

Supplementary Figure 1 – Alignment of Abbassa *amh*, *amhy*, and *amhΔy* open reading frame (ORF) and their encoded amino acid sequences. Coding sequence conservation is shaded and encoded amino acids are marked as alternating bold to demarcate exon boundaries. Missense single nucleotide polymorphisms contributing to amino acid change is marked in blue on the encoded amino acid sequence.

		10.....20.....30.....40.....50.....60
Abbassa_amh	1	ATGTTGGGTCTGCTCGTTCCTTTACAGCGAGGCGCTGACACTCTGCTGGACCCTGCAACCG
Abbassa_amhy	1	ATGTTGGGTCTGCTCGTTCCTTTACAGCGAGGCGCTGACACTCTGCTGGACCCTGCAACCG
Abbassa_amhΔy	1	ATGTTGGGTCTGCTCGTTCCTTTACAGCGAGGCGCTGACACTCTGCTGGACCCTGCAACCG
		<u> M L G L L V L Y S E A L T L C W T L Q P </u>
		<u> M L G L L V L Y S E A L T L C W T L Q P </u>
		<u> M L G L L V L Y S E A L T L C W T L Q P </u>
		70.....80.....90.....100.....110.....120
Abbassa_amh	61	GCCCAGGACCCCCACAGTAACCGAGTACTCACTCCCATCAGCGAAGACCCCCATCATCACCA
Abbassa_amhy	61	GCCCAGGACCCCCACAGTAACCGAGTACTCACTCCCATCAGCGAAGACCCCCATCATCACCA
Abbassa_amhΔy	61	GCCCAGGACCCCCACAGTAACCGAGTACTCACTCCCATCAGCGAAGACCCCCATCATCACCA
		<u> A Q D P T V T E Y S L P S A K T P S S P </u>
		<u> A Q D P T V T E Y S L P S A K T P S S P </u>
		<u> A Q D P T V T E Y S L P S A K T P S S P </u>
		130.....140.....150.....160.....170.....180
Abbassa_amh	121	TCATCATCCTCAGCAGCAGCGCCTCATGCTGCACCATGCTTCGTGGAGGACATCTTTGCA
Abbassa_amhy	121	TCATCATCCTCAGCAGCAGCGCCTCATGCTGCACCATGCTTCGTGGAGGACATCTTTGCA
Abbassa_amhΔy	121	TCATCATCCTCAGCAGCAGCGCCTCATGCTGCACCATGCTTCGTGGAGGACATCTTTGCA
		<u> S S S S A A A P H A A P C F V E D I F A </u>
		<u> S S S S A A A P H A A P C F V E D I F A </u>
		<u> S S S S A A A P H A A P C F V E D I F A </u>
		190.....200.....210.....220.....230.....240
Abbassa_amh	181	GCGTTGCGTGATGGTGTGGGGGACAGCGGCGAACTGACAAACAGCAGTTTGGTTCTGTTT
Abbassa_amhy	181	GCGTTGCGTGATGGTGTGGGGGACAGCGGCGAACTGACAAACAGCAGTTTGGTTCTGTTT
Abbassa_amhΔy	181	GCGTTGCGTGATGGTGTGGGGGACAGCGGCGAACTGACAAACAGCAGTTTGGTTCTGTTT
		<u> A L R D G V G D S G E L T N S S L V L F </u>
		<u> A L R D G V G D S G E L T N S S L V L F </u>
		<u> A L R E G V G D S G E L T N S S L V L F </u>
		250.....260.....270.....280.....290.....300
Abbassa_amh	241	GGATTCTGCTCGCAGTCTGCCCCGCTCATCAGCCTCGGTCTCGTTAGACCTCGCTAACAAG
Abbassa_amhy	241	GGATTCTGCTCGCAGTCTGCCCCGCTCATCAGCCTCGGTCTCGTTAGACCTCGCTAACAAG
Abbassa_amhΔy	241	GGATTCTGCTCGCAGTCTGCCCCGCTCATCAGCCTCGGTCTCGTTAGACCTCGCTAACAAG
		<u> G F C S Q S A R S S A S V S L D L A N K </u>
		<u> G F C S Q S A R S S A S V S L D L A N K </u>
		<u> G F C S Q S A R S S A S V S L D L A N K </u>
		310.....320.....330.....340.....350.....360
Abbassa_amh	301	AAGAGCAGCTTGGAGGTTCTGCACCCAGCTGCAGTACACGTATCAGAGGAAGAGGAGCAA
Abbassa_amhy	301	AAGAGCAGCTTGGAGGTTCTGCACCCAGCTGCAGTACACGTATCAGAGGAAGAGGAGCAA
Abbassa_amhΔy	301	AAGAGCAGCTTGGAGGTTCTGCACCCAGCTGCAGTACACGTATCAGAGGAAGAGGAGCAA
		<u> K S S L E V L H P A A V H V S E E E E Q </u>
		<u> K S S L E V L H P A A V H V S E E E E Q </u>
		<u> K S S L E V L H P A A V H V S E E E E Q </u>
		370.....380.....390.....400.....410.....420
Abbassa_amh	361	GGAACAATCACGTTGACCTTTGACCTCCACGGCCTCCATCGCTCATGACAAACCCTGTG
Abbassa_amhy	361	GGAACAATCACGTTGACCTTTGACCTCCACGGCCTCCATCGCTCATGACAAACCCTGTG
Abbassa_amhΔy	361	GGAACAATCACGTTGACCTTTGACCTCCACGGCCTCCATCGCTCATGACAAACCCTGTG
		<u> G T I T L T F D L P R P P S L M T N P V </u>
		<u> G T I T L T F D L P R P P S L M T N P V </u>
		<u> G T I T L T F D L P R P P S L M T N P V </u>
		430.....440.....450.....460.....470.....480
Abbassa_amh	421	CTGCTCTTGGTCTTTGAAAATCCACTGGCACGAGGAGACCTGGAAGTTGCTTTCACTAGT
Abbassa_amhy	421	CTGCTCTTGGTCTTTGAAAATCCACTGGCACGAGGAGACCTGGAAGTTGCTTTCACTAGT
Abbassa_amhΔy	421	CTGCTCTTGGTCTTTGAAAATCCACTGGCACGAGGAGACCTGGAAGTTGCTTTCACTAGT
		<u> L L L V F E N P L A R G D L E V A F T S </u>
		<u> L L L V F E N P L A R G D L E V A F T S </u>
		<u> L L L V F E S P L A R G D L E V A F T S </u>
		490.....500.....510.....520.....530.....540
Abbassa_amh	481	CAGTTTCTGCAGCCTAACACGCAGGCTGTGTGCATTTTCAGGAGACACACAGTACGTACTG

Abbassa_amhy 481 CAGTTTCTGCAGCCTAACACGCAGGCTGTGTGCATTTTCAGGAGACACACAGTACGTACTG
Abbassa_amhΔy 481 CAGTTTCTGCAGCCTAACACGCAGGCTGTGTGCATTTTCAGGAGACACACAGTACGTACTG

Q F L Q P N T Q A V C I S G D T Q Y V L
Q F L Q P N T Q A V C I S G D T Q Y V L
Q F L Q P N T Q A V C I S G D T Q Y V L

.....550.....560.....570.....580.....590.....600

Abbassa_amh 541 CTGACAGGAAAAATCATCAGAGGGGAGTGTTAATGACAGGTGGCAGATTACGGCTCAGACA
Abbassa_amhy 541 CTGACAGGAAAAATCATCAGAGGGGAGTGTTAATGACAGGTGGCAGATTACGGCTCAGACA
Abbassa_amhΔy 541 CTGACAGGAAAAATCATCAGAGGGGAGTGTTAATGACAGGTGGCAGATTACGGCTCAGACA

L T G K S S E G S V N D R W Q I T A Q T
L T G K S S E G S V N D R W Q I T A Q T
L T G K S S E G S V N D R W Q I T A Q T

.....610.....620.....630.....640.....650.....660

Abbassa_amh 601 AAACCTCCCTCATATGAAGCAAAACCTAAAAAGCATCTTGATTGGTGAAAAATCAGGAAGT
Abbassa_amhy 601 AAACCTCCCTCATATGAAGCAAAACCTAAAAAGCATCTTGATTGGTGAAAAATCAGGAAGT
Abbassa_amhΔy 601 AAACCTCCCTCATATGAAGCAAAACCTAAAAAGCATCTTGATTGGTGAAAAATCAGGAAGT

K L P H M K Q N L K S I L I G E K S G S
K L P H M K Q N L K S I L I G E K S G S
K L P H M K Q N L K S I L I G E K S G S

.....670.....680.....690.....700.....710.....720

Abbassa_amh 661 AACATCAGCATGAGTCCACTTCTACTTTTCTCCGGCGGAACGGGAACGATAACGAGATGT
Abbassa_amhy 661 AACATCAGCATGAGTCCACTTCTACTTTTCTCCGGCGGAACGGGAACGATAACGAGATGT
Abbassa_amhΔy 661 AACATCAGCATGAGTCCACTTCTACTTTTCTCCGGCGGAACGGGAACGATAACGAGATGT

N I S M S P L L L F S G G T G T D T R C
N I S M S P L L L F S G G T G T D T R C
N I S M S P L L L F S G G T G T D T R C

.....730.....740.....750.....760.....770.....780

Abbassa_amh 721 GCTTCAGGCTCGCCCCCGGCATCTCTGCAAACCTCCTTCCTTTGTGAGATGAAACGCTTC
Abbassa_amhy 721 GCTTCAGGCTCGCCCCCGGCATCTCTGCAAACCTCCTTCCTTTGTGAGATGAAACGCTTC
Abbassa_amhΔy 721 GCTTCAGGCTCGCCCCCGGCATCTCTGCAAACCTCCTTCCTTTGTGAATGTCGATGA---

A S G S P P A S L Q T S F L C E M K R F
A S G S P P A S L Q T S F L C E M K R F
A S G S P P A S L Q T S F L C E C R *

.....790.....800.....810.....820.....830.....840

Abbassa_amh 781 CTGGGTGCTGTTCTCCCTCAGGAACACTTCACGTCCCCTCCACTTCCTCTGGACTCCTTA
Abbassa_amhy 781 CTGGGTGCTGTTCTCCCTCAGGAACACTTCACGTCCCCTCCACTTCCTCTGGACTCCTTA
Abbassa_amhΔy 768 -----

L G A V L P Q E H F T S P P L P L D S L
L G A V L P Q E H F T S P P L P L D S L
- - - - - - - - - - - - - - - - - -

.....850.....860.....870.....880.....890.....900

Abbassa_amh 841 CAGTCTCTGCCTCCCCCTCTCGCTTGGCTTATCCTCCAGCGAGACCCTGCTGGCAGTAATG
Abbassa_amhy 841 CAGTCTCTGCCTCCCCCTCTCGCTTGGCTTATCCTCCAGCGAGACCCTGCTGGCAGTAATG
Abbassa_amhΔy 768 -----

Q S L P P L S L G L S S S E T L L A V M
Q S L P P L S L G L S S S E T L L A V M
- - - - - - - - - - - - - - - - - -

.....910.....920.....930.....940.....950.....960

Abbassa_amh 901 ATCAACTCCACAGCTCCCACAGTCTTTGGCTTCACGAGCTGGGGCTCCGTGTTGCCGGTG
Abbassa_amhy 901 ATCAACTCCACAGCTCCCACAGTCTTTGGCTTCACGAGCTGGGGCTCCGTGTTGCCGGTG
Abbassa_amhΔy 768 -----

I N S T A P T V F G F T S W G S V L P V
I N S T A P T V F G F T S W G S V L P V
- - - - - - - - - - - - - - - - - -

.....970.....980.....990.....1000.....1010.....1020

Abbassa_amh 961 TGCCACGGAGAGCTGGCCCTGTCTGCTGCACTGTTAGAGGAGCTCAGACAGAGACTGGAC
Abbassa_amhy 961 TGCCACGGAGAGCTGGCCCTGTCTGCTGCACTGTTAGAGGAGCTCAGACAGAGACTGGAC
Abbassa_amhΔy 768 -----

C H G E L A L S A A L L E E L R Q R L D
C H G E L A L S A A L L E E L R Q R L D
- - - - -

Abbassa_amh 10211030.....1040.....1050.....1060.....1070.....1080
Abbassa_amhy 1021 CAGACTTTGGTGCAAATGACAGAAATAATCAGAGAGGAAGAGGTTTCACTGGGAGCCAAG
Abbassa_amhΔy 768 CAGACTTTGGTGCAAATGACAGAAATAATCAGAGAGGAAGAGGTTTCACTGGGAGCCAAG

Q T L V Q M T E I I R E E E V S L G A K
Q T L V Q M T E I I R E E E V S L G A K
- - - - -

Abbassa_amh 10811090.....1100.....1110.....1120.....1130.....1140
Abbassa_amhy 1081 GAGAGCCTGGGGAGGCTCAAAGAACTGAGTGC GTTACAGGAGAAAGAACATGCCACAGGA
Abbassa_amhΔy 768 GAGAGCCTGGGGAGGCTCAAAGAACTGAGTGC GTTACAGGAGAAAGAACATGCCACAGGA

E S L G R L K E L S A L Q E K E H A T G
E S L G R L K E L S A L Q E K E H A T G
- - - - -

Abbassa_amh 11411150.....1160.....1170.....1180.....1190.....1200
Abbassa_amhy 1141 GGGAGTCAGTTCCGTGTGTTTCTTCTGCTGAAGGCTCTGCAGACGGTGGCCCCAAACGTAC
Abbassa_amhΔy 768 GGGAGTCAGTTCCGTGTGTTTCTTCTGCTGAAGGCTCTGCAGACGGTGGCCCCAAACGTAC

G S Q F R V F L L L K A L Q T V A Q T Y
G S Q F R V F L L L K A L Q T V A Q T Y
- - - - -

Abbassa_amh 12011210.....1220.....1230.....1240.....1250.....1260
Abbassa_amhy 1201 GACGCGCAAAGAAAAC TGCGGGCCACCAGAGCAGACCCCA GTTTCGTCAGTGAGGGGCGGC
Abbassa_amhΔy 768 GACGCGCAAAGAAAAC TGCGGGCCACCAGAGCAGACCCCA GTTTCGTCAGTGAGGGGCGGC

D A Q R K L R A T R A D P S S S V R G G
D A Q R K L R A T R A D P S S S V R G G
- - - - -

Abbassa_amh 12611270.....1280.....1290.....1300.....1310.....1320
Abbassa_amhy 1261 GTCTGTGGGCTGAAGGCTCTCACC GTGTCCCTGACAAAGCTTCTTGTCGGCCCAAGCAGC
Abbassa_amhΔy 768 GTCTGTGGGCTGAAGGCTCTCACC GTGTCCCTGACAAAGCTTCTTGTCGGCCCAAGCAGC

V C G L K A L T V S L T K L L V G P S S
V C G L K A L T V S L T K L L V G P S S
- - - - -

Abbassa_amh 13211330.....1340.....1350.....1360.....1370.....1380
Abbassa_amhy 1321 GCAAACATTAACAATTGCCACGGCTCCTGCACGTTCCCTCTGACCAACGGCAACAACCAC
Abbassa_amhΔy 768 GCAAACATTAACAATTGCCACGGCTCCTGCACGTTCCCTCTGACCAACGGCAACAACCAC

A N I N N C H G S C T F P L T N G N N H
A N I N N C H G S C A F P L T N G N N H
- - - - -

Abbassa_amh 13811390.....1400.....1410.....1420.....1430.....1440
Abbassa_amhy 1381 GCCATCCTGCTCAACTCCCACATCGAGACCGGCAACGCGGATGAGCGTTTCGCCCTGCTGT
Abbassa_amhΔy 768 GCCATCCTGCTCAACTCCCACATCGAGACCGGCAACGCGGATGAGCGTTTCGCCCTGCTGT

A I L L N S H I E T G N A D E R S P C C
A I L L N S H I E T G N A D E R S P C C
- - - - -

Abbassa_amh 14411450.....1460.....1470.....1480.....1490.....1500
Abbassa_amhy 1441 GTGCCCCGTGGCATAACGAAGCCCTGGAGGTTGTGGACTGGAACGCAGATGGGACCTTCATC
Abbassa_amhΔy 768 GTGCCCCGTGGCATAACGAAGCCCTGGAGGTTGTGGACTGGAACGCAGATGGGACCTTCATC

V P V A Y E A L E V V D W N A D G T F I
V P V A Y E A L E V V D W N A D G T F I
- - - - -

.....:1510.....:1520.....:1530.....:1540.....:
TCCATCAAGCCAGATGCGGTTGCGAGGGAGTGTGGATGCCGCTAG
TCCATCAAGCCAGATGCGGTTGCGAGGGAGTGTGGATGCCGCTAG

S I K P D A V A R E C G C R *
S I K P D A V A R E C G C R *

Abbassa_amh 1501
Abbassa_amhy 1501
Abbassa_amhΔy 768