

Table 1: The key loss of function *DPYD* gene variants that should be assessed in patients prior to treatment.

| Common name | Nucleotide variant, amino acid change, ID number | | Enzyme activity (relative to normal) | ^b Minor allele frequency (global) | Recommended dosage adjustment for heterozygote carriers (partial deficiency ^c) |
|---------------------------|---|--|--------------------------------------|--|--|
| *2A | c.1905+1G>A exon 14 skipping rs3918290 | Non-functional protein missing aa residues 581-635. | None | 0.0043 | 50% |
| *13 | c.1679T>G I560S rs55886062 | Missense mutation affects the cofactor binding and substantially decreases activity. | None | 0.0006 | 50% |
| *9B | c.2846 A>T D949V rs67376798 | SNP affects the electron transfer mechanism, which is key for activity. Low function protein. | Decreased | 0.0052 | >25% |
| Hap-B3^a | c.1129-5923C>G Intronic rs75017182 | Intronic variant which affects pre-mRNA splicing. Truncated non-functional protein. | Decreased | 0.0048 | >25% |

^aThe haplotype includes c.1236G>A & c.483+18G>A (rs56038477 & rs56276561, with MAF=0.0181 & 0.0153 respectively). ^bLittle is known about the minor allele frequency of these variants in people of Māori or Pacific Island ancestry. Individuals of East Asian ancestry have very low prevalence of HapB3 (MAF>0.0000) and *2A (MAF=0.0000) compared with Europeans or South Asians (MAF=0.000 and 0.0034, respectively). There is an additional loss of function variant observed in people of African ancestry (rs115232898, Y186C, with MAF=0.0183). ^cDosages should not be increased to standard dosage at subsequent cycles based on treatment tolerance. 5-FU and capecitabine use is *contraindicated* in individuals who are homozygous loss of function variant for these alleles (complete deficiency). However, recent studies have demonstrated that extremely low doses (<1% of a standard dose) achieve suitable therapeutic 5-FU plasma concentrations and are safe.¹⁸ Individuals who are compound heterozygote (carrier of more than one of these variant alleles) should be considered as having a complete enzyme deficiency.