

Supplementary Figure 3 – Alignment of Abbassa *amh*, *amhy*, and *amhΔy* 5' UTR and gene promoter region. Nucleotide sequence conservation is shaded and 346 bp Abbassa *amh* 5' UTR sequence shown for reference. Green nucleotides on *amhΔy* sequence indicate the 46 bp 5' UTR. The 165 bp deletion in *amhΔy* gene promoter and 3 bp 'TCT' insertion in *amhy* gene promoter marked in red. The deletions at > 1.6 kb in *amhy* and *amhΔy* are marked in green.

Abbassa_amh_h2tg0001191	9936	10810.....10820.....10830.....10840.....10850.....10860
Abbassa_amhΔy_h1tg0002121	9676	AATAACCACATGCATGCATTTTCCATTCAAAGTTAACGAGTTATTAATTAATCAGCTGA
Abbassa_amh_5'UTR	1	-----
Abbassa_amhy_h1tg0002121	9936	AATAACCACATGCATGCATTTTCCATTCAAAGTTAACGAGTTATTAATTAATCAGCTGA
Abbassa_amh_h2tg0001191	9996	10870.....10880.....10890.....10900.....10910.....10920
Abbassa_amhΔy_h1tg0002121	9736	GCGGCGTCTGACCGGTTACTGTGGGGTCCTGGGCCGGTTGCAGGGTCCAGCAGAGTGTCA
Abbassa_amh_5'UTR	1	-----
Abbassa_amhy_h1tg0002121	9996	GCGGCGTCTGACCGGTTACTGTGGGGTCCTGGGCCGGTTGCAGGGTCCAGCAGAGTGTCA
Abbassa_amh_h2tg0001191	10056	10930.....10940.....10950.....10960.....10970.....10980
Abbassa_amhΔy_h1tg0002121	9796	GCGCCTCGCTGTAAAGAACGAGCAGACCCAAACATGTTTGCACTGTCTGCGTGTGCGGT
Abbassa_amh_5'UTR	1	-----
Abbassa_amhy_h1tg0002121	10056	GCGCCTCGCTGTAAAGAACGAGCAGACCCAAACATGTTTGCACTGTCTGCGCGTGCCTGTG
Abbassa_amh_h2tg0001191	10116	10990.....11000.....11010.....11020.....11030.....11040
Abbassa_amhΔy_h1tg0002121	9856	TGTGGTCAGATCTCTCACAGGATGGGAGTTACATCCTCAGACCTCCCCTTCTCACCACCT
Abbassa_amh_5'UTR	26	TGTGGTCAGATCTCTCTCACAGGATGGGAGTTACATCCTCAGACCTCCCCTTCTCACCACCT
Abbassa_amhy_h1tg0002121	10116	TGTGGTCAGATCTCTCACAGGATGGGAGTTACATCCTCAGACCTCCCCTTCTCACCACCT
Abbassa_amh_h2tg0001191	10176	11050.....11060.....11070.....11080.....11090.....11100
Abbassa_amhΔy_h1tg0002121	9916	GGGGTCCCCTTTCTGCCAAAATAGCAGCACTGTGTGTCTTGATGACTGAGATTGTCAGT
Abbassa_amh_5'UTR	86	GGGGTCCCCTTTCTGCCAAAATAGCAGCACTGTGTGTCTTGATGACTGAGATTGTCAGT
Abbassa_amhy_h1tg0002121	10176	GGGGTCCCCTTTCTGCCAAAATAGCAGCACTGTGTGTCTTGATGACTGAGATTGTCAGT
Abbassa_amh_h2tg0001191	10236	11110.....11120.....11130.....11140.....11150.....11160
Abbassa_amhΔy_h1tg0002121	9976	ATTTGAGGTATTTTAACCTGCTTGTGGAGAACATTCTAAAATCAGACAGCAAACGGGACA
Abbassa_amh_5'UTR	146	ATTTGAGGTATTTTAACCTGCTTGTGGAGAACATTCTAAAATCAGACAGCAAACGGGACA
Abbassa_amhy_h1tg0002121	10236	ATTTGAGGTATTTTAACCTGCTTGTGGAGAACATTCTAAAATCAGACAGCAAACGGGACA
Abbassa_amh_h2tg0001191	10296	11170.....11180.....11190.....11200.....11210.....11220
Abbassa_amhΔy_h1tg0002121	10036	CGGAGGTAAACAGAAGACGACTTTGGACACACTGAACATCCTTATCTAGCAGACACAAAC
Abbassa_amh_5'UTR	206	CGGAGGTAAACAGAAGACGACTTTGGACACACTGAACATCCTTATCTAGCAGACACAAAC
Abbassa_amhy_h1tg0002121	10296	CGGAGGTAAACAGAAGACGACTTTGGACACACTGAACATCCTTATCTAGCAGACACAAAC
Abbassa_amh_h2tg0001191	10356	11230.....11240.....11250.....11260.....11270.....11280
Abbassa_amhΔy_h1tg0002121	10096	AGGTCCCGGAAAGAAAGTTTCTCACGAACCTTTCATAGAATACACAGGCTGAAAGATGA
Abbassa_amh_5'UTR	266	AGGTCCCGGAAAGAAAGTTTCTCACGAACCTTTCATAGAATACACAGGCTGAAAGATGA
Abbassa_amhy_h1tg0002121	10356	AGGTCTCAGAAAGAAAGTTTCTCACGAACCTTTCATAGAATACACAGGCTGAAAGATGA
Abbassa_amh_h2tg0001191	10416	11290.....11300.....11310.....11320.....11330.....11340
Abbassa_amhΔy_h1tg0002121	10156	AGAGTGCTGTTTAATGTTTCGTGGCTGCAGAGCTAATATGCACGCTGCTTAACTTAACCC
Abbassa_amh_5'UTR	326	AGAGTGCTGTTTAATGTTTC-----
Abbassa_amhy_h1tg0002121	10416	AGAGTGCTGTTTAATGTTTCGTGGCTGCAGAGCTAATATGCACGCTGCTTAACTTAACCC
Abbassa_amh_h2tg0001191	10476	11350.....11360.....11370.....11380.....11390.....11400
Abbassa_amhΔy_h1tg0002121	10216	TCTCGAGGCAGGCGTTGCCGATTTGCAACAGTTAAAAACTAACAACCTGATTACCCTACA
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	10476	TCTCGAGGCAGGCGTTGCCGATTTGCAACAGTTAAAAACTAACAACCTGATTACCCTACA
Abbassa_amh_h2tg0001191	10536	11410.....11420.....11430.....11440.....11450.....11460
Abbassa_amhΔy_h1tg0002121	10276	TACATATTTTATGAGTCTTTTTTTTTTTTGTATAATTTTCCCAAAATATCAGATTTTTC
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	10536	TACATATTTTATGAGTCTTTTTTTTTTTTGTATAATTTTCCCAAAATATCAGATTTTTC
Abbassa_amh_h2tg0001191	10596	11470.....11480.....11490.....11500.....11510.....11520
Abbassa_amhΔy_h1tg0002121	10336	TGTAACATAAACTTAATTTGAGCCTGAGAGGGTTAAACAAAGAGGACAGTAACTGGAG
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	10596	TGTAACATAAACTTAATTTGAGCCTGAGAGGGTTAAACAAAGAGGACAGTAACTGGAG
		11530.....11540.....11550.....11560.....11570.....11580

Abbassa_amh_h2tg0001191	10656	GTTTGCTTCCATCACGTCGACAACAAAGCTCAAAACGATTTTAAAGAAACACTTTGCATT
Abbassa_amhΔy_h1tg0002121	10396	GTTTGCTTCCATCACGTCGACAACAAAGCTCAAAACGATTTTAAAGAAACACTTTGCATT
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	10656	GTTTGCTTCCATCATGTCGACAACAAAGCTCAAAACGATTTTAAAGAAACACTTTGCATT
		11590.....11600.....11610.....11620.....11630.....11640
Abbassa_amh_h2tg0001191	10716	TTGGTAAATCTGCTTACTTGTGCTTTGGACTGATGAC---TCCTCTTAGAGAGACTGCT
Abbassa_amhΔy_h1tg0002121	10456	T-----
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	10716	TTGGTAAATCTGCTTACTTGTGCTTTGGACTGATGACTCTCTCTTAGAGAGACTGCT
		11650.....11660.....11670.....11680.....11690.....11700
Abbassa_amh_h2tg0001191	10773	GGCAGAAAGCCTTGAAGGGAACTTCAGCCACATCCACTGTTTTTCATCTTTCTGTTTCT
Abbassa_amhΔy_h1tg0002121	10457	-----
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	10776	GGCAGAAAGCCTTGAAGGGAACTTCAGCCACATCCACTGTTTTTCATCTTTCTGTTTCT
		11710.....11720.....11730.....11740.....11750.....11760
Abbassa_amh_h2tg0001191	10833	CTAAGCGGGGATGTCCAACATCAGGCCAGGGGCTAGAATCACCAGCAATGACTCCAA
Abbassa_amhΔy_h1tg0002121	10457	-----CAGCAATGACTCCAA
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	10836	CTAAGCGGGGATGTCCAACATCAGGCCAGGGGCTAGAATCACCAGCAATGACTCCAA
		11770.....11780.....11790.....11800.....11810.....11820
Abbassa_amh_h2tg0001191	10893	CCCAGCTCACTTGAAGGATGGCATAAATTTTGGAC-----CTTTTAACGTGTA
Abbassa_amhΔy_h1tg0002121	10472	CCCAGCTCACTTGAAGGATGGCATAAATTTTGGAC-----CTTTTAACGTGTA
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	10896	CCCAGCTCACTTGAAGGATGGCAAAATTTGCCAGCACAAAACACCCCTTTGCATATATA
		11830.....11840.....11850.....11860.....11870.....11880
Abbassa_amh_h2tg0001191	10939	TTTTCTTA---AATTTTATGGCTTTTCCTGCTAATAAAGAACTCTGCCACATGTTTCATGC
Abbassa_amhΔy_h1tg0002121	10518	TTTTCTTA---AATTTTATGGCTTTTCCTGCTAATAAAGAACTCTGCCACATGTTTCATGC
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	10956	TATGTATATATATTTATATACTTATATATATTTATATAGACTGTATATAGTTACTTATTT
		11890.....11900.....11910.....11920.....11930.....11940
Abbassa_amh_h2tg0001191	10996	TACACC-----AAAGTGATTACAATTA-----CATGACAAAAAAGT
Abbassa_amhΔy_h1tg0002121	10575	TACACC-----AAAGTGATTACAATTA-----CATGACAAAAAAGT
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	11016	TACATACCTTTCTGTTTATGACGGAGATGTACAATTAAGAAAACCTTATGTACAAAAACA
		11950.....11960.....11970.....11980.....11990.....12000
Abbassa_amh_h2tg0001191	11033	TCCTGT-TTTTTTTCACCATCTGCTCCAGAAATTAGTTTTTTCTGTGAATATTAC-----
Abbassa_amhΔy_h1tg0002121	10612	TCCTGT-TTTTTTTCACCATCTGCTCCAGAAATTAGTTTTTTCTGTGAATATTAC-----
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	11076	GTGTGT-TCTTGTTCACCAACAGC-----GGGCCGATGTATGTTTAAACATTACAGGGG
		12010.....12020.....12030.....12040.....12050.....12060
Abbassa_amh_h2tg0001191	11086	-----ACATTTATTTATTTATAATGGAAAATTTCTTTGATTTCAA
Abbassa_amhΔy_h1tg0002121	10666	-----ACATTTATTTATTTATGATGGAAAATTTCTTTGATTTCAA
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	11130	CCCCCGTGGCCGTCGCTCGGGCCCCGAGCCGGCTGCACGAGAGCA---CTTTGATCCAAA
		12070.....12080.....12090.....12100.....12110.....12120
Abbassa_amh_h2tg0001191	11126	GATTCAAACCTCTTTATTGTC-----ATGTGTCCAAAGA-----AAAAAGGCATTTTC--
Abbassa_amhΔy_h1tg0002121	10706	GATTCAAACCTGTTTATTGTC-----ATGTGTCCAAAGA-----AAAAAGGCATTTTC--
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	11187	GGT---GCGCTCTACAGTTGTACACGATGCATTCAAAGAACGAGACAAATAGCATATTAA
		12130.....12140.....12150.....12160.....12170.....12180
Abbassa_amh_h2tg0001191	11172	-TCTGTGCAATGAAACTT-----TTGCTTTGC-----TGTCACCCACAGAT
Abbassa_amhΔy_h1tg0002121	10752	-TCTGTGCAATGAAACTT-----TTGCTTTGC-----TGTCACCCACAGAT
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	11243	ATATGAGAAAGGAAATGCCAAAAAACGCTTTTACAAATGTCCCTGTGTACAGCACCAAGT
		12190.....12200.....12210.....12220.....12230.....12240
Abbassa_amh_h2tg0001191	11213	GCCGG-----TTAATATTTACAGTAGAATAGAACAGATAAATACAAATA-----
Abbassa_amhΔy_h1tg0002121	10793	GCCGG-----TTAATATTTACAATAGAATAGAACAGATAAATACAAATA-----
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	11303	ACTTGACTTGTTTTGTATGTTTTCATT---ACAGAATAAATAAGATCAGGCATAGTCCA
		12250.....12260.....12270.....12280.....12290.....12300
Abbassa_amh_h2tg0001191	11258	-----GCACAAATAAATAAGACAGAA

Abbassa_amhΔy_h1tg0002121 10838 -----GCACAAATAAATAAGACAGAA
Abbassa_amh_5'UTR 29 -----
Abbassa_amhy_h1tg0002121 11359 AACTTAGCACCATTGTTTTTCAGACTGTGAGTCAAGTACACACACTAATGGAATTCTACA
.....:12310.....:12320.....:12330.....:12340.....:12350.....:12360
Abbassa_amh_h2tg0001191 11280 AAGGAGACAAATTATTGAAGTGTGAAACATAGATGTGTGCA----AAAGAGCTTATAGC-
Abbassa_amhΔy_h1tg0002121 10860 AAGGAGACAAATTATTGAAGTGTGAAACAGAGATGTGTGCA----AAAGAGCTTATAGC-
Abbassa_amh_5'UTR 29 -----
Abbassa_amhy_h1tg0002121 11419 ATGTCACACAAATTCAGGATTTAAAAAATAAAGGCAATGGAAGACCGACAGCA
.....:12370.....:12380.....:12390.....:12400.....:12410.....:12420
Abbassa_amh_h2tg0001191 11334 TTAATATGCTGGCTTAA--TATGCAGGATGACCTGATGTGCAAAAAATTATT--ATTAA
Abbassa_amhΔy_h1tg0002121 10914 TTAATATGCTGGCTTAA--TATGCAGGATGACCTGATGTGCAAAAAATTATT--ATTGA
Abbassa_amh_5'UTR 29 -----
Abbassa_amhy_h1tg0002121 11479 TAAATATAATCATCTAAATATCCACAACATATACAGT---CAGAGAATTAATCACATTCA
.....:12430.....:12440.....:12450.....:12460.....:12470.....:12480
Abbassa_amh_h2tg0001191 11389 TGTT-----CAAAAATAGGTCAGCTTGTTTGACTCTGATGGCA-----
Abbassa_amhΔy_h1tg0002121 10969 TGTT-----CAAAAATAGGTCAGCTTGTTTGACTCTGATGGCA-----
Abbassa_amh_5'UTR 29 -----
Abbassa_amhy_h1tg0002121 11536 TAGTACAAACATCGTTTACAAAAACAAATTAACACCGTTT--TTTAAAAAGCAAAACAAAGA
.....:12490.....:12500.....:12510.....:12520.....:12530.....:12540
Abbassa_amh_h2tg0001191 11427 -GTGGGGAAGAAGGC--GTTGTTGAGTCTGGATGTTCTGGATTTCACACTTCTAAACCTC
Abbassa_amhΔy_h1tg0002121 11007 -GTGGGGAAGAAGGC--GTTGTTGAGTCTGGATGTTCTGGATTTCACACTTCTAAACCTC
Abbassa_amh_5'UTR 29 -----
Abbassa_amhy_h1tg0002121 11594 GGTGTGAAACAAGTCCAGTAGTTGTTGTGCTTATGGTCAA-----CTATGTTTTT
.....:12550.....:12560.....:12570.....:12580.....:12590.....:12600
Abbassa_amh_h2tg0001191 11484 CGCCCCGAGGGCAGAAGTGTGAACAGTCCGTGTGGGGATGTGTGGGGTCTTTGAGGATG
Abbassa_amhΔy_h1tg0002121 11064 CGCCCCGAGGGCAGAAGTGTGAACAGTCCATGTTGGGGATGTGTGGGGTCTTTGAGGATG
Abbassa_amh_5'UTR 29 -----
Abbassa_amhy_h1tg0002121 11644 CCCAGTGTCTGAGGATTGTCATGTCATGACTGTGTGTGTGTGTGTGTGTTAAACTA
.....:12610.....:12620.....:12630.....:12640.....:12650.....:12660
Abbassa_amh_h2tg0001191 11544 GAGGCAG-----CTCTCCTTTGGACTCTGCGATGGTAGATGCT
Abbassa_amhΔy_h1tg0002121 11124 GAGGCG-----CTCTCCTCTGGACTCTGCGATGGTAGATGCT
Abbassa_amh_5'UTR 29 -----
Abbassa_amhy_h1tg0002121 11704 AACGCAGTAAATTTTCACATATCAGTCCACTTTCATTTAAAC-CTGCATTTCTTAACA--
.....:12670.....:12680.....:12690.....:12700.....:12710.....:12720
Abbassa_amh_h2tg0001191 11582 GTGCAGAGAGGGCAGCGGAGTCTGATTATCTTCCCTGCAGTTGTTATCACTCTCTGCAG
Abbassa_amhΔy_h1tg0002121 11162 GTGCAGAGAGGGCAGCGGAGTCTGATTATCTTCCCTGCAGTTGTTATCACTCTCTGCAG
Abbassa_amh_5'UTR 29 -----
Abbassa_amhy_h1tg0002121 11761 --GCACGATAAATATCAATGCATGG----ATCTCTGCCCTTATGCTTAGCTTACAAAG
.....:12730.....:12740.....:12750.....:12760.....:12770.....:12780
Abbassa_amh_h2tg0001191 11642 GTGATTGCAGTCCATGGCAGTAGTGCTGCCGTATCATGCAGTGATGCAGCTGGTCAGTGT
Abbassa_amhΔy_h1tg0002121 11222 GTGATTGCGGTCCATGGCAGTAGTGCTGCCATATCATGCAGTGATGCAGCTGGTCAGTGT
Abbassa_amh_5'UTR 29 -----
Abbassa_amhy_h1tg0002121 11814 AGGAAT-----ATTCTCTGCTGCCGTTT-----GTGT
.....:12790.....:12800.....:12810.....:12820.....:12830.....:12840
Abbassa_amh_h2tg0001191 11702 GCTCTCCACAATGCAGCTGT--AGAACCTGCTGAGGATCATACCAAATTTCTCAGCCTC
Abbassa_amhΔy_h1tg0002121 11282 GCTCTCCACAATGCAGCTGT--AGAACCTGCTGAGGATCATACCAAATTTCTCAGCCTC
Abbassa_amh_5'UTR 29 -----
Abbassa_amhy_h1tg0002121 11840 GA-CTTCACAAACCGACGGGAAAGAAACGGTTAATAAATACAC-----GCAAA
.....:12850.....:12860.....:12870.....:12880.....:12890.....:12900
Abbassa_amh_h2tg0001191 11760 CTCAGGAAATGCAGCCATTCTGAGCCTTCTTGACAGCTGTGTGGTGTTCAGTGTCCAG
Abbassa_amhΔy_h1tg0002121 11340 CTCAGGAAATGCAGCCGTTCTGAGCCTTCTTGACAGCTGTGTGGTGTTCAGTGTCCAG
Abbassa_amh_5'UTR 29 -----
Abbassa_amhy_h1tg0002121 11887 CTCACTGAACCTCTGTTGTTCTTGACATGTGATTGAGCTGTTCGCTGAACCTTAACAGA
.....:12910.....:12920.....:12930.....:12940.....:12950.....:12960
Abbassa_amh_h2tg0001191 11820 GTGATGTCCACAGAAATGTAGACGCCAGGTATCTAAAGCTGCTCACCCCTCTCCACTTCA
Abbassa_amhΔy_h1tg0002121 11400 GTGATGTCCACAGAAATGTAGACGCCAGGTATCTAAAGCTGCTCACCCCTCTCCACTTCA
Abbassa_amh_5'UTR 29 -----
Abbassa_amhy_h1tg0002121 11947 GCAG---CCACAGTGA-----CGGGTGGCTGAAGAGCACATTTCAATTTTTTTTA
.....:12970.....:12980.....:12990.....:13000.....:13010.....:13020
Abbassa_amh_h2tg0001191 11880 AGGCCCCGATAAACCGCGGCTGGTGAGGCCTCCTCTTCTTCTCGTGTCCACTATCATC
Abbassa_amhΔy_h1tg0002121 11460 AGGCCCCGATAAACCGCGGCTGGTGAGGCCTCCTCTTCTTCTCGTGTCCACTATCATC

Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	11994	AAACAGATGTTAATGTACAA----GACGCTGCATTGCATTATTGGCACCCACAGGCATG
		13030.....13040.....13050.....13060.....13070.....13080
Abbassa_amh_h2tg0001191	11940	TCCTTTGTCT-TGTCAGTGTGAGGGTGAGGTTGTTGTCTCACACCATGACACCAGACC
Abbassa_amhΔy_h1tg0002121	11520	TCCTTTT-----
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	12049	TTATTAAATTATCCTCAAAATAAGGCCAAATCAACATCCGCAGATGTTTTCTCATTTCC
		13090.....13100.....13110.....13120.....13130.....13140
Abbassa_amh_h2tg0001191	11999	GGCCACCTCTCTCCTGTAAGCCGCTTCGTCCCTCCAGTGATGCGACGGATCACTGCAGT
Abbassa_amhΔy_h1tg0002121	11526	-----
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	12109	TCTCATCCTT-----
		13150.....13160.....13170.....13180.....13190.....13200
Abbassa_amh_h2tg0001191	12059	GCCATCTGAGAACCTTCAAAATGATGTTATCTTTGTTGGAGGTGACACAGTCGTGAGCGTA
Abbassa_amhΔy_h1tg0002121	11526	-----
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	12119	-----
		13210.....13220.....13230.....13240.....13250.....13260
Abbassa_amh_h2tg0001191	12119	CAGGGTGTAGAGGATGGGACTGAGGACTTTTGACATTACAT-----TATATATGGAAAA
Abbassa_amhΔy_h1tg0002121	11526	-----
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	12119	-----TGGGAGATTTGTCTGATTATTGCTAACATTAAATATCTGACATTAGCAGAAAA
		13270.....13280.....13290.....13300.....13310.....13320
Abbassa_amh_h2tg0001191	12173	ACTGAGACGTAGAGTTGAGGTTGCACTTTCTTATATTAAGATTCACATGTAGTTAAGCTT
Abbassa_amhΔy_h1tg0002121	11526	-----
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	12172	ACAGAAACA-----
		13330.....13340.....13350.....13360.....13370.....13380
Abbassa_amh_h2tg0001191	12233	CTTTACTCTGACAGAGCGGGCGTTTCACTGGTCAGGCACACTTAAGACCAAAGTGGGCT
Abbassa_amhΔy_h1tg0002121	11526	-----
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	12181	-----
		13390.....13400.....13410.....13420.....13430.....13440
Abbassa_amh_h2tg0001191	12293	GAATGTGGCCACGATCCACAATCAGTTGGACATCCCTGCCTTCAGGCTAACCATCTCCTG
Abbassa_amhΔy_h1tg0002121	11526	-----
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	12181	-----
		13450.....13460.....13470.....13480.....13490.....13500
Abbassa_amh_h2tg0001191	12353	CCCCCGGCTCCGTGTGTAATGTACGATCACTAGTGACACTACTAAACACTGTAAAGG
Abbassa_amhΔy_h1tg0002121	11526	-----
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	12181	-----
		13510.....13520.....13530.....13540.....13550.....13560
Abbassa_amh_h2tg0001191	12413	CTTTTATTCTACTCTAAATAAAAGTCTGATCTGTTTTTATAAGACATATTATGAG-CATA
Abbassa_amhΔy_h1tg0002121	11526	-----ATTCTACTCTAAATAAAAGTCTGATCTGTTTTTATAAGACATATTATGAG-CATA
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	12181	-----ACTTAACCTTAAAGGAATAGCTACAAAATATTTA----ATATTTTGTGAGACAGA
		13570.....13580.....13590.....13600.....13610.....13620
Abbassa_amh_h2tg0001191	12472	TTAAAGAGTAGCGGACCAAGGACAGATCCCTGAGGAACCTCCCTGACTCAATTTTGAT
Abbassa_amhΔy_h1tg0002121	11580	TTAAAGAATAGCGGACCAAGGACAGATCCCTGAGGAAC---TCCTGACTCAATTTTGAT
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	12232	AGGAGTCAGAGCAAGCCAAA-----CAGACAATCTAATTATTATTATTGGCTTTGAA
		13630.....13640.....13650.....13660.....13670.....13680
Abbassa_amh_h2tg0001191	12532	TTGATCAACTAAAACATGAAACCTTCAGTACTTCACCAGTTAAACCAACTGAAC-----
Abbassa_amhΔy_h1tg0002121	11636	TTGATCAACTAAAACATGAAACCTTCAGTACTTCACCAGTTAAACCAACTGAAC-----
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	12283	TTAAGCACCAACAACCTCA---TTCAGTTTGTTCACAAATGTAAATATGAAAACACAGTA
		13690.....13700.....13710.....13720.....13730.....13740
Abbassa_amh_h2tg0001191	12586	---CATGAAGTCTTTGAATGAAAAAGCCAAAATGTGCAATGAATTCAAAGCCAGTGTTT
Abbassa_amhΔy_h1tg0002121	11690	---CATGAAGTCTTTGAATGAAAAAGCCAAAGATGTGCAATGAATTCAAAGCCAGTGTTT
Abbassa_amh_5'UTR	29	-----

Abbassa_amhy_h1tg0002121	12339	AATACAGTAAATC-----ATGAACATGGCAGGGGTGCACACTAAACAC-AAGCAAGGCTT
		:13750.....:13760.....:13770.....:13780.....:13790.....:13800
Abbassa_amh_h2tg0001191	12642	GCAAA--TGCAGTTTTGAATCGTTATTTTCAGAGTCCAAATTTAAAAAACTGAAAAAAT
Abbassa_amhΔy_h1tg0002121	11746	GCAAA--TGCAGTTTTGAATCGTTATTTTCAGAGTCCAAATTTAAAAAACTGAAGAAAT
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	12393	GTACATCTTCTGCTATGTGAGCTTAATAATCCAGTGCGAAGTT----AGACCAAAAAAGT
		:13810.....:13820.....:13830.....:13840.....:13850.....:13860
Abbassa_amh_h2tg0001191	12700	TAACTATTACAGCTCATAAAAAACAT-TACAGCAGCACCC-----
Abbassa_amhΔy_h1tg0002121	11804	TAACTATTACAGCTCATAAAAAACAT-TACAGCAGCACCCAGAGTCATTTTAGCATTTCTA
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	12448	TCCTCATTTTGTGTACGCAACCAATATACTGCAACAATAACAGAATTTCTC-----
		:13870.....:13880.....:13890.....:13900.....:13910.....:13920
Abbassa_amh_h2tg0001191	12738	-----TAACTATTGCAAACCAG---GAAATAATCTGGTTTATAAG--GAC
Abbassa_amhΔy_h1tg0002121	11863	AAATTATAAGAAAAGTAACATATTGCAAACCAG---GAAATAATCTGGTTTATAAG--GAC
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	12497	-ACCGGGGGAGGAAATAACGCATGCACACAAAAGCAAAAGGTGCTTGACGTCCTGAGCAGAG
		:13930.....:13940.....:13950.....:13960.....:13970.....:13980
Abbassa_amh_h2tg0001191	12778	TGCAGTCTTTTAACACTTTTATAT-----TAATGTTTTT
Abbassa_amhΔy_h1tg0002121	11918	TGCAGTCTTTTAACACTTTTATAT-----TAATGTTTTT
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	12556	TTCAATGAACGGCTCTGTGTGTGTGTCTGAGTGTGTGTGACTCGTCAAGTCAAACTTTG
		:13990.....:14000.....:14010.....:14020.....:14030.....:14040
Abbassa_amh_h2tg0001191	12813	AAGTACAAAATATACTGCTATTTGTTTTATTTTGCTTAATTTTCATTCAGTTAATATCTT
Abbassa_amhΔy_h1tg0002121	11953	AAGTACAAAATATACTGCAATTTGTTTTATTTTGCTTAATTTTCATTCAGTTAATATCTT
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	12616	GGGGGGGAAGTAGATCCTGGTTTATCCTG--TCGTTAAATGATAATTC-----TTTTTT
		:14050.....:14060.....:14070.....:14080.....:14090.....:14100
Abbassa_amh_h2tg0001191	12873	TTTCTAATTTTTAGAGAAGCTTTGTGG-----AAAAGAACTGTTTCG
Abbassa_amhΔy_h1tg0002121	12013	TTTCTAATTTTTAGAGAAGCTTTGTGG-----AAAAGAACTGTTTCG
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	12668	TTTCTGATTTTTGCTGAATCCAGTTGCTATAATTGGCACCAGAACAAAGAACTACATA
		:14110.....:14120.....:14130.....:14140.....:14150.....:14160
Abbassa_amh_h2tg0001191	12915	GGAGCAAAATATTTTCAGTTCCAATCCG-----CTTTAGTTTGTTTCATAACTGAA
Abbassa_amhΔy_h1tg0002121	12055	GGAGCAAAATATTTTCAGTTCCAATCCG-----CTTTAGTTTGTTTCATAACTGAA
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	12728	TGAACAGATTAGATAGCACCTTAAATTCAAACACAATATTTAAGTTTCACTCAGAGCTGGA
		:14170.....:14180.....:14190.....:14200.....:14210.....:14220
Abbassa_amh_h2tg0001191	12967	-----ATGTCATTAAATTTATTTTCATCTATCTCAGATGAGAAATGAA--
Abbassa_amhΔy_h1tg0002121	12107	-----ATGTCATTAAATTTATTTTCATCTATCTCAGATGAGAAATGAA--
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	12788	CAACAGCCAGACTGTAAACACTACTCCACACCAAACATGACAGT-ACCTATGAATTC
		:14230.....:14240.....:14250.....:14260.....:14270.....:14280
Abbassa_amh_h2tg0001191	13009	--TCAGATTGTTTCATCA-----ACTGTGTG-GTCTGCCTGCAT-----TT
Abbassa_amhΔy_h1tg0002121	12149	---TCAGATTGTTTCATCA-----ACTGTGTG-GTCTGCCTGCAT-----TT
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	12847	TGCTCAGGGTGACCATAGTGGTGGTTAGTGTGTGTGTTTGTTGTGTGTGTGTGTGTGTGTG
		:14290.....:14300.....:14310.....:14320.....:14330.....:14340
Abbassa_amh_h2tg0001191	13046	TGGGTGAACCTTACCATTAAAGGTCATGGGAAGAGAATGGGTTATCTTAATGAACCCACAC
Abbassa_amhΔy_h1tg0002121	12186	TGGGTGAACCTTACCATTAAAGGTCATGGGAAGAGAATGGGTTATCTTAATGAACCCACAC
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	12907	TG
		:14350.....:14360.....:14370.....:14380.....:14390.....:14400
Abbassa_amh_h2tg0001191	13106	TGGAGATCTGGAAGCATTACAGCTGGAAGACGAGCAGGAACATGTTGTCAGAGGGGAGAC
Abbassa_amhΔy_h1tg0002121	12246	TGGAGATCTGGAAGCATTACAGCTGGAAGACGAGCAGGAACATGTTGTCAGAGGGGAGAC
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	12953	-----GTACAGAAGC---CGGTCTTGGAGCGCATTGGGTTAGTGCAGAGTTTGAAGCACCC

		14410.....14420.....14430.....14440.....14450.....14460
Abbassa_amh_h2tg0001191	13166	CTGAGTGGCTTCGAGGAGCTGTTACTCCCTCAGCATTCTCACAGCTGCAGGCTTGTGT
Abbassa_amhΔy_h1tg0002121	12306	CTGAGCGGCTTCGAGGAGCTGTTACTCCCTCAGCATTCTCACAGCTGCAGGCTTGTGT
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	13005	GTGAATGAGGAGAGTGCCTTGGTCCACACCTGGACATTGTGATAGTT---TATTTAATGT
		14470.....14480.....14490.....14500.....14510.....14520
Abbassa_amh_h2tg0001191	13226	GCAGACAGTC-----AAGGTCTCGGAGCCATTGTGGACGTTTCCCCCG
Abbassa_amhΔy_h1tg0002121	12366	GCAGACAGTC-----AAGGTCTCGGAGCCATTGTGGACGTTTCCCCCG
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	13062	TGAGGTAGTTTTCATCAATTACCTGAAACATTCAAAGACAGACGAGGACATC-----
		14530.....14540.....14550.....14560.....14570.....14580
Abbassa_amh_h2tg0001191	13271	GTGATAAAGCCAAGGTTCCACATACCTTATAAATC---ATCAGTGAGGAATGCGAGGAAA
Abbassa_amhΔy_h1tg0002121	12411	GTGATAAAGCCAAGGTTCCACATACCTTATAAATC---ATCAGTGAGGAATGCGAGGAAA
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	13114	ATGAGTGATTCTTAAGGCTTCCAGAAATAACACAGCAAAAACACAGACAGCTGATTGAGGA
		14590.....14600.....14610.....14620.....14630.....14640
Abbassa_amh_h2tg0001191	13328	TGTTTCATTGTATCAAGGCGGTGTTGAAGC-----ACACCAGC---CT
Abbassa_amhΔy_h1tg0002121	12468	TGTTTCATTGTATCAAGGCGGTGTTGAAGC-----ACACCAGC---CT
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	13174	TCTAAACCCTAACAAGTTCAAAATCAAAGTCTTTACTTTTAATCTAACACCTACTTCTCT
		14650.....14660.....14670.....14680.....14690.....14700
Abbassa_amh_h2tg0001191	13368	GGATGTTTTTCAGTCACA-----CTTGTTGGGAACAGGAATGCACTTT
Abbassa_amhΔy_h1tg0002121	12508	GGATGTTTTTCAGTCACA-----CTTGTTGGGAACAGGAATGCACTTT
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	13234	TACCTTGTTCAATCAGACAAACAGCTTGCAAGACACATGGAAAACAGGCATCCTGTCTC
		14710.....14720.....14730.....14740.....14750.....14760
Abbassa_amh_h2tg0001191	13411	GATGAAAAAGTA-----ATCAACATCTACACTCC-----TGTT-----T
Abbassa_amhΔy_h1tg0002121	12551	GATGAAAAAGTA-----ATCAACATCTACACTCC-----TGTT-----T
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	13294	TCTCACTCCCTACCAGCCTCTCTCGCTCACCCCTCTATCCACCCTCAGATTGTTCTCCGCC
		14770.....14780.....14790.....14800.....14810.....14820
Abbassa_amh_h2tg0001191	13445	CTCCCCATCATGTATTCACTCTCTACAGTAGCACACTTAAGTTTTCAGGTTGGAAAAA
Abbassa_amhΔy_h1tg0002121	12585	CTCCCCATCATGTATTCACTCTCTACAGTAGCACACTTAAGTTTTCAGGTTGGAAAAA
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	13354	CTTCCCCTCTCCTCTCCCCTTCCCCTCAGCCCCAAACC---CTATCTAGGTGGGAGCT
		14830.....14840.....14850.....14860.....14870.....14880
Abbassa_amh_h2tg0001191	13505	GGACAAAAACACAGAAGACATACATTTCTGGGGAATCTCAT---CTGTCCATGTTGTA
Abbassa_amhΔy_h1tg0002121	12645	GGACAAAAACACAGAAGACATACATTTCTGGGGAATCTCAT---CTGTCCATGTTGTA
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	13410	GGGGAG-----CTGGGAGGTGGTGAGGTACCATGCATGCTCTG
		14890.....14900.....14910.....14920.....14930.....14940
Abbassa_amh_h2tg0001191	13560	AGGTTGTAFCCTCATTACCCGAAGCCAAAGC-----CGGTAACCGGGGAACGCCACAG
Abbassa_amhΔy_h1tg0002121	12700	AGGTTGTAFCCTCATTACCCGAAGCCAAAGC-----CGGTAACCGGGGAACGCCACAG
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	13449	AGTCC---TCCACATGCTCCAGCACCACCAGAACTGCTGGTCGGTGGCGGAGGGGCGAG
		14950.....14960.....14970.....14980.....14990.....15000
Abbassa_amh_h2tg0001191	13614	GCCTGGCTTCAGGTGGAAAGCTTCAGTGC--ACGGACCTTTTGGGAGGCTTCTCTGAGG
Abbassa_amhΔy_h1tg0002121	12754	GCCTGGCTTCAGGTGGAAAGCTTCAGTGC--ACGGGCTTTTGGGAGGCTTCTCTGAGG
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	13506	A-----CGGGGGGAGTAGTGCACATGCAATGGAC---GAGAG-----GAGG

Abbassa_amh_h2tg0001191	13672	15010.....15020.....15030.....15040.....15050.....15060
Abbassa_amhΔy_h1tg0002121	12812	CATCACAGGCATTTCGACACAGAATAAGGTAACACGTCGTGT-----GAACTGAAGCAG
Abbassa_amh_5'UTR	29	CATCACAGGCATTTCGACACAGAATAAGGTAACACGTCGTGT-----GAACTGAAGCAG
Abbassa_amhy_h1tg0002121	13544	AGGCAGAGGAGGCTGAGAGAGAGGAAGAGGACAGGGATGCAGCAGCAGAGACAGAAGCAG
Abbassa_amh_h2tg0001191	13724	15070.....15080.....15090.....15100.....15110.....15120
Abbassa_amhΔy_h1tg0002121	12864	CAGAAGCTGTTTGTTTTTACAGACCTCACTGGACCATTATCCTCAAGTTAGTGACTGA
Abbassa_amh_5'UTR	29	CAGAAGCTGTTTGTTTTTACAGACCTCACTGGACCATTATCCTCAAGTTAGTGACTGA
Abbassa_amhy_h1tg0002121	13604	CAGAGGTAGAGGATG-----AGATGGAGAGGGATGATTGTGCTCTCTGTGGTGAGAGA
Abbassa_amh_h2tg0001191	13783	15130.....15140.....15150.....15160.....15170.....15180
Abbassa_amhΔy_h1tg0002121	12923	AGCAGCTCTCTTATGC-AGGACTACATTATGTTTATTATAACGTTCTCCATTCTTTTTTA
Abbassa_amh_5'UTR	29	AGCAGCTCTCTTATGC-AGGACTACATT--GTTTATTATAACGTTCTCCATTCTTTTTTA
Abbassa_amhy_h1tg0002121	13659	GGAGAGGGAAGACGCGAGGAGTGGAGGAGTCTGATCGAG-----
Abbassa_amh_h2tg0001191	13842	15190.....15200.....15210.....15220.....15230.....15240
Abbassa_amhΔy_h1tg0002121	12980	AAGCTGACATATTTTTTAAACAAT----GTCATTAATTGTGGTTTTTTAATCATCCATC
Abbassa_amh_5'UTR	29	AAGCTGACATATTTTTTAAACAAT----GTCATTAATTGTGGTTTTTTAATCATCCATC
Abbassa_amhy_h1tg0002121	13700	-----AAGACGCTGGGGAATCAGAGTGCCTGGATGTCGATGAGGAGGG
Abbassa_amh_h2tg0001191	13897	15250.....15260.....15270.....15280.....15290.....15300
Abbassa_amhΔy_h1tg0002121	13035	AATTTTCATATCCATCTCTCTGATTGAGGCTTCGAGGAGGGCA-----
Abbassa_amh_5'UTR	29	AATTTTCATATCCATCTCTCTGATTGAGGCTTCGAGGAGGGCA-----
Abbassa_amhy_h1tg0002121	13743	GACGCTATG-----CAGGGGTGAGGAGGGGACAGGGAGAGCGTGGGAGG
Abbassa_amh_h2tg0001191	13939	15310.....15320.....15330.....15340.....15350.....15360
Abbassa_amhΔy_h1tg0002121	13077	---GGACACAGTGAACAGGCT--GTTACTCTTTCTCAGGGCTGACACACACA-----
Abbassa_amh_5'UTR	29	---GGACACAGTGAACAGGCT--GTTACTCTTTCTCAGGGCTGA-----
Abbassa_amhy_h1tg0002121	13788	AGAGGGGCTATGCAGGACCGACTGCGTGCGGCTGTGCTGGGCTGGATAACGAGAGGGG
Abbassa_amh_h2tg0001191	13987	15370.....15380.....15390.....15400.....15410.....15420
Abbassa_amhΔy_h1tg0002121	13117	CACACACACACACACACACACCCATCAC-----TAATGATGCTG
Abbassa_amh_5'UTR	29	CACACACACACACACACACACCCATCAC-----TAATGATGCTG
Abbassa_amhy_h1tg0002121	13848	CATAGGCGAGGACACGGGCGCCAGGCGCGTGGAGGCTGGCTGGGGAGTGGTGCTTGCTG
Abbassa_amh_h2tg0001191	14026	15430.....15440.....15450.....15460.....15470.....15480
Abbassa_amhΔy_h1tg0002121	13156	ACTTCTCAAAAACTCGAGTATCTTATACAGAGAAGCATTTTTTTAATCAATTTATTTTACA
Abbassa_amh_5'UTR	29	ACTTCTCAAAAACTCGAGTATCTTATACAGAGACGCATTTTTTTAATCAATTTATTTTACA
Abbassa_amhy_h1tg0002121	13908	GGTTTGGGAGGA---GTTAGAGGAAGAGGAGGAGAGAGACTGAGCAGAGACTTG----
Abbassa_amh_h2tg0001191	14086	15490.....15500.....15510.....15520.....15530.....15540
Abbassa_amhΔy_h1tg0002121	13216	TCGCAGGCCACATGCAGC-----CCACTTTGAACCTTTTGTGAACCGGACCAGTGAAG
Abbassa_amh_5'UTR	29	TCGCAGGCCACATGA-----ACTTTGAACCTTTTGTGAACCGGACCAGAGAAG
Abbassa_amhy_h1tg0002121	13960	---AGGCCTCCTGAGGTGGGAGCGTTGCCCAAACTGATGGGAGGACACTGAGGGAA-
Abbassa_amh_h2tg0001191	14138	15550.....15560.....15570.....15580.....15590.....15600
Abbassa_amhΔy_h1tg0002121	13263	CTTCCCTTTCTGTCTCTGTGAAGAGGTTTACCTACACATTGACCTCAGAGAGCT----
Abbassa_amh_5'UTR	29	CTTCCCTTTCTGTCTCTGTGAAGAGGTTTACCTACACATTGACCTCAGAGAGCT----
Abbassa_amhy_h1tg0002121	14015	-----CCACGTGGTGAATAACCTGCAAATCATACAGCAGAAATGAGGGGA

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.....15610.....15620.....15630.....15640.....15650.....15660
Abbassa_amh_h2tg0001191 14193 -----GTGGAAACAGGA-AGTGCAGTTTCAACCA---
Abbassa_amhΔy_h1tg0002121 13318 -----GTGGAAACAGGA-AGTGCAGTTTCAACCA---
Abbassa_amh_5'UTR 29 -----
Abbassa_amhy_h1tg0002121 14062 GGAGGAGGAGGAGGAGGAGGCGAGAGAGTGGAGACAAGAGAGAGCAGTGGCAAAAAGAG

.....15670.....15680.....15690.....15700.....15710.....15720
Abbassa_amh_h2tg0001191 14221 -----CA
Abbassa_amhΔy_h1tg0002121 13346 -----CA
Abbassa_amh_5'UTR 29 -----
Abbassa_amhy_h1tg0002121 14122 CAGGGGTGGGGACAGAGAGAGAAGCAAGGGCTGAGCCAGGTTGTGCAAGCGCCAAGCA

.....15730.....15740.....15750.....15760.....15770.....15780
Abbassa_amh_h2tg0001191 14223 TATCT-----GTTTTCTACT-----C
Abbassa_amhΔy_h1tg0002121 13348 TATCT-----GTTTTCTACT-----C
Abbassa_amh_5'UTR 29 -----
Abbassa_amhy_h1tg0002121 14182 AGTCTGAGACAAGCACACAGAAAGCAAACAGAGCTCAGTCCACTGGAAATGTACGGAGCC

.....15790.....15800.....15810.....15820.....15830.....15840
Abbassa_amh_h2tg0001191 14240 AATTAAGAAAGTGCTGCTGTAATGAACTGAAGAAA-----TCTGTCAGCACAAACAG
Abbassa_amhΔy_h1tg0002121 13365 AATTAAGAAAGTGCTGCTGTAATGAACTGAAGAAA-----TCTGTCAGCACAAACAG
Abbassa_amh_5'UTR 29 -----
Abbassa_amhy_h1tg0002121 14242 AATTCAGCGCAGCCAGTGTAACG--CTGCAGGAAGTGAAATGACTTCTGATGCACTAACAC

.....15850.....15860.....15870.....15880.....15890.....15900
Abbassa_amh_h2tg0001191 14290 ATACTGTGGAC-----CAGCTGTA-----AAAACAAACTGCTA-----
Abbassa_amhΔy_h1tg0002121 13415 ATACTGTGGAC-----CAGCTGTA-----AAAACAAACTGCTA-----
Abbassa_amh_5'UTR 29 -----
Abbassa_amhy_h1tg0002121 14300 ACCCGGGCAAAACGCACACGCCAGCAGCGTGACCTGCATGAAATCAAACGGTCACTCGCGC

.....15910.....15920.....15930.....15940.....15950.....15960
Abbassa_amh_h2tg0001191 14324 -----TAGTAGATTAAAAAAA-ATTTCTTTAAGGGTTATATATTTGTTGGTTACT
Abbassa_amhΔy_h1tg0002121 13449 -----TAGTAGATTAAAAAAAATTTCTTTAAGGGTTATATATTTGTTGGTTACT
Abbassa_amh_5'UTR 29 -----
Abbassa_amhy_h1tg0002121 14360 TTTGTTATTAATGATTTCAATGAAAGTTTTGTGAAAATGTCACATTTCCGAGC-----

.....15970.....15980.....15990.....16000.....16010.....16020
Abbassa_amh_h2tg0001191 14375 TTGTCTTTTCATTAGGAAAAACTATCAAACTTGTGGAAGTTCACATTTTGCCTCGAGTG
Abbassa_amhΔy_h1tg0002121 13501 TTGTCTTTTCATTAGGAAAAACTATCAAACTTGTGGAAGTTCACATTTTGCCTCGAGCG
Abbassa_amh_5'UTR 29 -----
Abbassa_amhy_h1tg0002121 14415 --GTGTCTCCCTGCATTACCTAAACAGCCAGTCCACGTCAAAGTATGGCAGCACAGCG

.....16030.....16040.....16050.....16060.....16070.....16080
Abbassa_amh_h2tg0001191 14435 GGCCAGATTGGAGTCTTTGCGGGCGCACTTGGCATTACAAGGTAAATGCCGCCTACCTG
Abbassa_amhΔy_h1tg0002121 13561 GGCCAGATTGGAGTCTTTGCGGGCGCACTTGGCATTACAAGGTAAATGCCGCCTACCTG
Abbassa_amh_5'UTR 29 -----
Abbassa_amhy_h1tg0002121 14473 AGTCACAGT-----TTTGCTTCTCACCT-----GTCTTGCTGCCCTCGGG

.....16090.....16100.....16110.....16120.....16130.....16140
Abbassa_amh_h2tg0001191 14495 TGAAGTCTACTAACTGAGGATTTAGGTAGCGGGCTCCAACATGGTTCAGGTATGAAGA
Abbassa_amhΔy_h1tg0002121 13621 TGAAGTCT---ACTGAGGATTTAGGTAGCGGGCTCCAACATGGTTCAGGTATGAAGA
Abbassa_amh_5'UTR 29 -----
Abbassa_amhy_h1tg0002121 14515 CAAAGCTC-----CAGGAGGGATTTCAAC---GTACAGGTTTCCTCC

.....16150.....16160.....16170.....16180.....16190.....16200
Abbassa_amh_h2tg0001191 14555 TATCAGCATGACACCCCTCTTCCGTCACGG-----CAAACCAAATGGACTCAGACA
Abbassa_amhΔy_h1tg0002121 13677 TATCAGCATGACACCCCTCTTCCGTCACGG-----CAAACCAAATGGACTCAGACA
Abbassa_amh_5'UTR 29 -----
Abbassa_amhy_h1tg0002121 14554 TTTCAGCGC----CGCCCTCCAGACACAGTGCTTTCTTTCAGAGCGCGCGGGCTCAAAGA

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		16210.....16220.....16230.....16240.....16250.....16260
Abbassa_amh_h2tg0001191	14605	-----AAGTTCACCTCC-----AAACGTAAACTCAATAT
Abbassa_amhΔy_h1tg0002121	13727	-----AAGTTCACCTCC-----AAACGTAAACTCAATAT
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	14610	GTAAG AAGCGCACTCT GTCTATTGGCAGGGGAAGGCTCCTCAAGAA CCAGC ACT CTGAGCAT
		16270.....16280.....16290.....16300.....16310.....16320
Abbassa_amh_h2tg0001191	14633	TATAAGAAA---CATTTTATTAATTATCATAAATCGCAGGGGAG-AAAAAAAAACATTAA
Abbassa_amhΔy_h1tg0002121	13755	TATAAGAAA---CATTTTATTAATTATCATAAATCGCAGGGGAGAAAAAAAAACATTAA
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	14670	CCTGG GAAAGTGTAGTTTAGGTTATGTTAA AAATGAA ACTGC CATACC AGCAAGGACAA
		16330.....16340.....16350.....16360.....16370.....16380
Abbassa_amh_h2tg0001191	14689	TTCCATTTTTTCATTATAACATCTTAGGATAAAAGCACCAACATCAACAGTAACAATGT
Abbassa_amhΔy_h1tg0002121	13812	TTCCATTTTTTCATTATAACATCTTAGGATAAAAGCACCAACATC-AACAGTAACAATGT
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	14730	TTCTGTATTT-----CTTTTAAAGCTTTCATCACTTACAG----AATAGAACAGC
		16390.....16400.....16410.....16420.....16430.....16440
Abbassa_amh_h2tg0001191	14749	TTCCATGAAAAACCGAGGGCGTTT TGG AAAGTAGGTTTGCCATTATTGCACCTCAAACCTT
Abbassa_amhΔy_h1tg0002121	13871	TTCCATGAAAAACCGAGGGCGTTT TGG AAAGTAGGTTTGCCATTATTGCACCTCAAACCTT
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	14776	TTAGCTGAAAGATTGCGATCCG TTGG -----TCATTCCCTCG CCACCT
		16450.....16460.....16470.....16480.....16490.....16500
Abbassa_amh_h2tg0001191	14809	GCCCTGGCTTCACCAATCAGAGA---GCACTATACACATCCTGTAGGTC---ACGCGTG
Abbassa_amhΔy_h1tg0002121	13931	GCCCTGGCTTCACCAATCAGAGA---GCACTATACACATCCTGTAGGTC---ACGCGTG
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	14821	GGGAT--CTCAGGGGTGG GAGAGGGGCATC AGGAGCAC ACAGAGGC CCCGAGACGGG
		16510.....16520.....16530.....16540.....16550.....16560
Abbassa_amh_h2tg0001191	14862	TCCTTGAAATGTTACCCCCAATTC AAAGAGGGATTCAAACAAGACACCGAACCTCCTCCTT
Abbassa_amhΔy_h1tg0002121	13984	TCCTTGAAATGTTACCCCCAATTC AAAGAGGGATTCAAACAAGACACCGAACCTCCTCCTT
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	14879	TTACTGCA-----ACAGCGGGAGCACCTCAGAGGACTGGAGATACT----
		16570.....16580.....16590.....16600.....16610.....16620
Abbassa_amh_h2tg0001191	14922	AGAGACGCAAAATCTAGACAGAGGCATTTGTGAGATGAGGAAGATGCTGAAAGTCGT TGCC
Abbassa_amhΔy_h1tg0002121	14044	AGAGACGCAAAATCTAGACAGAGGCATTTGTGAGATGAGGAAGATGCTGAAAGTCGT TGCC
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	14920	-GGAAAGCGAAACAAACAAGTGGTTTATGTCACACCACCACATTACTGA-----TGCC
		16630.....16640.....16650.....16660.....16670.....16680
Abbassa_amh_h2tg0001191	14982	ATTTACAGCTTCT--CGAGATCAGATCGCTCAT AAAGCTCGGACTGATTGT CGGGGGTG
Abbassa_amhΔy_h1tg0002121	14104	ATTTACAGCTTCT--CGAGATCAGATCGCTCAT AAAGCTCGGACTGATTGT CGGGGGTG
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	14972	TCACT AAA ACTGT TAACA ATTTTATGTCAGCTGTCAGT CAAATAT TGACCAC CAACTATG
		16690.....16700.....16710.....16720.....16730.....16740
Abbassa_amh_h2tg0001191	15040	GGGGTGT-----ACGTGC CGGCAGGACTGTGTCTGAGGAGATC
Abbassa_amhΔy_h1tg0002121	14162	GGGGTGT-----ACGTGC CGGCAGGACTGTGTCTGAGGAGATC
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	15032	AGAAACTGTTTGTTTTTTGTCTCACAAGAC ACATCGAGGCTACGGCTTCTGCACACTTC
		16750.....16760.....16770.....16780.....16790.....16800
Abbassa_amh_h2tg0001191	15078	TGATGAGGGCAGCTGATACATTTTACCTTG-----AAATACACTGACTGAAGGGTGGC
Abbassa_amhΔy_h1tg0002121	14200	TGATGAGGGCAGCTGATACATTTTACCTTG-----AAATACACTGACTGAAGGGTGGC
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	15092	TGCTGC GGGCACTTTAAGCTTGTTCACAGTTCTC ACAGGA ACCTGCCAGAGAACAGG

Abbassa_amh_h2tg0001191	15131	16810.....16820.....16830.....16840.....16850.....16860
Abbassa_amhΔy_h1tg0002121	14253	CCTGGTCCCTGAGTTGGGTCGTAGAGGGACTTTGTCTATGCCACCTGAAGGTAAATTACCGT
Abbassa_amh_5'UTR	29	CCTGGTCCCTGAGTTGGGTCGTAGAGGGACTTTGTCTATGCCACCTGAAGGTAAATTACCGT
Abbassa_amhy_h1tg0002121	15152	CTATTTTTTCCTCTAGCCGCTAGCCTACTTTAGCTCTTCAC-----TCACCGC
Abbassa_amh_h2tg0001191	15191	16870.....16880.....16890.....16900.....16910.....16920
Abbassa_amhΔy_h1tg0002121	14313	AACATGCAGCAGATTAGGAAACTTGTTCCTTCAAGCAGTGTGGGAGTTCTCTGAGTTAAG
Abbassa_amh_5'UTR	29	AACATGCAGCAGATTAGGAAACTTGTTCCTTCAAGCAGTGTGGGAGTTCTCTGAGTTAAG
Abbassa_amhy_h1tg0002121	15201	GTCA--CTGCAGTTTAAGAGACTGGGACAAAACAATACTGATCAGCCGTTCT--AATTCAG
Abbassa_amh_h2tg0001191	15251	16930.....16940.....16950.....16960.....16970.....16980
Abbassa_amhΔy_h1tg0002121	14373	ACCTTTGGCAGGATTTTCAGTAAACAGCCT---TGACTGCAAAGCTCT-----
Abbassa_amh_5'UTR	29	ACCTTTGGCAGGATTTTCAGTAAACAGCCT---TGACTGCAAAGCTCT-----
Abbassa_amhy_h1tg0002121	15257	CGCTGTCAAGCAGCTCTCTCAGATTTAGCTTGCTGTGACTGCATACATTTACAGCTTTGAG
Abbassa_amh_h2tg0001191	15296	16990.....17000.....17010.....17020.....17030.....17040
Abbassa_amhΔy_h1tg0002121	14418	-GAAAGATTATCTACGAATAATGTACCAGGATGCAGTATGATGCAGAAGCTGCACAGCTTT
Abbassa_amh_5'UTR	29	-GAAAGATTATCTACGAATAATGTACCAGGATGCAGTATGATGCAGAAGCTGCACAGCTTT
Abbassa_amhy_h1tg0002121	15317	CGAAGGCCCTGTTCACTGGGATTCTATTAGGAACAATAAT-----AACAGCGCGC---
Abbassa_amh_h2tg0001191	15355	17050.....17060.....17070.....17080.....17090.....17100
Abbassa_amhΔy_h1tg0002121	14477	AAAGCCAAATCACACCCAGAAATACTTTTAAAAACTATAAAGCTGCCTAAATCTG-TA
Abbassa_amh_5'UTR	29	AAAGCCAAATCACACCCAGAAATACTTTTAAAAACTATAAAGCTGCCTAAATCTG-TA
Abbassa_amhy_h1tg0002121	15367	-AAACACCATCACA-CACAGGGATGCTCTC-----TTACGCAATGCCACCAATGCGCTA
Abbassa_amh_h2tg0001191	15414	17110.....17120.....17130.....17140.....17150.....17160
Abbassa_amhΔy_h1tg0002121	14536	TGTAATGAATGGAAT-----ACCTCCACCTTCCTCAAAGTGCTCTGACAGGCACGTAC
Abbassa_amh_5'UTR	29	TGTAATGAATGGAAT-----ACCTCCACCTTCCTCAAAGTGCTCTGACAGGCACGTAC
Abbassa_amhy_h1tg0002121	15420	CATGTTGAGCAGAGGTGTGGAAACAGTGTCAATCGCAGTGTGTAATATCAAATTATGA
Abbassa_amh_h2tg0001191	15468	17170.....17180.....17190.....17200.....17210.....17220
Abbassa_amhΔy_h1tg0002121	14590	ACCCCT-----GCCTCCGCCCGCGGTGTCCCTCCAGATTAAAGATTCAAAGG
Abbassa_amh_5'UTR	29	ACCCCT-----GCCTCCGCCCGCGGTGTCCCTCCAGATTAAAGATTCAAAGG
Abbassa_amhy_h1tg0002121	15480	TCTCACAGAGGATTGGGGATTTTAACCAAATGCAGTTACTCGCT----AAATCCGGTAA
Abbassa_amh_h2tg0001191	15516	17230.....17240.....17250.....17260.....17270.....17280
Abbassa_amhΔy_h1tg0002121	14638	TTAGACTGGGCTGTGAGAAAGCCACCAGGTGAGCTTGTGTCTAAGATTCTTAAACATA
Abbassa_amh_5'UTR	29	TTAGACTGGGCTGTGAGAAAGCCACCAGGTGAGCTTGTGTCTAAGATTCTTAAACATA
Abbassa_amhy_h1tg0002121	15535	TCAGATTAGG---AAAGGAAGCCACTTGCCATCCT---TGCAGAACCCCTTAACGCCT
Abbassa_amh_h2tg0001191	15576	17290.....17300.....17310.....17320.....17330.....17340
Abbassa_amhΔy_h1tg0002121	14698	AAACCCCTGCAGCACAAACAGGAGGAGAGTAGTATTTCATCAATAGCTGCGATTTCCTTGTTT
Abbassa_amh_5'UTR	29	AAACCCCTGCAGCACAAACAGGAGGAGAGTAGTATTTCATCAATAGCTGCGATTTCCTTGTTT
Abbassa_amhy_h1tg0002121	15587	CCTTTTCTGCGATTTAAAGAGAACACAAAGTTCTTCAGTCAGTTCTGCGCTTTAGCATTCCTT
Abbassa_amh_h2tg0001191	15636	17350.....17360.....17370.....17380.....17390.....17400
Abbassa_amhΔy_h1tg0002121	14758	TAA-----GTGAAGGAGAGCACCGTGCTGTCTGACTAGTAGTATTAAAACTGACA
Abbassa_amh_5'UTR	29	TAA-----GTGAAGGAGAGCACCGTGCTGTCTGACTAGTAGTATTAAAACTGACA
Abbassa_amhy_h1tg0002121	15647	TGAGACTGACATGTGAACAGTAG-GCAGTGCTGCGCA-----ATGACGCCCTGACG

Abbassa_amh_h2tg0001191	15687	17410.....:17420.....:17430.....:17440.....:17450.....:17460
Abbassa_amhΔy_h1tg0002121	14809	GAAATCTGAAGACACAATCAAAAGCATAACATGTAACCT-GCAATTCGTATCAAAACACCAA-
Abbassa_amh_5'UTR	29	GAAATCTGAAGACACAATCAAAAGCATAACATGTAACCT-GCAATTCGTATCAAAACACCAA-
Abbassa_amhy_h1tg0002121	15697	GTCATCTTAG-----TAAAAACAGCTGCTGTGAATAGTGTTTGTAGGAGACTCTGCT
Abbassa_amh_h2tg0001191	15745	:17470.....:17480.....:17490.....:17500.....:17510.....:17520
Abbassa_amhΔy_h1tg0002121	14867	GAATAAGAAATCA----AAACGCATCGACAATAATTACAAAATACCTCTCAGTGCTGG
Abbassa_amh_5'UTR	29	GAATAAGAAATCA----AAACGCATCGACAATAATTACAAAATACCTCTCAGTGCTGG
Abbassa_amhy_h1tg0002121	15749	GTAAATGAACATCATTGTAAAGGACATCTGCAATAAATCTCATGCAATCCATC-----
Abbassa_amh_h2tg0001191	15801	:17530.....:17540.....:17550.....:17560.....:17570.....:17580
Abbassa_amhΔy_h1tg0002121	14923	TAACAAATGGACTAGTCTTAATCTTAAATGACTTTTCTCTTCACTTGCACACGAGTGCA
Abbassa_amh_5'UTR	29	TAACAAATGGACTAGTCTTAATCTTAAATGACTTTTCTCTTCACTTGCACACGAGTGCA
Abbassa_amhy_h1tg0002121	15801	TAGCAGAGAATCATCTTTAATCCCATG----TTCTAGCCTGCACTGTTAGACACTTCAA
Abbassa_amh_h2tg0001191	15861	:17590.....:17600.....:17610.....:17620.....:17630.....:17640
Abbassa_amhΔy_h1tg0002121	14983	CGGGACAGGA-----GTTTTATTTT-----TCTATAAAGCTTTGATTATT
Abbassa_amh_5'UTR	29	CGGGACAGGA-----GTTTTATTTT-----TCTATAAAGCTTTGATTATT
Abbassa_amhy_h1tg0002121	15856	TGTAGTATGACATTTGCAATGTGGGTTTTATTTTAGCTCACCTAACACGTTCTGGCT---
Abbassa_amh_h2tg0001191	15901	:17650.....:17660.....:17670.....:17680.....:17690.....:17700
Abbassa_amhΔy_h1tg0002121	15023	ACACTAATATTCCCTTAGATATGCGCTGGCAAGTGAAAAATTAAAAAAAACCAA-----
Abbassa_amh_5'UTR	29	ACACTAATATTCCCTTAGATATGCGCTGGCAAGTGAAAAATTAAAAAAA--ACCAA-----
Abbassa_amhy_h1tg0002121	15913	-----TTCAACAAAGAAAAATTAGCAGCTTAAAAATGTAACAGTCTTTAATGTGG
Abbassa_amh_h2tg0001191	15956	:17710.....:17720.....:17730.....:17740.....:17750.....:17760
Abbassa_amhΔy_h1tg0002121	15076	--ACAAAAACACACACGTACAACTGAGCTTTAGTGTAAATCCCACTATCAGAG-----
Abbassa_amh_5'UTR	29	--ACAAAA--ACACACGTACAACTGAGCTTTAGTGTAAATCCCACTATCAGAG-----
Abbassa_amhy_h1tg0002121	15964	GGTTAAATTTACACAAGTTTAAAT--ACATTTGATTTTATCAGGTGGTCAAAATGAAAA
Abbassa_amh_h2tg0001191	16007	:17770.....:17780.....:17790.....:17800.....:17810.....:17820
Abbassa_amhΔy_h1tg0002121	15125	---GAAAAAGGAAGCCT-GTCTGATCT--CACTCACACACACACACACTAAGACAAGT
Abbassa_amh_5'UTR	29	---GAAAAAGGAAGCCT-GTCTGATCTCACACACACACACACACACTAAGACAAGT
Abbassa_amhy_h1tg0002121	16022	GAATGAAAGAAAAGGCCTAGCCTTCTCT--TA-----AGGTAAACAGAGAC
Abbassa_amh_h2tg0001191	16060	:17830.....:17840.....:17850.....:17860.....:17870.....:17880
Abbassa_amhΔy_h1tg0002121	15180	GTTTCACATCAGCTCACGCGGCGAGGTACGCGCTCGTCAGTAAGACGTCTACAGGCGGTG
Abbassa_amh_5'UTR	29	GTTTCACATCAGCTCACGCGGCGAGGTACGCGCTCGTCAGTAAGACGTCTACAGGCGGTG
Abbassa_amhy_h1tg0002121	16066	TTTTTACCTTGG-----GAAGGGGGAGGCTATTAGCTGCTATA-----ATAGATGATG
Abbassa_amh_h2tg0001191	16120	:17890.....:17900.....:17910.....:17920.....:17930.....:17940
Abbassa_amhΔy_h1tg0002121	15240	TGTGTAAAGAGGCTGACGCGCAGTTCTGTATGCACCGGTGAAGATTTTGA-----TTG
Abbassa_amh_5'UTR	29	TGTGTAAAGAGGCTGACGCGCAGTTCTGTATGCACCGGTGAAGATTTTGA-----TTG
Abbassa_amhy_h1tg0002121	16114	T-----TATTTTAATGCATGCTTTATTATGGAAGGTGTGATGTTAAACCAGCCTTA
Abbassa_amh_h2tg0001191	16173	:17950.....:17960.....:17970.....:17980.....:17990.....:18000
Abbassa_amhΔy_h1tg0002121	15293	TAAGGTCTGA----ACTGCCCTCGCTTGGAAACAGAAGCACCATTTTTCCTGCAGAATCT
Abbassa_amh_5'UTR	29	TAAGGTCTGA----ACTGCCCTCGCTTGGAAACAGAAGCACCATTTTTCCTGCAGAATCT
Abbassa_amhy_h1tg0002121	16167	TCACACATGATAGCTATGTGTCAGCATATTTATAAAGGCATCTTTT-----CAAGCTTT

Abbassa_amh_h2tg0001191	16229	18010.....18020.....18030.....18040.....18050.....18060
Abbassa_amhΔy_h1tg0002121	15349	GGGTTGGTAAAAA---ATTAAACACCAAAACAAACAAAA--AAACAACAATAAATC
Abbassa_amh_5'UTR	29	GGGTTGGTAAAAA---ATTAAACACCAAAACAAACAAAA--AACCAACAATAAATC
Abbassa_amhy_h1tg0002121	16221	GGCTTAAAGAGAAACACTATTATATAATGTACATATATAAATATCTAACCATGACAATTA
Abbassa_amh_h2tg0001191	16283	18070.....18080.....18090.....18100.....18110.....18120
Abbassa_amhΔy_h1tg0002121	15403	AAAGAAGTGAAAATACCTGAAACAAGTGATAACAGTTCTAGTACTG-----GAAT
Abbassa_amh_5'UTR	29	AAAGAAGTGAAAATACCTGAAACAAGTGATAACAGTTCTAGTACTG-----GAAT
Abbassa_amhy_h1tg0002121	16281	CATAACAATTACATAGCCGAAACAGCTGAACAC--TCTTGCACTGCCACTGCAAAGAGA
Abbassa_amh_h2tg0001191	16333	18130.....18140.....18150.....18160.....18170.....18180
Abbassa_amhΔy_h1tg0002121	15453	CTGGTGGCGTTTGAGCCGC-----
Abbassa_amh_5'UTR	29	CTGGTGGCGTTTGAGCCGC-----
Abbassa_amhy_h1tg0002121	16338	TTAGGGGCTGCAGAGCGGCGTAACAAGTTAGTATTAGTTAACAGTAATAACCTTGGCTAT
Abbassa_amh_h2tg0001191	16352	18190.....18200.....18210.....18220.....18230.....18240
Abbassa_amhΔy_h1tg0002121	15472	-----CGCACCTTTGTGTAATAAACACACAGCCT-----CTGAGTTTGT
Abbassa_amh_5'UTR	29	-----CGCACCTTTGTGTAATAAACACACAGCCT-----CTGAGTTTGT
Abbassa_amhy_h1tg0002121	16398	CACAGGTTAGTGTATACTTTCTTGGGTGATGGATGCCGAACCTTTCACAGCTATCTTTGA
Abbassa_amh_h2tg0001191	16391	18250.....18260.....18270.....18280.....18290.....18300
Abbassa_amhΔy_h1tg0002121	15511	GGCTGCGGGCGATGTGTGTGTGTGTGTG-----TGTGTGTGT-----
Abbassa_amh_5'UTR	29	GGCTGCGGGCGATGTGTGTGTGTGTGTG-----TGTGTGTGTGTGTGTGTGTGTGT
Abbassa_amhy_h1tg0002121	16458	GAGTAACACAGTCATTATCTATTTTTGGTACTGCAAGATGTGTGCTTAATAATTTTATA
Abbassa_amh_h2tg0001191	16428	18310.....18320.....18330.....18340.....18350.....18360
Abbassa_amhΔy_h1tg0002121	15560	-----TTTCAGGTGCTGATCTGCAGCCATGTTAAGGTC
Abbassa_amh_5'UTR	29	GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTTCAGGTGCTGATCTGCAGCCATGTTAAGGTC
Abbassa_amhy_h1tg0002121	16518	ATATAGCAATAATAATTTTCATAAATGTTCCAAAGA-----CGCAGAAATGTCTACAGC
Abbassa_amh_h2tg0001191	16461	18370.....18380.....18390.....18400.....18410.....18420
Abbassa_amhΔy_h1tg0002121	15620	CTCTGGTGGCAATGCTTTGCTCTGCTCAGCTTCAAGCCTCCTGTTACAGGGTGAA---T
Abbassa_amh_5'UTR	29	CTCTGGTGGCAATGCTTTGCTCTGCTCAGCTTCAAGCCTCCTGTTACAGGGTGAA---T
Abbassa_amhy_h1tg0002121	16573	CGGTTTCTCACAAGTCTAGGAAATGCACA---CTAAACTGCTCAAGCTGGACAAAAGCT
Abbassa_amh_h2tg0001191	16517	18430.....18440.....18450.....18460.....18470.....18480
Abbassa_amhΔy_h1tg0002121	15676	TTAAGGGTCACAATGCCAGCACCAAAACACCCCTTTTCACATATATATGTATATATATTTA
Abbassa_amh_5'UTR	29	TTAAGGGTCACAATGCCAGCACCAAAACACCCCTTTTCACATATATATGTATATATATTTA
Abbassa_amhy_h1tg0002121	16629	CTACAGCTCAGAGGACCAAAATAAACTGGACTTTGGAT-CGTCTCTTTAAATA---TCA
Abbassa_amh_h2tg0001191	16577	18490.....18500.....18510.....18520.....18530.....18540
Abbassa_amhΔy_h1tg0002121	15736	TATACTTATATATATTTATATAGACTGTATATAGTTACTTATTTTATATACCTTCTGTGTT
Abbassa_amh_5'UTR	29	TATACTTATATATATTTATATAGACTGTATATAGTTACTTATTTTATATACCTTCTGTGTT
Abbassa_amhy_h1tg0002121	16685	CATGCTCAAAATATTATGA-----TATATGAGAATTTTATTATGCAACACTATA--
Abbassa_amh_h2tg0001191	16637	18550.....18560.....18570.....18580.....18590.....18600
Abbassa_amhΔy_h1tg0002121	15796	TATGATGGAGATGTACAA---TTAAAGAAAACCTTATGTACAAAACAGTGTGTCTTGTTC
Abbassa_amh_5'UTR	29	TATGATGGAGATGTACAA---TTAAAGAAAACCTTATGTACAAAACAGTGTGTCTTGTTC
Abbassa_amhy_h1tg0002121	16734	-----GGATTTCCACAGTATTTAGGGCTGGTTGATATGGAAACACA-CGTGTCTTGTGT

		18610.....18620.....18630.....18640.....18650.....18660
Abbassa_amh_h2tg0001191	16694	ACCAACAGCGGGCC--GATGTATGTTTAAACATTAAACAGGGGC-----
Abbassa_amhΔy_h1tg0002121	15853	ACCAACAGCGGGCC--GATGTATGTTTAAACAATAACAGGGGCCCCCGTGGCCGTCGC
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	16787	CCCATTGTCTGCCTCCAGGTTTCCATATGGGACGGCTTCA-----
		18670.....18680.....18690.....18700.....18710.....18720
Abbassa_amh_h2tg0001191	16736	----CCCCGTGGCCGTCGCTCGGGCCCCGAGCCGGCTGCACGAGAGCACTTTCATCCAA
Abbassa_amhΔy_h1tg0002121	15910	TCGGGCCCCGTGGCCGTCGCTCGGGCCCCGAGCCGGCTGCACGAGAGCACTTTCATCCAA
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	16827	----CCCGGTGGTGG-----GGATCTGAAGAAGTCCGAGCGATAA-----GAA
		18730.....18740.....18750.....18760.....18770.....18780
Abbassa_amh_h2tg0001191	16791	AGGTGGCGTCTACAGTTGTACACGATGCATTTC--AAAGAACGAGACAATAGCATATTAAA
Abbassa_amhΔy_h1tg0002121	15970	AGGTGGCGTCTACAGTTGTACACGATGCATTTC--AAAGAACGAGACAATAGCATATTAAA
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	16866	GGAGGAAGAAGCCAGCTGCTAATAAAGCAATCTGAAACCAAAATCAAGCATAAAACA
		18790.....18800.....18810.....18820.....18830.....18840
Abbassa_amh_h2tg0001191	16849	TATGAGAAAGGAAATGCCAAAAACGGCTTTACAAATGTCCCTGTGTACAGCACCAAGTA
Abbassa_amhΔy_h1tg0002121	16028	TATGAGAAAGGAAATGCCAAAAACGGCTTTACAAATGTCCCTGTGTACAGCACCAAGTA
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	16926	TATACTGTAGCTTATGTAGCTGAATGGC--TACGAA-----CACAGAACTTTAAGTA
		18850.....18860.....18870.....18880.....18890.....18900
Abbassa_amh_h2tg0001191	16909	CTTGACTTGTTTTTGATGTTTTCATTACAGAATAAATAAGATCAGGCATAGTCCAAACTT
Abbassa_amhΔy_h1tg0002121	16088	CTTGACTTGTTTTTGATGTTTTCATTACAGAATAAATAAGATCAGGCATAGTCCAAACTT
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	16976	G-----ACTTTGCATTTAATTATTACAAGTTTGAGAAGGCTATATTTTCATCC--TTTT
		18910.....18920.....18930.....18940.....18950.....18960
Abbassa_amh_h2tg0001191	16969	AGCACCATTGTTTTTCAGACTGTGAGTCAAGTACACACACACTAATGCATTCTACAATGTC
Abbassa_amhΔy_h1tg0002121	16148	AGCACCATTGTTTTTCAGACTGTGAGTCAAGTACACACACACTAATGCATTCTACAATGTC
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	17027	AACAGTTTAACTTTAACT-----CAGAAACATTATTCCAATTAGAAATATT
		18970.....18980.....18990.....19000.....19010.....19020
Abbassa_amh_h2tg0001191	17029	AACACAATTCAGGATTT-----AAAAAAAAAAAAAAAAAAAAAAAAAAGGCAAA
Abbassa_amhΔy_h1tg0002121	16208	AACACAATTCAGGATTTAAAAAAAAAAAAAAAAAAAAAAAAAAGGCAAA
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	17075	TTCAAAAT-----GACAAAA-----
		19030.....19040.....19050.....19060.....19070.....19080
Abbassa_amh_h2tg0001191	17077	TGGAAAGACCGAC-----
Abbassa_amhΔy_h1tg0002121	16268	TGGAAAGACCGACAGCATAAATATAATCATCTAAATTATCCACAACCTATACAGTCAGAGA
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	17090	-----
		19090.....19100.....19110.....19120.....19130.....19140
Abbassa_amh_h2tg0001191	17090	-----
Abbassa_amhΔy_h1tg0002121	16328	ATGAATCACATTACAGTACAAACATTGTTTACAAAACAAATTACACCGTTTTTTAAAA
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	17090	-----
		19150.....19160.....19170.....19180.....19190.....19200
Abbassa_amh_h2tg0001191	17090	-----
Abbassa_amhΔy_h1tg0002121	16388	AGCAAACAAAGAGGTGTGAAACAAGTCCAGTAGTTTGTGTGGTTATGGTCAACTATGTT
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	17090	-----

		19210.....19220.....19230.....19240.....19250.....19260
Abbassa_amh_h2tg0001191	17090	-----
Abbassa_amhΔy_h1tg0002121	16448	TTCCCAGTGTGTGAGGATTTGCATGCATGACTGTGTGTGTATGTGTGTTTAACTAAA
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	17090	-----
		19270.....19280.....19290.....19300.....19310.....19320
Abbassa_amh_h2tg0001191	17090	-----
Abbassa_amhΔy_h1tg0002121	16508	CGCAGTAAATTTTCACATATCAGTCCACTTTCATTTAACCTGCATTTCCCTAACAGCAGC
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	17090	-----
		19330.....19340.....19350.....19360.....19370.....19380
Abbassa_amh_h2tg0001191	17090	-----
Abbassa_amhΔy_h1tg0002121	16568	GATAAATATGAATGCATGGATCTCTGCTGTTATGCTTAGCTTACAAAGAGGAATATTCT
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	17090	-----
		19390.....19400.....19410.....19420.....19430.....19440
Abbassa_amh_h2tg0001191	17090	-----
Abbassa_amhΔy_h1tg0002121	16628	GCTGCCGTTTGTGTGACTTCACAAACCGACGGGAAAGAAACGGTTAATAAATACACGCAA
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	17090	-----
		19450.....19460.....19470.....19480.....19490.....19500
Abbassa_amh_h2tg0001191	17090	-----
Abbassa_amhΔy_h1tg0002121	16688	ACTCACTGAACTCTGTTGTTCTTGGACATGTGGATTTCAGCTGTTTCGCTGAACCTTAACAG
Abbassa_amh_5'UTR	29	-----
Abbassa_amhy_h1tg0002121	17090	-----
		..
Abbassa_amh_h2tg0001191	17090	--
Abbassa_amhΔy_h1tg0002121	16748	AG
Abbassa_amh_5'UTR	29	--
Abbassa_amhy_h1tg0002121	17090	--