

WT -277 AAGAACCACATTCTATTTGGGGTCAACATATTGAAAGCATAATGATATGCTGTTGATATC
SD AAGAACCACATTCTATTTGGGGTCAACATATTGAAAGCATAATGATATGCTGTTGATATC
NT AAGAACCACATTCTATTTGGGGTCAACATATTGAAAGCATAATGATATGCTGTTGAAATC
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WT -217 ATATACCTTTGAAATTAGTTGTGCATTTCTGTAATGTGCTCAACAGGTAGTCTCTTTGCT
SD ATATACCTTTGAAATTAGTTGTGCATTTCTGTAATGTGCTCAACAGGTAGTCTCTTTGCT
NT ATATACCTTTGAAATTAGTTGTGCATTTCTGTCATGGGCTCAACAGGTAGTCTCTTTGCT
***** **

WT -157 TTTTGCCGCCCTGCTTCCCTTGAAGAGTCGAAAGCTTTTTCCAGCTGAGAAGTCACTTGT
SD TTTTGCCGCCCTGCT--CCCTGAAAGAGTCGAAAGCTTTTTCCAGCTGAGAAGTCACTTGT
NT TTTTGCCGCCCTGCTTCCCTTGAAGAGTCGAAAGCTTTTTCCAGCTGAGAAGTCACTTGT

WT -97 TGATTTGCTGGAAGAGCAGCAGAGTCCAGAGAAAAAGACTCGGTTGTTGTAGCGCTTAT
SD TGATTTGCTGGAAGAGCAGCAGAGTCCAGAGAAAAAGACTCGGTTGTTGTAGCGCTTAT
NT TGATTTGCTGGAAGAGCAGCAGAGTCCAGAGAAAAAGACTCGGTTGTTGTAGCGCTTAT

WT -37 CGCGGGTTCTACGTCTATATAAGACCGATGCTCATGCAGTCTGAATTTGTACAGTTTGAAG
SD CGCGGGTTCTACGTCTATATAAGACCGATGCTCATGCAGTCTGAATTTGTACAGTTTGAAG
NT CGCGGGTTCTACGTCTATATAAGACCGATGCTCATGCAGTCTGAATTTGTACAGTTTGAAG

WT 24 GTGTGCATCGAGTAGTTTCGCAAATATTTACCACCTTTTAGAAATTTGTGATTTTCAATAC
SD GTGTGCATCGAGTAGTTTCGCAAATATTTACCACCTTTTAGAAATTTGTGATTTTCAATAC
NT GTGTGCATCGAGTAGTTTCGCAAATATTTACCACCTTTTAGAAATTTGTGATTTTCAATAC

WT 84 CAAAAGTTAGACTAGAGATTCTCAATATGTGGACCATTTCTCTGACGATCCTAATCGCGG
SD CAAAAGTTAGACTAGAGATTCTCGATATGTGGACCATTTCTCTGACGATCCTAATCGCGG
NT CAAAAGTTAGACTAGAGATTCTCAATATGTGGACCATTTCTCTGACGATCCTAATCGCGG

WT 144 GTCTGCTGTACAGATATGTGAAGCGGCACTACACTCACTGGCAGCGATTGGGAGTCGATG
SD GTCTGCTGTACAGATATGTGAAGCGGCACTACACTCACTGGCAGCGATTGGGAGTCGATG
NT GTCTGCTGTACAGATATGTGAAGCGGCACTACACTCACTGGCAGCGATTGGGAGTCGATG

WT 204 AGGAGCCGGCAAAGATTCCCTTTGGCGTAATGGATACTGTCATGAAGCAGGAACGAAGTT
SD AGGAGCCGGCAAAGATTCCCTTTGGCGTAATGGATACTGTCATGAAGCAGGAACGAAGTT
NT AGGAGCCGGCAAAGATTCCCTTTGGCGTAATGGATACTGTCATGAAGCAGGAACGAAGTT

WT 264 TGGGCATGGCTCTGGCTGATATATACGCCCGGCACGAGGGCAAATCGTTGGCATATACA
SD TGGGCATGGCTCTGGCTGATATATACGCCCGGCACGAGGGCAAATCGTTGGCATATACA
NT TGGGCATGGCTCTGGCTGATATATACGCCCGGCACGAGGGCAAATCGTTGGCATATACA

WT 324 TGTGTAACAAACGAAGTATCCTGATCCGAGATGCCCAATTGGCTCGCCAAATCATGACCA
SD TGTGTAACAAACGAAGTATCCTGATCCGAGATGCCCAATTGGCTCGCCAAATCATGACCA
NT TGTGTAACAAACGAAGTATCCTGATCCGAGATGCCCAATTGGCTCGCCAAATCATGACCA

WT 384 GCGATTTCCAGTTTCCACGATCGCGGGGTGTACGTGGACGAGGATAAGGACCCGTTGT
SD GCGATTTCCAGTTTCCACGATCGCGGGGTGTACGTGGACGAGGATAAGGACCCGTTGT
NT GCGATTTCCAGTTTCCACGATCGCGGGGTGTACGTGGACGAGGATAAGGACCCGTTGT

WT 444 CGGCCAACCTTTTTAACCTAAGAGGTGCTTCATGGCGAAATCTACGTCAGAACTTACGC
SD CGGCCAACCTTTTTAACCTAAGAGGTGCTTCATGGCGAAATCTACGTCAGAACTTACGC
NT CGGCCAACCTTTTTAACCTAAGAGGTGCTTCATGGCGAAATCTACGTCAGAACTTACGC

WT 504 CGTCGTTCTCCTCCGGCAAATAAAGGGCATGTTCCGGCACCATCGACGACGTGGGCGATA
SD CGTCGTTCTCCTCCGGCAAATAAAGGGCATGTTCCGGCACCATCGACGACGTGGGCGATA
NT CGTCGTTCTCCTCCGGCAAATAAAGGGCATGTTCCGGCACCATCGACGACGTGGGCGATA

WT 564 AGTTGGTGCAGCATTTGGAGGGGGCCCTTGACCAAAGCGATGAAGTGGAGATCAAGGATG
SD AGTTGGTGCAGCATTTGGAGGGGGCCCTTGACCAAAGCGATGAAGTGGAGATCAAGGATG
NT AGTTGGTGCAGCATTTGGAGGGGGCCCTTGACCAAAGCGATGAAGTGGAGATCAAGGATG

WT 624 TGATGACCACGTATGCGGTGGACATCATTGGGTCAGTCATTTTTGGCTTGGAGATAGACA
SD TGATGACCACGTATGCGGTGGACATCATTGGGTCAGTCATTTTTGGCTTGGAGATAGACA
NT TGATGACCACGTATGCGGTGGACATCATTGGGTCAGTCATTTTTGGCTTGGAGATAGACA

WT 684 GCTTCCGAAATCCAAAAAACGAGTTCCGCGAGATCAGCAGCTCTACGTCTAGGGATGAAT
SD GCTTCCGAAATCCAAAAAACGAGTTCCGCGAGATCAGCAGCTCTACGTCTAGGGATGAAT
NT GCTTCCGAAATCCAAAAAACGAGTTCCGCGAGATCAGCAGCTCTACGTCTAGGGATGAAT

WT 744 CTCTGCTGCTGAAGATTCACAATATGTCCATGTTTCATTTGTCCACCgtgagttcaaaaat
SD CTCTGCTGCTGAAGATTCACAATATGTCCATGTTTCATTTGTCCACCgtgagttcaaaaat
NT CTCTGCTGCTGAAGATTCACAATATGTCCATGTTTCATTTGTCCACCgtgagttcaaaaat

WT 804 aaccagggtatataatgttgggaatctttatctatatttataactaaatgttacagG
SD aaccagggtatataatgttgggaatctttatctatatttataactaaatgttacagG
NT aaccagggtatataatgttgggaatctttatctatatttataactaaatgttacagG

WT 864 ATTGCTAAGCTAATGAACCGCTTGGGCTACGAAAGCCGCATTTCTGACATCCCTGCGAGAC
SD ATTGCTAAGCTAATGAACCGCTTGGGCTACGAAAGCCGCATTTCTGACATCCCTGCGAGAC
NT ATTGCTAAGCTAATGAACCGCTTGGGCTACGAAAGCCGCATTTCTGACATCCCTGCGAGAC

WT 924 ATGATGAAGCGCACAATCGAGTTCCGGGAGGAGCACAACGTGGTGCGAAAGGACATGCTG
SD ATGATGAAGCGCACAATCGAGTTCCGGGAGGAGCACAACGTGGTGCGAAAGGACATGCTG
NT ATGATGAAGCGCACAATCGAGTTCCGGGAGGAGCACAACGTGGTGCGAAAGGACATGCTG

WT 984 CAGCTGCTGATCCGCCCTCCGAAATACGGGCAAGATTGGCGAGGACGACGACCAGGTGTGG
SD CAGCTGCTGATCCGCCCTCCGAAATACGGGCAAGATTGGCGAGGACGACGACCAGGTGTGG
NT CAGCTGCTGATCCGCCCTCCGAAATACGGGCAAGATTGGCGAGGACGACGACCAGGTGTGG

WT 1044 GACATGGAAACCGCACAGGAGCAGCTGAAGTCTATGTTCGATCGAGAAGATTGCCGCCAG
SD GACATGGAAACCGCACAGGAGCAGCTGAAGTCTATGTTCGATCGAGAAGATTGCCGCCAG
NT GACATGGAAACCGCACAGGAGCAGCTGAAGTCTATGTTCGATCGAGAAGATTGCCGCCAG

WT 1104 GCATTCTGTTCTACGTGGCGGGCTCGGAATCCACAGCTGCGGCGTCTGCCTTCACTCTC
SD GCATTCTGTTCTACGTGGCGGGCTCGGAATCCACAGCTGCGGCGTCTGCCTTCACTCTC
NT GCATTCTGTTCTACGTGGCGGGCTCGGAATCCACAGCTGCGGCGTCTGCCTTCACTCTC

WT 1164 TACGAGCTGTCCATGTATCCGGAAGTGTGAAGGAGGCGCAAGAAGAAGTGGATGCTGTG
SD TACGAGCTGTCCATGTATCCGGAAGTGTGAAGGAGGCGCAAGAAGAAGTGGATGCTGTG
NT TACGAGCTGTCCATGTATCCGGAAGTGTGAAGGAGGCGCAAGAAGAAGTGGATGCTGTG

WT 1224 CTGATGAAGCACAATCTGAAGCCCAAGGATAGGTTACCTACGAGGCGGTGCAGGACTTA
SD CTGATGAAGCACAATCTGAAGCCCAAGGATAGGTTACCTACGAGGCGGTGCAGGACTTA
NT CTGATGAAGCACAATCTGAAGCCCAAGGATAGGTTACCTACGAGGCGGTGCAGGACTTA

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WT   1284   AAGTTTCTGGACATCTGCATCATGGgtgggtttcacatagcattcagtttcaacgatcct
SD   1284   AAGTTTCTGGACATCTGCATCATGGgtgggtttcacatagcattcagtttcaacgatcct
NT   1284   AAGTTTCTGGACATCTGCATCATGGgtgggtttcacatagcattcagtttcaacgatcct
*****

WT   1344   tagttaaacgtatTTTTTgcagAAACCATTCGCAAATACCCCGGGCTACCATTCTCAATC
SD   1344   tagttaaacgtatTTTTTgcagAAACCATTCGCAAATACCCCGGGCTACCATTCTCAATC
NT   1344   tagttaaacgtatTTTTTgcagAAACCATTCGCAAATACCCCGGGCTACCATTCTCAATC
*****

WT   1404   GAGAGTGCACCGAAGATTATCCCGTACCTGGAAC TAATCACATCATAGCCAAGGGAACAC
SD   1404   GAGAGTGCACCGAAGATTATCCCGTACCTGGAAC TAATCACATCATAGCCAAGGGAACAC
NT   1404   GAGAGTGCACCGAAGATTATCCCGTACCTGGAAC TAATCACATCATAGCCAAGGGAACAC
*****

WT   1464   CCATTCTGATCTCGCTCTTTGGCATGCAGCGTGATCCCGTCTATTTTCCCAATCCCAATG
SD   1464   CCATTCTGATCTCGCTCTTTGGCATGCAGCGTGATCCCGTCTATTTTCCCAATCCCAATG
NT   1464   CCATTCTGATCTCGCTCTTTGGCATGCAGCGTGATCCCGTCTATTTTCCCAATCCCAATG
*****

WT   1524   GCTACGATCCCCATCGCTTCGATTCAAATAACATGAACTACGATCAGGCAGCTTATATGC
SD   1524   GCTACGATCCCCATCGCTTCGATTCAAATAACATGAACTACGATCAGGCAGCTTATATGC
NT   1524   GCTACGATCCCCATCGCTTCGATTCAATAACATGAACTACGATCAGGCAGCTTATATGC
*****

WT   1584   CTTTGGAGAGGGTCCTAGGCACTGCATAGgtaaagatgtgttttgtaccagtggctcttg
SD   1584   CTTTGGAGAGGGTCCTAGGCACTGCATAGgtaaagatgtgttttgtaccagtggctcttg
NT   1584   CTTTGGAGAGGGTCCTAGGCACTGCATAGgtaaagatgtgttttgtaccagtggctcttg
* *****

WT   1644   tcttcttctgatcctgttctcttaattctttgccccaaagCTCTTCGCATGGGAAAAGTC
SD   1644   tcttcttctgatcctgttctcttaattctttgccccaaagCTCTTCGCATGGGAAAAGTC
NT   1644   tcttcttctgatcctgttctcttaattctttgccccaaagCTCTTCGCATGGGAAAAGTC
*****

WT   1704   AACTCCAAGGTGGCGGTGGCTAAGATTTTGGCCAATTTTGATCTGGTTCAATCTCCACGC
SD   1704   AACTCCAAGGTGGCGGTGGCTAAGATTTTGGCCAATTTTGATCTGGTTCAATCTCCACGC
NT   1704   AACTCCAAGGTGGCGGTGGCTAAGATTTTGGCCAATTTTGATCTGGTTCAATCTCCACGC
*****

WT   1764   AAGGAGGTGGAGTTCCGTTTCGATGCCGCCCTGTTTTAGTGACCAAGGAGCCGTTGAAG
SD   1764   AAGGAGGTGGAGTTCCGTTTCGATGCCGCCCTGTTTTAGTGACCAAGGAGCCGTTGAAG
NT   1764   AAGGAGGTGGAGTTCCGTTTCGATGCCGCCCTGTTTTAGTGACCAAGGAGCCGTTGAAG
*****

WT   1824   CTGCGCTTGACCAAGAGAAAAGTAAATCAAAAATATGTGGCTATTGTATG-----TAA
SD   1824   CTGCGCTTGACCAAGAGAAAAGTAAATCAAAAATATGTGGCTATTGTATG-----TAA
NT   1824   CTGCGCTTGACCAAGAGAAAAGTAAATCAAAAATATGTGGCTAAAAGCGAATATACTATAT
*****

WT   1876   TTGCAATTTGTATGTATAGATATATATCGATACTCAAATAAATTAATACATTGGTTTTAT
SD   1876   TTGCAATTTGTATGTATAGATATATATCGATACTCAAATAAATTAATACATTGGTTTTAT
NT   1876   AATAAATTTTATGTATAGATATATATCGATACTCAAATAAATTAATACATTGGTTTTAT
*****

WT   1936   TGATCATCTACCAAGATAAT
SD   1936   TGATCATCTACCAAGATAAT
NT   1936   TGATCATCTACCAAGATAAT
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Figure S2 Nucleotide sequence of *Cyp6d2* alleles. Nucleotide positions relative to *Cyp6d2* transcription start site are indicated. Red: untranslated regions, Blue: protein coding regions, Black uppercase: upstream intergenic region, Black lowercase: introns. Asterisk below sequence indicates all three alleles are identical at this position. Highlighted SNPs predicted to change amino acid sequence. Two stocks for each allele were sequenced to confirm changes: WT (*P{SUPor-P}KG06046*, *P{SUPor-P}KG01596*), SD (*P{SUPor-P}KG02287*, *P{SUPor-P}KG06675*), NT (*Mi{ET1}CG3746*, *P{GT1}CG42565*). Alignment performed using Clustal Omega (Sievers et al. 2011) and boundaries are as defined by FlyBase.

Sievers F, Wilm A, Dineen D, Gibson TJ, Karplus K, Li W, Lopez R, McWilliam H, Remmert M, Ding JSO, et al. 2011. Fast, scalable generation of high-quality protein multiple sequence alignments using Clustal Omega. *Molecular Systems Biology* 7: 1–6.