufficient evidence, confidence, or agreement to provide a recommendation to guide clinical practice at this time

The strength of the 5-fluorouracil dosing recommendations (**Table 2, main manuscript**) is based on the fact that some variants (c.1905+1G>A, c.1679T>G, c.2846A>T, c.1129–5923C>G) clearly affect DPD activity, and DPD activity is clearly related to 5-fluorouracil clearance, and 5-fluorouracil exposure is associated with its toxic effects. Therefore, reduction of 5-fluorouracil dosage in patients with these variants can prevent severe and possibly life-threatening toxicities, as has been demonstrated for c.1905+1G>A (17). The strength of the capecitabine dosing recommendations is based on the fact that this prodrug of 5- fluorouracil is metabolized by DPD in the same manner.

Resources to Incorporate Pharmacogenetics into an Electronic Health Record with Clinical Decision Support

Clinical decision support (CDS) tools integrated within electronic health records (EHRs) can help guide clinical pharmacogenetics at the point of care (18-22). See

https://cpicpgx.org/guidelines/guideline-for-fluoropyrimidines-and-dpyd/ for resources to support the adoption of CPIC guidelines within an EHR. Based on the capabilities of various EHRs and local preferences, we recognize that approaches may vary across organizations. Our intent is to synthesize foundational knowledge that provides a common starting point for incorporating the use of *DPYD* genotype results to guide fluoropyrimidine dosing in an EHR.

Effectively incorporating pharmacogenetic information into an EHR to optimize drug therapy should have some key attributes. Pharmacogenetic results, an interpreted phenotype, and a concise interpretation or summary of the result must be documented in the EHR (23, 24). To incorporate a phenotype in the EHR in a standardized manner, genotype test results provided by the laboratory must be consistently translated into an interpreted phenotype (**Table 1, main manuscript**). Because clinicians must be able to easily find the information, the interpreted phenotype may be documented as a problem list entry or in a patient summary section; these phenotypes are best stored in the EHR at the "person level" rather than at the date-centric "encounter level". Additionally, results should be entered as standardized and discrete terms to facilitate using them to provide point-of-care CDS (18, 25).

Because pharmacogenetic results have lifetime implications and clinical significance, results should be placed into a section of the EHR that is accessible independent of the test result date to allow clinicians to quickly find the result at any time after it is initially placed in the EHR. To facilitate this process, CPIC is providing gene-specific information figures and tables that include full diplotype to phenotype tables, diagram(s) that illustrate how *DPYD* pharmacogenetic test results could be entered into an EHR, example EHR consultation/genetic test interpretation language and widely used nomenclature systems for genes relevant to the CPIC guideline (see https://cpicpgx.org/guidelines/guideline-for-fluoropyrimidines-and-dpyd/) (26).

Point-of-care CDS should be designed to effectively notify clinicians of prescribing implications at any time after the test result is entered into the EHR. CPIC is also

providing gene-drug specific tables that provide guidance to achieve these objectives with diagrams that illustrate how point-of-care CDS should be entered into the EHR, example pre- and post-test alert language, and widely used nomenclature systems for drugs relevant to the CPIC guideline (see https://cpicpgx.org/guidelines/guideline-for-fluoropyrimidines-and-dpyd/).

Supplemental Table S1. Evidence linking *DPYD* genotype with DPD phenotype and dihydropyrimidine toxicity

DPYD	Parameter	Major findings	References	Type of	Level of
*allele	1 al allietei	wajor munigs	References	experiment	Evidence ^{c,}
rsID				al model	d d
				ai illouei	_
nucleotide change ^a					
protein change ^b					
*2A	Activity	AG is associated with	Supports Statement: <i>Statistically</i>	Clinical, Ex	Moderate
		decreased DPD activity as	Significant:	vivo	
rs3918290		compared to GG	Wei, et al. (1996)(27)		
			Kuilenburg, et al. (2016)(28)		
c.1905+1G>A			Nie, et al. (2017)(29)		
			Same Direction of Association:		
			Sistonen, et al. (2014)(30)		
		Within cell lines, AA is	Supports Statement: <i>Statistically</i>	In vitro	High
		associated with decreased	Significant:		
		DPD activity as compared to	Offer, et al. (2013)(31)		
		GG			
		AA + AG were observed in	Supports Statement:	Clinical, Ex	High
		individuals with decreased	Holopainen, et al. (1997)(32)	vivo	
		DPD activity	Vreken, et al. (1997)(33)		
			Van Kuilenburg, <i>et al.</i> (1997)(34)		
			Ridge, et al. (1998)(35)		
			Van Kuilenburg, <i>et al.</i> (1999)(36)		
			van Kuilenburg, <i>et al.</i> (2001)(37)		
			Johnson, et al. (2002)(38)		
			Maring, et al. (2002)(39)		
			van Kuilenburg, <i>et al.</i> (2002)(40)		
			Van Kuilenburg, <i>et al.</i> (2002)(41)		
			Al-Sanna'a, et al. (2005)(42)		

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		Ezzeldin, et al. (2005)(43)		
		Largillier, <i>et al.</i> (2006)(44)		
		Magne, et al. (2007)(45)		
		Loganayagam, <i>et al.</i> (2010)(46)		
		van Kuilenburg, <i>et al.</i> (2010)(47)		
		Thomas, et al. (2016)(48)		
		Does Not Support Statement:		
		Collie-Duguid, et al. (2000)(49)		
		Loganayagam, et al. (2010)(46)		
Dose	AG is associated with	Supports Statement: <i>Statistically</i>	Clinical	Moderate
	decreased capecitabine dose	Significant:		
	as compared to GG	Deenen, et al. (2011)(50)		
	Individuals with AG received	Supports Statement:	Clinical	Weak
	a decreased dose of	Joerger, et al. (2015)(51)		
	capecitabine			
Efficacy	AG is associated with a	Supports Statement: <i>Statistically</i>	Clinical	Weak
_	decreased acute lymphoblastic	Significant:		
	leukemia complete remission	Zhao, et al. (2016)(52)		
	rate as compared to GG			
	AA + AG are not associated	McLeod, et al. (2010)(53)	Clinical	Moderate
	with progression-free, disease-	Deenen, et al. (2011)(50)		
	free, event-free or overall	Cai, et al. (2014)(54)		
	survival times or confirmed	Zhao, et al. (2016)(52)		
	response rate as compared to			
	GG			
Metabolism	AG is associated with	Supports Statement: Statistically	Clinical, Ex	High
	decreased metabolism of	Significant:	vivo	J
	fluorouracil as compared to	Boisdron-Celle, <i>et al.</i> (2007)(55)		
	GG	van Kuilenburg, et al. (2008)(56)		
		Gentile, et al. (2016)(57)		

	Individuals with AG were	Supports Statement:	Clinical	Moderate
	observed to have decreased	Maring, et al. (2002)(58)		
	metabolism of fluorouracil	Joerger, et al. (2015)(51)		
Towisite	AA + AG are associated with	Commence Charles and Charles at a The	Clinical	TT: -1.
Toxicity		Supports Statement: Statistically	Cillical	High
	increased risk or severity of	Significant (overall toxicity):		
	fluoropyrimidine toxicity as	Van Kuilenburg, <i>et al.</i> (2002)(59)		
	compared to GG	Salgueiro, <i>et al.</i> (2004)(60)		
		Boisdron-Celle, <i>et al.</i> (2007)(55)		
		Schwab, et al. (2008)(61)		
		Deenen, et al. (2011)(50)		
		Lee, et al. (2014)(62)		
		Toffoli, et al. (2015)(63)		
		Statistically Significant		
		(myelosuppression):		
		Schwab, et al. (2008)(61)		
		Kleibl, et al. (2009)(64)		
		Kristensen, et al. (2010)(65)		
		Rosmarin, et al. (2014)(66)		
		Cai, et al. (2014)(54)		
		Statistically Significant (hand-		
		foot syndrome):		
		Cai, et al. (2014)(54)		
		Statistically Significant		
		(diarrhea):		
		Deenen, et al. (2011)(50)		
		Cai, et al. (2014)(54)		
		Statistically Significant		
		(mucositis):		
		Schwab, et al. (2008)(61)		

Kleibl, et al. (2009)(64) Statistically Significant	

AA + AG were observed in	Supports Statement:	Clinical	High
individuals with	Wei, et al. (1996)(27)		_
fluoropyrimidine toxicity	Van Kuilenburg, <i>et al.</i> (1997)(34)		
	van Kuilenburg, <i>et al.</i> (2000)(70)		
	van Kuilenburg, <i>et al.</i> (2001)(37)		
	Raida, et al. (2001)(71)		
	Johnson, et al. (2002)(38)		
	Maring, et al. (2002)(58)		
	Van Kuilenburg, <i>et al.</i> (2002)(41)		
	Steiner, et al. (2005)(72)		
	Ezzeldin, et al. (2005)(43)		
	Largillier, et al. (2006)(44)		
	Morel, et al. (2006)(73)		
	Saif, et al. (2007)(74)		
	Salgado, et al. (2007)(75)		
	Magne, et al. (2007)(45)		
	Sulzyc-Bielicka, et al.(2008)(76)		
	Gross, et al. (2008)(77)		
	Loganayagam, et al. (2010)(46)		
	Boige, et al. (2010)(78)		
	Ceric, et al. (2010)(79)		
	van Kuilenburg, <i>et al.</i> (2010)(47)		
	Savva-Bordalo, et al. (2010)(80)		
	Cellier, et al. (2011)(147)		
	Loganayagam, et al. (2013)(13)		
	Suarez Martinez-Falero, et al.		
	(2014)(81)		
	Joerger, et al. (2015)(51)		
	Thomas, et al. (2016)(48)		
	Roberto, et al. (2017)(82)		

*13	Activity	GT is associated with	Supports Statement: Statistically	Clinical, Ex	Moderate
		decreased DPD activity as	Significant:	vivo	
rs55886062		compared to TT	Offer, et al.(2013)(5)		
			Nie, et al. (2017)(29)		
c.1679T>G			Same Direction of Association:		
			Sistonen, et al. (2014)(30)		
p.I560S		Within cell lines, GG is	Supports Statement: Statistically	In vitro	High
		associated with decreased	Significant:		
		DPD activity was compared to	Offer, et al. (2013)(31)		
		TT			
		GT was observed in	Supports Statement:	Clinical, Ex	High
		individuals with decreased	Collie-Duguid, <i>et al.</i> (2000)(49)	vivo	
		DPD activity	Johnson, et al. (2002)(38)		
			van Kuilenburg, <i>et al.</i> (2002)(40)		
			Ezzeldin, et al. (2005)(43)		
			Thomas, et al. (2016)(48)		
	Toxicity	GT is associated with	Supports Statement: Same	Clinical	High
		increased risk or severity of	Direction of Association (overall		
		fluoropyrimidine toxicity as	toxicity):		
		compared to TT	Rosmarin, et al. (2015)(9)		
			Froehlich, <i>et al.</i> (2015)(3)		
			Lee, et al. (2014)(62)		
			Toffoli, et al. (2015)(63)		
			Does Not Support Statement:		
			Amstutz, et al. (2009)(2)		
			Deenen, et al. (2011)(50)		
			Boige, et al. (2016)(69)		
		GT was observed in	Supports Statement:	Clinical	High
		individuals with	Collie-Duguid, <i>et al.</i> (2000)(49)		
		fluoropyrimidine toxicity	Johnson, et al. (2002)(38)		
			Ezzeldin, et al. (2005)(43)		

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			Morel, et al. (2006)(73)		
			Loganayagam, <i>et al</i> . (2010)(46)		
			Cellier, et al. (2011)(83)		
			Loganayagam, et al. (2013)(13)		
			Dhelens, et al. (2016)(84)		
			Thomas, et al. (2016)(48)		
rs67376798	Activity	The AT genotype/the T allele	Supports Statement: <i>Statistically</i>	Clinical, Ex	Moderate
		is associated with decreased	Significant:	vivo	
c.2846A>T		DPD activity as compared to	Seck, et al. (2005)(85)		
		the AA genotype	Same Direction of Association:		
p.D949V			Sistonen, et al. (2014)(30)		
			Kuilenburg, et al. (2016)(28)		
			Nie, et al. (2017)(29)		
			Does Not Support Statement:		
			Offer, et al. (2013)(5)		
		Within cell lines, the T allele	Supports Statement: <i>Statistically</i>	In vitro	High
		is associated with decreased	Significant:		
		DPD activity as compared to	Offer, et al. (2014)(86)		
		AA	Kuilenburg, et al. (2016)(28)		
		The AT genotype/the T allele	Supports Statement:	Clinical, Ex	Moderate
		was observed in individuals	van Kuilenburg, <i>et al.</i> (2002)((40)	vivo	
		with decreased DPD activity	Loganayagam, <i>et al.</i> (2010)(46)		
			Thomas, et al. (2016)(48)		
			Does Not Support Statement:		
			Loganayagam, et al. (2010)(46)		

Dose	The AT genotype is associated with decreased capecitabine dose as compared to the AA genotype	Supports Statement: Statistically Significant: Deenen, et al. (2011)(50)	Clinical	Moderate
Efficacy	The AT genotype is not associated with disease-free survival as compared to the AA genotype	Lee, et al. (2014)(62)	Clinical	Moderate
Metabolism	The AT genotype is associated with decreased metabolism of fluorouracil as compared to the AA genotype	Supports Statement: Statistically Significant: Boisdron-Celle, et al. (2007)(55) Same Direction of Association: Gentile, et al. (2016)(57)	Clinical, Ex vivo	Moderate
Toxicity	The AT genotype/the T allele is associated with increased risk or severity of fluoropyrimidine toxicity as compared to the AA genotype	Supports Statement: Statistically Significant (overall toxicity): Boisdron-Celle, et al. (2007)(55) Schwab, et al. (2008)(61) Deenen, et al. (2011)(50) Rosmarin, et al. (2014)(66) Lee, et al. (2014)(62) Toffoli, et al. (2015)(63) Boige, et al. (2016)(69) Statistically Significant (diarrhea): Deenen, et al. (2011)(50) Joerger, et al. (2015)(51)	Clinical	High

			Same Direction of Association (overall toxicity): Rosmarin, et al. (2015)(9) Froehlich, et al. (2015)(3)		
		The AT genotype/the T allele was observed in individuals with fluoropyrimidine toxicity	Supports Statement: van Kuilenburg, et al. (2000)(70) Morel, et al. (2006)(73) Gross, et al. (2008)(77) Loganayagam, et al. (2010)(46) Obi, et al. (2011)(87) Cellier, et al. (2011)(83) Loganayagam, et al. (2013)(13) Thomas, et al. (2016)(48) Kuilenburg, et al. (2016)(28) Does Not Support Statement: Kristensen, et al. (2010)(65)	Clinical	High
HapB3 rs75017182 + rs56038477 + rs56276561	Activity	HapB3 is associated with decreased DPD activity	Supports Statement: Statistically Significant: Sistonen, et al. (2014)(30) Nie, et al. (2017)(29) Same Direction of Association: Offer, et al. (2013)(5)	Ex vivo, Clinical	Moderate
c.1129-5923C>G + c.1236G>A (p.E412E) + c.483+18G>A		HapB3 was observed in individuals with decreased DPD activity	Supports Statement: van Kuilenburg, et al. (2010)(47) Meulendijks, et al. (2016)(88) Does Not Support Statement: Seck, et al. (2005)(85)	Ex vivo	Moderate

Dose	HapB3 was observed in	Supports Statement:	Clinical	Weak
	individuals who required a	Meulendijks, <i>et al.</i> (2016)(88)		
	fluoropyrimidine dose	Does Not Support Statement:		
	reduction	Meulendijks, <i>et al.</i> (2016)(88)		
Toxicity	HapB3 is associated with	Supports Statement: <i>Statistically</i>	Clinical	High
,	increased risk or severity of	Significant (overall toxicity):		
	fluoropyrimidine toxicity	Amstutz, et al. (2009)(2)		
		van Kuilenburg, <i>et al.</i> (2010)(47)		
		Froehlich, et al. (2015)(3)		
		Statistically Significant		
		(diarrhea):		
		Deenen, et al. (2011)(50)		
		Statistically Significant		
		(neutropenia):		
		Lee, et al. (2016)(89)		
		Same Direction of Association		
		(overall toxicity):		
		Schwab, et al. (2008)(61)		
		Deenen, et al. (2011)(50)		
		Rosmarin, et al. (2014)(66)		
		Rosmarin, et al. (2015)(9)		
		Lee, et al. (2016)(89)		
		Boige, et al. (2016)(69)		
		Does Not Support Statement:		
		Kleibl, et al. (2009)(64)		
		Loganayagam, et al. (2013)(13)		
		Falvella, et al. (2015)(90)		
	HapB3 was observed in	Supports Statement:	Clinical	Weak
	individuals with	van Kuilenburg, <i>et al.</i> (2010)(47)		
	fluoropyrimidine toxicity	Meulendijks, et al. (2016)(88)		

*2A (rs3918290, c.1905+1G>A) + rs67376798 (c.2846A>T, p.D949V) + *13 (rs55886062, c.1679T>G, p.I560S)	Toxicity	When the 1905+1 A allele and 2846 T allele are assessed together, with or without the 1679 G allele, they are associated with increased risk or severity of fluoropyrimidine toxicity	Does Not Support Statement: Meulendijks, et al. (2016)(88) Supports Statement: Statistically Significant (overall toxicity): Morel, et al. (2006)(73) Saif, et al. (2013)(91) Statistically Significant (gastrointestinal events): Capitain, et al. (2008)(92)	Clinical	High
*2A (rs3918290, c.1905+1G>A) + rs67376798 (c.2846A>T, p.D949V) + *13 (rs55886062, c.1679T>G, p.I560S) + HapB3	Toxicity	When the 1905+1 A allele, the rs67376798 T allele and the HapB3 haplotype are assessed together, with or without the 1679 G allele, they are associated with increased risk or severity of fluoropyrimidine toxicity	Supports Statement: Statistically Significant (overall toxicity): Jennings, et. al (2013)(93) Froehlich, et al (2015)(3)	Clinical	High
*2A (rs3918290, c.1905+1G>A) +	Toxicity	When the 1905+1 A allele, 2846 T allele, 1679 G allele and 1601 A allele are assessed	Supports Statement: Statistically Significant (overall toxicity): Loganayagam, et al. (2013)(13)	Clinical	Moderate

rs67376798 (c.2846A>T, p.D949V) + *13 (rs55886062, c.1679T>G, p.I560S) + *4 (rs1801158, c.1601G>A, p.S534N)		together they are associated with increased risk or severity of fluoropyrimidine toxicity			
*2A (rs3918290, c.1905+1G>A) + rs67376798 (c.2846A>T, p.D949V) + HapB3	Activity	When the 1905+1 A allele, 2846 T allele and the HapB3 haplotype are assessed together they are associated with decreased DPD activity	Supports Statement: Statistically Significant: Sistonen, et al. (2014)(30) Kuilenburg, et al. (2016)(28)	Clinical, Ex vivo	Moderate
*4 rs1801158 c.1601G>A	Activity	AG/the A allele is associated with decreased DPD activity as compared to GG	Supports Statement: Statistically Significant: Seck, et al. (2005)(85) Same Direction of Association: Sistonen, et al. (2014)(30) Kuilenburg, et al. (2016)(28) Does Not Support Statement:	Clinical, Ex vivo	Weak
c.1601G>A p.S534N			Sistonen, et al. (2014)(30)		

	AG was observed in	Supports Statement:	Clinical, Ex	Weak
	individuals with decreased	Collie-Duguid, et al. (2000)(49)	vivo	
	DPD activity	Gross, et al. (2003)(94)		
		Thomas, et al. (2016)(48)		
		Does Not Support Statement:		
		Ridge, et al. (1998)(35)		
	Within cell lines, the A allele	Supports Statement: Statistically	In vitro	Weak
	is associated with decreased	Significant:		
	DPD activity as compared to	Kuilenburg, et al. (2016)(28)		
	GG			
	Within cell lines AA is	Supports Statement: Statistically	In vitro	Weak
	associated with increased	Significant:		
	DPD activity as compared to	Offer, et al. (2013)(31)		
	the G allele			
Metabolism	AG is not associated with	Gentile, et al. (2016)(57)	Ex vivo	Weak
	altered fluorouracil			
	metabolism as compared to			
	GG			
Toxicity	The A allele is associated with	Supports Statement: Same	Clinical	Weak
	increased risk or severity of	Direction of Association:		
	fluoropyrimidine toxicity as	Froehlich, et al. (2015)(3)		
	compared to GG	Loganayagam, et al. (2013)(13)		
		Rosmarin, et al. (2014)(66)		
		Rosmarin, et al. (2015)(9)		
		Does Not Support Statement:		
		Schwab, et al. (2008)(61)		
		Kleibl, et al. (2009)(64)		
		Amstutz, et al. (2009)(2)		
		Deenen, et al. (2011)(50)		
		Froehlich, et al. (2015)(3)		

			Toffoli, et al. (2015)(63) Boige, et al. (2016)(69)		
		AG was observed in individuals with fluoropyrimidine toxicity	Supports Statement: Collie-Duguid, et al. (2000)(49) Gross, et al. (2003)(94) Lazar, et al. (2004)(95) van Kuilenburg, et al. (2010)(47)	Clinical	Weak
*5 rs1801159	Activity	AG + GG are not associated with altered DPD activity as compared to AA	He, et al. (2008)(96) Offer, et. al. (2013)(5) Sistonen, et al. (2014)(30) Kuilenburg, et al. (2016)(28)	Clinical, Ex vivo	High
c.1627A>G p.I543V		Within cell lines, the GG or the G allele are not associated with altered DPD activity as compared to AA	Offer, et al. (2013)(31) Kuilenburg, et al. (2016)(28)	In vitro	High
		AG + GG were observed in individuals with decreased DPD activity	Supports Statement: Collie-Duguid, et al. (2000)(49) Gross, et al. (2003)(94) Ezzeldin, et al. (2005)(43) Thomas, et al. (2016)(48) Does Not Support Statement: Ridge, et al. (1998)(35) Collie-Duguid, et al. (2000)(49) Seck, et al. (2005)(85) Ezzeldin, et al. (2005)(43)	Clinical, Ex vivo	Weak

Metabolism	AG + GG are associated with decreased metabolism of fluorouracil as compared to AA	Supports Statement: Statistically Significant: Zhang, et al. (2007)(97) Teh, et al. (2013)(98) Same Direction of Association: Gentile, et al. (2016)(57) Does Not Support Statement: Rudek, et al. (2013)(99)	Clinical, Ex vivo	Weak
Efficacy	AG + GG are associated with increased overall survival time, or increased response to fluoropyrimidine treatment as compared to AA	Supports Statement: Statistically Significant: Grau, et al. (2008)(100) Joerger, et al. (2015)(51) Does Not Support Statement: McLeod, et al. (2010)(53)	Clinical	Weak
	AG + GG are associated with decreased response to fluoropyrimidine treatment as compared to AA	Supports Statement: Statistically Significant: Zhang, et al. (2012)(101)	Clinical	Weak
	AG + GG are not associated with progression-free survival time as compared to AA	McLeod, et al. (2010)(53) Farina-Sarasqueta, et al. (2010)(102)	Clinical	Weak

,	Toxicity	AG + GG are associated with	Supports Statement: <i>Statistically</i>	Clinical	Weak
	5	risk or severity of	Significant (nausea/vomiting):		
		fluoropyrimidine toxicity as	Zhang, et al. (2007)(97)		
		compared to AA	Statistically Significant		
		T T T T T T T T T T T T T T T T T T T	(leukopenia):		
			Zhang, et al. (2007)(97)		
			Same Direction of Association:		
			Rosmarin, <i>et al.</i> (2014)(66)		
			Does Not Support Statement:		
			Gross, et al. (2003)(94)		
			Cho, et al. (2007)(103)		
			Schwab, et al. (2008)(61)		
			Kleibl, et al. (2009)(64)		
			Amstutz, et al. (2009)(2)		
			McLeod, et al. (2010)(53)		
			Deenen, et al. (2011)(50)		
			, , , ,		
			Zhang, et al. (2012)(101)		
			Teh, et al. (2013)(98)		
			Rosmarin, et al. (2015)(9)		
			Froehlich, et al. (2015)(3)		
			Joerger, et al. (2015)(51)		
			Toffoli, et al. (2015)(63)		
			Boige, et al. (2016)(69)	~	
		AG + GG were observed in	Supports Statement:	Clinical	Weak
		individuals with	Collie-Duguid, <i>et al.</i> (2000)(49)		
		fluoropyrimidine toxicity	van Kuilenburg, <i>et al.</i> (2000)(70)		
			Lazar, et al. (2004)(95)		
			Ezzeldin, et al. (2005)(43)		
			Kim, et al. (2010)(104)		
			van Kuilenburg, <i>et al.</i> (2010)(47)		
			Zaanan, et al. (2014)(105)		

			Thomas, et al. (2016)(48)		
			Does Not Support Statement:		
			Collie-Duguid, <i>et al.</i> (2000)(49)		
*6	Activity	AG/the A allele is associated	Supports Statement: Statistically	Ex vivo	weak
		with decreased DPD activity	Significant:		
rs1801160		as compared to GG	Offer, et al. (2013)(5)		
			Same Direction of Association:		
c.2194G>A			Kuilenburg, et al. (2016)(28)		
		Within cell lines, the AA	Supports Statement: Statistically	In vitro	weak
p.V732I		genotype or the A allele are	Significant:		
		associated with decreased	Kuilenburg, <i>et al.</i> (2016)(28) Does		
		DPD activity as compared to	Not Support Statement:		
		GG	Offer, et al. (2013)(31)		
		AA + AG were observed in	Supports Statement:	Clinical, Ex	weak
		individuals with decreased	Collie-Duguid, <i>et al.</i> (2000)(49)	vivo	
		DPD activity	Thomas, et al. (2016)(48)		
		-	Does Not Support Statement:		
			Collie-Duguid, <i>et al.</i> (2000)(49)		
			Seck, et al. (2005)(85)		
	Metabolism	AA + AG are associated with	Supports Statement: <i>Statistically</i>	Ex vivo	weak
		decreased metabolism of	Significant:		
		fluorouracil as compared to	Gentile, et al. (2016)(57)		
		GG			

Efficac	AA + AG are not associated with complete remission rate, event-free survival or response to fluoropyrimidine treatment as compared to GG	Zhang, et al. (2012)(101) Zhao, et al. (2016)(52)	Clinical	weak
Toxicit	AA + AG are associated with increased risk or severity of fluoropyrimidine toxicity as compared to GG	Supports Statement: Statistically Significant (overall toxicity): Boige, et al. (2016)(69) Statistically Significant (myelosuppression): Kleibl, et al. (2009)(64) Boige, et al. (2016)(69) Statistically Significant (diarrhea): Deenen, et al. (2011)(50) Same Direction of Association: Does Not Support Statement: Schwab, et al. (2008)(61) Amstutz, et al. (2009)(2) Deenen, et al. (2011)(50) Zhang, et al. (2012)(101) Rosmarin, et al. (2015)(9) Froehlich, et al. (2015)(3) Toffoli, et al. (2016)(52)	Clinical	weak
	AA + AG were observed in individuals with	Supports Statement: Collie-Duguid, <i>et al.</i> (2000)(49)	Clinical	weak
	fluoropyrimidine toxicity	van Kuilenburg, et al. (2000)(70) Thomas, et al. (2016)(48)		

			Del Re, et al. (2015)(106) Does Not Support Statement: Thomas, et al. (2016)(48)		
*9A	Activity	The CC + CT genotypes are associated with increased	Supports Statement: Statistically Significant:	Clinical, Ex vivo	weak
rs1801265		DPD activity as compared to	Offer, et al. (2013)(5)	VIVO	
		TT	Sistonen, et al. (2014)(30)		
c.85T>C			Does Not Support Statement: He, et al. (2008)(96)		
p.C29R			Kuilenburg, et al. (2016)(28)		
1		Within cell lines, CC is	Supports Statement: <i>Statistically</i>	In vitro	weak
		associated with increased	Significant:		
		DPD activity as compared to TT	Offer, et al. (2013)(31)		
		Within cell lines, the C allele	Supports Statement: <i>Statistically</i>	In vitro	weak
		is associated with decreased	Significant:		
		DPD activity as compared to TT	Kuilenburg, et al. (2016)(28)		
		CC + CT were observed in	Supports Statement:	Clinical, Ex	weak
		individuals with decreased	Vreken, et al. (1997)(33)	vivo	
		DPD activity	Van Kuilenburg, <i>et al.</i> (1999)(36)		
			Van Kuilenburg, <i>et al.</i> (1999)(107)		
			Collie-Duguid, <i>et al.</i> (2000)(49)		
			van Kuilenburg, <i>et al.</i> (2002)(40)		
			Gross, et al. (2003)(94)		
			Ezzeldin, <i>et al.</i> (2005)(43)		
			Thomas, et al. (2016)(48)		
			Does Not Support Statement:		
			Collie-Duguid, et al. (2000)(49)		
			Johnson, et al. (2002)(38)		

		Gross, et al. (2003)(94) Seck, et al. (2005)(85) Ezzeldin, et al. (2005)(43)		
Metabolism	CC is associated with decreased metabolism of fluorouracil as compared to CT + TT	Supports Statement: Gentile, et al. (2016)(57) Does Not Support Statement: Boisdron-Celle, et al. (2007)(55) Zhang, et al. (2007)(97)	Clinical, Ex vivo	weak
Efficacy	CC + CT are associated with decreased event-free survival time and decreased response to fluorouracil treatment as compared to TT	Supports Statement: Statistically Significant: Zhao, et al. (2016)(52)	Clinical	weak
	CC + CT is not associated with overall survival, progression-free survival or response to fluoropyrimidine treatment as compared to TT	Grau, et al. (2008)(100) McLeod, et al. (2010)(53) Joerger, et al. (2015)(51)	Clinical	moderate

Toxicit	y CC are associated with risk or	Supports Statement: Statistically	Clinical	weak
	severity of fluoropyrimidine	Significant (nausea/vomiting):		
	toxicity as compared to TT	Zhang, et al. (2007)(97)		
		Statistically Significant (hand-		
		foot syndrome):		
		Joerger, et al. (2015)(51)		
		Statistically Significant		
		(diarrhea):		
		Joerger, et al. (2015)(51)		
		Statistically Significant		
		(infection):		
		Zhao, et al. (2016)(52)		
		Statistically Significant		
		(nephrotoxicity):		
		Zhao, et al. (2016)(52)		
		Statistically Significant		
		(hepatotoxicity):		
		Zhao, et al. (2016)(52)		
		Same Direction of Association		
		(overall toxicity):		
		Froehlich, et al. (2015)(3)		
		Does Not Support Statement:		
		Gross, et al. (2003)(94)		
		Boisdron-Celle, <i>et al.</i> (2007)(55)		
		Morel, et al.(2006)(73)		
		Schwab, et al. (2008)(61)		
		Amstutz, et al. (2009)(2)		
		McLeod, et al. (2010)(53)		
		Deenen, et al. (2011)(50)		
		Dhawan, et al. (2013)(68)		
		Rosmarin, et al. (2014)(66)		

	Rosmarin, et al. (2015)(9) Boige, et al. (2016)(69)		
CC + CT are associated with decreased risk of gastrointestinal toxicity as compared to TT	Supports Statement: Statistically Significant: Kleibl, et al. (2009)(64)	Clinical	weak
CC + CT were observed in individuals with fluoropyrimidine toxicity	Supports Statement: Collie-Duguid, et al. (2000)(49) van Kuilenburg, et al (2000)(70) Lazar, et al. (2004)(95) Kim, et al. (2010)(104) van Kuilenburg, et al. (2010)(47) Kristensen, et al. (2010)(65) Zaanan, et al. (2014)(105) Saif, et al. (2014)(6) Baskin, et al. (2015)(108) Thomas, et al. (2015)(106) Does Not Support Statement: Kristensen, et al. (2010)(65) Thomas, et al. (2016)(48)	Clinical	weak

rs2297595	Activity	The AG + GG genotypes are	Seck, et al. (2005)(85)	Ex vivo	weak
		not associated with altered	Offer, et al. (2013)(5)		
c.496A>G		DPD activity as compared to	Kuilenburg, et al. (2016)(28)		
		the AA genotype			
p.M166V					
		Within cell lines, the G allele	Supports Statement: <i>Statistically</i>	In vitro	weak
		is associated with decreased	Significant:		
		DPD activity as compared to	Kuilenburg, <i>et al.</i> (2016)(28)		
		the AA genotype			
		Within cell lines, the G allele	Supports Statement: Statistically	In vitro	weak
		is associated with increased	Supports Statement: Statistically Significant:	III VIIIO	weak
		DPD activity as compared to	Offer, et al. (2014)(86)		
		the A allele	Offer, et al. (2014)(80)		
		the A affele			
		The AG genotype was	Supports Statement:	Clinical, Ex	weak
		observed in individuals with	Gross, et al. (2003)(94)	vivo	
		decreased DPD activity	Thomas, et al. (2016)(48)		
			Does Not Support Statement:		
			Johnson, et al. (2002)(38)		
	Metabolism	The AG + GG genotypes are	Supports Statement: Statistically	Ex vivo	weak
		associated with decreased	Significant:		
		metabolism of fluorouracil as	Gentile, et al. (2016)(57)		
		compared to the AA genotype			

Efficacy	The AG genotype is not associated with response to fluoropyrimidine treatment as compared to the AA genotype	Zhang, et al. (2012)(101)	Clinical	weak
Toxicity	The AG + GG genotypes are associated with risk or severity of fluoropyrimidine toxicity as compared to the AA genotype	Supports Statement: Statistically Significant (overall toxicity): Gross, et al. (2008)(77) Falvella, et al. (2015)(90) Statistically Significant (diarrhea): Deenen, et al. (2011)(50) Statistically Significant (handfoot syndrome): Deenen, et al. (2011)(50) Same Direction of Association: Deenen, et al. (2011)(50) Does Not Support Statement for overall toxicity: Schwab, et al. (2008)(61) Amstutz, et al. (2009)(2) Zhang, et al. (2012)(101) Loganayagam, et al. (2013)(13) Rosmarin, et al. (2014)(66) Rosmarin, et al. (2015)(9) Froehlich, et al. (2015)(63) Boige, et al. (2016)(69)	Clinical	weak

		The AG + GG genotypes are associated with a decreased risk of neutropenia as compared to the AA genotype	Supports Statement: Statistically Significant: Kleibl, et al. (2009)(64)	Clinical	weak
		The AG genotype/the G allele was observed in individuals with fluoropyrimidine toxicity	Supports Statement: van Kuilenburg, et al. (2000)(70) Gross, et al. (2003)(94) van Kuilenburg, et al. (2010)(47) Kristensen, et al. (2010)(65) Thomas, et al. (2016)(48) Does Not Support Statement: Kristensen, et al. (2010)(65)	Clinical	weak
			Thomas, et al. (2016)(48)		
rs115232898 c.557A>G	Activity	The AG genotype is associated with decreased DPD activity as compared to the AA genotype	Supports Statement: Statistically Significant: Offer, et al. (2013)(5)	Ex vivo	Moderate
p.Y186C		Within cell lines, the GG genotype/the G allele is associated with decreased DPD activity as compared to the AA genotype	Supports Statement: Statistically Significant: Offer, et al. (2014)(109) Offer, et al. (2014)(86)	In vitro	Moderate
		The AG genotype/the G allele was observed in individuals with decreased DPD activity	Supports Statement: Ezzeldin, et al. (2005)(43) Zaanan, et al. (2014)(105)	Clinical, Ex vivo	Moderate

	Toxicity	The AG genotype was observed in individuals with fluoropyrimidine toxicity	Supports Statement: Zaanan, et al. (2014)(105) Saif, <i>et al.</i> (2014)(6)	Clinical	Weak
rs61622928 c.1218G>A	Activity	The AG genotype/the A allele is not associated with altered DPD activity as compared to the GG genotype	Offer, et al. (2013)(5) Kuilenburg, et al. (2016)(28)	Ex vivo	weak
p.M406I		Within cell lines, the A allele is not associated with altered DPD activity as compared to the G allele	Offer, et al. (2014)(86) Kuilenburg, et al. (2016)(28)	In vitro	weak
		The AG genotype/the A allele was observed in an individual with decreased DPD activity	Supports Statement: Ezzeldin, et al. (2005)(43) Thomas, et al. (2016)(48)	Clinical, Ex vivo	weak
rs17376848 c.1896T>C p.F632F	Activity	The CC + CT genotypes are not associated with altered DPD activity as compared to the TT genotype	He, et al. (2008)(96) Offer, et al. (2013)(5)	Clinical, Ex vivo	weak
		The CT genotype/the C allele were observed in individuals with decreased DPD activity	Supports Statement: Collie-Duguid, et al. (2000)(49) Ezzeldin, et al. (2005)(43) Does Not Support Statement: Collie-Duguid, et al. (2000)(49)	Ex vivo	weak

Metabolisn	The CC + CT genotypes are associated with decreased metabolism of fluorouracil as compared to the TT genotype	Supports Statement: Statistically Significant: Teh, et al. (2013)(98)	Clinical	weak
Toxicity	The CT genotype/the C allele is associated with risk or severity of fluoropyrimidine toxicity as compared to the TT genotype	Supports Statement: Statistically Significant (overall toxicity): Kristensen, et al. (2010)(65) Falvella, et al. (2015)(90) Statistically Significant (neutropenia): Teh, et al. (2013)(98) Statistically Significant (stomatitis): Joerger, et al. (2015)(51) Does Not Support Statement: Schwab, et al. (2008)(61) Kleibl, et al. (2009)(64) Amstutz, et al. (2009)(2) Deenen, et al. (2011)(50) Froehlich, et al. (2015)(3) Toffoli, et al. (2015)(63) Boige, et al. (2016)(69)	Clinical	weak
	The CT genotype was observed in individuals with fluoropyrimidine toxicity	Supports Statement: Gross, et al. (2003)(94)	Clinical	weak

*2B rs1801159 + rs3918290	Activity	The *2B/*4 genotype was observed in an individual with decreased DPD activity	Supports Statement: Ridge, et al. (1998)(35)	Ex vivo	weak
1627A>G (I543V) + 1905+1G>A	Toxicity	The *2B/*4 genotype was observed in an individual with fluoropyrimidine toxicity	Supports Statement: Ridge, et al. (1998)(35)	Clinical	weak
*3 rs72549303 c.1898delC	Activity	Within cell lines, the del allele is associated with decreased DPD activity as compared the C allele	Supports Statement: Statistically Significant: Offer, et al. (2014)(86)	In vitro	weak
p.P633Qfs		The C/del + del/del genotypes were observed in individuals with decreased DPD activity	Supports Statement: Vreken, et al. (1997)(110) Vreken, et al. (1997)(33) Van Kuilenburg, et al. (1999)(36)	Clinical, Ex vivo	weak
*7 rs72549309	Activity	Within cell lines, the del allele is associated with decreased DPD activity as compared to the TCAT allele	Supports Statement: Statistically Significant: Offer, et al. (2014)(86)	In vitro	weak
c.295_298delTCAT p.F100Sfs		The del/del genotype was observed in individuals with DPYD deficiency	Supports Statement: Van Kuilenburg, et al. (1999)(36)	Clinical	weak

*8 rs1801266 c.703C>T	Activity	Within cell lines, the T allele is associated with decreased DPD activity as compared to the C allele	Supports Statement: Statistically Significant: Offer, et al. (2014)(86)	In vitro	weak
p.R235W		The T allele was observed in individuals with decreased DPD activity	Supports Statement: Vreken, et al. (1997)(110) Vreken, et al. (1997)(33) Van Kuilenburg, et al. (1999)(36)	Clinical, Ex vivo	weak
	Toxicity	The T allele was observed in an individual without fluoropyrimidine toxicity	Supports Statement: Kristensen, et al. (2010)(65)	Clinical	weak
*9B rs1801267 + rs1801265	Activity	*9B/*9B/the *9B allele was observed in individuals with decreased DPD activity	Supports Statement: Vreken, et al. (1997)(110) Vreken, et al. (1997)(33) Van Kuilenburg, et al. (1999)(36)	Clinical, Ex vivo	weak
c.2657G>A + c.85T>C p.R886H + p.C29R		Within cell lines, the A allele of the rs1801267 variant (part of *9B) is not associated with altered DPD activity as compared to the G allele	Offer, et al. (2014)(86)	In vitro	weak
	Toxicity	The A allele of the rs1801267 variant (part of *9B) is not associated with risk of fluoropyrimidine toxicity as compared to the G allele	Boige, et al. (2016)(69)	Clinical	weak

*10	Activity	Within cell lines, the T allele is associated with decreased	Supports Statement: Statistically Significant:	In vitro	weak
rs1801268		DPD activity as compared to the G allele	Offer, et al. (2014)(86)		
c.2983G>T p.V995F		The TT genotype was observed in an individual with decreased DPD activity	Supports Statement: Van Kuilenburg, <i>et al.</i> (1999) (36)	Clinical	weak
*11 rs72549306	Activity	The T allele was observed in individuals with decreased DPD activity	Supports Statement: Kouwaki, et al. (1998)(111)	Ex vivo	weak
c.1003G>T p.V335L		The T allele was observed to result in decreased DPD activity in <i>E.coli</i> lysates	Supports Statement: Kouwaki, <i>et al.</i> (1998)(111)	In vitro	weak
		Within cell lines, the T allele is not associated with altered DPD activity as compared to the G allele	Offer, et al. (2014)(86)	In vitro	weak
	Toxicity	The T allele was observed in an individual with fluoropyrimidine toxicity	Supports Statement: Kouwaki, <i>et al.</i> (1998)(111)	Clinical	weak
*12	Activity	The *12 allele was observed in individuals with decreased DPD activity		Ex vivo	weak

rs80081766 + rs78060119 c.62G>A + c.1156G>T		The T allele of the rs78060119 variant (part of *12) was observed to result in undetectable DPD activity in <i>E.coli</i> lysates	Supports Statement: Kouwaki, <i>et al</i> . (1998)(111)	In vitro	weak
p.R21Q + p.E386X		The A allele of the rs80081766 variant (part of *12) was not observed to result in altered DPD activity in <i>E.coli</i> lysates	Kouwaki, <i>et al</i> . (1998)(111)	In vitro	weak
		Within cell lines, the T allele of the rs78060119 variant (part of *12) is associated with decreased DPD activity as compared to the G allele	Supports Statement: Statistically Significant: Offer, et al. (2014)(86)	In vitro	weak
		Within cell lines, the A allele of the rs80081766 variant (part of *12) is not associated with altered DPD activity as compared to the G allele	Offer, et al. (2014)(86)	In vitro	weak
	Toxicity	The *12 allele was observed in an individual with fluoropyrimidine toxicity	Supports Statement: Kouwaki, et al. (1998)(111)	Clinical	weak

		The GG genotype of the rs78060119 variant (part of *12) is not associated with risk or severity of fluoropyrimidine toxicity as compared to the TT or GT genotypes	Zhao, et al. (2016)(52)	Clinical	weak
rs111858276 c.1484A>G p.D495G	Activity	Within cell lines, the G allele is associated with decreased DPD activity as compared to the A allele	Supports Statement: Statistically Significant: Offer, et al. (2014)(86)	In vitro	weak
rs112766203 c.2279C>T p.T760I	Activity	Within cell lines, the T allele is associated with decreased DPD activity as compared to the C allele	Supports Statement: Statistically Significant: Offer, et al. (2014)(86)	In vitro	weak
rs114096998 c.3067C>A p.P1023T	Activity	Within cell lines, the A allele is associated with increased DPD activity as compared to the C allele	Supports Statement: Statistically Significant: Offer, et al. (2014)(86)	In vitro	weak

rs115632870 c.151-69G>A	Activity	The AG genotype is associated with decreased DPD activity as compared to the GG genotype	Supports Statement: Statistically Significant: Offer, et al. (2013)(5)	Ex vivo	weak
rs12022243 1906-14763G>A	Toxicity	The A allele is associated with increased severity of fluoropyrimidine toxicity as compared to the G allele	Supports Statement: Statistically Significant: Rosmarin, et al. (2015)(9)	Clinical	weak
rs12132152 g.97523004G>A ^e	Toxicity	The A allele is associated with increased severity of fluoropyrimidine toxicity as compared to the G allele	Supports Statement: Statistically Significant: Rosmarin, et al. (2015)(9)	Clinical	weak
rs76387818 g.97539400G>A ^e	Toxicity	The A allele is associated with increased severity of fluoropyrimidine toxicity as compared to the G allele	Supports Statement: Statistically Significant: Rosmarin, et al. (2015)(9)	Clinical	weak

rs7548189 c.1906-19696G>T	Toxicity	The T allele is associated with increased severity of fluoropyrimidine toxicity as compared to the G allele	Supports Statement: Same Direction of Association: Rosmarin, et al. (2015)(9)	Clinical	weak
rs137999090 c.2021G>A p.G674D	Activity	Within cell lines, the A allele is associated with decreased DPD activity as compared to the G allele	Supports Statement: Statistically Significant: Offer, et al. (2014)(86)	In vitro	weak
rs138616379 c.1775G>A p.R592Q	Activity	Within cell lines, the A allele is associated with decreased DPD activity as compared to the G allele	Supports Statement: Statistically Significant: Offer, et al. (2014)(86)	In vitro	weak
rs141044036 c.2872A>G p.K958E	Activity	Within cell lines, the G allele is associated with decreased DPD activity as compared to the A allele	Supports Statement: Statistically Significant: Offer, et al. (2014)(86)	In vitro	weak

rs143154602 c.1057C>T p.R353C	Activity	Within cell lines, the T allele is associated with decreased DPD activity as compared to the C allele	Supports Statement: Statistically Significant: Offer, et al. (2014)(86)	In vitro	weak
rs143986398 c.274C>G p.P92A	Activity	Within cell lines, the G allele is associated with decreased DPD activity as compared to the C allele	Supports Statement: Statistically Significant: Offer, et al. (2014)(86)	In vitro	weak
rs145773863 c.1777G>A p.G593R	Activity	Within cell lines, the A allele is associated with decreased DPD activity as compared to the G allele	Supports Statement: Statistically Significant: Offer, et al. (2014)(86)	In vitro	weak
rs146356975 c.868A>G p.K290E	Activity	Within cell lines, the G allele is associated with decreased DPD activity as compared to the A allele	Supports Statement: Statistically Significant: Offer, et al. (2014)(86)	In vitro	weak

rs147601618 c.1796T>C	Toxicity	The CT genotype was observed in an individual with fluoropyrimidine toxicity	Supports Statement: Ofverholm, et al. (2010)(112)	Clinical	weak
p.M599T					
	Activity	Within cell lines, the C allele is not associated with DPD activity as compared to the T allele	Offer, et al. (2014)(86)	In vitro	weak
rs183105782 c.910T>C p.Y304H	Activity	Within cell lines, the C allele is associated with decreased DPD activity as compared to the T allele	Supports Statement: Statistically Significant: Offer, et al. (2014)(86)	In vitro	weak
rs183385770 c.1024G>A p.D342N	Activity	Within cell lines, the T allele is associated with decreased DPD activity as compared to the C allele	Supports Statement: Statistically Significant: Offer, et al. (2014)(86)	In vitro	weak

rs186169810 c.1314T>G p.F438L	Activity	Within cell lines, the G allele is associated with decreased DPD activity as compared to the T allele	Supports Statement: Statistically Significant: Offer, et al. (2014)(86)	In vitro	weak
rs188052243 c.2678A>G p.N893S	Activity	Within cell lines, the G allele is associated with decreased DPD activity as compared to the A allele	Supports Statement: Statistically Significant: Offer, et al. (2014)(86)	In vitro	weak
rs190577302 c.1054C>G p.L352V	Activity	Within cell lines, the G allele is associated with decreased DPD activity as compared to the C allele	Supports Statement: Statistically Significant: Offer, et al. (2014)(86)	In vitro	weak
rs200687447 c.2482G>A p.E828K	Activity	Within cell lines, the A allele is associated with increased DPD activity as compared to the G allele	Supports Statement: Statistically Significant: Offer, et al. (2014)(86)	In vitro	weak

rs367619008 187A>G p.K63E	Toxicity	The AG genotype was observed in an individual with fluoropyrimidine toxicity	Supports Statement: Kleibl, et al. (2009)(64)	Clinical	weak
rs376073289 c.623G>A p.R208Q	Toxicity	The AG genotype was observed in an individual with fluoropyrimidine toxicity	Supports Statement: Thomas, et al. (2016)(48)	Clinical	weak
		The A allele is not associated with risk of fluoropyrimidine toxicity	Schwab, et al. (2008)(61)	Clinical	weak
rs45589337 c.775A>G p.K259E	Activity	Within cell lines, the G allele is not associated with altered DPD activity as compared to the A allele	Offer, et al. (2014)(86)	In vitro	weak

	The G allele is not associated with altered DPD activity as compared to the AA genotype	Sistonen, et al. (2014)(30)	Clinical	weak
	The AG genotype was observed in an individual without altered DPD activity	Supports Statement: Gross, et al. (2003)(94)	Ex vivo	weak
Toxicity	The AG genotype was observed in an individual with fluoropyrimidine toxicity	Supports Statement: Gross, et al. (2003)(94)	Clinical	weak
	The AG genotype/the G allele is not associated with risk or severity of fluoropyrimidine toxicity as compared to the AA genotype	Schwab, et al. (2008)(61) Rosmarin, et al. (2015)(9) Froehlich, et al. (2015)(3)	Clinical	weak

rs55674432 c.2639G>T p.G880V	Activity	Within cell lines, the T allele is associated with decreased DPD activity as compared to the G allele	Supports Statement: Statistically Significant: Offer, et al. (2014)(86)	In vitro	weak
rs56293913 c.1129-15T>C	Activity	The CC + CT genotypes are not associated with altered DPD activity as compared to the TT genotype	Offer, et al. (2013)(5) Sistonen, et al. (2014)(30)	Clinical, Ex vivo	weak
	Toxicity	The CC + CT genotypes are associated with increased severity of fluoropyrimidine toxicity as compared to the TT genotype	Supports Statement: Statistically Significant: Gross, et al. (2008)(77) Same Direction of Association: Amstutz, et al. (2009)(2) Deenen, et al. (2011)(50)	Clinical	weak
rs568132506 c.257C>T p.P86L	Activity	The CT + TT genotypes were observed in individuals with decreased DPD activity	Supports Statement: van Kuilenburg, et al. (2002)(40) Thomas, et al. (2016)(48)	Clinical, Ex vivo	weak

	Toxicity	The CT genotype was observed in an individual with fluoropyrimidine toxicity	Supports Statement: Thomas, et al. (2016)(48)	Clinical	weak
rs59086055 c.1774C>T p.R592W	Activity	Within cell lines, the T allele is associated with decreased DPD activity as compared to the C allele	Supports Statement: Statistically Significant: Offer, et al. (2014)(86)	In vitro	weak
rs60139309 c.2582A>G p.K861R	Activity	Within cell lines, the G allele is associated with increased DPD activity as compared to the A allele	Supports Statement: Statistically Significant: Offer, et al. (2014)(86)	In vitro	weak
rs61757362 c.2948C>T p.T983I	Activity	Within cell lines, the T allele is associated with decreased DPD activity as compared to the C allele	Supports Statement: Statistically Significant: Offer, et al. (2014)(86)	In vitro	weak

rs72547601 c.2933A>G p.H978R	Activity	Within cell lines, the G allele is associated with decreased DPD activity as compared to the A allele	Supports Statement: Statistically Significant: Offer, et al. (2014)(86)	In vitro	weak
		The GG genotype was observed in an individual with decreased DPD activity	Supports Statement: van Kuilenburg, et al. (2002)(40)	Ex vivo	weak
rs72549304 c.1475C>T p.S492L	Activity	Within cell lines, the T allele is associated with decreased DPD activity as compared to the C allele	Supports Statement: Statistically Significant: Offer, et al. (2014)(86)	In vitro	weak
		The TT genotype was observed in an individual with decreased DPD activity	Supports Statement: van Kuilenburg, et al. (2002)(40)	Ex vivo	weak
rs72549305 c.1108A>G p.I370V	Activity	·	Offer, et al. (2014)(86)	In vitro	weak
		The GG genotype was observed in an individual with decreased DPD activity	Supports Statement: van Kuilenburg, et al. (2002)(40)	Ex vivo	weak

rs72549307 c.632A>G p.Y211C	Activity	Within cell lines, the G allele is associated with decreased DPD activity as compared to the A allele	Supports Statement: Statistically Significant: Offer, et al. (2014)(86)	In vitro	weak
		The GG genotype was observed in an individual with decreased DPD activity	Supports Statement: (van Kuilenburg, <i>et al.</i> (2002)(40)	Ex vivo	weak
	Toxicity	The G allele is not associated with risk or severity of fluoropyrimidine toxicity	Froehlich, et al. (2015)(3)	Clinical	weak
rs72549308 c.601A>C p.S201R	Activity	Within cell lines, the C allele is associated with decreased DPD activity as compared to the A allele	Supports Statement: Statistically Significant: Offer, et al. (2014)(86)	In vitro	weak
rs72549310 c.61C>T p.R21X	Activity	Within cell lines, the T allele is associated with decreased DPD activity as compared to the C allele	Supports Statement: Statistically Significant: Offer, et al. (2014)(86)	In vitro	weak
rs72728438 c.1974+75A>G	Activity	The AG genotype is associated with decreased DPD activity as compared to the AA genotype	Supports Statement: Statistically Significant: Offer, et al. (2013)(5)	Ex vivo	weak

rs777425216 c.1651G>A	Toxicity	The AG genotype was observed in an individual with fluoropyrimidine toxicity	Supports Statement: Rosmarin, et al. (2015)(9)	Clinical	weak
p.A551T					
rs150036960 c.46C>G	Activity	Within cell lines, the G allele is not associated with altered DPD activity as compared to	Offer, et al. (2014)(86)	In vitro	weak
p.L16V		the C allele.			
rs150385342	Activity	Within cell lines, the A allele is not associated with altered	Offer, et al. (2014)(86)	In vitro	weak
c.313G>A		DPD activity as compared to the G allele.			
p.A105T					
rs141462178	Activity	Within cell lines, the G allele is not associated with altered	Offer, et al. (2014)(86)	In vitro	weak
c.343A>G		DPD activity as compared to the A allele.			
p.M115V					
rs200562975	Activity	Within cell lines, the G allele is not associated with altered	Offer, et al. (2014)(86)	In vitro	weak
c.451A>G		DPD activity as compared to the A allele.			
p.N151D					

rs139834141 c.498G>A p.M166I	Activity	Within cell lines, the A allele is not associated with altered DPD activity as compared to the G allele.	Offer, et al. (2014)(86)	In vitro	weak
rs150437414 c.929T>C p.L310S	Activity	Within cell lines, the C allele is not associated with altered DPD activity as compared to the T allele.	Offer, et al. (2014)(86)	In vitro	weak
rs145112791 c.934C>T p.L312F	Activity	Within cell lines, the T allele is not associated with altered DPD activity as compared to the C allele.	Offer, et al. (2014)(86)	In vitro	weak
rs201018345 c.967G>A p.A323T	Activity	Within cell lines, the A allele is not associated with altered DPD activity as compared to the G allele.	Offer, et al. (2014)(574)	In vitro	weak
rs143815742 c.1181G>T p.R394L	Activity	Within cell lines, the T allele is not associated with altered DPD activity as compared to the G allele.	Offer, et al. (2014)(86)	In vitro	weak

rs140602333 c.1180C>T p.R394W	Activity	Within cell lines, the T allele is not associated with altered DPD activity as compared to the C allele.	Offer, et al. (2014)(86)	In vitro	weak
rs200064537 c.1260T>A p.N420K	Activity	Within cell lines, the A allele is not associated with altered DPD activity as compared to the T allele.	Offer, et al. (2014)(86)	In vitro	weak
rs764666241 c.1278G>T p.M426I	Activity	Within cell lines, the T allele is not associated with altered DPD activity as compared to the G allele.	Offer, et al. (2014)(86)	In vitro	weak
rs142512579 c.1294G>A p.D432N	Activity	Within cell lines, the A allele is not associated with altered DPD activity as compared to the G allele.	Offer, et al. (2014)(86)	In vitro	weak
rs72975710 c.1349C>T p.A450V	Activity	Within cell lines, the T allele is not associated with altered DPD activity as compared to the C allele.	Offer, et al. (2014)(86)	In vitro	weak

rs144395748	Activity	Within cell lines, the G allele is not associated with altered	Offer, et al. (2014)(86)	In vitro	weak
c.1358C>G		DPD activity as compared to the C allele.			
p.P453R		The GG genotype is not associated with altered DPD activity as compared to the CG genotype.	Offer, et al. (2013)(5)	Ex vivo	weak
rs199549923	Activity	Within cell lines, the A allele	Offer, et al. (2014)(86)	In vitro	weak
c.1403C>A		is not associated with altered DPD activity as compared to the C allele.			
p.T468N					
rs138391898	Activity	Within cell lines, the A allele	Offer, et al. (2014)(86)	In vitro	weak
c.1519G>A		is not associated with altered DPD activity as compared to the G allele.			
p.V507I		une e unerer			
rs148994843	Activity	Within cell lines, the A allele is not associated with altered	Offer, et al. (2014)(86)	In vitro	weak
c.1543G>A		DPD activity as compared to the G allele.			
p.V515I					
rs190951787	Activity	Within cell lines, the G allele is not associated with altered	Offer, et al. (2014)(86)	In vitro	weak
c.1577C>G		DPD activity as compared to the C allele.			
p.T526S					

rs142619737 c.1615G>A p.G539R	Activity	Within cell lines, the A allele is not associated with altered DPD activity as compared to the G allele.	Offer, et al. (2014)(86)	In vitro	weak
rs201615754 c.1682G>T p.R561L	Activity	Within cell lines, the T allele is not associated with altered DPD activity as compared to the G allele.	Offer, et al. (2014)(86)	In vitro	weak
rs3918289 c.1905C>G p.N635K	Activity	Within cell lines, the G allele is not associated with altered DPD activity as compared to the C allele.	Offer, et al. (2014)(86)	In vitro	weak
rs55971861 c.1906A>C p.I636L	Activity	Within cell lines, the C allele is not associated with altered DPD activity as compared to the A allele.	Offer, et al. (2014)(86)	In vitro	weak
rs138545885 c.1990G>T p.A664S	Activity	Within cell lines, the T allele is not associated with altered DPD activity as compared to the G allele.	Offer, et al. (2014)(86)	In vitro	weak

rs145548112 c.2161G>A p.A721T	Activity	Within cell lines, the A allele is not associated with altered DPD activity as compared to the G allele.	Offer, et al. (2014)(86)	In vitro	weak
rs146529561 c.2186C>T p.A729V	Activity	Within cell lines, the T allele is not associated with altered DPD activity as compared to the C allele.	Offer, et al. (2014)(86)	In vitro	weak
rs60511679 c.2195T>G p.V732G	Activity	Within cell lines, the G allele is not associated with altered DPD activity as compared to the T allele.	Offer, et al. (2014)(86)	In vitro	weak
rs56005131 c.2303C>A p.T768K	Activity	Within cell lines, the A allele is not associated with altered DPD activity as compared to the C allele.	Offer, et al. (2014)(86)	In vitro	weak

rs199634007 c.2336C>A p.T779N	Activity	Within cell lines, the A allele is not associated with altered DPD activity as compared to the C allele.	Offer, et al. (2014)(86)	In vitro	weak
rs201035051 c.2623A>C p.K875Q	Activity	Within cell lines, the C allele is not associated with altered DPD activity as compared to the A allele.	Offer, et al. (2014)(86)	In vitro	weak
rs147545709 c.2656C>T p.R886C	Activity	Within cell lines, the T allele is not associated with altered DPD activity as compared to the C allele.	Offer, et al. (2014)(86)	In vitro	weak
rs145529148 c.2915A>G p.Q972R	Activity	Within cell lines, the G allele is not associated with altered DPD activity as compared to the A allele.	Offer, et al. (2014)(86)	In vitro	weak
rs72547602 c.2921A>T p.D974V	Activity	Within cell lines, the T allele is not associated with altered DPD activity as compared to the A allele.	Offer, et al. (2014)(86)	In vitro	weak

rs139459586 c.2978T>G p.L993R	Activity	Within cell lines, the G allele is not associated with altered DPD activity as compared to the T allele.	Offer, et al. (2014)(86)	In vitro	weak
rs202144771 c.2977C>T p.L993F	Activity	Within cell lines, the T allele is not associated with altered DPD activity as compared to the C allele.	Offer, et al. (2014)(86)	In vitro	weak
rs140114515 c.3049G>A p.V1017I	Activity	Within cell lines, the A allele is not associated with altered DPD activity as compared to the G allele.	Offer, et al. (2014)(86)	In vitro	weak
rs148799944 c.3061G>C p.V1021L	Activity	Within cell lines, the C allele is not associated with altered DPD activity as compared to the G allele.	Offer, et al. (2014)(86)	In vitro	weak
rs6670886 c.525G>A p.S175S	Activity	The A allele is not associated with altered DPD activity as compared to the G allele.	Offer, et al. (2013)(5)	Ex vivo	weak

rs3790387 c.763-118A>G	Activity	The AG + GG genotypes are not associated with altered DPD activity as compared to the AA genotype.	Offer, et al. (2013)(5) Kuilenburg, et al. (2016)(28)	Ex vivo	weak
		The G allele is not associated with altered DPD activity as compared to the A allele.	Sistonen, et al. (2014)(30)	Clinical	weak
rs112550271 c.850+41T>C	Activity	The CT genotype is not associated with altered DPD activity as compared to the TT genotype.	Offer, et al. (2013)(5) Kuilenburg, et al. (2016)(28)	Ex vivo	weak
rs2811202 c.958+134T>G	Activity	The GG + GT genotypes are not associated with altered DPD activity as compared to the TT genotype.	Offer, et. al. (2013)(5)	Ex vivo	weak
rs61789183 c.1340-106T>A	Activity	The AA + AT genotypes are not associated with altered DPD activity as compared to the TT genotype.	Offer, et al. (2013)(5) Kuilenburg, et al. (2016)(28)	Ex vivo	weak
rs57918000 c.1371C>T p.N457N	Activity	The CT genotype is not associated with altered DPD activity as compared to the CC genotype.	Offer, et al. (2013)(5)	Ex vivo	weak

rs2786783 c.1740+39C>T	Activity	The CT + TT genotypes are not associated with altered DPD activity as compared to the CC genotype.	Offer, et al. (2013)(5) Sistonen, et al. (2014)(30)	Ex vivo, Clinical	weak
rs2811178 1740+40A>G	Activity	The AG + GG genotypes are not associated with altered DPD activity as compared to the AA genotype.	Offer, et al. (2013)(5) Sistonen, et al. (2014)(30)	Ex vivo, Clinical	weak
rs12137711 c.2300-39G>A	Activity	The AG genotype is not associated with altered DPD activity as compared to the GG genotype.	Offer, et al. (2013)(5)	Ex vivo	weak
rs41309171 c.234-123G>C	Activity	The CG genotype is not associated with altered DPD activity as compared to the GG genotype.	Sistonen, et al. (2014)(30)	Clinical	weak
rs138924556 c.850+91C>T	Activity	The CT genotype is not associated with altered DPD activity as compared to the CC genotype.	Sistonen, et al. (2014)(30)	Clinical	weak

rs368600943	Activity	The GT genotype is not	Sistonen, et al. (2014)(30)	Clinical	weak
		associated with altered DPD			
c.1129-28G>T		activity as compared to the			
		GG genotype.			

^aNucleotide changes according to reference sequence NM_000110.3 unless otherwise specified

^bProtein changes according to reference sequence NP_000101.2

^cRating Scheme for Quality of Evidence as per (16)

^dSome of the small case series, although not strong individually, collectively do support a strong recommendation.

^eNucleotide changes according to NC_000001.10

^fLikely HapB3 causal variant. Proxy SNPs are c.1236G>A (rs56038477, E412E), c.483+18G>A (rs56276561) and c.959-51T>G (rs115349832). c.680+139G>A (rs6668296) is not exclusive to HapB3 and therefore not a suitable proxy.

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