

***6 1707delT *45 1716G>A**

Cyp2D6 1756 CACCTTGC GCAACTTGGGCCTGGGCAAGAAGTCGCTGGAGCAGTGGGTGACCAGGAGGCC
Cyp2D7 1753
Cyp2D8 2672C.....G.....
consensus 2701 *****.*****.*****.*****

***6 Rev - *4 Fwd *8 1758 G>T**

Cyp2D6 1816 CGCCTGCCTTTGTGC**CGCCTTCGCCAACCACTCCGG**TGGGTGATGGGCAGAAGGGCACAA
Cyp2D7 1813G...AG.....C
Cyp2D8 2732C.....G...AG..A.....G.....
consensus 2761 *****.*****.***.***.*****.*****.

Cyp2D6 1876 AGCGGAACTGGGAAGGCGGGGACGGGAAGGCGACCCCTTACCCGCATCTCCC**ACCCC**
Cyp2D7 1873A.....M.....
Cyp2D8 2792T..A...T.....G.....G.....
consensus 2821 *****.***.***.***.*****.*****.*****.*****

***4 1846G>A *40 1863_1864ins(TTTCGCCCC)₂ *4 Rev**

Cyp2D6 1936 **CARGACGCCCTTTTCGCCCCAACGGTCTCTTGGACAAAGCCGTGAGCAACGTGATCGCCT**
Cyp2D7 1933SS.....
Cyp2D8 2852A.....C...C..A.....G.C.....
consensus 2881 *****.*****.*****.***.***.*****.***.*****.*****

Exon 4

Cyp2D6 1996 **CCCTCACCTGCGGGCGCCGCTTTCGAGTACGACGACCCCTCGCTTCCTCAGGCTGCTGGACC**
Cyp2D7 1993
Cyp2D8 2912Y.....A.....
consensus 2941 *****.*****.*****.*****.*****.*****.*****

***20 1973_1974InsG**

Cyp2D6 2056 **TAGCTCAGGAGGGACTGAAGGAGGAGTCGGGCTTTCTGCGCGAGGTGCGGAGCGAGAGA**
Cyp2D7 2053G.....YY.....C.....A..G.-
Cyp2D8 2972A-.....T.....RCT.....Y.A..A..T.....G..
consensus 3001 *****.*****.*****.*****.***.***.***.***.***.***.***.***

Cyp2D6 2115 CCGAGGAGTCTCTGCAGGGCGAGCTCCCGAGAGGTGCCGGGGCTGGACTGGGGCCTCGGA
Cyp2D7 2112 -----...T.....T.....C..
Cyp2D8 3031 ...CA.G.....T.....A...C.GCC..A...CA.
consensus 3061***.*****.*****.*****.***.***.***.***.***.***.***

Cyp2D6 2175 AGAGCAGGATTTGCATAGATGGGTTTGGGAAAGGACATTCCAGGAGACCCCACTGT---A
Cyp2D7 2164 ..G.....R.....---
Cyp2D8 3091 G.....G.....GT.....A...G.T....CTAG.
consensus 3121 .*.*****.*****.*****.*****.*****.*****.*****.*****

Cyp2D6 2232 AGAAGGGCCTGGAGGAGGAGGGGACATCTCAGACATGGTCGTGGGAGAGGTGTGCCCGGG
Cyp2D7 2221
Cyp2D8 3151 G.....T.....A.....T.C.....
consensus 3181 .*****.*****.*****.*****.*****.*****.*****.*****

Cyp2D6 2292 TCAGGGGGCACCAGGAGAGGCCAAGGACTCTGTACCTCCTATCCACGTCAGAGATTTCGA
Cyp2D7 2281-..CG.....TGK.....
Cyp2D8 3211A..A.....C...G.....G.....A.TG.....T..
consensus 3241 *****.***.*****.*****.***.***.*****.***.*****.***

Cyp2D6 2352 TTTT-AGGTTTCTCCTCTGG-----GCAAGGAGAGAG--GGTGGAGGCTGGCACTT
Cyp2D7 2340-...Y.....-----AG.....
Cyp2D8 3271T.....CAGCCAGG.....--.....
consensus 3301 ****.****.*****.*****.*****.*****.*****.*****

***41 Rev**

Cyp2D6 3108 **TTGCTGGGACACC**CGGGGCTCCAAGCACAGGCTTGACCAGGATCCTGTAAGCCTGACCTC
Cyp2D7 3100 .A.....T.C.....G..G.....C.....A..T..
Cyp2D8 4042 .A.....R..A.....G.....T.....A.....
consensus 4081 *.*****.***.***.*****.***.*****.*****.***.***

Cyp2D6 3168 CTCCAACATAGGAGGCAAGAAGGAGTGTGAGGGCCGACCCCCTGGGTGCTGACCCATTG
Cyp2D7 3160C...S.A.G.--.....-----
Cyp2D8 4102C.....G.--.....T..-T.....
consensus 4141 *****.*****.***.***.*****.*****.*****.*****.*****

Exon 7 *29 3183G>A
***36 Cyp2D6->2D7 hybrid point**

Cyp2D6 3228 TGGGGACGCATGCTGTCCAG**CCGTGTCCAACAGGAGATCGACGAC**GTGATAGGGCAGG
Cyp2D7 3207T.....
Cyp2D8 4159G.....---.....A.....
consensus 4201 *****.*****.*****.*****.*****.*****.*****.*****

***56 3201C>T**

Cyp2D6 3288 **TGCGG**GACCAGAGATGGGTGACCAGGCTCACATGCCCTACACCACTGCCGTGATTTCATG
Cyp2D7 3267R.....Y..
Cyp2D8 4216 ..T..T.....G.....G.....C..
consensus 4261 **.***.*****.*****.*****.*****.*****.*****.***

***42 3259_3260insGT**

Cyp2D6 3348 **AGCT**GCAGCGCTTTGGGGACATCGTCCCCCTGGGTGTGACCCATATGACATCCCGTGACA
Cyp2D7 3327R.....R.....R.....
Cyp2D8 4276
consensus 4321 *****.*****.*****.*****.*****.*****.*****.*****

Cyp2D6 3408 **TCGAAGTACAGGGCTTCCGCATCCCTAAG**TAGGCCTGGCGCCCTCCTCACCCAGCTCA
Cyp2D7 3387
Cyp2D8 4336A.....
consensus 4381 *****.*****.*****.*****.*****.*****.*****.*****

Cyp2D6 3468 GCACCAGCMCCTGGTGATAGCCCCAGCATGGCTACTGCCAGGTGGGCCCACTCTAGGAAC
Cyp2D7 3447 ...Y...C.....R.....
Cyp2D8 4396C.....Y.....C.....G.....
consensus 4441 ***.****.*****.****.*****.*****.*****.*****.*****

Cyp2D6 3528 CCTGGCCACCTAGTCCTCAATGCCACCACACTGACTGTCCCCACTTGGGTGGGGGGTCCA
Cyp2D7 3507R.....R.....
Cyp2D8 4456C.....TC.....AG.C.....T.....G..
consensus 4501 *****.*****.*****.*****.*****.*****.*****.*****

Cyp2D6 3588 GAGTATAGGCAGGGCTGGCCTGTCCATCCAGAGCCCCGTCTAGTGGGA-GACAAACCA
Cyp2D7 3567A.....Y..
Cyp2D8 4516A.....A.G..G....
consensus 4561 *****.*****.*****.*****.*****.*****.***.***.***

Cyp2D6 3647 GGACCTGCCAGAATGTTGGAGGACCC-AACRCCTGCAGGGAGAGGGGGCAGTGTGGGTGC
Cyp2D7 3627-G.G.....
Cyp2D8 4576C..TA...T.....T..C...C..
consensus 4621 *****.***.*****.*****.*****.*****.***.*****.***

Cyp2D6 3706 CTCTGAGAGGTGTGACTGCGCCCTGCTGTGGGTGCGGAGAGGTACTGTGGAGCTTCTCG
Cyp2D7 3686
Cyp2D8 4636 TC.CAG.....CR.....G..C.....
consensus 4681 ..*...*****.*****.*****.*****.*****.*****

Cyp2D6 3766 GGCGCAGGACTAGTTGACAGAGTCCAGCTGTGTGCCAGGCAGTGTGTGTCCCCGTGTGT
 Cyp2D7 3746
 Cyp2D8 4696 ...A.....T.....C
 consensus 4741 ***.*****.

Cyp2D6 3826 TTGGTGGCAGGGGTCCCAGCATCCTAGAGTCCAGTCCCCTCTCACCTGCATCTYCTG
 Cyp2D7 3806C...
 Cyp2D8 4756
 consensus 4801 ****.*****.

Exon 8

Cyp2D6 3886 CCCAGGGAACGACACTCATCACCACCTGTCATCGGTGCTGAAGGATGAGGCCGTCTGGG
 Cyp2D7 3866R
 Cyp2D8 4810G.T..TG...T.....
 consensus 4861 *****.*.*.*.***.*****.

Cyp2D6 3946 AGAAGCCCTTCCGCTTCCACCCCGAACACTTCTGGATGCCAGGGCCACTTTGTGAAGC
 Cyp2D7 3926
 Cyp2D8 4870Y.....
 consensus 4921 *****.*****.

Cyp2D6 4006 CGGAGGCCTTCCCTGCCTTTCTCAGCAGGTGCCTGKGGGAGCCCGGCTCCCTGTCCCCTT
 Cyp2D7 3986T.....
 Cyp2D8 4930 Y.....T.....
 consensus 4981 .*****.*****.

Cyp2D6 4066 CCGTGGAGTCTTGACAGGGTATCACCCAGGAGCCAGGCTCACTGACGCCCTCCCCTCCC
 Cyp2D7 4046
 Cyp2D8 4990G.....
 consensus 5041 *****.*****.

Exon 9

Cyp2D6 4126 CACAGGCCCGTGCATGCCTCGGGG-AGCCCTGGCCCGCATGGAGCTCTTCTCTTCT
 Cyp2D7 4106-.....
 Cyp2D8 5050SC.....R.....
 consensus 5101 *****.*****.*****.

*18 4125_4133dupGTGCCACT

*36 conv. fra 2D6 til 2D7->

Cyp2D6 4185 TCACCTCCCTGCTGCAGCACTTCCAGCTTCTC GTGCCACTGGACAGCCCCGGC CCAGCC
 Cyp2D7 4165C...G..G.C.....
 Cyp2D8 5110CR.....
 consensus 5161 *****.***.*.*.*****.

Cyp2D6 4245 ACCATGGTGTCTTTGCTTTCCTGGTGASCCCATCCCCCTATGAGCTTTGTGCTGTGCCCC
 Cyp2D7 4225 ..TC.C....G.CAGC..T.....C.....Y.....
 Cyp2D8 5170 ..TC.C....G.C.GC..T.....CG.....
 consensus 5221 **.*.*****.*.....**.******.*****.*****.

Cyp2D6 4305 GCTAGAATGGGGTACCTAGTCCCCAGCCTGCTCCCTAGCCAGAGGCTCTAATGTACAATA
 Cyp2D7 4285
 Cyp2D8 5230G-----TC..TG-.A.C..GT.....
 consensus 5281 *****.*.....*****.***.*.*.*.*.*****.

Cyp2D6 4365 AAGCAATGTGGTAGTTCCAA
 Cyp2D7 4345
 Cyp2D8 5269 ..TT.G.C.A..G.C...--
 consensus 5341 **.*.*.*.*.*.***.

Alignment of *CYP2C19* and *CYP2C9*

Nomenclature:

Forward Primer

Reverse primer

Overlapping primers (Forward/Reverse)

Probe region

SNP/deletion targeted i assays

>*CYP2C19**2 NG_008384 23581-24841 – rs2444285 19154G>A

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Cyp2C19      1  ATAATTGTATGATTTTACAGAAGTCATTTAACTGCTCTGGTGCACAGTTGGAATTTGAAG
Cyp2c9       1  .....G.....T.....
consensus    1  *****.*****.*****.*****.*****.*****.*****.*****

Cyp2C19     61  TATCTTTGAGCCCCCTCCCACTTCTAAAATACTAATTCAATTTTCAGAGGCTGCTTGATAGA
Cyp2c9      61  .....C.....
consensus   61  *****.*****.*****.*****.*****.*****.*****.*****

Cyp2C19    121  AATCAATATAGCAGGGACTATCTTTGTAGTATCAATCAGGTTGTGCAAACCTCTTTTAACC
Cyp2c9     121  .....T.....G.....C.....C....T.....
consensus  121  *****.*****.*****.*****.*****.*****.*****.*****

Cyp2C19    181  TATGCTATCATCTCCAAAATGTTAATGTAGTAATTCATACCATCTTATATTTCAAGATTG
Cyp2c9     181  .....G.....A.....C..G.....G.....A
consensus  181  *****.*****.*****.*.*****.*****.*****.*****.*****

Cyp2C19    241  TAGAGAAGAATTGTTGTAAAAGTAAGAGAATTAATATAAAGATGCTTTTATACTATCAA
Cyp2c9     241  .....---.....C.....C.....A..
consensus  241  *****.*****.*****.*****.*****.*****.*****.*****

Cyp2C19    301  AAGCAGGTATAAGTCTAGGAAATGATTATCATCT-----TTGATTCTCTTGTCAGAA
Cyp2c9     298  ...G...C.G.....GGTTAGAA....C...G.....
consensus  301  **.***.*.*****.*****.*****.*****.*****.*****

Cyp2C19    353  TTTTCTTTCTCAAATCTTGTATAATCAGAGAATTACTACACATGTACAATAAAAATTTCC
Cyp2c9     358  .....T.....T.....
consensus  361  *****.*****.*****.*****.*****.*****.*****.*****

Cyp2C19    413  CCATCAAGATATACAATATATTTTATTTATATTTATAGTTTTAAATTACAACCAGAGCTT
Cyp2c9     418  .....C.G...T.....
consensus  421  *****.*****.*****.*****.*****.*****.*****.*****

Cyp2C19    473  GGCATATTGTATCTATACCTTTTATTAATGCTTTTAAATTAATAAATTATTGTTT-TCTC
Cyp2c9     478  ..T...G...G...G.T.....AT.....-....
consensus  481  **.***.***.***.*.*****.*****.*****.*****.*****.*****

                                     Cyp2C19*2 - 19154G>A
Cyp2C19    532  TTAGATATGCAATAATTTTCCCACTATCATTGATTATTTCCCGGGAACCCATAACAAATT
Cyp2c9     537  .....C.....T.TC.....C.....T..C.....
consensus  541  *****.*****.*.*****.*****.*****.*****.*****.*****

Cyp2C19    592  ACTTAAAAACCTTGCTTTTATGGAAAGTGATATTTGGAGAAAGTAAAAGAACACCAAGA
Cyp2c9     597  .....G.....A....T.....A.....
consensus  601  *****.*****.*****.*****.*****.*****.*****.*****

Cyp2C19    652  ATCGATGGACATCAACAACCCTCGGGACTTTTATTGATTGCTTCCTGATCAAATGGAGAA
Cyp2c9     657  ...A.....G.....A.....G.....
consensus  661  **.***.***.***.*.*****.*****.*****.*****.*****.*****

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Cyp2C19 712 GGTA AAAATGTTAACAAAAGCTTAGTTATGTGACTGCTTGC GTATTTGTGATT CATTGACT
Cyp2c9 717A.....T.A.....TG.....
consensus 721 *****.*****.*****.*****.*****.*****.*****

Cyp2C19 772 AGTTTTGTGTTTACTACGGATGTTTAAACAGGTCAAGGAGTAATGCTTGAGAAGCATATTT
Cyp2c9 777C.....A.....T.....TC.....C-....
consensus 781 ****.*****.*****.*****.*****.*****.*****.***

Cyp2C19 832 AAGTTTTTTATTGTATGCATGAATATCCAGTAAGCATCATAGAAAATGTAAAATTAATTG
Cyp2c9 836A.....-----
consensus 841 *****.*****.*****.*****.*****.*****.*****

Cyp2C19 892 TTAAATAATTAGAATACATAGAAGAAATTGTTTAGATAAAATATAATCTATCTGAACAATA
Cyp2c9 -----
consensus 901
Cyp2C19 952 AGGATGTCAGGATAGGAAAAGCTCTGTTCTGCAGCTTCCAGTGAGATCAGCACAGGAGGA
Cyp2c9 -----
consensus 961
Cyp2C19 1012 ACTTAAATTTAAAAGAAAATAAAAAACATCTCCATCAAAAAGTGAGTGAAGGATATGAAC
Cyp2c9 -----
consensus 1021
Cyp2C19 1072 AGACACTTTTCAAAGAAGTCATTGGAGAAATGCAAATAAAAAACAACAATGAGATACCAT
Cyp2c9 -----
consensus 1081
Cyp2C19 1132 CTCATGCCAGTTAGAATGGCGATCATTA AAAAGTCAGGATATAACAGATGCTGAAGAGGA
Cyp2c9 -----
consensus 1141
Cyp2C19 1192 TGTGGAAAATAGAAATGTTTTTACTCTGTTTGTGGGAGCGTAAATTAGTTCAATCATTG
Cyp2c9 -----
consensus 1201
Cyp2C19 1252 TGGAAGGCA
Cyp2c9 -----
consensus 1261

>CYP2C19*3 region gj|460417326:22561-23561 – rs4986893 – 22948G>A

Cyp2C19 1 AAATTTAGCATTTGAGCAACCATTATTTAACCAGCTAGGCTGTAATTGTTAATTCGAGAT
Cyp2C9 1A.....T.....G..C..C..AG...
consensus 1 *****.*****.*****.*****.*****.*****.*****

Cyp2C19 61 TAATGTAAAAGTGATGTGTTGATTTTATGCATGCCAAACTCTTTTTTGCTTTTAAGGGAA
Cyp2C9 61A.....G.....G.....
consensus 61 *****.*****.*****.*****.*****.*****.*****

Cyp2C19 121 TTCATAGGTAAGATATTACTTAAAATTTCTAAACTATTATTATCTGTTAACWAATATGAA
Cyp2C9 121 ..TG.....-----.....C.....A....C--.
consensus 121 **..*****.*****.*****.*****.*****.*****.*****

Cyp2C19 181 GTGTTTTATATCTAATGTTTACTCATATTTTAAATTTGTTTCCAATCATTAGCTTCACC
Cyp2C9 170A....A.AG.....-.....T...T.....C.....
consensus 181 *****.*****.*****.*****.*****.*****.*****.*****

Cyp2C19 241 CTGTGATCCCACTTTCATCCTGGGCTGTGCTCCCTGCAATGTGATCTGCTCCATTATTTT
 Cyp2C9 229
 consensus 241 *****

Cyp2C19 301 CCAGAAACGTTTCGATTATAAAGATCAGCAATTTCTTAACTTGATGGAAAAATTGAATGA
 Cyp2C9 289 ...T.....T.....A.....G.....
 consensus 301 ***.*****.*****.*****.*****.*****.*****.*****

Cyp2C19*3 17948G>A

Cyp2C19 361 AAASATCAGGATTGTAAGCACCCCTGATSCAGGTAAGGCCAAGTTTTTTGCTTCCTGA
 Cyp2C9 349 ...C...A...T.G...G...G...C.....A.....
 consensus 361 ***.***.***.*.***.***.***.***.*****.*****.*****

Cyp2C19 421 GAAACCACCTTACAGTCTTTTTTTT-CTGGGAAATCC-AAAATTCTATATTGACCAAGCCCT
 Cyp2C9 409TTC.....T...AC.....C.....C..G..T.....T..
 consensus 421 *****.***.***.***.***.***.***.***.***.***.***.***.***.***

Cyp2C19 479 GAAGTACATTTTTGAATACTACAGTCTTGCCCTAGACAGCCATGGGGTGAATATCTGGAAA
 Cyp2C9 469 ...K.G.....C.....T.....G..
 consensus 481 ***.*.*****.*****.*****.*****.*****.*****.***

Cyp2C19 539 AGATGGCAAAGTTCCTTTATTTTATGCACAGGAAATGAATATCCCAATATAGATCAGGCTT
 Cyp2C9 529 ...C...C...CC.....TG.....A...GC.T.....GC.T.AT..
 consensus 541 ***.***.***.***.***.***.***.***.***.***.***.***.***.***

Cyp2C19 599 CTAAGCCCATTAGCTCCCTGATCAGTGTTTTTTCCACTAAACTCCAAAGCCCTGTTTCTA
 Cyp2C9 589C....A.....TG.....G.....
 consensus 601 *****.***.***.***.***.***.***.***.***.***.***.***.***.***

Cyp2C19 659 TAAAGTACTTTGGTGACAGCCCCAAAGCGTGTATATCACTCCATGGACATCCAGGCAC
 Cyp2C9 649T.....T.....C...G.....T.....
 consensus 661 *****.***.***.***.***.***.***.***.***.***.***.***.***.***

Cyp2C19 719 TTTGGAGTCTTCCATTACTACAAGGCTTGTCCCTTCAATTCACACTTTGTCATATTGTGT
 Cyp2C9 709G..C.....A.....A.....G...A...
 consensus 721 *****.***.***.***.***.***.***.***.***.***.***.***.***.***

Cyp2C19 779 GACAGAAATATCCTAATCTAAAAGACATTATCTCCTTCAAGGACAGAGAATATTTGGAAC
 Cyp2C9 769 .G.....T.....T..T.GG.....G..
 consensus 781 *.*****.*****.*****.***.*.*****.***

Cyp2C19 839 CACAGAAGCTGCCAAGAAACACTGAATAGGGCAGAGGTGTTTGATGTCTCAGTTGGGATT
 Cyp2C9 829 ..T.....G.....A.....C
 consensus 841 **.*****.*****.*****.*****.*****.***

Cyp2C19 899 CTAGCTGATGAGACAGCTGG-TTAGGAATGAAAAAATTATTGTTTTTTTGGTGTATGAAC
 Cyp2C9 889T.....G.....C.....G...A.....
 consensus 901 *****.***.***.***.***.***.***.***.***.***.***.***.***

Cyp2C19 958 CATAAACAGACATCACACTTTTACCCTGTGCTGAATTGGCATGT
 Cyp2C9 949A.....GC.....
 consensus 961 *****.***.***.***.***.***.***.***.***

>CYP2C19*4 region gi|460417326:4561-5561 – rs28399504 – 5001A>G

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Cyp2C19      1  TTTTAAATATACAAGGCATAGAATATGGCCATTTCCGTTAAATCATAAATTCCCAACTGG
Cyp2C9       1  .....T.....T.....
consensus    1  *****.*****.*****
Cyp2C19     61  TTATTAATCTAAGAATTCAGAATTTTAAGTAATTGTTTTGCATCAGATTGTTTACTTCA
Cyp2C9       61  .....G.....C.....A.....
consensus    61  *****.*****.*****.*****
Cyp2C19     121  GTGCTCTCAATTATGACGGTGCATTGGAACCACTTGGGTTAACATTTTTTTGTTTTTATT
Cyp2C9       121  .....T.....A.....TC.....G...---.....
consensus    121  *****.*****.*****.*****.***...*****
Cyp2C19     181  ACCAATACCTAGGCTTCAACCTAGTACAATGAAACCAGAATGTACAGAGTGGGCACTGGG
Cyp2C9       178  .....C.....A.....G.....TG.....A..A..A
consensus    181  *****.*****.*****.*****.*****.***.***.
Cyp2C19     241  ACGAAGGAGAACAAGACCAAGGACATTTTATTTTTATCTCTATCAGTGGGTCAAAGTCC
Cyp2C9       238  .....G.....
consensus    241  *****.*****
Cyp2C19     301  TTTCAGAAGGAGCATATAGTGGGCCTAGGTGATTGGCCACTTTATCCATCAAAGAGGCAC
Cyp2C9       298  .....A.....T..A.....
consensus    301  *****.*****.***.*****
Cyp2C19     361  ACACACTTAATTAGCATGGAGTGTATAAAAAGCTTGGAGTGCAAGCTCACGGTTGTCTT
Cyp2C9       358  ...--CG.....G.....T.....
consensus    361  ***.***.*****.*****.*****
Cyp2C19*4 5001A>G
Cyp2C19     421  AACAAGAGGAGAAGGCTTCAATGGATCCTTTTGTGGTCCTTGTGCTCTGTCTCTCATGTT
Cyp2C9       416  .....A.....T..C.....
consensus    421  *****.*****.***.*****
Cyp2C19     481  TGCTTCTCCTTTCAATCTGGAGACAGAGCTCTGGGAGAGGAAAACCTCCCTCCTGGCCCYA
Cyp2C9       476  .....C.....C.
consensus    481  *****.*****.
Cyp2C19     541  CTCCTCTCCCAGTGATTGGAATATCCTACAGATAGATATTAAGGATGTCAAGCAAATCCT
Cyp2C9       536  .....G.....CA.....
consensus    541  *****.*****.*****
Cyp2C19     601  TAACCAATGTAAGTATGCTCCTTCAGTGGCTTGCAAAAGGTAAGTAAATTCACCTGTATT
Cyp2C9       596  .....
consensus    601  *****
Cyp2C19     661  TTTTAAATAAAGTATATCCCTAGAGGTACAATGTTACAAGAGATCATTGTAAAGTAAAT
Cyp2C9       656  .....G.....-.....G..A..G.....
consensus    661  *****.*****.*****.***.*****
Cyp2C19     721  ACTTTGAAAGGCTTTTGTTCCTTTTCCAGTCTGTTCAGTGTCAAGAAATAGTGAATGAAA
Cyp2C9       715  .....
consensus    721  *****
Cyp2C19     781  TAATATATTTTGTATTAGAGAAAGATTTAGGTCTTTGCATGTTAAATTCAGAATAACAA
Cyp2C9       775  CC..G.....G.G.....G.....G.....A.....
consensus    781  ..**.*.....*.....*****.*****.*****

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Cyp2C19      841 ACTGTCAATAGTTTCAAATGTTGTGTTCCCTTCTTTATTTTCATAGCCATTTGCTAGAATTT
Cyp2C9       835 G-.....A.C.....C.....A.....T.....
consensus    841 ..*****.*.*****.*****.*****.*****

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Cyp2C19      901 TTGGCTGAGGGTAAACAGTAAGGGAAGTGTGTTATTAGAGATTTTATTAAATAAGTCC
Cyp2C9       894 .....A.....TG.....-----
consensus    901 *****.******.******.....

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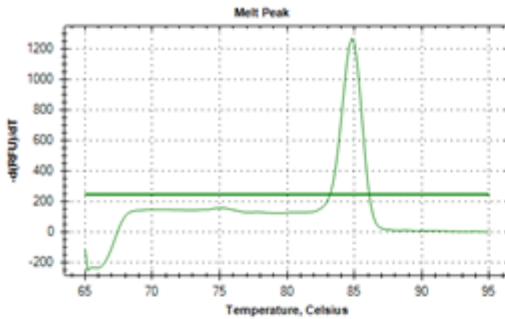
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Cyp2C19      961 TCTACTATATTAGCCATGTGTTTTATTTCAGAATAGCCGTGA
Cyp2C9       -----
consensus    961 .....

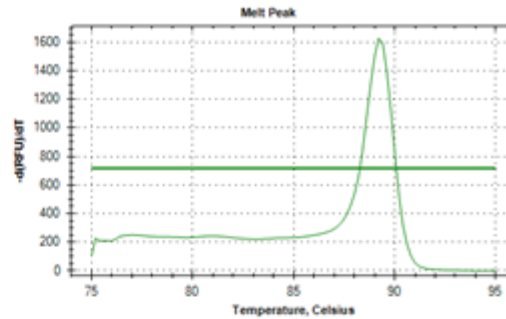
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CYP2D6 : Specificity of primers analysed by meltcurves

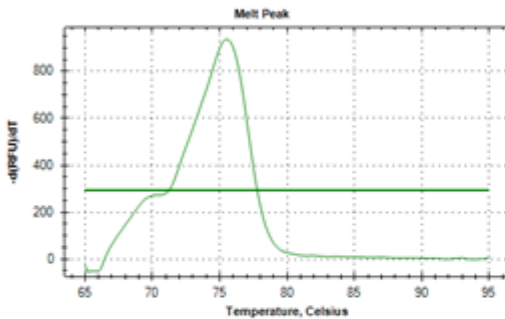
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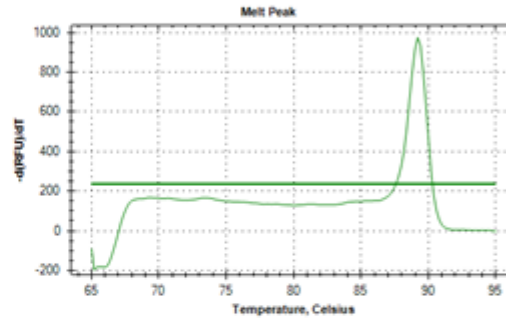
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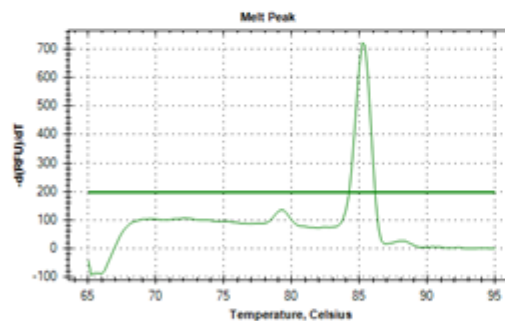
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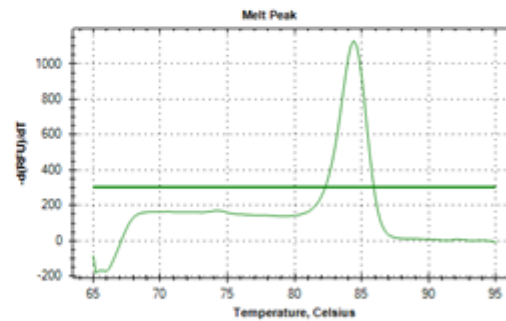
Allele *17



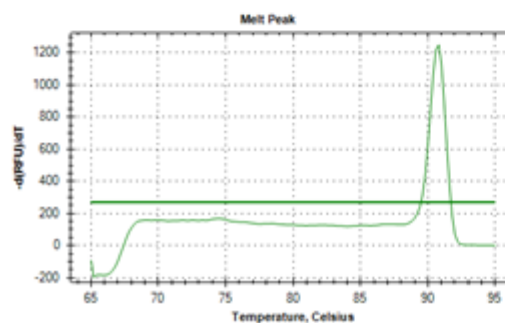
Allele *4



Allele *41

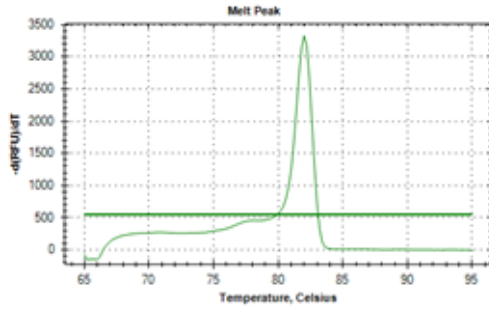


Allele *6

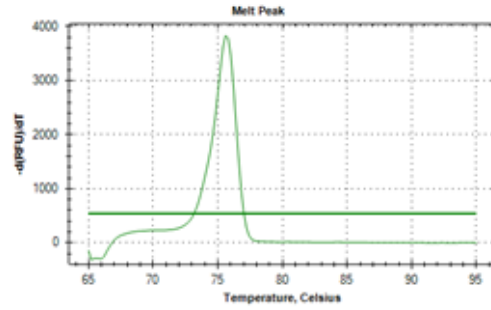


CYP2C19 : Specificity of primers analysed by meltcurves

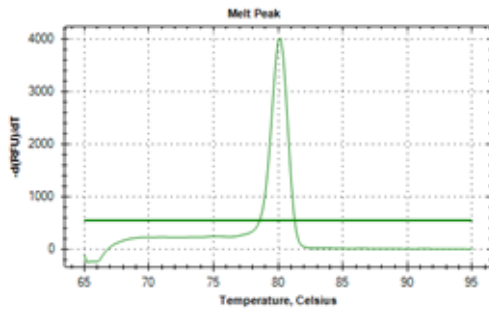
Allele *2



Allele *4



Allele *3

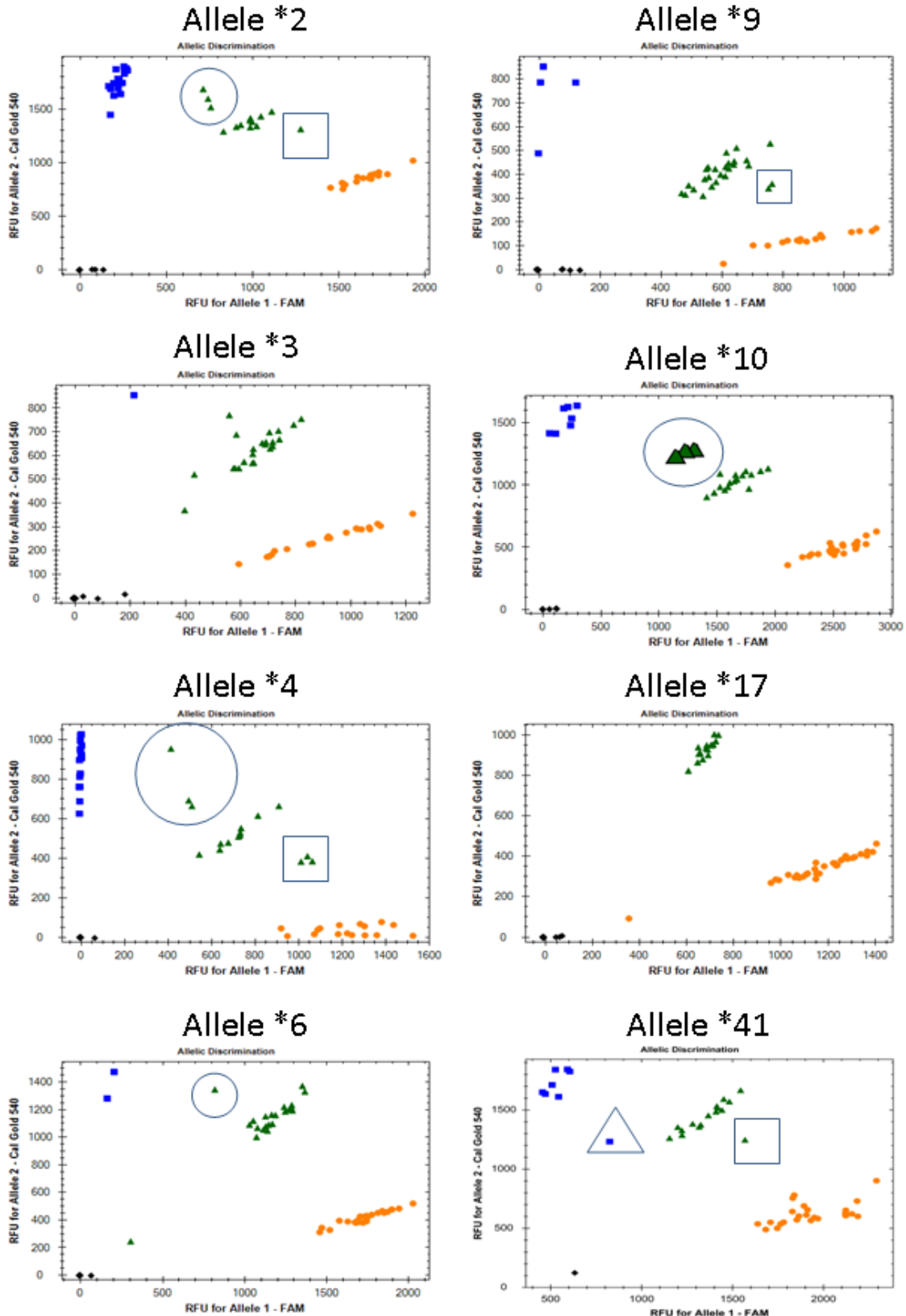


CYP2D6 : Allelic discrimination plots generated during validation

Circled samples : Samples containing copy number variations (CNV) of SNP/Mutation

Samples in squares : Samples containing copy number variations of wildtype allele.

For most validations multiple NTC controls were included.



CYP2C19 : Allelic discrimination plots generated during validation

