

# Supplementary materials

CLUSTAL O(1.2.4) multiple sequence alignment

|             |  |     |
|-------------|--|-----|
| can-iso-001 | ATGGCTATTGTTGAAACTGTCATTGATGGCATTAAATATTTTTTGTGCAATATTGTTATA | 60  |
| XM_711668.2 | ATGGCTATTGTTGAAACTGTCATTGATGGCATTAAATATTTTTTGTGTCCTTAGTGTACA | 60  |
| can-iso-017 | ATGGCTATTGTTGAAACTGTCATTGATGGCATTAAATATTTTTTGTGTCCTTAGTGTACA | 60  |
|             | ***** ** *****   |     |
| can-iso-001 | CGACATATCAGTATATATTAGGGGTCCCTCTGTTTACAACCTTGTATGGCAATATTTT   | 120 |
| XM_711668.2 | CAACAGATCAGTATATATTAGGGGTCCATTTGTTTACAACCTAGTATGGCAATATTTA   | 120 |
| can-iso-017 | CAACAGATCAGTATATATTAGGGGTCCATTTGTTTACTACTTATATGGCTATATTTA    | 120 |
|             | * ** ***** ***** ***** ***** *****                           |     |
| can-iso-001 | CTTTCATTCAGAAATGATAGATCTCCATTACAGTTTATTGGAATCCTTGGTTGGTTCT   | 180 |
| XM_711668.2 | TATTCATTAAGAAAAGATAGAGCTCCATTAGTGTTTATTGGATTCTTGGTTGGTTCT    | 180 |
| can-iso-017 | TATTCATTAAGAAAAGATAGAGCTCCATTATGTTTATTGGATTCTTGGTTGGTTCT     | 180 |
|             | ***** ***** ***** ***** ***** ***** *****                    |     |
| can-iso-001 | GCAGCTTCATATGGTCAACAACCTTATGAATTTTCGAATCATGTCGTCAAAAGTATGGT  | 240 |
| XM_711668.2 | GCAGCTTCATATGGTCAACAACCTTATGAATTTTCGAATCATGTCGTCAAAAGTATGGT  | 240 |
| can-iso-017 | GCAGCTTCATATGGTCAACAACCTTATGAATTTTCGAATCATGTCGTCAAAAGTATGGT  | 240 |
|             | *****  |     |
| can-iso-001 | GATGATTTTTCATTTATGTTATTAGGGAAAATTATGACGGTTTATTAGTCCAAAAGGT   | 300 |
| XM_711668.2 | GATGATTTTTCATTTATGTTATTAGGGAAAATTATGACGGTTTATTAGTCCAAAAGGT   | 300 |
| can-iso-017 | GATGATTTTTCATTTATGTTATTAGGGAAAATTATGACGGTTTATTAGTCCAAAAGGT   | 300 |
|             | *****  |     |
| can-iso-001 | CATGAATTTGTTTCAATGCTAAATTATCTGATGTTTCTGTTGAAGAAGCTTATAAGCAT  | 360 |
| XM_711668.2 | CATGAATTTGTTTCAATGCTAAATTATCTGATGTTTCTGCTGAAGATGCTTATAAACAT  | 360 |
| can-iso-017 | CATGAATTTGTTTCAATGCTAAATTATCTGATGTTTCTGTTGAAGAAGCTTATAAGCAT  | 360 |
|             | ***** ***** ***** ***** ***** *****                          |     |
| can-iso-001 | TTAACTACTCCAGTTTTCGGTACAGGGTTATTTATGATTGTCCAAATCTAGATTAATG   | 420 |
| XM_711668.2 | TTAACTACTCCAGTTTTCGGTAAAGGGTTATTTATGATTGTCCAAATCCAGATTAATG   | 420 |
| can-iso-017 | TTAACTACTCCAGTTTTCGGTACAGGGTTATTTATGATTGTCCAAATCTAGATTAATG   | 420 |
|             | *****  |     |
| can-iso-001 | GAACAAAAAACTTGCTAAATTGCTTTGACTACTGATTCATTTAAAAGATATGTTCCCT   | 480 |
| XM_711668.2 | GAACAAAAAACTTGCTAAATTGCTTTGACTACTGATTCATTTAAAAGATATGTTCCCT   | 480 |
| can-iso-017 | GAACAAAAAACTTGCTAAATTGCTTTGACTACTGATTCATTTAAAAGATATGTTCCCT   | 480 |
|             | *****  |     |
| can-iso-001 | AAGATTAGAGAAGAAATTTGAATTATTTGTTACTGATGAAAGTTCAAATTGAAAGAA    | 540 |
| XM_711668.2 | AAGATTAGAGAAGAAATTTGAATTATTTGTTACTGATGAAAGTTCAAATTGAAAGAA    | 540 |
| can-iso-017 | AAGATTAGAGAAGAAATTTGAATTATTTGTTACTGATGAAAGTTCAAATTGAAAGAA    | 540 |
|             | *****  |     |
| can-iso-001 | AAAACATGCGGTTGCCAATGTTATGAAAACCAACCAGAAATTAATTTTCACTGCT      | 600 |
| XM_711668.2 | AAAACATGCGGTTGCCAATGTTATGAAAACCAACCAGAAATTAATTTTCACTGCT      | 600 |
| can-iso-017 | AAAACATGCGGTTGCCAATGTTATGAAAACCAACCAGAAATTAATTTTCACTGCT      | 600 |
|             | *****  |     |
| can-iso-001 | TCAAGATCTTTATTTGGTGATGAAATGAGAAGAATTTTGACCGTTCATTTGCTCAATTA  | 660 |
| XM_711668.2 | TCAAGATCTTTATTTGGTGATGAAATGAGAAGAATTTTGACCGTTCATTTGCTCAACTA  | 660 |
| can-iso-017 | TCAAGATCTTTATTTGGTGATGAAATGAGAAGAATTTTGACCGTTCATTTGCTCAATTA  | 660 |
|             | ***** **   |     |
| can-iso-001 | TATCTGATTTAGATAAAGGTTTACCCTATTAATTTGTTTCCCTAATTTACCTTTA      | 720 |
| XM_711668.2 | TATCTGATTTAGATAAAGGTTTACCCTATTAATTTGTTTCCCTAATTTACCTTTA      | 720 |
| can-iso-017 | TATCTGATTTAGATAAAGGTTTACCCTATTAATTTGTTTCCCTAATTTACCTTTA      | 720 |
|             | *****  |     |
| can-iso-001 | CCTCATTATTGGAGACGTGATGCTGCTCAAAGAAAATCTCTGCTACTTATATGAAAGAA  | 780 |
| XM_711668.2 | CCTCATTATTGGAGACGTGATGCTGCTCAAAGAAAATCTCTGCTACTTATATGAAAGAA  | 780 |
| can-iso-017 | CCTCATTATTGGAGACGTGATGCTGCTCAAAGAAAATCTCTGCTACTTATATGAAAGAA  | 780 |
|             | *****  |     |

Supplementary Figure 1: *ERG11* gene nucleotide MSA between the wild-type and the fluconazole-resistant isolates

|             |  |      |
|-------------|--|------|
| can-iso-001 | ATTAAACTGAGAAGAACGTTGGTGATATTGATCCAAATCGTGATTTAATTGATTCCCTTA                                       | 840  |
| XM_711668.2 | ATTAAACTGAGAAGAACGTTGGTGATATTGATCCAAATCGTGATTTAATTGATTCCCTTA                                       | 840  |
| can-iso-017 | ATTAAACTGAGAAGAACGTTGGTGATATTGATCCAAATCGTGATTTAATTGATTCCCTTA<br>*****                              | 840  |
| can-iso-001 | TTGATTCATTCAACTTATAAAGATGGTGTGAAAATGACTGATCAAGAAATTGCTAATCTT                                       | 900  |
| XM_711668.2 | TTGATTCATTCAACTTATAAAGATGGTGTGAAAATGACTGATCAAGAAATTGCTAATCTT                                       | 900  |
| can-iso-017 | TTGATTCATTCAACTTATAAAGATGGTGTGAAAATGACTGATCAAGAAATTGCTAATCTT<br>*****                              | 900  |
| can-iso-001 | TTAATTGGTATTCTTATGGGTGGTCAACATACTTCTGCTTCTACTTCTGCTTGGTTCCTTG                                      | 960  |
| XM_711668.2 | TTAATTGGTATTCTTATGGGTGGTCAACATACTTCTGCTTCTACTTCTGCTTGGTTCCTTG                                      | 960  |
| can-iso-017 | TTAATTGGTATTCTTATGGGTGGTCAACATACTTCTGCTTCTACTTCTGCTTGGTTCCTTG<br>*****                             | 960  |
| can-iso-001 | TTACATTTAGGTGAAAAACCTCATTTACAAGATGTTATTTATCAAGAAGTTGTTGAATTA                                       | 1020 |
| XM_711668.2 | TTACATTTAGGTGAAAAACCTCATTTACAAGATGTTATTTATCAAGAAGTTGTTGAATTA                                       | 1020 |
| can-iso-017 | TTACATTTAGGTGAAAAACCTCATTTACAAGATGTTATTTATCAAGAAGTTGTTGAATTA<br>*****                              | 1020 |
| can-iso-001 | TTGAAAGAAAAAGGTGGTGATTTGAATGATTTGACTTATGAAGATTACAAAAATTACCA  | 1080 |
| XM_711668.2 | TTGAAAGAAAAAGGTGGTGATTTGAATGATTTGACTTATGAAGATTACAAAAATTACCA  | 1080 |
| can-iso-017 | TTGAAAGAAAAAGGTGGTGATTTGAATGATTTGACTTATGAAGATTACAAAAATTACCA<br>*****                               | 1080 |
| can-iso-001 | TCAGTCAATTACACTATTAAGGAAAACCTCTAGAATGCATATGCCATTACATTTCTATTTTT                                     | 1140 |
| XM_711668.2 | TCAGTCAATTACACTATTAAGGAAAACCTCTAGAATGCATATGCCATTACATTTCTATTTTT                                     | 1140 |
| can-iso-017 | TCAGTCAATTACACTATTAAGGAAAACCTCTAGAATGCATATGCCATTACATTTCTATTTTT<br>*****                            | 1140 |
| can-iso-001 | AGAAAAGGTACTAACCATTAGGATTCCTGGAACCAATTATATGGTCCAAAAGGTCAT  | 1200 |
| XM_711668.2 | AGAAAAGGTACTAACCATTAGGATTCCTGGAACCAATTATATGGTCCAAAAGGTCAT  | 1200 |
| can-iso-017 | AGAAAAGGTACTAACCATTAGGATTCCTGGAACCAATTATATGGTCCAAAAGGTCAT<br>**** * ***** * * **** * ***** * ***** | 1200 |
| can-iso-001 | TATGTTTTAGCTTCTCCAGGTAATGCTCATACTAGTGAAGATATTTTGATAACCCTGAA  | 1260 |
| XM_711668.2 | TATGTTTTAGCTTCTCCAGGTAATGCTCATACTAGTGAAGATATTTTGATAACCCTGAA  | 1260 |
| can-iso-017 | AATGATTTAGCTTCTCCAGGTAATGCTCATACTAGTGAAGATATTTTGATAACCCTGAA<br>* * * * * *****                     | 1260 |
| can-iso-001 | GATTTTGATCCAACCTAGATGGGATACGCTGCTGCCAAAGCTAATTCTGTTTCATTTAAC                                       | 1320 |
| XM_711668.2 | GATTTTGATCCAACCTAGATGGGATACGCTGCTGCCAAAGCTAATTCTGTTTCATTTAAC                                       | 1320 |
| can-iso-017 | GATTTTGATCCAACCTAGATGGGATACGCTGCTGCCAAAGCTAATTCTGTTTCATTTAAC<br>*****                              | 1320 |
| can-iso-001 | TCTTCTGATGAAGTTGATTATGGGTTTGGGAAAAGTTTCTAAGGGGTTTCTTACCTTAT  | 1380 |
| XM_711668.2 | TCTTCTGATGAAGTTGATTATGGGTTTGGGAAAAGTTTCTAAGGGGTTTCTTACCTTAT  | 1380 |
| can-iso-017 | TCTTCTGATGAAGTTGATTATGGGTTTGGGAAAAGTTTCTAAGGGGTTTCTTACCTTAT<br>*****                               | 1380 |
| can-iso-001 | TTACCATTGGTGGTGGTAGACATAGATGTATTGGGGAACAATTTGCTTATGTTCAAATTA                                       | 1440 |
| XM_711668.2 | TTACCATTGGTGGTGGTAGACATAGATGTATTGGGGAACAATTTGCTTATGTTCAAATTA                                       | 1440 |
| can-iso-017 | TTACCATTGGTGGTGGTAGACATAGATGTATTGGGGAACAATTTGCTTATGTTCAAATTA<br>*****                              | 1440 |
| can-iso-001 | GGAACCATTTAACTACTTTTGTTTATAACTTAAGATGGACTATTGATGGTTATAAAGTG  | 1500 |
| XM_711668.2 | GGAACCATTTAACTACTTTTGTTTATAACTTAAGATGGACTATTGATGGTTATAAAGTG  | 1500 |
| can-iso-017 | GGAACCATTTAACTACTTTTGTTTATAACTTAAGATGGACTATTGATGGTTATAAAGTG<br>*****                               | 1500 |
| can-iso-001 | CCTGACCCTGATTATAGTTCAATGGTGGTTTTACCTACTGAACCAGCAGAAATCATTGG  | 1560 |
| XM_711668.2 | CCTGACCCTGATTATAGTTCAATGGTGGTTTTACCTACTGAACCAGCAGAAATCATTGG  | 1560 |
| can-iso-017 | CCTGACCCTGATTATAGTTCAATGGTGGTTTTACCTACTGAACCAGCAGAAATCATTGG<br>*****                               | 1560 |
| can-iso-001 | GAAAAAGAGAACTTGTATGTTTTAA  | 1587 |
| XM_711668.2 | GAAAAAGAGAACTTGTATGTTTTAA  | 1587 |
| can-iso-017 | GAAAAAGAGAACTTGTATGTTTTAA<br>*****   | 1587 |

Cont'd Supplementary Figure 1: *ERG11* gene nucleotide MSA between the wild-type and the fluconazole-resistant isolates

CLUSTAL O(1.2.4) multiple sequence alignment

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can-iso-001      MAIVETVIDGINYFLSNIVIRHISILLGVPLVYNFVWQYFLSFRNDRSPLQFYWNPWFGS 60
XM_711668.2     MAIVETVIDGINYFLSLSVTQQISILLGVPPVYNLWQYLYSLRKDRAPLVFYWIPWFGS 60
can-iso-017     MAIVETVIDGINYFLSLSVTQQISILLGVPPVYLLWLYLYSLRKDRAPLLFYWIPWFGS 60
***** * :;*****:* *:* * :;:*:* * * * * *

can-iso-001      AASYGQQPYEFFESCQRKYGDVFSFMLLGKIMTVYLGPKGHEFVFNAKLSDVSVEEAYKH 120
XM_711668.2     AASYGQQPYEFFESCQRKYGDVFSFMLLGKIMTVYLGPKGHEFVFNAKLSDVSAEDAYKH 120
can-iso-017     AASYGQQPYEFFESCQRKYGDVFSFMLLGKIMTVYLGPKGHEFVFNAKLSDVSVEEAYKH 120
*****_*;****

can-iso-001      LTPVFGTGVYDCPN SRLMEQKKLAKFALTTDSFKRYVPKIREEILNYFVTDESFKLKE 180
XM_711668.2     LTPVFGKGVYDCPN SRLMEQKKFAKALTTDSFKRYVPKIREEILNYFVTDESFKLKE 180
can-iso-017     LTPVFGTGVYDCPN SRLMEQKKLAKFALTTDSFKRYVPKIREEILNYFVTDESFKLKE 180
*****_*;*****;*****

can-iso-001      KTHGVANVMKTQPEITIFTASRSLFGDEMRRIFDRSFAQLYSDLKGF TPI NFVFPNLPL 240
XM_711668.2     KTHGVANVMKTQPEITIFTASRSLFGDEMRRIFDRSFAQLYSDLKGF TPI NFVFPNLPL 240
can-iso-017     KTHGVANVMKTQPEITIFTASRSLFGDEMRRIFDRSFAQLYSDLKGF TPI NFVFPNLPL 240
*****

can-iso-001      PHYWRRDAAQKKISATYMK EIKLRRERGDIDPNRDLIDSLLIHSTYKDGVKMTDQEIANL 300
XM_711668.2     PHYWRRDAAQKKISATYMK EIKLRRERGDIDPNRDLIDSLLIHSTYKDGVKMTDQEIANL 300
can-iso-017     PHYWRRDAAQKKISATYMK EIKLRRERGDIDPNRDLIDSLLIHSTYKDGVKMTDQEIANL 300
*****

can-iso-001      LIGILMGGQHTSASTSAWFLHLGKPHLQDVIYQEVVELLKEKGGDLNDLTYEDLQKLP 360
XM_711668.2     LIGILMGGQHTSASTSAWFLHLGKPHLQDVIYQEVVELLKEKGGDLNDLTYEDLQKLP 360
can-iso-017     LIGILMGGQHTSASTSAWFLHLGKPHLQDVIYQEVVELLKEKGGDLNDLTYEDLQKLP 360
*****

can-iso-001      SVNYTIKENS RMHMLHSIFRKGTNPLGPPGTNYMVPKGHYVLASPGNAHTSERYFDNPE 420
XM_711668.2     SVNNTIKETLRMHMPLHSIFRKVTNPLRIPETNYIVPKGHYVLVSPGYAHTSERYFDNPE 420
can-iso-017     SVNYTIKEPS RMHMLHSIFRRVTNPLRIPETHYIDPKGHNDLASPGYAHTSERYFDNPE 420
*** **** * * * * * : * * * : * * * : * * * * *

can-iso-001      DFDPTRWDTAAAKANSV SFNSSDEV DYGFGKVKSGVSSPYLPPGGRRHRCIGEQFAYVQL 480
XM_711668.2     DFDPTRWDTAAAKANSV SFNSSDEV DYGFGKVKSGVSSPYLPPGGRRHRCIGEQFAYVQL 480
can-iso-017     DFDPTRWDTAAAKANSV SFNSSDEV DYGFGKVKSGVSSPYLPPGGRRHRCIGEQFAYVQL 480
*****

can-iso-001      GTILTTFVYNLRWTIDGYKVPDPDYSSMVVLPTEPAEIIWEKRETCMF 528
XM_711668.2     GTILTTFVYNLRWTIDGYKVPDPDYSSMVVLPTEPAEIIWEKRETCMF 528
can-iso-017     GTILTTFVYNLRWTIDGYKVPDPDYSSMVVLPTEPAEIIWEKRETCMF 528
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**Supplementary Figure 2:** CYP51 amino acid MSA between the wild-type and the fluconazole-resistant isolates

CLUSTAL O(1.2.4) multiple sequence alignment

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can-iso-028      ATGGCTATTGTTGAAACTGTCATTGATGGCATTAAATATTTTTTTGAACCATAGTGTACAA      60
XM_711668.2     ATGGCTATTGTTGAAACTGTCATTGATGGCATTAAATATTTTTTTGTC CCTTAGTGTACAA      60
can-iso-029/dog ATGGCTATTGTTGAAACTGTCATTGATGGCATTAAATATTTTTTTGTTGATAATTGTATA      60
*****
can-iso-028      CAACAGATCAGTATGTTATTAGGGGTTCCATTTGTTTACTACTTAGTATGTTGTTATTTA      120
XM_711668.2     CAACAGATCAGTATGTTATTAGGGGTTCCATTTGTTTACAACCTAGTATGGCAATATTTA      120
can-iso-029/dog CAACATATCAGTATGTTATTAGGGGTTCCCTTTGTTTACTACTTAGTCTGTTGTTTTTA      120
*****
can-iso-028      TATTCATTAAGAAATGATAGATCTCCTTATGGGTTTATTCGACTTCCTGGTTTGGTTCT      180
XM_711668.2     TATTCATTAAGAAAAGATAGAGCTCCATTTAGTGTTTTATGGATTCCCTGGTTTGGTTCT      180
can-iso-029/dog TATTCATTAAGAAATGATAGATCTCCTTTATGTTTATTCGATTCCCTGGTTTGGTTCT      180
*****
can-iso-028      GCAGCTTCATATGGTCAACAACCTTATGAATTTTTCGAATCATGTCGCAAAAGTATGGT      240
XM_711668.2     GCAGCTTCATATGGTCAACAACCTTATGAATTTTTCGAATCATGTCGCAAAAGTATGGT      240
can-iso-029/dog GCAGCTTCATATGGTCAACAACCTTATGAATTTTTCGAATCATGTCGCAAAAGTATGGT      240
*****
can-iso-028      GATGTAATTTTCATTTATGTTATTAGGGAAAATATGACGGTTTATTTAGTCCAAAAGGT      300
XM_711668.2     GATGTAATTTTCATTTATGTTATTAGGGAAAATATGACGGTTTATTTAGTCCAAAAGGT      300
can-iso-029/dog GATGTAATTTTCATTTATGTTATTAGGGAAAATATGACGGTTTATTTAGTCCAAAAGGT      300
*****
can-iso-028      CATGAATTTGTTTTAATGCTAAATATCTGATGTTTCTGCTGAAGATGCTTATAAACAT      360
XM_711668.2     CATGAATTTGTTTTAATGCTAAATATCTGATGTTTCTGCTGAAGATGCTTATAAACAT      360
can-iso-029/dog CATGAATTTGTTTTAATGCTAAATATCTGATGTTTCTGCTGAAGATGCTTATAAACAT      360
*****
can-iso-028      TTAACTACTCCAGTTTTCGGTAAAGGGGTTATTTATGATTGTCCAAATCCAGATTAATG      420
XM_711668.2     TTAACTACTCCAGTTTTCGGTAAAGGGGTTATTTATGATTGTCCAAATCCAGATTAATG      420
can-iso-029/dog TTAACTACTCCAGTTTTCGGTAAAGGGGTTATTTATGATTGTCCAAATCCAGATTAATG      420
*****
can-iso-028      GAACAAAAAAATTTGCTAAATTTGCTTTGACTACTGATTCATTTAAAAGATATGTTCTCT      480
XM_711668.2     GAACAAAAAAATTTGCTAAATTTGCTTTGACTACTGATTCATTTAAAAGATATGTTCTCT      480
can-iso-029/dog GAACAAAAAAATTTGCTAAATTTGCTTTGACTACTGATTCATTTAAAAGATATGTTCTCT      480
*****
can-iso-028      AAGATTAGAGAAGAAATTTGAATTTATTTGTTACTGATGAAAGTTTCAAATGAAAGAA      540
XM_711668.2     AAGATTAGAGAAGAAATTTGAATTTATTTGTTACTGATGAAAGTTTCAAATGAAAGAA      540
can-iso-029/dog AAGATTAGAGAAGAAATTTGAATTTATTTGTTACTGATGAAAGTTTCAAATGAAAGAA      540
*****
can-iso-028      AAAACTCATGGGGTTGCCAATGTTATGAAAACCAACCAGAAATTAATTTTCACTGCT      600
XM_711668.2     AAAACTCATGGGGTTGCCAATGTTATGAAAACCAACCAGAAATTAATTTTCACTGCT      600
can-iso-029/dog AAAACTCATGGGGTTGCCAATGTTATGAAAACCAACCAGAAATTAATTTTCACTGCT      600
*****
can-iso-028      TCAAGATCTTTATTTGGTGATGAAATGAGAAGAATTTTGACCGTTCATTGCTCAACTA      660
XM_711668.2     TCAAGATCTTTATTTGGTGATGAAATGAGAAGAATTTTGACCGTTCATTGCTCAACTA      660
can-iso-029/dog TCAAGATCTTTATTTGGTGATGAAATGAGAAGAATTTTGACCGTTCATTGCTCAACTA      660
*****
can-iso-028      TATTCTGATTTAGATAAAGGTTTACCCTATTAATTTTGTTCCTAATTTACCTTTA      720
XM_711668.2     TATTCTGATTTAGATAAAGGTTTACCCTATTAATTTTGTTCCTAATTTACCTTTA      720
can-iso-029/dog TATTCTGATTTAGATAAAGGTTTACCCTATTAATTTTGTTCCTAATTTACCTTTA      720
*****
can-iso-028      CCTCATTATTGGAGACGTGATGCTGCTCAAAGAAAATCTCTGCTACTTATATGAAAGAA      780
XM_711668.2     CCTCATTATTGGAGACGTGATGCTGCTCAAAGAAAATCTCTGCTACTTATATGAAAGAA      780
can-iso-029/dog CCTCATTATTGGAGACGTGATGCTGCTCAAAGAAAATCTCTGCTACTTATATGAAAGAA      780
*****
can-iso-028      ATTAAACTGAGAAGAGAACGTGGTGATATTGATCCAAATCGTGATTTAATTGATTCCTTA      840
XM_711668.2     ATTAAACTGAGAAGAGAACGTGGTGATATTGATCCAAATCGTGATTTAATTGATTCCTTA      840
can-iso-029/dog ATTAAACTGAGAAGAGAACGTGGTGATATTGATCCAAATCGTGATTTAATTGATTCCTTA      840
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**Supplementary Figure 3: *ERG11* gene nucleotide MSA between the wild-type and the fluconazole susceptible isolates**

|                 |  |      |
|-----------------|--|------|
| can-iso-028     | ATTAAACTGAGAAGAGAACGTGGTGATATTGATCCAAATCGTGATTTAATTGATTCCTTA   | 840  |
| XM_711668.2     | ATTAAACTGAGAAGAGAACGTGGTGATATTGATCCAAATCGTGATTTAATTGATTCCTTA   | 840  |
| can-iso-029/dog | ATTAAACTGAGAAGAGAACGTGGTGATATTGATCCAAATCGTGATTTAATTGATTCCTTA<br>*****  | 840  |
| can-iso-028     | TTGATTCATTCAACTTATAAAGATGGTGTGAAAATGACTGATCAAGAAATGCTAATCTT  | 900  |
| XM_711668.2     | TTGATTCATTCAACTTATAAAGATGGTGTGAAAATGACTGATCAAGAAATGCTAATCTT  | 900  |
| can-iso-029/dog | TTGATTCATTCAACTTATAAAGATGGTGTGAAAATGACTGATCAAGAAATGCTAATCTT<br>*****   | 900  |
| can-iso-028     | TTAATTGGTATTCCTTATGGGTGGTCAACATACTTCTGCTTCTACTTCTGCTTGGTTCTTG  | 960  |
| XM_711668.2     | TTAATTGGTATTCCTTATGGGTGGTCAACATACTTCTGCTTCTACTTCTGCTTGGTTCTTG  | 960  |
| can-iso-029/dog | TTAATTGGTATTCCTTATGGGTGGTCAACATACTTCTGCTTCTACTTCTGCTTGGTTCTTG<br>*****   | 960  |
| can-iso-028     | TTACATTTAGGTGAAAAACCTCATTTACAAGATGTTATTTATCAAGAAGTTGTTGAATTA   | 1020 |
| XM_711668.2     | TTACATTTAGGTGAAAAACCTCATTTACAAGATGTTATTTATCAAGAAGTTGTTGAATTA   | 1020 |
| can-iso-029/dog | TTACATTTAGGTGAAAAACCTCATTTACAAGATGTTATTTATCAAGAAGTTGTTGAATTA<br>*****  | 1020 |
| can-iso-028     | TTGAAAGAAAAAGGTGGTGATTTGAATGATTTGACTTATGAAGATTTACAAAAATTACCA   | 1080 |
| XM_711668.2     | TTGAAAGAAAAAGGTGGTGATTTGAATGATTTGACTTATGAAGATTTACAAAAATTACCA   | 1080 |
| can-iso-029/dog | TTGAAAGAAAAAGGTGGTGATTTGAATGATTTGACTTATGAAGATTTACAAAAATTACCA<br>*****  | 1080 |
| can-iso-028     | TCAGTCAATAACACTATTACGAAACTCTCAGAATGCATATGCCATTACATTCATTTTT   | 1140 |
| XM_711668.2     | TCAGTCAATAACACTATTACGAAACTCTCAGAATGCATATGCCATTACATTCATTTTT   | 1140 |
| can-iso-029/dog | TCAGTCAATTACACTATTATGAAACTCTCAGAATGCATATGCCATTACATTCATTTTT<br>***** ***** ***** ***** ***** ***** ***** *****    | 1140 |
| can-iso-028     | AGAAGAGTTACTATCCCATTAATAGATCCTGAATCAAAATTTTATTGATCCAAAAGGTCAT  | 1200 |
| XM_711668.2     | AGAAAAGTTACTAACCATTAAAGATCCCTGAAACCAATTATATTGTTCCAAAAGGTCAT  | 1200 |
| can-iso-029/dog | AGAAAAGTTACTATCCCATTAAGAAATTCCTGAATCCAATTATATTGATCCAAAAGGTCAT<br>**** ***** ***** * ***** * **** ***** *****     | 1200 |
| can-iso-028     | TATGTTTTAGTTCTTCCAGGTTATGCTCATACTAGTGAAAGATATTTTGATAACCCTGAA   | 1260 |
| XM_711668.2     | TATGTTTTAGTTCTTCCAGGTTATGCTCATACTAGTGAAAGATATTTTGATAACCCTGAA   | 1260 |
| can-iso-029/dog | TATGTTTTAGTTCTTCCAGGTTATGCTCATACTAGTGAAAGATATTTTGATAACCCTGAA<br>***** ***** ***** ***** ***** ***** ***** *****  | 1260 |
| can-iso-028     | GATTTTGATCCAAC TAGATGGGATACTGCTGCTGCCAAAGCTAATTCTGTTTCATTTAAC  | 1320 |
| XM_711668.2     | GATTTTGATCCAAC TAGATGGGATACTGCTGCTGCCAAAGCTAATTCTGTTTCATTTAAC  | 1320 |
| can-iso-029/dog | GATTTTGATCCAAC TAGATGGGATACTGCTGCTGCCAAAGCTAATTCTGTTTCATTTAAC<br>***** ***** ***** ***** ***** ***** ***** ***** | 1320 |
| can-iso-028     | TCTTCTGATGAAGTTGATTATGGGTTTGGGAAAGTTTCTAAAGGGGTTTCTTACCTTAT  | 1380 |
| XM_711668.2     | TCTTCTGATGAAGTTGATTATGGGTTTGGGAAAGTTTCTAAAGGGGTTTCTTACCTTAT  | 1380 |
| can-iso-029/dog | TCTTCTGATGAAGTTGATTATGGGTTTGGGAAAGTTTCTAAAGGGGTTTCTTACCTTAT<br>***** ***** ***** ***** ***** ***** ***** *****   | 1380 |
| can-iso-028     | TTACCATTGGTGGTGGTAGACATAGATGATTGGGGAACAATTTGCTTATGTTCAATTA   | 1440 |
| XM_711668.2     | TTACCATTGGTGGTGGTAGACATAGATGATTGGGGAACAATTTGCTTATGTTCAATTA   | 1440 |
| can-iso-029/dog | TTACCATTGGTGGTGGTAGACATAGATGATTGGGGAACAATTTGCTTATGTTCAATTA<br>***** ***** ***** ***** ***** ***** ***** *****    | 1440 |
| can-iso-028     | GGAACCATTTTAACTACTTTTGTTTATAATTTAAGATGGACTATTGATGGTTATAAAGTG   | 1500 |
| XM_711668.2     | GGAACCATTTTAACTACTTTTGTTTATAATTTAAGATGGACTATTGATGGTTATAAAGTG   | 1500 |
| can-iso-029/dog | GGAACCATTTTAACTACTTTTGTTTATAATTTAAGATGGACTATTGATGGTTATAAAGTG<br>***** ***** ***** ***** ***** ***** ***** *****  | 1500 |
| can-iso-028     | CCTGACCCTGATTATAGTTCAATGGTGGTTTTACCTACTGAACCAGCAGAAATCATTGG  | 1560 |
| XM_711668.2     | CCTGACCCTGATTATAGTTCAATGGTGGTTTTACCTACTGAACCAGCAGAAATCATTGG  | 1560 |
| can-iso-029/dog | CCTGACCCTGATTATAGTTCAATGGTGGTTTTACCTACTGAACCAGCAGAAATCATTGG<br>***** ***** ***** ***** ***** ***** ***** *****   | 1560 |
| can-iso-028     | GAAAAAGAGAAACTTGTATGTTTTAA   | 1587 |
| XM_711668.2     | GAAAAAGAGAAACTTGTATGTTTTAA   | 1587 |
| can-iso-029/dog | GAAAAAGAGAAACTTGTATGTTTTAA<br>*****  | 1587 |

**Cont'd Supplementary Figure 3: *ERG11* gene nucleotide MSA between the wild-type and the fluconazole susceptible isolates**



CLUSTAL O(1.2.4) multiple sequence alignment

```
can-iso-029/dog      MAIVETVIDGINYFLFDNCIQHISILLGVPLVIYLVCCFLYSLRNDRSPLLFYSIPWFGS      60
XM_711668.2         MAIVETVIDGINYFLSLSVTQQISILLGVPPVYNLVWQYLYSLRKKDRAPLVFYWIWPFWS      60
can-iso-028         MAIVETVIDGINYFLNHSVTQQISMLLGVPFVYLVCCYLYSLRNDRSPYGFIRLPWFGS      60
*****          .  *:::*****: *  *  :*****:*:*  *  :*****

can-iso-029/dog      AASYGQQPYEFPFESCRQKYGDVFSFMLLGKIMTVYLGPKGHEFVFNKLSDVSAEDAYKH      120
XM_711668.2         AASYGQQPYEFPFESCRQKYGDVFSFMLLGKIMTVYLGPKGHEFVFNKLSDVSAEDAYKH      120
can-iso-028         AASYGQQPYEFPFESCRQKYGDVFSFMLLGKIMTVYLGPKGHEFVFNKLSDVSAEDAYKH      120
*****

can-iso-029/dog      LTPVFGKGVYDCPN SRLMEQKKFAKFAITDTSFKRYVPKIREEILNYFVTDESFKLKE      180
XM_711668.2         LTPVFGKGVYDCPN SRLMEQKKFAKFAITDTSFKRYVPKIREEILNYFVTDESFKLKE      180
can-iso-028         LTPVFGKGVYDCPN SRLMEQKKFAKFAITDTSFKRYVPKIREEILNYFVTDESFKLKE      180
*****

can-iso-029/dog      KTHGVANVMKTQPEITIFTASRSLFGDEMRRIFDRSFAQLYSDLDKGFTPINFVFPNLPL      240
XM_711668.2         KTHGVANVMKTQPEITIFTASRSLFGDEMRRIFDRSFAQLYSDLDKGFTPINFVFPNLPL      240
can-iso-028         KTHGVANVMKTQPEITIFTASRSLFGDEMRRIFDRSFAQLYSDLDKGFTPINFVFPNLPL      240
*****

can-iso-029/dog      PHYWRRDAAQKKISATYMKI IKLRRERGDIDPNRDLIDSLLIHSTYKDGVKMTDQEIANL      300
XM_711668.2         PHYWRRDAAQKKISATYMKI IKLRRERGDIDPNRDLIDSLLIHSTYKDGVKMTDQEIANL      300
can-iso-028         PHYWRRDAAQKKISATYMKI IKLRRERGDIDPNRDLIDSLLIHSTYKDGVKMTDQEIANL      300
*****

can-iso-029/dog      LIGILMGGQHTSASTSAWFLHLGKPHLQDVVIYQEVVLLKKEGGDLNDLTYEDLQKLP      360
XM_711668.2         LIGILMGGQHTSASTSAWFLHLGKPHLQDVVIYQEVVLLKKEGGDLNDLTYEDLQKLP      360
can-iso-028         LIGILMGGQHTSASTSAWFLHLGKPHLQDVVIYQEVVLLKKEGGDLNDLTYEDLQKLP      360
*****

can-iso-029/dog      SVNYTIMETLRMHMPLHSIFRKYVPIPLRIPESNYIDPKGHYVLVSPGYAHTSERYFDNPE      420
XM_711668.2         SVNNTIKETLRMHMPLHSIFRKYVPIPLRIPETNYIVPKGHYVLVSPGYAHTSERYFDNPE      420
can-iso-028         SVNNTITETLRMHMPLHSIFRRVPIPLIDPESNFIDPKGHYVLVLPGYAHTSERYFDNPE      420
*** * ***** **::* *  *  *:::***** *****

can-iso-029/dog      DFDPTRWDTAAAKANSVFNSSDEVVDYGFQKVKVSGVSSPYLPFGGGRHRCIGEQPAYVQL      480
XM_711668.2         DFDPTRWDTAAAKANSVFNSSDEVVDYGFQKVKVSGVSSPYLPFGGGRHRCIGEQPAYVQL      480
can-iso-028         DFDPTRWDTAAAKANSVFNSSDEVVDYGFQKVKVSGVSSPYLPFGGGRHRCIGEQPAYVQL      480
*****

can-iso-029/dog      GTILTFVYNLRWTIDGYKVPDPDYSSMVVLPTEPAEIIWEKRETCMF      528
XM_711668.2         GTILTFVYNLRWTIDGYKVPDPDYSSMVVLPTEPAEIIWEKRETCMF      528
can-iso-028         GTILTFVYNLRWTIDGYKVPDPDYSSMVVLPTEPAEIIWEKRETCMF      528
*****
```

**Supplementary Figure 4:** CYP51 amino acid MSA between the wild-type and the fluconazole susceptible isolates

CLUSTAL O(1.2.4) multiple sequence alignment

```
5FSA -----MAIVETVIDGINYFLSLSVTQQISILLGVPFVYNLVNQYLYSLRKDRAPLVF 52
4WMZ MSATKSIKVEALEYVNIQLSHFLALPLAQRISLIIIIIPFIYNIWQLLYSLRKDRPPLVF 60
      :* * * :.:**:* :.:**:* :.:**:*:** * :***** **

5FSA YWIPWFGSAASYGQQPYEFPESCQRQKYGDVPSFMLLGKIMTVYLGPKGHEFVFNAKLSDV 112
4WMZ YWIPWVGSVVYGMKPYEFPFEECQKKYGDIFSFVLLGRVMTVYLGPKGHEFVFNAKLADV 120
      ***** ** :***** :.:**:*:**:* :.:**:*:**:* :*****:**

5FSA SAEDAYKHLTTPVFGKGIYDCPNSRLMEQKKFAKPAITDSFKRYVPKIREEILNYFVT 172
4WMZ SAEAAVAHLTTPVFGKGIYDCPNSRLMEQKKFVKGALTKEAFKSYVPLIAEEVYKYFRD 180
      *** ** ***** :***** :***** :***** :***** :*****

5FSA DESFKLKEKTHGVANVMKTQPEITIFTASRSLFGDEMRRIFDRSFAQLYSDDLKGFPTIN 232
4WMZ SKNFRLNERTTGTIDVMVTQPEMTIFTASRSLGKEMRAKLDTDFAYLYSDDLKGFPTIN 240
      .:.*:**:* * :. ** ***** :***** :***** :***** :*****

5FSA FVFPNLPLPHYWRRDAAQKKISATYMKIKSRRERGDIDPNRDLIDSLLIHSTYKDGVKM 292
4WMZ FVFPNLPLEHYRKRDAQKAISGTYSMLIKERRKNNDIQ-DRDLIDSLMKNSTYKDGVKM 299
      ***** ** :** ** * :***** :***** :***** :*****

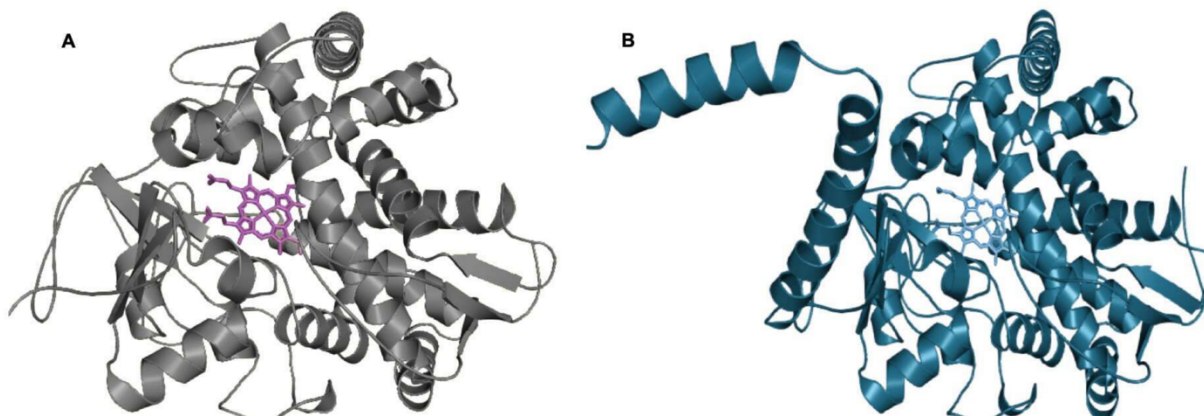
5FSA TDQEIANLLIGILMGGQHTSASTSAWFLHLGKPHLQDVIYQEVVELLKEKGGDLNDLT 352
4WMZ TDQEIANLLIGVLMGGQHTSAA TSAWILLHLAERP DVQQELYEEQMRVL---DGGKKELT 356
      ***** :***** :***** :***** :***** :***** :*****

5FSA YEDLQKLPSVNNNTIKETLRMHMPLHSIPRKVTNPLRIPETNYIVPKGHYVLVSPGYAHTS 412
4WMZ YDLLQEMPLLNQTIKETLRMHMPLHSIFRKVMKDMHVPNTSYVIVIPAGYHVLVSPGYTHLR 416
      * : ** :.* :***** ***** : : : : * : * :***** :*

5FSA ERYFDNPEDFDPTRWDTAAAKANSVSNSSDEVYGFQKVSQGVSSPYLPFGGGRHRCIG 472
4WMZ DEYFPNAHQFNIRWNNDSAS----SYVGEVDYGFQAIKGVSSPYLPFGGGRHRCIG 472
      :.* * :.* : ** :. :* :. :***** :***** :*****

5FSA EQPAYVQLGTLITTFVYNLRWTI-DGYKVPDPDYSSMVVLPTEPAEIIWEKRETCMP- 528
4WMZ EHFAYCQLGVLMSIFIRTLKWHYPEGKTVPPPDFTSMVTLPTGPAKIIWEKRNPQKI 530
      * : ** * : : : * : . * * : * . ** * : : ** * : ** * :***** :
```

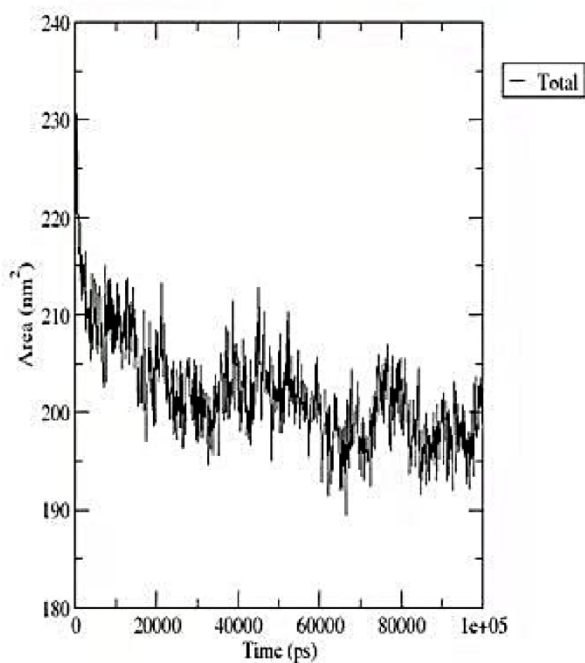
Supplementary Figure 5: CYP51 amino acid MSA between the wild-type *C. albicans* (5FSA) and *S. cerevisiae* (4WMZ).



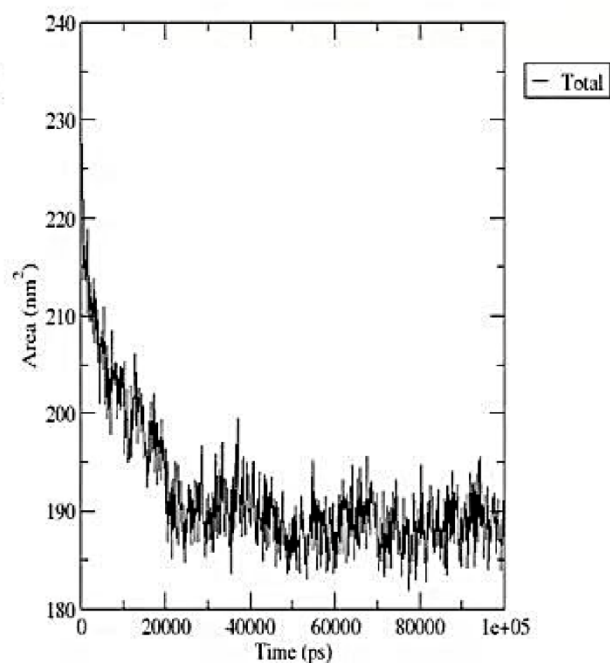
**Supplementary Figure 6:** Pre-alignment 3D structures of the *C. albicans* (grey cartoon) and *S. cerevisiae* (purple cartoon) CYP51. (A) shows the positioning of the heme molecule (purple) in the drug-binding site of the *C. albicans* CYP51 prior to alignment. (B) shows the positioning of the heme molecule (blue) in the drug-binding site of the *S. cerevisiae* CYP51 before alignment.



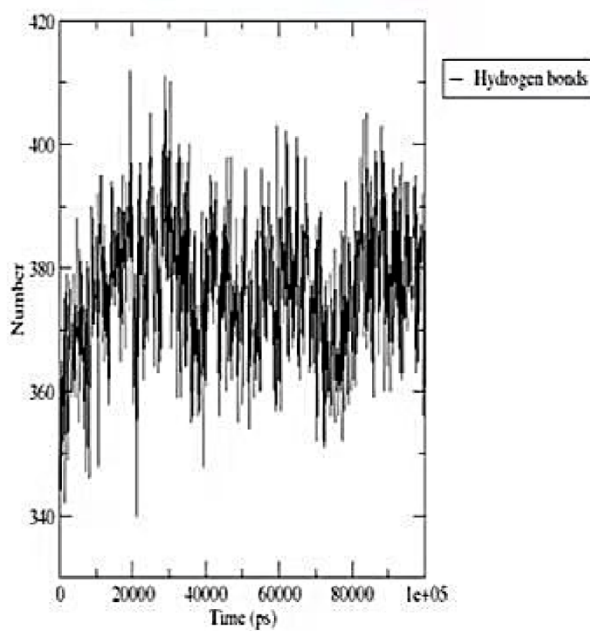
### WT Protein SASA Plot



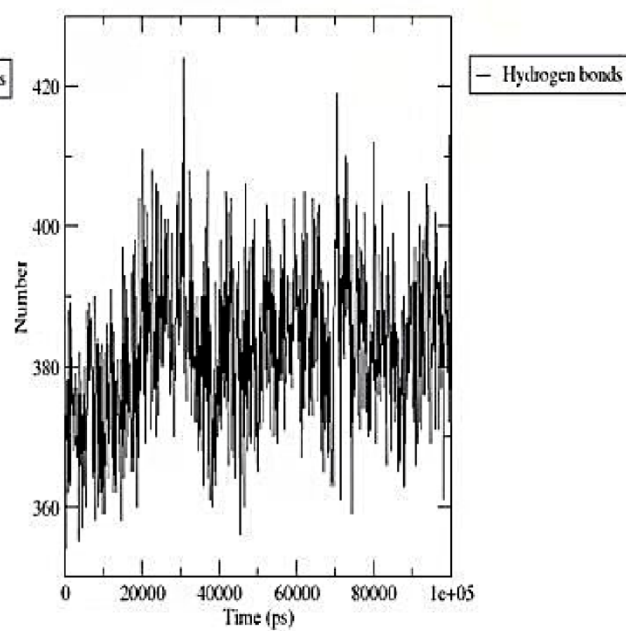
### MT Protein SASA Plot



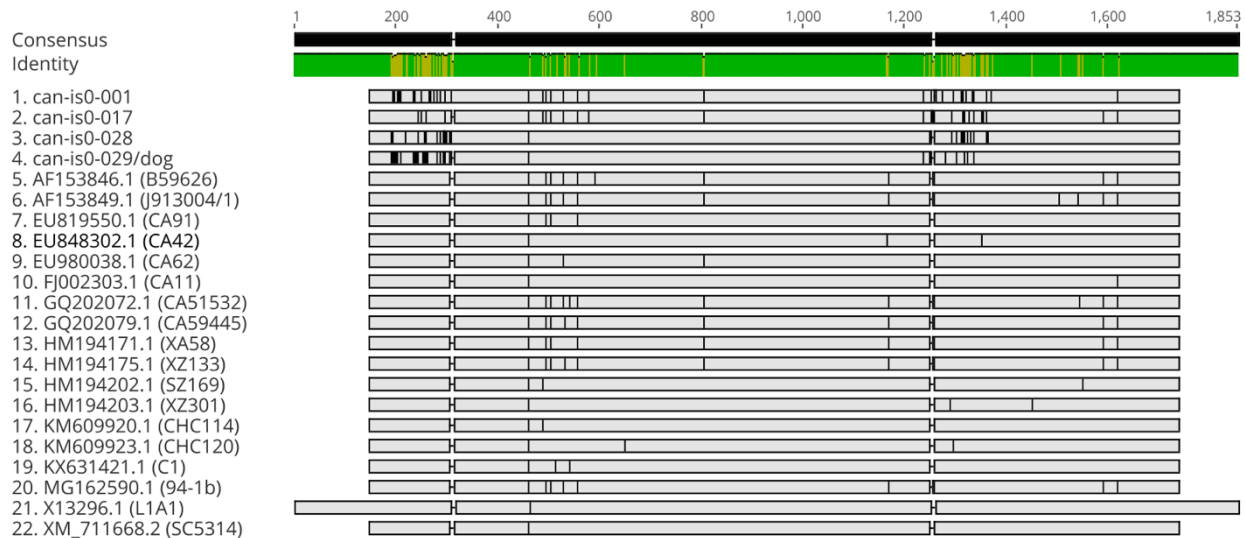
### WT Protein HBONDS Plot



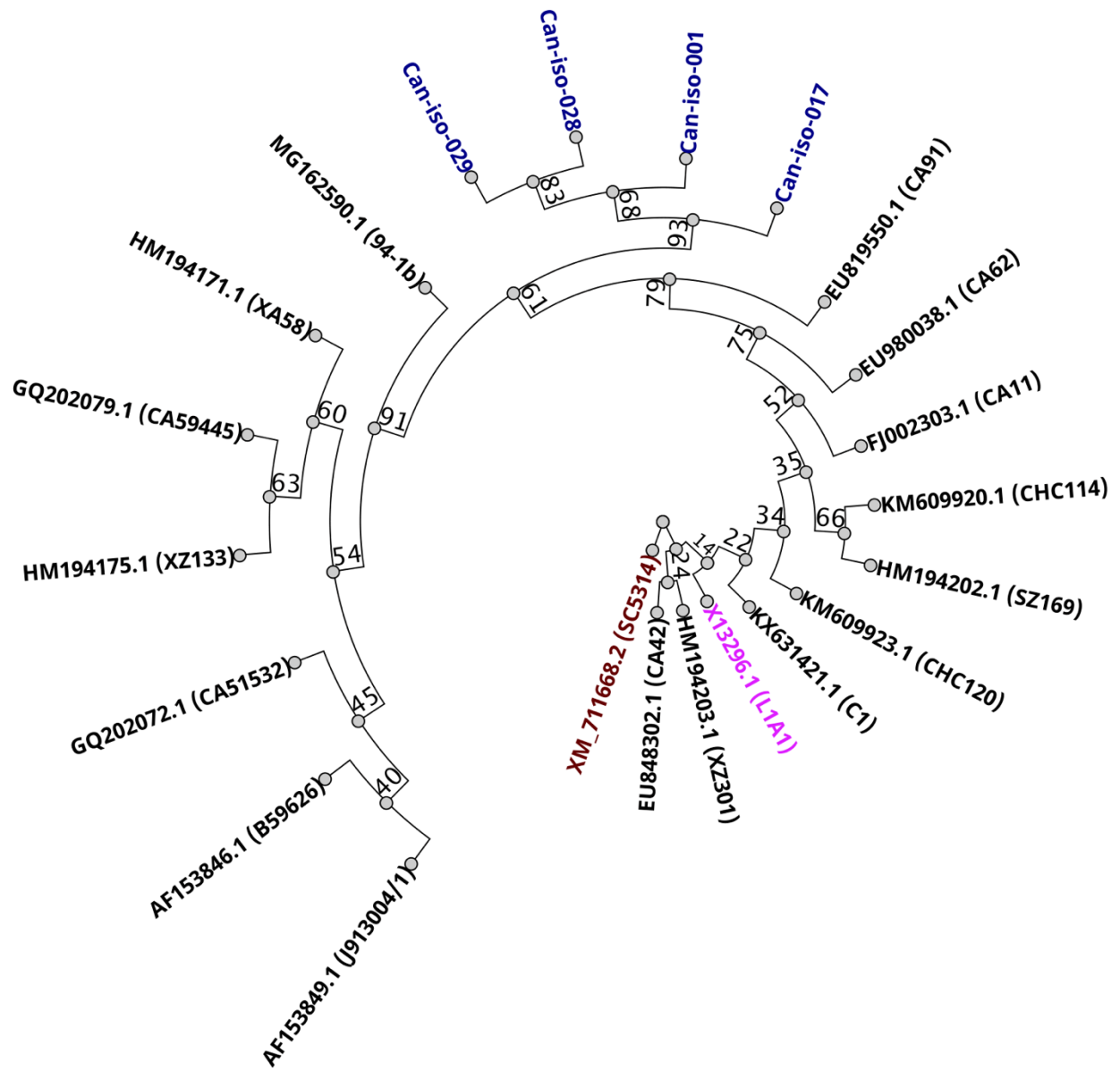
### MT Protein HBONDS Plot



**Supplementary Figure 7:** Analysis of the molecular dynamics simulation and trajectory of the wild-type and mutant protein-ligand complex. Plots of the solvent-accessible surface area (top), and the intramolecular hydrogen bonds (bottom) for the wild-type and mutant proteins respectively.



**Supplementary Figure 8:** Nucleotide MSA-phylogenetic map for the analysis between the sequences of interest



**Supplementary Figure 9:** A rooted phylogenetic relationship between the *ERG11* genes of the 4 *Candida* isolates sequenced in this study (in purple), and 17 pre-selected nucleotide sequences from the GenBank repository. Wild-type is in brown, and *ERG16* in pink.

**Supplementary Table 1** Molecular identification indices of pure cultures of *Candida* isolates

| <i>Candida</i> Species  | ITS1-ITS2 amplicon size (bp) | Size of Fragment (bp) after digest |
|-------------------------|------------------------------|------------------------------------|
| <i>C. albicans</i>      | 538                          | 299, 239                           |
| <i>C. krusei</i>        | 510                          | 262, 248                           |
| <i>C. glabrata</i>      | 880                          | 563, 317                           |
| <i>C. tropicalis</i>    | 528                          | 342, 186                           |
| <i>C. parapsilosis</i>  | 520                          | 520                                |
| <i>C. kefyr</i>         | 721                          | 721                                |
| <i>C. guillermondii</i> | 607                          | 372, 157, 82                       |
| <i>C. catenulata</i>    | 402                          | 402                                |
| <i>C. famata</i>        | 639                          | 639                                |

**Supplementary Table 2** Identification and characterization of yeast samples using conventional methods

| S/N | Sample    | Growth on SDA and germ tube test |
|-----|-----------|----------------------------------|
| 1   | h-HVS-001 | +ve (+ve to germ tube test)      |
| 2   | h-HVS-002 | +ve (+ve to germ tube test)      |
| 3   | h-HVS-003 | Growth Absent (-ve)              |
| 4   | h-HVS-004 | -ve                              |
| 5   | h-HVS-005 | -ve                              |
| 6   | h-HVS-006 | +ve (+ve to germ tube test)      |
| 7   | h-HVS-007 | +ve (+ve to germ tube test)      |
| 8   | h-HVS-008 | -ve                              |
| 9   | h-HVS-009 | -ve                              |
| 10  | h-HVS-010 | +ve (+ve to germ tube test)      |
| 11  | h-HVS-011 | +ve (+ve to germ tube test)      |
| 12  | h-HVS-012 | -ve                              |
| 13  | h-HVS-013 | -ve                              |
| 14  | h-HVS-014 | -ve                              |
| 15  | h-HVS-015 | -ve                              |
| 16  | h-HVS-016 | -ve                              |
| 17  | h-HVS-017 | +ve (+ve to germ tube test)      |
| 18  | h-HVS-018 | -ve                              |
| 19  | h-HVS-019 | +ve (+ve to germ tube test)      |
| 20  | h-HVS-020 | +ve (+ve to germ tube test)      |
| 21  | h-HVS-021 | +ve (+ve to germ tube test)      |
| 22  | h-HVS-022 | -ve                              |
| 23  | h-HVS-023 | -ve                              |
| 24  | h-HVS-024 | -ve                              |

|    |           |                             |
|----|-----------|-----------------------------|
| 25 | h-HVS-025 | +ve (+ve to germ tube test) |
| 26 | h-HVS-026 | -ve                         |
| 27 | h-HVS-027 | +ve (+ve to germ tube test) |
| 28 | h-HVS-028 | +ve (+ve to germ tube test) |
| 29 | h-HVS-029 | +ve (+ve to germ tube test) |
| 30 | h-HVS-030 | -ve                         |
| 31 | h-HVS-031 | -ve                         |
| 32 | h-HVS-032 | -ve                         |
| 33 | h-HVS-033 | +ve (+ve to germ tube test) |
| 34 | h-HVS-034 | -ve                         |
| 35 | h-HVS-035 | +ve (+ve to germ tube test) |
| 36 | h-HVS-036 | +ve (+ve to germ tube test) |
| 37 | h-HVS-037 | +ve (+ve to germ tube test) |
| 38 | h-HVS-038 | +ve (+ve to germ tube test) |
| 39 | h-HVS-039 | +ve (+ve to germ tube test) |
| 40 | h-HVS-040 | +ve (+ve to germ tube test) |
| 41 | h-HVS-041 | +ve (+ve to germ tube test) |
| 42 | h-HVS-042 | -ve                         |
| 43 | h-HVS-043 | -ve                         |
| 44 | h-HVS-044 | +ve (+ve to germ tube test) |
| 45 | h-HVS-045 | -ve                         |
| 46 | h-HVS-046 | -ve                         |
| 47 | h-HVS-047 | -ve                         |
| 48 | h-HVS-048 | -ve                         |
| 49 | h-HVS-049 | +ve (+ve to germ tube test) |
| 50 | h-HVS-050 | +ve (+ve to germ tube test) |
| 51 | h-HVS-051 | -ve                         |



|    |           |                             |
|----|-----------|-----------------------------|
| 52 | h-HVS-052 | +ve (+ve to germ tube test) |
| 53 | h-HVS-053 | +ve (+ve to germ tube test) |
| 54 | h-HVS-054 | -ve                         |
| 55 | h-HVS-055 | +ve (+ve to germ tube test) |
| 56 | h-HVS-056 | -ve                         |
| 57 | h-HVS-058 | -ve                         |
| 58 | d-HVS-001 | +ve (+ve to germ tube test) |
| 59 | d-HVS-002 | -ve                         |
| 60 | d-HVS-003 | -ve                         |
| 61 | d-HVS-004 | -ve                         |
| 62 | d-HVS-005 | +ve (+ve to germ tube test) |
| 63 | d-HVS-006 | +ve (+ve to germ tube test) |
| 64 | d-HVS-007 | +ve (+ve to germ tube test) |

**h-HVS – Human High Vaginal Swab**

**d-HVS – Dog High Vaginal Swab**

**Supplementary Table 3** Active site residues of the *C. albicans* CYP51 that are involved in specific interactions with the bound heme molecule and Posaconazole

| Ligands      | Hydrophobic interactions                                   | Hydrogen bonds       | Salt bridges                    |
|--------------|--|----------------------|---------------------------------|
| Heme         | LEU-370, PRO-375,<br>PHE-463, ILE-471, PHE-<br>475         | TYR-118, TYR-<br>132 | LYS-143,<br>ARG-381,<br>HIS-468 |
| Posaconazole | LEU-121, PHE-126,<br>PRO-230, PHE-233,<br>LEU-376, PHE-380 | TYR-132              | Nil                             |

**Supplementary Table 4** Active site residues of the *S. cerevisiae* CYP51 that are involved in specific interactions with the bound heme molecule and Fluconazole

| Ligands     | Hydrophobic interactions   | Hydrogen bonds   | Salt bridges              |
|-------------|--|------------------|---------------------------|
| Heme        | LYS-151, VAL-311, THR-318, LEU-374, PRO-379, LEU-383, PHE-463, ILE-471, PHE-475, ALA-476 | TYR-140, HIS-468 | LYS-151, ARG-385, HIS-468 |
| Fluconazole | PHE-134  | TYR-126          | Nil                       |

**Supplementary Table 5** Unrooted phylogenetic relationship between the *ERG11* genes of the 4 *Candida* isolates sequenced in this study, and 17 pre-selected nucleotide sequences from GenBank repository.

|    | AF153846.1          | AF153849.1 | Can-iso-001 | Can-iso-017 | Can-iso-028 | Can-iso-029 | EU819550.1 | EU848302.1 | EU980038.1 | FJ002303.1 | GQ202072.1 | GQ202079.1 | HM194171 | HM194175 | HM194202 | HM194203 | KM609920 | KM609923 | KX631421.1 | MG162590 | X13296.1 | (L:XM_711668.2 [SC5314]) |       |
|----|---------------------|------------|-------------|-------------|-------------|-------------|------------|------------|------------|------------|------------|------------|----------|----------|----------|----------|----------|----------|------------|----------|----------|--------------------------|-------|
| 1  |                     |            |             |             |             |             |            |            |            |            |            |            |          |          |          |          |          |          |            |          |          |                          |       |
| 2  | AF153846.1 (B59626) | 0.002      | 0.033       | 0.012       | 0.019       | 0.028       | 0.005      | 0.008      | 0.007      | 0.007      | 0.002      | 0.002      | 0.001    | 0.002    | 0.008    | 0.007    | 0.008    | 0.008    | 0.008      | 0.002    | 0.007    | 0.007                    |       |
| 3  | AF153849.1          | 0.002      | 0.034       | 0.012       | 0.02        | 0.029       | 0.006      | 0.008      | 0.007      | 0.008      | 0.003      | 0.003      | 0.002    | 0.003    | 0.009    | 0.008    | 0.009    | 0.009    | 0.009      | 0.009    | 0.003    | 0.008                    | 0.008 |
| 4  | Can-iso-001         | 0.033      | 0.034       | 0.029       | 0.027       | 0.036       | 0.031      | 0.033      | 0.032      | 0.033      | 0.034      | 0.033      | 0.032    | 0.033    | 0.034    | 0.033    | 0.034    | 0.034    | 0.034      | 0.034    | 0.031    | 0.033                    | 0.033 |
| 5  | Can-iso-017         | 0.012      | 0.012       | 0.029       | 0.015       | 0.024       | 0.009      | 0.012      | 0.011      | 0.012      | 0.012      | 0.012      | 0.011    | 0.011    | 0.012    | 0.012    | 0.013    | 0.013    | 0.013      | 0.01     | 0.012    | 0.012                    |       |
| 6  | Can-iso-028         | 0.019      | 0.02        | 0.027       | 0.015       | 0.012       | 0.017      | 0.02       | 0.018      | 0.019      | 0.02       | 0.019      | 0.018    | 0.019    | 0.02     | 0.019    | 0.02     | 0.02     | 0.02       | 0.02     | 0.018    | 0.019                    | 0.019 |
| 7  | Can-iso-029         | 0.028      | 0.029       | 0.036       | 0.024       | 0.012       | 0.026      | 0.028      | 0.027      | 0.028      | 0.029      | 0.028      | 0.027    | 0.028    | 0.029    | 0.028    | 0.029    | 0.029    | 0.029      | 0.029    | 0.026    | 0.028                    | 0.028 |
| 8  | EU819550.1          | 0.005      | 0.006       | 0.031       | 0.009       | 0.017       | 0.026      | 0.003      | 0.002      | 0.003      | 0.006      | 0.005      | 0.004    | 0.005    | 0.004    | 0.003    | 0.004    | 0.004    | 0.004      | 0.004    | 0.004    | 0.003                    | 0.003 |
| 9  | EU848302.1          | 0.008      | 0.008       | 0.033       | 0.012       | 0.02        | 0.028      | 0.003      | 0.002      | 0.001      | 0.008      | 0.008      | 0.007    | 0.007    | 0.002    | 0.001    | 0.002    | 0.002    | 0.002      | 0.002    | 0.006    | 0.001                    | 0.001 |
| 10 | EU980038.1          | 0.007      | 0.007       | 0.032       | 0.011       | 0.018       | 0.027      | 0.002      | 0.002      | 0.002      | 0.007      | 0.006      | 0.006    | 0.006    | 0.002    | 0.001    | 0.002    | 0.003    | 0.003      | 0.005    | 0.001    | 0.001                    |       |
| 11 | FJ002303.1          | 0.007      | 0.008       | 0.033       | 0.012       | 0.019       | 0.028      | 0.003      | 0.001      | 0.002      | 0.008      | 0.007      | 0.007    | 0.007    | 0.001    | 0.001    | 0.001    | 0.002    | 0.002      | 0.006    | 0.001    | 0.001                    |       |
| 12 | GQ202072.1          | 0.002      | 0.003       | 0.034       | 0.012       | 0.02        | 0.029      | 0.006      | 0.008      | 0.007      | 0.008      | 0.003      | 0.002    | 0.002    | 0.009    | 0.008    | 0.009    | 0.009    | 0.009      | 0.009    | 0.003    | 0.008                    | 0.008 |
| 13 | GQ202079.1          | 0.002      | 0.003       | 0.033       | 0.012       | 0.019       | 0.028      | 0.005      | 0.008      | 0.006      | 0.007      | 0.003      | 0.001    | 0        | 0.008    | 0.007    | 0.008    | 0.008    | 0.008      | 0.002    | 0.007    | 0.007                    |       |
| 14 | HM194171            | 0.001      | 0.002       | 0.032       | 0.011       | 0.018       | 0.027      | 0.004      | 0.007      | 0.006      | 0.007      | 0.002      | 0.001    | 0        | 0.007    | 0.006    | 0.007    | 0.008    | 0.008      | 0.008    | 0.001    | 0.006                    | 0.006 |
| 15 | HM194175            | 0.002      | 0.003       | 0.033       | 0.011       | 0.019       | 0.028      | 0.005      | 0.007      | 0.006      | 0.007      | 0.002      | 0        | 0        | 0.008    | 0.007    | 0.008    | 0.008    | 0.008      | 0.002    | 0.007    | 0.007                    |       |
| 16 | HM194202            | 0.008      | 0.009       | 0.034       | 0.012       | 0.02        | 0.029      | 0.004      | 0.002      | 0.002      | 0.001      | 0.009      | 0.008    | 0.007    | 0.008    | 0.001    | 0        | 0.002    | 0.002      | 0.006    | 0.001    | 0.001                    |       |
| 17 | HM194203            | 0.007      | 0.008       | 0.033       | 0.012       | 0.019       | 0.028      | 0.003      | 0.001      | 0.001      | 0.001      | 0.008      | 0.007    | 0.006    | 0.007    | 0.001    | 0.001    | 0.001    | 0.001      | 0.006    | 0        | 0                        |       |
| 18 | KM609920            | 0.008      | 0.009       | 0.034       | 0.012       | 0.02        | 0.029      | 0.004      | 0.002      | 0.002      | 0.001      | 0.009      | 0.008    | 0.007    | 0.008    | 0        | 0.001    | 0.002    | 0.002      | 0.006    | 0.001    | 0.001                    |       |
| 19 | KM609923            | 0.008      | 0.009       | 0.034       | 0.013       | 0.02        | 0.029      | 0.004      | 0.002      | 0.003      | 0.002      | 0.009      | 0.008    | 0.008    | 0.008    | 0.002    | 0.001    | 0.002    | 0.002      | 0.007    | 0.001    | 0.001                    |       |
| 20 | KX631421.1          | 0.008      | 0.009       | 0.034       | 0.013       | 0.02        | 0.029      | 0.004      | 0.002      | 0.003      | 0.002      | 0.009      | 0.008    | 0.008    | 0.008    | 0.002    | 0.001    | 0.002    | 0.002      | 0.007    | 0.001    | 0.001                    |       |
| 21 | MG162590            | 0.002      | 0.003       | 0.031       | 0.01        | 0.018       | 0.026      | 0.004      | 0.006      | 0.005      | 0.006      | 0.003      | 0.002    | 0.001    | 0.002    | 0.006    | 0.006    | 0.006    | 0.007      | 0.007    | 0.006    | 0.006                    |       |
| 22 | X13296.1 (L         | 0.007      | 0.008       | 0.033       | 0.012       | 0.019       | 0.028      | 0.003      | 0.001      | 0.001      | 0.001      | 0.008      | 0.007    | 0.006    | 0.007    | 0.001    | 0        | 0.001    | 0.001      | 0.001    | 0.006    | 0                        |       |
| 23 | XM_711668           | 0.007      | 0.008       | 0.033       | 0.012       | 0.019       | 0.028      | 0.003      | 0.001      | 0.001      | 0.001      | 0.008      | 0.007    | 0.006    | 0.007    | 0.001    | 0        | 0.001    | 0.001      | 0.001    | 0.006    | 0                        |       |