

Supplementary Materials:

Figure S1. The nucleotide, deduced amino acid, and the promoter sequences of *cyp19a1a* (**a-b**) and *cyp19a1b* (**c-d**). (**a, c**) The nucleotide and amino acid sequences are numbered on the left. The start codon and stop codon are in red bold, the mRNA instability (ATTTA) is displayed as wavy line, and poly-adenylation signal sequence (AATAA) is underlined with underscore. The signal peptide is highlighted with blue background, and the conserved P450 domain are showed with gray background; (**b, d**) The putative TSS is marked in bold, and designated as +1, the putative TFBS are highlighted with different symbols, and the putative CpG islands are yellow-shaded and the CpG sites are in the box.

Figure S2. The alignment of amino acid sequences of *cyp19a1a* and *cyp19a1b* in *C. maculata*. The dark shade indicates 100% identity.

Figure S3. The alignments of amino acid sequences of aromatase protein sequences from 26 species. The dark shade indicates 100% identity.

Figure S4. The relationship between the CpG methylation levels and the expression levels of aromatase gene in the gonads of XX-F and XY-M individuals at different developmental stages. (**a**) *cyp19a1a* in ovary; (**b**) *cyp19a1b* in ovary; (**c**) *cyp19a1a* in testis; (**d**) *cyp19a1b* in testis.

Figure S1

(a)

1 M D L I P A C E R A M T
1 attgcttgttgggtctctgaagtcgtgtgcagattgtgtcaagtcctccctcct**ATGG**GATCTGATCCTTGTGTGAACGGGCCATGACT
13 P V G L K A I E A D L V S V S L N T T T V E S P G I S I A T
91 CCTGTAGGTTTGAAGCTATAGAAGCAGACCTGGTCTCTGTTTCTTTGAACACCACTACGGTTGAGTCACCAAGGCATTTCCATAGCAACC
43 R T L I L L V C L L L F A W S H T D K N N V P G P S F C L G
181 CGGACACTGATACTGCTTGTGTGTCTGCTGCTGCTTCGCCCTGGAGCCACACAGACAAGAACAATGTTCCAGGTCCTTCCTTTTGTCTGGGT
73 L G P I L S Y V R F M W T G I G T A S N Y Y N N K Y G D I V
271 TTGGGGCCAATTCTGTCATATGTGAGATTCATGTGGACTGGTATAGGCACCTGCCAGCACTACTACAACAACAAGTACGGAGATATTGTC
103 R V W I N G E E T L V I S R S S A V H H V L K N G Q Y T C R
361 AGAGTCTGGATCAATGGAGAGGAGACCCTCGTAATCAGCAGATCGTCAGCAGTGCACCATGTACTGAAAAATGGACAATACACTTGCCGT
133 F G S K Q G L S C I G M N E R G I I F N N N V V L W K K I R
451 TTTGGGAGCAAAACAGGGACTCAGCTGCATTGGCATGAATGAGAGAGGCATCATATTTAACAACAATGTAGTCTGTGTGAAAAAATACGC
163 T Y F T K A L T G P G L Q Q T V E V C V S S M Q T H L D K L
541 ACCTATTACCAAGACATCAGAGTCCGGGGTGCAGCAGACAGTGAAGTCTGTGCTCCTCCATGCAAGTCCAGGAGAGTCCAGGAGT
193 G S L N H A D V L S L R C T V I D I S N R L F L G V P V D
631 GGCAGTTTGAATCATGCGGATGTCTTAGTTTGTGCGCTGCACCGTGATCGACATCTCCAACAGACTCTTCTGGGCGTACCTGTCTGAT
223 E K E L L M K I Q K Y F E T W Q N V L I K P D I Y F K C D W
721 GAGAAAGAGTGTCTGATGAAGATTGAGAAGTATTTTGAACATGGCAGAAATGTGTGATCAAACAGACATCTACTCAAGTGTGACTGG
253 I Q Q R H R K T A Q E L Q D A I E S L V E Q K R R E M G Q A
811 ATTCACAAAGGCAGAGAACTGCCAGGAGCTGCAGGATGCCATAGAGAGCCTGTAGAACAGAGAAGAGAAATGGGGCAGGCT
283 D K L D N I N F T A E L I F A Q N H S E L S A E D V R Q C V
901 GATAAACTGGACAACATCAACTTTACCGCTGAGCTGATATTTGCACAGAACCACAGCAGCTGTCTGCTGAGGATGTGAGGCAGTGTGTG
313 L E M V I A A P D T L S I S L Y F M L L L L K Q N P D V E I
991 TTGGAGATGGTGATTGCAGCACCAGGACACTCTGTCCATCAGCCTCTATTTTATGCTGCTGCTTCTCAAACAGAATCCAGATGTGGAGTTG
343 Q L L Q E I D T V V G Q R Q L Q N E H L Q R L Q M L E S F I
1081 CAGTTGTCACAGGATAGACACAGTTGTAGGTCAGAGACAACCTTCAGAGGTTGCAGATGCTGGAGAGCTTCATC
373 N E C L R F H P V V D I T M R R A L S D D I I D G Y R V P K
1171 AATGAATGCTTGCCTTCCACCCTGTGGTGGACATCACCATGCGCCGAGCCCTGTCTGATGACATCATAGATGGCTACAGGTTCCAAAA
403 G T N I I L N T G R M H R T E F F L K Q N E F S L E N F E K
1261 GGCACAAATATCATCTCAATACTGGCCGAATGCACCGGACAGAGTTTTTCTCAACAAAAATGAATTCAGTCTGGAGAAGTTTGAAAAA
433 N T P R R Y F Q P F G S G P R S C V G K H I A M V M M K S I
1351 AATACCCCTCGTCTGTTACTTCCAGCCATTGCGTTCCAGGCCCGGATCCTGTGTTGGCAAGCATATGCCATGCTGATGAATTCGATC
463 L V T L L S R Y S V C L H K G L T L D C L P Q T N N L S Q Q
1441 CTGGTGACATTGCTCTCCCGGTACTCAGTTTGCCTCCATAAGGGTTTGACCTGGACTGCCTCCACAGACAAACACCTCTCCAGCAG
493 P V E H H Q E A E H L S M R F L P R Q R G S E S T *
1531 CCTGTAGAGCATCACCAGGAGGCTGAACACCTCAGCATGAGATTCTTACCAGACAGAGAGGTAGCGAGTCCACA**TAG**tgagatactgac
1621 cttatgttgcattctatacatattatgcaaaggacatccattataatctccattactacatctttcattattgttaagctaaactaaagttt
1711 catatttttgtgtattcaataaataatgtgtacgatgaaatgtacgtttcagacatcctaataactaaagcaaatgttaattttgttgcca
1801 atattgtgttttgttgccttcatttggatgttttgaaatgtaatggtttcagactaagaacatcttttattttacatgtaagaactgggt
1891 atcagtgtaaaaatccctttttctgtttatattttaaactggtttttcattttttaaacaatgttcaaattatatgcttttttcattaccatt
1981 agcagcatgaaagacataaataaagtgtattttttataaataaaagcgaaaaataaaaaaaaaaaaaaaaaaaaaa

(b)

-1019 tgcgcacagtcaggcatttcaccagtgacattcttggattcgaactgtggcggtgagtgattcacagagtttccctttatacagaattta
DMRT
-909 ttaataaatggaaacaaggcagagcacagtgagcactctgtcacatacaaaaaatagactaaacacaccttaggagtttggataaaat
SOX
-819 gtgtctgtcacacaaaagggtccacagatgaaatctgaaattatataatattacattttatataataatagaaaaatagtttcaatgggtct
GATA
-709 ttcaaatatcaactgctcttcaggtaatgtgtggtgttttagtggtacagtacagtcaccacacaccacagagaaaaacgcaacggctgcca
-619 ctgatgtgcatacagatatttttggctcgtaaaattttgttgaggaaatctaaagatggcagtagctctgctctccatctactggttag
SOX
-509 tctgatggaggaaattcaaaatgatcatcaaagtaaacttttaaagggttgaatgggtgttgcgtgatcaattattttaaaaatacag
DMRT
-419 caaaaaatgttcactttgtcttgttttatataaagaaaaatgaaggaaaaacaggagtgtaagaatggagaatttaattctatttggacaga
GATA
-309 taaagctaataaataaataaacaacaatttttcccttgctttcacagaccaggtgctctattgtagagatttccagcgcagttcttttgg
-219 atgttgaaaggaggatttatacttgctcatatcaccaaaacgtgcaatacactaaattaaatcccatctccttcaagagtgaggcaca
CRE SOX
-129 acctaactctcaagggttacaagagtattgttttacaattttcccccctctgttggcttttgcctttaccctgacctggctcgttaaccagc
SOX FOXL
-39 gctgactgcctataaagagaaaaagcctcactgcatcgggttgattgcttgttgggtctctgaagtccgtgtgcagattgtgtcaagtctcc
TATA Box +1
51 ctccct**ATGG**GATCTGATCTCTGCTTGTGAACGGGCCATGACTCCTGTAGGTTTGAAGCTATAGAAGCAGACCTGGTCTCTGTTTCTTTG
141 AACACCACTA**CG**GTTGAGTCACCAAGGCATTTCCATAGCAACC**CG**GACACTGATACTGCTGTTTGTCTGCTGCTGTT**CG**CCTGGAGCCAC
231 ACAGACAAGAAACAATGTTCAGgtaggatttagtggaacatttgagattttttcttctgtgttgatgccaagtattttactattttatgt
SOX SOX

(c)

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1 cttaaccaaggatttataaaatcgtgaatcagtgcaatttcttttagttggagaataccgatcatctttacaacaagtggaggaagcgctcg
91 tgttcttctcaaactgcgccctaagctgtcaggagtagtaacacacagaagcaagggttgactggttgactggtgagagacacttt
181 atgagcacaagcaaaaggttcatttacagacagacagcaggagtagcgagctggctcaggtgtgtgtgtactcggctggagtataaaggg
1 M V G D T V T A I L L L L L L L L L L L L
271 aatcctgtccctggggaagcacaccatcggtcccATGGTGGGTGATACAGTCACTGCGATTCTGCTTCTTCTGCTGCTGCTGCTGCTGCT
20 L F T T W S R R N R S H I P G P R F L A G L G P Y L S Y A R
361 GCTGTTTACCACCTGGAGCAGAAGAAACCGCTCACATATACCAGGTCTCGTTTCTAGCAGGACTGGTCTTATCTCTCCTATGCCAG
50 F I W T G I G T A S N Y Y S N K Y G S V V R V W I N G E E T
451 ATTTATCTGGACTGGGATTGGAACAGCAAGCAACTACTACAGCAACAAATATGGCAGTGTGTCCGGGTCTGGATTAATGGCGAGGAGAC
80 L I L S R S S A V Y H V L R S A Q Y T A R F G S K K G L E C
541 CCTAATTCTGAGCAGGTCTCTGCACTGTACCATTGTTTGGAGGAGTCCCACTACACGGCCAGATTGGGAGTAAAAAGGGGCTGGAGTG
110 I G M E G A R G I I F N S D V P L W K K V R A Y F S K A L T T G
631 TATTGGGATGGAAGGAAGGGGTATCATTTTCAACAGTGATGTTTCTCTATGGAAAAAGTCAGAGCATATTCTCCAAAGCTCTGACAGG
140 P G L Q R T V A I C V S S T A K H L D N L Q E M T D S S G H
721 CCCCCCTCCAGAGAACAGTGGCAATTTGTGTGAGCTCCACAGCCAAGCATCTGGACAATCTGCAGGAGATGACCGACTCGTCTGGACA
170 V D T L N L L R A I V V D I S N R L F L G V P L N E K D F L
811 TGTGGACACTCTCAATCTGCTCAGAGCCATAGTGGTGGACATCTCCAACAGGCTTTTCTTGGAGTGCCGCTAAACGAGAAAGACTTTCT
200 T K I Q N Y F D T W Q A V L I K P D I F F K I G W L Y N K H
901 GACGAAAATCCAAAACACTTTGACACCTGGCAAGCAGTTCTAATAAAGCCTGATATATTCTTTAAGATTGGATGGCTGTACAACAAGCA
230 K R A A Q E L Q D A M E S L L E I K R Q V I N E S E K L D D
991 CAAAAGAGCAGCCCAAGAGCTGCAAGATGCGATGGAGAGCCTTCTAGAAATCAAAGACAAGTTATTAATGAATCTGAAAAGCTGGATGA
260 N L D F A T E L I L A Q N H G E L S A D N V R Q C V L E M V
1081 TAATCTTGACTTTGCAACAGAGCTCATCTTGGCCAGAACCCAGGAGAGCTTTCAGCAGATAACGTCAGGCAGTGTGTGCTGGAGATGGT
290 I A A P D T L S I S L F F M L M L L K Q N P D V E L R I V E
1171 GATCGCAGACCTGACACTTTTCCATCAGCCTTTTCTTATGTTGATGTGCTGAAACAAAACCCAGATGTAGAACTGAGGATAGTGGA
320 E M N T V L S E K A V E N I D Y Q V L K V L E I F I N E C L
1261 GGAGATGAACACTGTCTTGAGTGAGAAAGCTGTTGAAAACATTGATTATCAAGTCTTGAAAGTGCTGGAGATTTTCATCAATGAGTGT
350 R F H P V V D F T M R K A L E D D N I E G T K I R K G T N I
1351 GAGATTTCATCCTGTGGTCGATTTCACAATGCGAAAAGCTCTGGAGGATGACAACATCGAAGGCACAAAAATTAGAAAAGGAACCAACAT
380 I L N I G L M H K T E F F P K P K D F N L M N F D K T V P S
1441 CATTCTCAACATTGGTCTCATGCTAAGACTGAGTCTTCCCAAAACAAAAGATTCAACCTGATGAACCTTGACAAAACAGTGCCACAG
410 R F F Q P F G C G P R S C V G K N I A M V M M K A I L V T L
1531 TCGTTTCTTCCAGCCCTTCGGCTGTGGCCTCGTTTCTGTGTGGGCAAAACATCGCCATGGTGATGATGAAGGCCATCTTGGTCACTCT
440 L S R Y T V C P R Q G C T V N N I R Q T N N L S Q Q P V E D
1621 GTTGTCCCGTTACACAGTGTGTCTCGTCAAGGCTGCACTGTCAACAACATCCGGCAGACCAACAACCTGTGCGCAGCAGCCTGTGGAGGA
470 E H S I A M C F I P R T T Q H S Q L *
1711 CGAGCACAGCCTGGCCATGTGCTTCATCCCTCGGACAACACAACACAGTCACTCTGAaacacagggatgctgttacacatcggtgaaa
1801 acgctagtattatataagtgtagttaggcctgctgggctggtataataaatgcttcaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa
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(d)

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-1054 actatgaatagaaaaactgctttttttgttcgttttgaatctgttttggtggtttcaaagcaatgttatctggcctgttcagtgttgctg
SOX GATA
-964 tcatgtaattggtactttagtagcccgagtggtcagtggtctaaagcaaccagtatagtgaaggcttaaccaaggatttataaatacgtgagtc
-874 agtgcaatttcttttagttggagaataacgatcatctttacaacaagtgagggaagcgtcgtgttcttctcaaactgcctcctaagctgtc
-784 aggagtagtaacacacagaagcagtaagttatccttttggtaatttggttaaaacaaatttaacttagaatttaattggaagtaaaaaat
-694 ataagataactactaaaatttcagtttcagttttctgtcacttactctcaatcattcatatgtgacatttttatatttctaataatatt
SOX
-604 caggaattcagttttgactcagagtttgcacaaatttttacaaaattctaattgtgggcggcaacaatttgtgctttgcaaaatgatatttc
SOX
-514 agtttttacattgagaaagggatctcttttaaacttgaaattcatacgaacacaccttaatgcagtttcttaaagaagctcattactgtaaa
-424 ttgtcaagggaacattaaactttctcgaccactgtgcacaatttgaaaaatgatgaaaaatctcattgttttttactaaaattaaagt
SOX
-344 ttgatgtgaaacactaatcacacgtcagagcattatgtgggtatatttgttcgtgcaggtgtaagtacaggctggtgtgtgttacatt
CRE
-244 ccagcattgaagagtattatttagcagtaaatagaaaggctgtccacagattaagggttcttctgtgtgtgcttgaatgaatgaatgaatgaa
-154 tgaatgagagggggttgactggtgtactggtgagagacactttatgagcacaagcaagggttcatttacagacagacagcaggagtag
-64 cgagctggctcaggtgtgtgtgtactcggctggtgttataaagggaatcctgtccctggggaagcacaccatcggtcccATGGTGGTGA
TATA Box +1
26 TACAGTCACTGCGATTCTGCTTCT
DMRT
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Figure S2

1 10 20 30 40 50 60 70
 Cyp19a1a MDLIPACERAMTPVGLKAIEADLVSVSLNTTTVESPGISIASTRLLILLVCLLLFAWSHTDKNNVPGPSFC
 Cyp19a1bMVGDTVTAIL.....LLLLLLLLFTTWSRRNRSHIPGPRFL
 80 90 100 110 120 130 140
 Cyp19a1a LGLGLPILSYVRFMTWTGIGTASNYYNKKYGDIVRVWINGEETLVISSSSAVHVLKNGQYTCRFGSKQGLS
 Cyp19a1b AGLGLPILSYARFIWTGIGTASNYYSNKYGSVVRVWINGEETLILSSSSAVHVLRSQAQYTCRFGSKKGL
 150 160 170 180 190 200
 Cyp19a1a CIGMNERGIIFNNNVVLWKKIRTYFTKALTGPGLOQTVEVCVSSMQTHLDDKLGSLN...HADVLSLLRC
 Cyp19a1b CIGMEGRGIIFNSDVPVLWKKVRAYFSKALTGPGLOQRTVAICVSSSTAKHLDNLQEMTDSSGHVDLTNLLRA
 210 220 230 240 250 260 270
 Cyp19a1a TVVDISNRLFLGVPVDEKELLMKIQKYFETWQNVLIKPDIIYFKCDWIIQQRHRKTAQELQDAIESLVEQKR
 Cyp19a1b TVVDISNRLFLGVPVLNEKDFLTKIQNYFETWQAVLIKPDIFFKIGWLYNKHKRAAQELQDAMESLLEIKR
 280 290 300 310 320 330 340
 Cyp19a1a REMQQADKLDN.INFTAEELIFAQNHSELSAEDVRQCVLEMVIAAPDTLSSISLYFMLLLKQNPDELQLL
 Cyp19a1b QVINESEKLDNLDLFATEELILAQNHSELSADNVRQCVLEMVIAAPDTLSSISLYFMLLLKQNPDELRI
 350 360 370 380 390 400 410
 Cyp19a1a QEDTIVVGQRQLQNEHLQRLQMLESFINECLRFHPVVDITMRRALSDDIIDGYRVPKGTNIILNTGRMHR
 Cyp19a1b EEMNTVLSEKAVERNIDYQVLKVLEIFINECLRFHPVVDFTMRKALEDDNIEGTKIRKGTNIILNIGLMHK
 420 430 440 450 460 470 480
 Cyp19a1a TEFELKQNEFSELENFEKNTPRRYFQPFQSGPRSCVGVKHIAMVMMKSIILVTLLSRYSVCLHKGILTLDCLPQ
 Cyp19a1b TEFELPKPKDFNLNMFDKTVPSPRFQPFQSGPRSCVGVKNIAMVMMKSIILVTLLSRYTVCPRQGCTVNNIRQ
 490 500 510
 Cyp19a1a TNNLSQOPVEHHQEAELLSMRFLLPRQSGEST Identity
 Cyp19a1b TNNLSQOPVEDEHS...LAMCFIPRTTOHSOL 57.5%

Figure S3

1 10 20 30 40 50 60 70 80

CmCyp19a1a .MDLIP.ACERAMPVPVGLKAIADL.VSVSLNTTIVTESPGISIAATR.LTLLV.LLLFAWSHTDKN.VVPG.PS.FC.LGLGPILSYVRFIWMIGT
 McCyp19a1a .MDLIP.ACERAMPVPVGLDAAADL.DVSSNNTAVGSAAGISVIAATR.ALMLLV.LLLVWNHTEKK.VVPG.PS.FC.LGLGPILSYVRFIWMIGT
 LcCyp19a1a .MDLIS.ACERAMPNPVGLDAMVTEL.VSPMPNATAVGSVPGISIAATR.LTLLV.LLLVWASHTDKK.VVPG.PS.FC.LGLGPILSYVRFIWMIGT
 OcCyp19a1a .MDLIS.ACEQAMPNPVGLDAMVARS.LCDLCKHPIDG..ISMAATR.LTLLV.LLLVWASHTDKK.VVPG.PS.FC.LGLGPILSYVRFIWMIGT
 OlCyp19a1a .MDLIP.ACDRMTSSS...CLVLAEL.VSIAPNTTVGLSPGIPMAATR.SLTLLV.LLLVWWSHSEKK.TVPG.PS.FC.LGLGPILSYVRFIWMIGT
 TrCyp19a1a .MDLI...CDWAMAAGVLADEVL...VSVSPNATEASPSSGSAATR.ALITLL.LLLVWWSHTEKK.VVPG.PS.FC.LGLGPILSYVRFIWMIGT
 SsCyp19a1a .MDLLSPVCGRAMEAVCLDTV.IADLLVSELNRNATASQGVNLCATG.SLIMLL.LLLLAWRHTDKN.VVPG.PF.FC.LGVGPILSYVRFIWMIGT
 CaCyp19a1a .MKQVHLGEAVLELLMGQAHNSSYGAGDNVSGAMAT.LL.LLL.LLLLAIRHHWTEKDHVPG.PF.FC.LGLGPILSYVRFIWMIGT
 CcCyp19a1a MAGELLPCPG..MKPVLHSEAPLDLLMGQAHNSYGAGDNVSGAMAT.LL.LLL.LLLLAIRHHWTEKDHVPG.PF.FC.LGLGPILSYVRFIWMIGT
 DrCyp19a1a MAGDLLQPCG..MKPVLHSEAPLDLLRGHANTGTGAGDNACGATAT.LL.LLL.LLLLAIRHHWTEKDHVPG.PF.FC.LGLGPILSYVRFIWMIGT
 IpCyp19a1a MAAHVFPMCERTKRPVHFSEITVMEILLREARNGTDPRYENPRGIT.L.LLL.LLLVLLVWNHREKKCSIPG.PS.FC.LGLGPILSYVRFIWMIGT
 HfCyp19a1a MAAHIANKCECRKPLFSEQVMEILLREHRNGTNPQENPTGIT..LL.LLL.LLLVLLVWNHREKKCSIPG.PS.FC.LGLGPILSYVRFIWMIGT
 OlCyp19a1b MIQOEOTLDE...LFHS.VSQVITFL.LL.LLL.LLLFINTWRQSHLSIPG.PF.FC.LGLGPILSYVRFIWMIGT
 OcCyp19a1b MLPVEELTAGP...MVADRASEVTAIVLL.LL.LLL.LLLFINTWRQSHLSIPG.PF.FC.LGLGPILSYVRFIWMIGT
 CmCyp19a1b MYGDTVT..AILLL.LLL.LLLFINTWRQSHLSIPG.PF.FC.LGLGPILSYVRFIWMIGT
 McCyp19a1b MKRMLPLETLTISP...MVDDTISP.LL.LLL.LLLFINTWRQSHLSIPG.PF.FC.LGLGPILSYVRFIWMIGT
 LcCyp19a1b MLVIFKTSRGSTGFLKLHNSLSGVGKIDTR.PF.FC.LGLGPILSYVRFIWMIGT
 TrCyp19a1b MKPKETLNLITASGPTPLPLPLMMMLLMMMLLFTWNRQSHVPG.PF.FC.LGLGPILSYVRFIWMIGT
 SsCyp19a1b MATS...IVDDTSMSEALL.LL.LLL.LLLITWCLNTSHIPG.PF.FC.LGLGPILSYVRFIWMIGT
 CaCyp19a1b MEEVLKGTVNFAA...TVQVTLMALTGT.LL.LLL.LLLHRIFTAKNWRNQSIPG.PG.WLGLGPIMSYVRFIWMIGT
 CcCyp19a1b MMEQVVKGPVNIAA...AVQVTLMALTGT.LL.LLL.LLLHRIFTAKNWRNQSIPG.PG.WLGLGPIMSYVRFIWMIGT
 DrCyp19a1b MMEHVVKDANVIGA...VVGQTLTLTGT.LL.LLL.LLLHRIFTAKNWRNQSIPG.PG.WLGLGPIMSYVRFIWMIGT
 IpCyp19a1b MELQNVSDVMA...VMEGRGLCVISALFL.LL.LLL.LLLTAYNRRNKSLTPG.PY.WLGLGPILSYVRFIWMIGT
 HfCyp19a1b MELQNVSDVMA...ALDATGFKVGSALLFL.LL.LLL.LLLTAYNRRNKSLTPG.PY.WLGLGPILSYVRFIWMIGT
 AbCyp19a1 MKQVLEERISKMLVPVHHNITDIVPEMSSGTTA..ILSL.LL.LLLVWLNCKAKASIPG.PF.FC.MGIGIALLSYVRFIWMIGT
 LoCyp19a1 MKQVPLDNVVMKMQNPVSHNITDIVPEMSSGATA..IL.LL.LL.LLLVWLNCKAKASIPG.PF.FC.MGIGIALLSYVRFIWMIGT
 BtCyp19a1 MVLEMLNPIHYNITSVPEAMPAATMPV.LL.LL.LLLVWLNCKAKASIPG.PF.FC.MGIGIALLSYVRFIWMIGT
 HsCyp19a1 MLLEVLNPIHYNITSVPEAMPAATMPV.LL.LL.LLLVWLNCKAKASIPG.PF.FC.MGIGIALLSYVRFIWMIGT
 MmCyp19a1 MFLEMLNPIHYNITSVPEAMPAATMPV.LL.LL.LLLVWLNCKAKASIPG.PF.FC.MGIGIALLSYVRFIWMIGT
 GgCyp19a1 MIPETLNLPLNY.FTSLVPDLMPVATVPV.II.LL.LL.LLLVWLNCKAKASIPG.PF.FC.MGIGIALLSYVRFIWMIGT
 NmCyp19a1 MVLETLNLMHYNITSVPEAMPAATMPV.LL.LL.LLLVWLNCKAKASIPG.PF.FC.MGIGIALLSYVRFIWMIGT
 ShCyp19a1 MVLETLNLMHYNITSVPEAMPAATMPV.LL.LL.LLLVWLNCKAKASIPG.PF.FC.MGIGIALLSYVRFIWMIGT
 XtCyp19a1 MEALNPVQYNSTEAPVTLATP.LL.LL.LL.LLLVWLNCKAKASIPG.PF.FC.MGIGIALLSYVRFIWMIGT
 XlCyp19a1 MEALNPVQYNSTEAPVTLATP.LL.LL.LL.LLLVWLNCKAKASIPG.PF.FC.MGIGIALLSYVRFIWMIGT
 CcCyp19a1 MRQFSLGDMVLQMSKAAQNLTITGVPEMSSGATVP.LL.LL.LL.LLLVWLNCKAKASIPG.PF.FC.MGIGIALLSYVRFIWMIGT
 HsaCyp19a1 MEMKEFAPDNKLQMSKAAQNLTITGVPEMSSGATVP.LL.LL.LL.LLLVWLNCKAKASIPG.PF.FC.MGIGIALLSYVRFIWMIGT
 CmCyp19a1

90 100 110 120 130 140 150 160 170 180

CmCyp19a1a ASNYYN.NK.YGDI.VR.VWINGEET.LL.VISRSSAVHVLKNGHYV.SRFSGKQGLSCIGMNER.GIIFNNNVVLWKKIRTYFTKATGPGLOQTVEVCVS
 McCyp19a1a ASNYYN.NK.YGDI.VR.VWINGEET.LL.VISRSSAVHVLKNGHYV.SRFSGKQGLSCIGMNER.GIIFNNNVVLWKKIRTYFTKATGPGLOQTVEVCVS
 LcCyp19a1a ASNYYN.NK.YGDI.VR.VWINGEET.LL.VISRSSAVHVLKNGHYV.SRFSGKQGLSCIGMNER.GIIFNNNVVLWKKIRTYFTKATGPGLOQTVEVCVS
 OcCyp19a1a ASNYYN.NK.YGDI.VR.VWINGEET.LL.VISRSSAVHVLKNGHYV.SRFSGKQGLSCIGMNER.GIIFNNNVVLWKKIRTYFTKATGPGLOQTVEVCVS
 OlCyp19a1a ASNYYN.NK.YGDI.VR.VWINGEET.LL.VISRSSAVHVLKNGHYV.SRFSGKQGLSCIGMNER.GIIFNNNVVLWKKIRTYFTKATGPGLOQTVEVCVS
 TrCyp19a1a ASNYYN.NK.YGDI.VR.VWINGEET.LL.VISRSSAVHVLKNGHYV.SRFSGKQGLSCIGMNER.GIIFNNNVVLWKKIRTYFTKATGPGLOQTVEVCVS
 SsCyp19a1a ASNYYN.NK.YGDI.VR.VWINGEET.LL.VISRSSAVHVLKNGHYV.SRFSGKQGLSCIGMNER.GIIFNNNVVLWKKIRTYFTKATGPGLOQTVEVCVS
 CaCyp19a1a ASNYYN.NK.YGDI.VR.VWINGEET.LL.VISRSSAVHVLKNGHYV.SRFSGKQGLSCIGMNER.GIIFNNNVVLWKKIRTYFTKATGPGLOQTVEVCVS
 CcCyp19a1a ASNYYN.NK.YGDI.VR.VWINGEET.LL.VISRSSAVHVLKNGHYV.SRFSGKQGLSCIGMNER.GIIFNNNVVLWKKIRTYFTKATGPGLOQTVEVCVS
 DrCyp19a1a ASNYYN.NK.YGDI.VR.VWINGEET.LL.VISRSSAVHVLKNGHYV.SRFSGKQGLSCIGMNER.GIIFNNNVVLWKKIRTYFTKATGPGLOQTVEVCVS
 IpCyp19a1a ASNYYN.NK.YGDI.VR.VWINGEET.LL.VISRSSAVHVLKNGHYV.SRFSGKQGLSCIGMNER.GIIFNNNVVLWKKIRTYFTKATGPGLOQTVEVCVS
 HfCyp19a1a ASNYYN.NK.YGDI.VR.VWINGEET.LL.VISRSSAVHVLKNGHYV.SRFSGKQGLSCIGMNER.GIIFNNNVVLWKKIRTYFTKATGPGLOQTVEVCVS
 OlCyp19a1b ASNYYN.NK.YGDI.VR.VWINGEET.LL.VISRSSAVHVLKNGHYV.SRFSGKQGLSCIGMNER.GIIFNNNVVLWKKIRTYFTKATGPGLOQTVEVCVS
 CmCyp19a1b ASNYYN.NK.YGDI.VR.VWINGEET.LL.VISRSSAVHVLKNGHYV.SRFSGKQGLSCIGMNER.GIIFNNNVVLWKKIRTYFTKATGPGLOQTVEVCVS
 LcCyp19a1b ASNYYN.NK.YGDI.VR.VWINGEET.LL.VISRSSAVHVLKNGHYV.SRFSGKQGLSCIGMNER.GIIFNNNVVLWKKIRTYFTKATGPGLOQTVEVCVS
 SsCyp19a1b ASNYYN.NK.YGDI.VR.VWINGEET.LL.VISRSSAVHVLKNGHYV.SRFSGKQGLSCIGMNER.GIIFNNNVVLWKKIRTYFTKATGPGLOQTVEVCVS
 TrCyp19a1b ASNYYN.NK.YGDI.VR.VWINGEET.LL.VISRSSAVHVLKNGHYV.SRFSGKQGLSCIGMNER.GIIFNNNVVLWKKIRTYFTKATGPGLOQTVEVCVS
 CaCyp19a1b ASNYYN.NK.YGDI.VR.VWINGEET.LL.VISRSSAVHVLKNGHYV.SRFSGKQGLSCIGMNER.GIIFNNNVVLWKKIRTYFTKATGPGLOQTVEVCVS
 CcCyp19a1b ASNYYN.NK.YGDI.VR.VWINGEET.LL.VISRSSAVHVLKNGHYV.SRFSGKQGLSCIGMNER.GIIFNNNVVLWKKIRTYFTKATGPGLOQTVEVCVS
 DrCyp19a1b ASNYYN.NK.YGDI.VR.VWINGEET.LL.VISRSSAVHVLKNGHYV.SRFSGKQGLSCIGMNER.GIIFNNNVVLWKKIRTYFTKATGPGLOQTVEVCVS
 IpCyp19a1b ASNYYN.NK.YGDI.VR.VWINGEET.LL.VISRSSAVHVLKNGHYV.SRFSGKQGLSCIGMNER.GIIFNNNVVLWKKIRTYFTKATGPGLOQTVEVCVS
 HfCyp19a1b ASNYYN.NK.YGDI.VR.VWINGEET.LL.VISRSSAVHVLKNGHYV.SRFSGKQGLSCIGMNER.GIIFNNNVVLWKKIRTYFTKATGPGLOQTVEVCVS
 OlCyp19a1b ASNYYN.NK.YGDI.VR.VWINGEET.LL.VISRSSAVHVLKNGHYV.SRFSGKQGLSCIGMNER.GIIFNNNVVLWKKIRTYFTKATGPGLOQTVEVCVS
 CmCyp19a1b ASNYYN.NK.YGDI.VR.VWINGEET.LL.VISRSSAVHVLKNGHYV.SRFSGKQGLSCIGMNER.GIIFNNNVVLWKKIRTYFTKATGPGLOQTVEVCVS
 LcCyp19a1b ASNYYN.NK.YGDI.VR.VWINGEET.LL.VISRSSAVHVLKNGHYV.SRFSGKQGLSCIGMNER.GIIFNNNVVLWKKIRTYFTKATGPGLOQTVEVCVS
 SsCyp19a1b ASNYYN.NK.YGDI.VR.VWINGEET.LL.VISRSSAVHVLKNGHYV.SRFSGKQGLSCIGMNER.GIIFNNNVVLWKKIRTYFTKATGPGLOQTVEVCVS
 TrCyp

Figure S4

