```
    M  S  L  A  G  E  V  C  L  I  T  G  A  F  G  F  L  G  Q  R  I  I  Q  L  L  L  Q  E  D  E  L  A  E  I  R  L  L  D  R  H
I ATGTCTCTTGCTGGGGAAGTTTGTCTCATTACTGGAGCGTTTGGATTCCTGGGACAAAGAATTATCCAGCTTCTGCTGCAGGAGGATGAGCTTGCAGAGATCAGGCTCCTTGACAGGCAC120
II
III

    V  R  P  D  I  L  E  S  L  E  E  F  R  G  Q  T  K  L  T  V  F  E  G  D  I  R  D  A  E  L  L  K  K  A  C  Q  H  V  S  L
 GTCAGGCCTGATATACTTGAATCTTTGGAAGAGTTTCGTGGCCAAACCAAGCTGACTGTGTTTGAGGGGGATATCAGAGATGCAGAGCTCCTCAAGAAAGCATGCCAGCATGTCAGCCTT240
I
II
III
    V  I  H  T  A  S  L  I  D  V  I  G  A  I  D  E  R  K  L  K  E  V  N  V  K  G  T  Q  F  L  L  E  A  C  I  Q  E  N  V  K
I GTGATCCACACAGCTTCGCTCATTGATGTCATAGGAGCTATAGACGAACGGAAACTAAAAGAAGTGAATGTAAAAGGTACCCAGTTCTTGCTGGAAGCCTGTATTCAAGAGAATGTGAAA360
II
III
    S  F  I  Y  T  S  S  I  E  V  A  G  P  N  T  R  G  D  P  V  I  N  G  N  E  D  T  V  Y  S  C  S  L  K  F  P  Y  S  K  T
I TCCTTCATCTACACCAGCAGCATTGAGGTGGCAGGTCCAAACACCCGGGGAGACCCTGTGATCAATGGGAATGAAGACACAGTTTATTCATGCTCCTTGAAATTTCCCTACAGCAAGACC480
II
III

    K  F  Q  A  E  Q  L  V  L  Q  V  N  G  E  V  L  R  S  Q  D  K  M  V  T  C  A  L  R  P  M  Y  I  Y  G  E  G  C  N  F  L
I AAGTTCCAAGCTGAACAGCTGGTTCTACAGGTCAATGGGGAGGTTCTCAGAAGTCAAGACAAAATGGTGACATGTGCCCTGCGGCCCATGTACATCTATGGGGAAGGCTGTAACTTCCTT600
II
III

    L  G  H  M  D  D  G  I  R  N  G  D  I  L  L  R  S  S  K  K  E  S  V  V  N  P  V  Y  V  G  N  V  A  W  A  H  I  L  A  A
I TTGGGCCACATGGATGACGGAATCAGAAACGGGGACATATTATTGCGTAGCTCTAAAAAGGAGTCTGTTGTGAACCCAGTGTACGTAGGCAATGTAGCCTGGGCCCATATTTTAGCAGCC720
II
III                                                G  G              C

    K  A  M  R  D  P  K  K  A  A  L  I  G  G  R  F  Y  F  I  S  D  D  T  P  H  V  S  Y  S  D  F  N  H  V  V  L  K  P  L  G
I AAAGCTATGAGGGATCCCAAGAAAGCTGCCTTGATTGGTGGTAGGTTCTACTTCATCTCAGATGACACTCCACATGTAAGCTACTCAGATTTCAACCACATGGTGTTAAAGCCATTGGGG840
II
III                                                                                                                G  [M]

    F  G  I  Q  E  R  L  A  L  P  L  P  L  L  L  F  L  T  L  L  L  E  M  V  Q  V  F  L  K  P  F  V  K  Y  T  P  R  M  N  R
I TTCGGGATTCAGGAGAGGCTCGCTCTCCCTCTGCCACTGCTGTTGTTCCTCACACTCCTTCTGGAGATGGTGCAGGTCTTTCTGAAACCTTTTGTGAAGTACACTCCCAGAATGAATCGC960
II                                                      G  [T]
III

    Q  L  L  I  M  L  N  T  Q  F  S  F  T  Y  K  K  A  Q  R  D  F  G  Y  T  P  K  Y  S  W  E  D  A  R  T  I  T  T  T  W  L
I CAGCTTCTCATCATGCTCAACACGCAGTTTAGCTTCACCTATAAAAAGGCCCAAAGGGATTTTGGTTACACTCCAAAGTACAGCTGGGAGGATGCTAGGACCATTACTACCACTTGGCTT1080
II
III                                                                                                                    C

    E  S  V  L  P  Q  H  R  A  L  L  K  T  H  *
I GAATCTGTTTTGCCACAGCACCGTGCACTTCTGAAAACACATTAA  1125
II
III
```

Supplemental Figure S1. Nucleotide and amino acid sequences of Amur sturgeon *hsd3b* type I–III. Nucleotide variations between these types and corresponding amino acid alterations are indicated.

```
     M   E   W   V   L   G   T   A   L   V   L   T   V   A   L   A   V   L   F   V   K   G   R   F   E   R   R   L   K   R   S   N   L   P   N   S   L   P   V   F
I ATGGAGTGGGTACTTGGTACTGCTTTGGTTCTCACTGTGGCACTTGCTGTGCTGTTCGTAAAAGGACGCTTCGAGAGGAGATTGAAGAGGTCCAATCTCCCCAACAGCCTGCCCGTGTTC
II                                                                                                                                                   A[K]
III                                                                                                                                                  A[K]
IV
V
VI

     P   L   I   G   S   L   L   S   L   R   S   D   L   Q   P   H   I   L   F   Q   R   L   Q   E   K   Y   G   N   I   Y   S   L   M   M   G   S   H   Y   V   V
I CCTCTAATTGGGAGCCTGCTGAGTCTGAGAAGCGACCTGCAGCCACACATTCTCTTTCAGCGGCTGCAGGAGAAATATGGCAACATCTACTCGCTCATGATGGGGTCTCACTATGTGGTG
II                                                                                                                  C
III                                                                                                                 C
IV
V       A   [I]
VI      A   [I]

     I   V   N   N   Y   Q   D   A   K   E   V   L   L   K   K   S   K   I   F   A   G   R   Q   R   T   V   T   T   D   I   L   S   R   E   G   K   D   I   A   F
I ATTGTGAATAACTACCAAGATGCCAAAGAGGTTTTACTGAAGAAGAGCAAAATCTTTGCTGGGAGACAAAGAACTGTGACTACAGACATTCTATCCAGGGAAGGGAAAGACATCGCGTTT
II                                G   C
III                               G   C
IV
V
VI

     G   D   Y   S   P   A   W   R   F   H   R   K   M   V   H   S   A   F   S   M   L   G   E   G   S   T   S   I   E   K   I   I   C   R   E   A   R   S   M   C
I GGAGACTACAGCCCGGCTTGGAGGTTTCACAGGAAGATGGTGCACTCGGCGTTCAGCATGCTTGGCGAAGGCTCAACCTCAATCGAGAAAATAATCTGTAGAGAAGCCCGCTCCATGTGC
II                                                      A
III                                                                                                                                                  T[I]
IV                                                                                                          A
V                                                                                                           A
VI

     Q   T   L   S   D   L   Q   S   T   A   I   D   L   A   P   E   L   T   R   A   V   T   N   V   V   C   S   L   C   F   N   S   S   Y   Q   R   G   D   P   E
I CAGACCCTATCCGACCTCCAGAGTACAGCCATCGACCTGGCGCCTGAACTGACCCGCGCTGTCACCAACGTGGTGTGTTCCTTGTGCTTCAACTCATCCTATCAACGCGGGGACCCCGAG
II
III
IV
V
VI                                                                                                          C [S]

     F   E   S   M   L   Q   Y   S   Q   G   I   V   D   T   V   A   K   G   S   L   V   D   I   F   P   W   L   Q   M   F   P   N   E   D   L   R   I   L   K   D
I TTTGAATCCATGCTCCAATACAGCCAGGGGATTGTGGACACCGTGGCTAAAGGCAGCCTGGTAGACATCTTTCCCTGGCTTCAGATGTTCCCCAATGAAGACCTCAGGATACTAAAAGAC
II
III
IV
V
VI

     C   I   A   V   R   D   T   L   L   Q   K   K   Y   D   E   H   K   A   D   Y   S   D   G   A   E   K   D   L   L   D   S   L   L   R   A   K   L   C   S   E
I TGCATTGCGGTCAGGGACACGCTCCTGCAGAAGAAGTATGACGAACACAAAGCTGACTACAGTGATGGTGCAGAGAAGGACCTGCTGGATTCCCTCCTGCGAGCCAAGCTCTGCTCCGAG
II
III
IV
V                                                                                                                                                    G[W]
VI

     N   N   N   T   R   A   R   E   V   G   L   T   D   D   H   L   L   M   T   V   G   D   I   F   G   A   G   V   E   T   T   T   T   V   M   K   W   A   I   A
I AACAACAACACGCGAGCAAGAGAAGTGGGGCTGACAGACGACCACCTACTCATGACCGTGGGAGACATCTTCGGGGCTGGAGTCGAGACCACCACCACTGTCATGAAGTGGGCCATTGCT
II                                                                                                                                                   C
III                                                                                                                                                  C
IV                                                                                                                                  A G T [V]A   [T]
V
VI

     Y   L   L   H   H   P   Q   V   Q   K   K   I   Q   E   E   I   D   S   T   I   G   L   D   R   H   P   N   L   S   D   R   G   S   L   P   Y   L   E   A   T
I TACCTCCTACACCACCCGCAGGTCCAGAAGAAGATCCAGGAGGAGATTGACAGTACGATTGGGTTGGACAGACACCCCAATCTGAGTGACAGGGGCAGTTTGCCCTACCTGGAAGCAACG
II
III
IV
V
VI

     I   R   E   V   L   R   I   R   P   V   S   P   L   L   I   P   H   V   A   L   T   H   S   S   I   G   A   F   T   I   P   K   G   T   Q   V   I   I   N   L
I ATTCGGGAGGTGCTACGGATCAGACCGGTCTCCCCCCTCCTCATCCCTCATGTGGCCCTCACACACTCCAGTATTGGAGCTTTTACTATCCCGAAAGGAACTCAAGTCATTATTAACCTT
II
III  A
IV
V
VI

     W   S   L   H   H   D   E   K   E   W   K   N   P   D   I   F   D   P   G   R   F   L   D   E   E   G   K   Q   V   Y   S   P   S   A   S   Y   L   P   F   G
I TGGTCCTTGCATCACGATGAAAAGGAATGGAAAAACCCAGACATATTTGACCCTGGTCGCTTTCTAGATGAAGAGGGGAAGCAAGTCTATTCCCCCTCTGCCAGCTACCTCCCATTTGGG
II
III
IV
V
VI

     A   G   V   R   V   C   L   G   Q   S   L   A   K   M   E   L   F   L   F   L   G   W   M   L   Q   Q   F   T   L   E   V   P   A   D   Q   P   L   P   N   L
I GCAGGGGTCCGGGTGTGTCTGGGGCAGTCACTAGCTAAGATGGAGCTCTTCCTGTTCCTGGGCTGGATGCTGCAGCAGTTCACCCTGGAGGTACCAGCCGATCAGCCCCTGCCTAACTTA
II                                                                                                                  T
III                                                                                                                 T
IV
V
VI

     Q   G   K   F   G   V   V   L   Q   P   Q   K   F   K   V   N   A   R   L   R   D   S   W   V   N   T   E   M   Y   H   *
I CAGGGCAAATTCGGAGTCGTCCTCCAGCCCCAGAAATTCAAAGTGAACGCCAGACTTAGGGATTCCTGGGTGAACACTGAAATGTACCACTGA
II
III
IV
V
VI
```

Supplemental Figure S2. Nucleotide and amino acid sequences of Amur sturgeon *cyp17a1* type I–VI. Nucleotide variations between these types and corresponding amino acid alterations are indicated.

```
    M  V  F  S  L  V  G  I  S  L  A  S  V  V  A  A  L  V  I  F  K  L  L  K  S  V  V  G  P  S  P  T  T  L  P  C  L  P  S  F
| ATGGTGTTTTCCTTGGTTGGCATCTCGCTGGCATCTGTAGTGGCTGCCTTGGTCATCTTCAAGCTCCTGAAGAGTGTGGTGGGCCCGTCACCGACCACACTGCCCTGTCTGCCCTCCTTC    120
||

    P  I  V  G  S  L  L  S  L  G  G  T  T  P  P  H  L  L  F  T  R  L  G  C  K  Y  G  G  L  F  G  L  Y  L  G  P  H  Y  T  V
| CCCATCGTGGGCAGCCTGCTCAGCCTGGGAGGCACCACCCCTCCCCACCTTCTCTTCACCAGGCTGGGGTGCAAGTATGGGGGCCTCTTTGGTCTGTACTTGGGGCCCCACTATACTGTG    240
||

    V  I  N  N  F  K  H  A  K  E  I  L  L  R  K  G  K  V  F  A  G  R  P  H  M  V  T  T  A  L  L  S  R  D  G  K  D  I  A  F
| GTGATCAACAATTTCAAACACGCCAAGGAGATCCTGCTGCGCAAAGGGAAGGTCTTCGCTGGGAGACCCCATATGGTGACAACAGCTCTGCTGAGCAGGGATGGGAAAGACATTGCATTC    360
||

    A  D  Y  S  P  L  W  K  F  H  R  K  L   V  H  S  A  F  T  M  F  G  E  G  T  S  K  L  E  T  I  V  C  Q  E  A  S  S  L  C
| GCTGACTACAGTCCTCTCTGGAAGTTCCACCGCAAGTTGG- TACACTCTGCATTCACTATGTTTGGAGAGGGCACCAGCAAACTTGAGACCATCGTTTGTCAGGAAGCCTCCAGCCTGTGC    480
||              - [I]  [L]  [S]  [G]  [S]  [S]  [T]  [A]  [S]  [W]  G

    S  F  L  M  D  N  L  E  T  P  L  D  P  G  L  G  L  S  Q  A  V  T  N  V  V  C  T  L  V  F  N  S  K  Y  Q  P  G  D  S  E
| TCCTTTTTGATGGATAATCTTGAAACCCCGCTGGACCCGGGACTAGGCCTGTCCCAAGCCGTCACCAACGTGGTGTGCACCCTCGTCTTCAACTCCAAATACCAGCCGGGGGACAGCGAG    600
||

    L  Q  S  V  M  D  Y  T  S  G  I  V  E  T  I  A  R  G  S  L  V  D  I  F  P  W  L  K  V  F  P  N  K  D  L  K  K  L  N  K
| CTCCAGAGTGTGATGGACTACACCAGCGGCATTGTGGAAACCATCGCCAGAGGAAGCCTAGTAGACATTTTCCCATGGCTTAAGGTGTTTCCTAATAAAGACTTAAAGAAACTGAACAAA    720
||

    C  I  Q  V  R  D  E  L  L  T  Q  K  L  E  E  H  K  A  T  Y  C  M  S  E  T  R  D  L  M  D  A  L  L  T  A  Q  R  G  P  T
| TGCATTCAAGTGCGAGATGAGTTGTTAACACAGAAACTGGAGGAACACAAGGCTACTTACTGTATGTCTGAGACACGGGACCTGATGGACGCCCTGCTCACAGCCCAGCGTGGCCCCACG    840
||                                                                                                  [A]

    E  S  R  G  L  E  E  T  S  F  S  D  D  H  V  L  M  I  A  A  D  A  F  G  A  G  V  E  T  T  A  T  T  L  K  W  M  I  A  F
| GAGAGCCGAGGCCTGGAGGAGACTAGTTTCAGTGATGATCACGTTCTGATGATCGCAGCTGATGCCTTCGGTGCTGGAGTGGAAACCACGGCAACCACTCTCAAGTGGATGATAGCCTTC    960
||

    L  L  H  H  P  E  V  Q  K  K  I  Q  Q  E  I  D  E  Q  I  G  W  N  R  H  P  G  L  S  D  R  R  L  L  P  Y  L  E  C  T  L
| TTGCTTCATCACCCTGAGGTCCAAAAAAAGATCCAGCAAGAAATTGATGAACAGATCGGATGGAATCGCCACCCAGGTCTGTCAGACCGGAGGCTGCTGCCGTACTTGGAGTGCACACTG    1080
||

    N  E  V  L  R  I  R  P  V  A  P  L  L  I  P  H  V  A  L  E  N  T  S  I  G  E  H  V  I  P  K  G  T  R  V  V  V  N  M  W
| AACGAGGTACTGAGAATAAGGCCGGTAGCCCCTCTGCTTATCCCTCATGTGGCCTTGGAAAATACCAGTATCGGAGAACATGTCATTCCTAAAGGTACACGTGTGGTTGTGAACATGTGG    1200
||

    S  I  H  H  D  P  R  E  W  E  D  P  D  S  F  I  P  E  R  F  L  D  S  K  G  Q  R  F  S  P  P  A  F  I  P  F  G  A  G  P
| TCCATTCACCACGACCCCCGGGAGTGGGAGGATCCTGACAGCTTTATTCCAGAGCGTTTTTTGGACAGCAAAGGGCAGCGTTTCTCTCCCCCAGCTTTCATCCCATTCGGCGCAGGGCCG    1320
||

    R  V  C  I  G  E  S  L  A  K  L  E  L  F  L  F  T  S  W  L  L  Q  H  F  S  F  F  C  P  P  G  A  P  L  P  N  L  E  G  R
| CGGGTCTGTATTGGGGAATCTCTGGCTAAGCTGGAGCTGTTTCTCTTCACCAGCTGGCTGCTCCAGCATTTCAGCTTTTTCTGCCCTCCTGGGGCCCCCCTGCCCAACCTTGAGGGGAGA    1440
||

    Y  G  V  V  L  Q  P  E  S  Y  R  V  C  V  R  S  R  H  D  W  R  T  K  N  K  D  *
| TATGGGGTAGTCCTGCAGCCAGAAAGCTACAGGGTGTGTGTCCGTTCGCGTCATGACTGGAGAACCAAAAACAAGGATTAA  1521
```

Supplemental Figure S3. Nucleotide and amino acid sequences of Amur sturgeon *cyp17a2* type I–II. Nucleotide variations between these types and corresponding amino acid alterations are indicated. (-) indicates the missing nucleotides.

Supplemental Table S1. Substrate specificity of amur sturgeon hsd3b type-II/III and cyp17a2 type-II

Substrate	Product	Conversion Rate		
		Amur sturgeon hsd3b type II	Amur sturgeon hsd3b type III	Amur sturgeon cyp17a2 type II
P5	17OHP5	n.d.	n.d.	n.d.
P5	DHEA	n.d.	n.d.	n.d.
P4	17OHP	n.d.	n.d.	n.d.
P4	A4	n.d.	n.d.	n.d.
P5	P4	9.4%	10.6%	n.d.
P4	P5	n.d.	n.d.	n.d.
17OHP5	17OHP	10.8%	10.1%	-
17OHP	17OHP5	n.d.	n.d.	-
DHEA	A4	13.2%	16.5%	-
A4	DHEA	-	-	-
A5	T	15.8%	17.4%	-
T	A5	-	-	-

Eight steroids were used as substrates. pregnenolone; P5, 17α-hydroxypregnenolone; 17OHP5, progesterone; P4, 17α-Hydroxyprogesterone; 17OHP, androstenedione; A4, testosterone; T dehydroepiandrosterone; DHEA, 5α-androstenediol; A5, n.d; no detection

Supplemental Table S2. Substrate specificity of amur sturgeon cyp17a1 type II–VI

Substrate	Product	Conversion Rate				
		Amur sturgeon cyp17a1 type-II	Amur sturgeon cyp17a1 type-III	Amur sturgeon cyp17a1 type-IV	Amur sturgeon cyp17a1 type-V	Amur sturgeon cyp17a1 type-VI
P5	17OHP5	1.2%	2.3%	1.2%	0.8%	1.2%
P5	DHEA	1.8%	2.8%	2.1%	1.3%	0.8%
P4	17OHP	3.2%	4.8%	3.2%	2.8%	2.1%
P4	A4	4.2%	5.6%	4.8%	6.6%	6%

Two steroids were used as substrates. pregnenolone; P5, 17α-hydroxypregnenolone; 17OHP5, progesterone; P4, 17α-Hydroxyprogesterone; 17OHP, androstenedione; A4