Figure S1. Alignment of cadherin cDNA sequences of pink bollworm from Akola, Maharashtra (AMH) with the susceptible allele *PgCad1* *s* (AY198374.1). Eight of the nine cDNA clones from three individuals (AMH-1, AMH-2, AMH-3) have no insertions or deletions. One cDNA clone (AMH-3\_16) has a single 3-bp deletion at base positions 72-74. Stars show nucleotides conserved in all of the sequences. The deletion is highlighted in gray.

AMH-3\_16 ATGGCGGGTGACGCCTGCATACTGGTGACGGTGCTTCTGACCTTCGCAACATCAGTTTTC 60

AMH-2\_4 ATGGCGGGTGACGCCTGCATACTGGTGACGGTGCTTCTGATCTTCGCAATATCAGTTTTC 60

AMH-2\_1 ATGGCGGGTGACGCCTGCATACTGGTGACGGTGCTTCTGATCTTCGCAATATCAGTTTTC 60

AMH-2\_5 ATGGCGGGTGACGCCTGCATACTGGTGACGGTGCTTCTGATCTTCGCAATATCAGTTTTC 60

AMH-3\_1 ATGGCGGGTGACGCCTGCATACTGGTGACGGTGCTTCTGGCCTTCGCAACATCAGTTTTC 60

AMH-3\_13 ATGGCGGGTGACGCCTGCATACTGGTGACGGTGCTTCTGACCTTCGCAACATCAGTTTTC 60

AY198374.1 ATGGCGGGTGACGCCTGCATACTGGTGACGGTGCTTCTGACCTTCGCAACATCAGTTTTC 60

AMH-1\_2 ATGGCGGGTGACGCCTGCATACTGGTGACGGTGCTTCTCACCTTCGCAACATCAGTTTTC 60

AMH-1\_7 ATGGCGGGTGACGCCTGCATACTGGTGACGGTGCTTCTGACCTTCGCAACATCAGTTTTC 60

AMH-1\_11 ATGGCGGGTGACGCCTGCATACTGGTGACGGTGCTTCTGACCTTCGCAACATCAGTTTTC 60

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AMH-3\_16 GGGCAAGAAAC---ATCGTCGAGATGTTACTACATGACTGACGCTATTCCGAGAGAACCG 117

AMH-2\_4 GGGCAAGAAACAGCATCGTCGAGATGTTACTACATGACTGACGCTATTCCGAGAGAACCG 120

AMH-2\_1 GGGCAAGAAACAGCATCGTCGAGATGTTACTACATGACTGACGCTATTCCGAGAGAACCG 120

AMH-2\_5 GGGCAAGAAACAGCATCGTCGAGATGTTACTACATGACTGACGCTATTCCGAGAGAACCG 120

AMH-3\_1 GGGCAAGAAACAGCATCGTCGAGATGTTACTACATGACTGACGCTATTCCGAGAGAACCG 120

AMH-3\_13 GGGCAAGAAACAGCATCGTCGAGATGTTACTACATGACTGACGCTATTCCGAGAGAACCG 120

AY198374.1 GGGCAAGAAACAACATCGTCGAGATGTTACTACATGACTGACGCTATTCCGAGAGAACCG 120

AMH-1\_2 GGGCAAGAAACAACATCGTCGAGATGTTACTACATGACTGACGCTATTCCGAGGGAACCG 120

AMH-1\_7 GGGCAAGAAACAGCATCGTCGAGATGTTACTACATGACTGACGCTATTCCGAGAGAACCG 120

AMH-1\_11 GGGCAAGAAACAGCATCGTCGAGATGTTACTACATGACTGACGCTATTCCGAGAGAACCG 120

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AMH-3\_16 AAACCGGATGATTTGCCTGATTTAGAATGGACTGGTGGATGGACCAACTGGCCTTTGATC 177

AMH-2\_4 AAACCGGATGATTTGCCTGATTTAGAATGGACTGGTGGATGGACCGACTGGCCTTTGATC 180

AMH-2\_1 AAACCGGATGATTTGCCTGATTTAGAATGGACTGGTGGATGGACCGACTGGCCTTTGATC 180

AMH-2\_5 AAACCGGATGATTTGCCTGATTTAGAATGGACTGGTGGATGGACCGACTGGCCTTTGATC 180

AMH-3\_1 AAACCGGATGATTTGCCTGATTTAGAATGGACTGGTGGATGGACCGACTGGCCTCTGATC 180

AMH-3\_13 AAACCGGATGATTTGCCTGATTTAGAATGGACTGGTGGATGGACCGACTGGCCTTTGATC 180

AY198374.1 AAACCGGATGATTTGCCTGATTTAGAATGGACTGGTGGATGGACCGACTGGCCTTTGATC 180

AMH-1\_2 AAACCGGATGATTTGCCTGACTTAGAATGGACTGGTGGATGGACCGACTGGCCTTTGATC 180

AMH-1\_7 AAACCGGATGATTTGCCTGATTTAGAATGGACTGGTGGATGGACCGACTGGCCTTTGATC 180

AMH-1\_11 AAACCGGATGATTTACCTGATTTAGAATGGACTGGTGGATGGACCGACTGGCCTTTGATC 180

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AMH-3\_16 CCGGCTGAGCCAAGAGACGACGTGTGCATAAACGGCTGGTACCCACAACTCACCAGCACT 237

AMH-2\_4 CCGGCTGAGCCAAGAGACGACGTGTGCATAAACGGCTGGTACCCACAACTCACCAGCACT 240

AMH-2\_1 CCGGCTGAGCCAAGAGACGACGTGTGCATAAACGGCTGGTACCCACAACTCACCAGCACT 240

AMH-2\_5 CCGGCTGAGCCAAGAGACGACGTGTGCATAAACGACTGGTACCCACAACTCACCAGCACT 240

AMH-3\_1 CCGGCTGAGCCAAGAGACGACGTGTGCATAAACGGCTGGTACCCACAACTCACCAGCACT 240

AMH-3\_13 CCGGCTGAGCCAAGAGACGACGTGTGCATAAACGGCTGGTACCCACAACTCACCAGCACT 240

AY198374.1 CCGGCTGAGCCAAGAGACGACGTGTGCATAAACGGCTGGTACCCACAACTCACCAGCACT 240

AMH-1\_2 CCGGCTGAGCCAAGAGACGACGTGTGCATAAACGGCTGGTACCCACAACTCACCAGCACT 240

AMH-1\_7 CCGGCTGAGCCAAGAGACGACGTGTGCATAAACGGCTGGTACCCACAACTCACCAGCACT 240

AMH-1\_11 CCGGCTGAGCCAAGAGACGACGTGTGCATAAACGGCTGGTACCCACAACTCACCAGCACT 240

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AMH-3\_16 TCTCTCGGCACCATCATCATCCACATGGAAGAGGAGATCGAGGGAGATGTTGCTATCGCT 297

AMH-2\_4 TCTCTCGGCACCATCATCATCCACATGGAAGAGGAGATCGAGGGAGATGTTGCTATCGCT 300

AMH-2\_1 TCTCTCGGCACCATCATCATCCACATGGAAGAGGAGATCGAGGGAGATGTTGCTATCGCT 300

AMH-2\_5 TCTCTCGGCACCATCATCATCCACATGGAAGAGGAGATCGAGGGAGATGTTGCTATCGCT 300

AMH-3\_1 TCTCTCGGCACCATCATCATCCACATGGAAGAGGAGATCGAGGGAGATGTTGCTATCGCT 300

AMH-3\_13 TCTCTCGGCACCATCATCATCCACATGGAAGAGGAGATCGAGGGAGATGTTGCTATCGCT 300

AY198374.1 TCTCTCGGCACCATCATCATCCACATGGAAGAGGAGATCGAGGGAGATGTTGCTATCGCT 300

AMH-1\_2 TCTCTCGGCACCATCATCATCCACATGGAAGAGGAGATCGAGGGAGATGTTGCTATCGCT 300

AMH-1\_7 TCTCTCGGCACCATCATCATCCACATGGAAGAGGAGATCGAGGGAGATGTTGCTATCGCT 300

AMH-1\_11 TCTCTCGGCACCATCATCATCCACATGGAAGAGGAGATCGAGGGAGATGTTGCTATCGCT 300

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AMH-3\_16 AAACTTAACTATGATGGTTCTGGAACCCCAGAAATTGTCCAGCCGATGGTTATAGGATCT 357

AMH-2\_4 AAACTTAACTATGATGGTTCTGGAACCCCAGAAATTGTCCAGCCGATGGTTATAGGATCT 360

AMH-2\_1 AAACTTTACTATGATGGTTCTGGAACCCCAGAAATTGTCCAGCCGATGGTTATAGGATCT 360

AMH-2\_5 AAACTTAACTATGATGGTTCTGGAACCCCAGAAATTGTCCAGCCGATGGTTATAGGATCT 360

AMH-3\_1 AAACTTAACTATGATGGTTCTGGAACCCCAGAAATTGTCCAGCCGATGGTTATAGGATCT 360

AMH-3\_13 AAACTTAACTATGATGGTTCTGGAACCCCAGAAATTGTCCAGCCGATGGTTATAGGATCT 360

AY198374.1 AAACTTAACTATGATGGTTCTGGAACCCCAGAAATTGTCCAGCCGATGGTTATAGGATCT 360

AMH-1\_2 AAACTTAACTATGATGGTTCTGGAACCCCAGAAATTGTCCAGCCGATGGTTATAGGATCT 360

AMH-1\_7 AAACTTAACTATGATGGTTCTGGAACCCCAGAAATTGTCCAGCCGATGGTTATAGGATCT 360

AMH-1\_11 AAACTTAACTATGATGGTTCTGGAACCCCAGAAATTGTCCAGCCGATGGTTATAGGATCT 360

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AMH-3\_16 TTTAACCTGCTAAGTCCAGAGATCCGGAATGAAAACGGGGCGTGGTACCTTTATATAACC 417

AMH-2\_4 TTTAACCTGCTAAGTCCAGAGATCCTGAATGAAAACGGGGCGTGGTACCTTTATATAACC 420

AMH-2\_1 TTTAACCTGCTAAGTCCAGAGATCCGGAATGAAAACGGGGCGTGGTACCTTTATATAACC 420

AMH-2\_5 TTTAACCTGCTAAGTCCAGGGATCCGGAATGAAAACGGGGCGTGGTACCTTTATATAACC 420

AMH-3\_1 TTTAACCTGCTAAGTCCAGAGATCCGGAATGAAAACGGGGCGTGGTACCTTTATATAACC 420

AMH-3\_13 TTTAACCTGCTAAGTCCAGAGATCCGGAATGAAAACGGGGCGTGGTACCTTTATATAACC 420

AY198374.1 TTTAACCTGCTAAGTCCAGAGATCCGGAATGAAAACGGGGCGTGGTACCTTTATATAACC 420

AMH-1\_2 TTTAACCTGCTAAGTCCAGGGATCCGGAATGAAAACGGGGCGTGGTACCTTTATATAACC 420

AMH-1\_7 TTTAACCTGCTAAGTCCAGAGATCCGGAATGAAAACGGGGCGTGGTACCTTTATATAACC 420

AMH-1\_11 TTTAACCTGCTAAGTCCAGAGATCCGGAATGAAAACGGGGCGTGGTACCTTTATATAACC 420

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AMH-3\_16 AATAGGCAAGATTATGAAACGCCAACAATGCGTCGGTATACATTCGACGTCCGAGTGCCA 477

AMH-2\_4 AATAGGCAAGATTATGAAACACCAACAATGCGTCGGTATACATTCGACGTCCGAGTGCCA 480

AMH-2\_1 AATAGGCAAGATTATGAAACACCAACAATGCGTCGGTATACATTCGACGTCCGAGTGCCA 480

AMH-2\_5 AATAGGCAAGATTATGAAACACCAACAATGCGTCGGTATACATTCGACGTCCGAGTGCCA 480

AMH-3\_1 AATAGGCAAGATTATGAAACACCAACAATGCGTCGGTATACATTCGACGTCCGAGTGCCA 480

AMH-3\_13 AATAGGCAAGATTATGAAACACCAACAATGCGTCGGTATACATTCGACGTCCGAGTGCCA 480

AY198374.1 AATAGGCAAGATTATGAAACACCAACAATGCGTCGGTATACATTCGACGTCCGAGTGCCA 480

AMH-1\_2 AATAGGCAAGATTATGAAACACCAACAATGCGTCGGTATACATTCGACGTCCGAGTGCCA 480

AMH-1\_7 AATAGGCAAGATTATGAAACACCAACAATGCGTCGGTATACATTCGACGTCCGAGTGCCA 480

AMH-1\_11 AATAGGCAAGATTATGAAACACCAACAATGCGTCGGTATACATTCGACGTCCGAGTGCCA 480

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AMH-3\_16 GACGAGACTCGTGCCGCACGAGTGAGTCTCTCCATCGAAAACATTGACGATAACGACCCT 537

AMH-2\_4 GACGAGACTCGTGCGGCACGAGTGAGTCTCTCCATCGAAAACATTGACGATAACGACCCT 540

AMH-2\_1 GACGAGACTCGTGCGGCACGAGTGAGTCTCTCCATCGAAAACATTGACGATAACGACCCT 540

AMH-2\_5 GACGAGACTCGTGCGGCACGAGTGAGTCTCTCCATCGAAAACATTGACGATAACGACCCT 540

AMH-3\_1 GACGAGACTCGTGCCGCACGAGTGAGTCTCTCCATCGAAAACATTGACGATAACGACCCT 540

AMH-3\_13 GACGAGACTCGTGCCGCACGAGTGAGTCTCTCCATCGAAAACATTGACGATAACGACCCT 540

AY198374.1 GACGAGACTCGTGCGGCACGAGTGAGTCTGTCCATCGAAAACATTGACGATAACGACCCT 540

AMH-1\_2 GACGAGACTCGTGCGGCACGAGTGAGTCCGTCCATCGAAAACATTGACGATAACGACCCT 540

AMH-1\_7 GACGAGACTCGTGCCGCACGAGTGAGTCTCTCCATCGAAAACATTGACGATAACGACCCT 540

AMH-1\_11 GACGAGACTCGTGCCGCACGAGTGAGTCTCTCCATCGAAAACATTGACGATAACGACCCT 540

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AMH-3\_16 ATCGTCAGGGTGCTAGACGCTTGCCAAGTGCCGGAATTGGGGGAGCCTCGACTAACTGAC 597

AMH-2\_4 ATCGTCAGGGTGCTAGACGCTTGCCAAGTGCCGGAATTGGGGGAGCCTCGACTAACAGAC 600

AMH-2\_1 ATCGTCAGGGTGCTAGACGCTTGCCAAGTGCCGGAATTGGGGGAGCCTCGACTAACAGAC 600

AMH-2\_5 ATCGTCAGGGTGCTAGACGCTTGCCAAGTGCCGGAATTGGGGGAGCCTCGACTAACAGAC 600

AMH-3\_1 ATCGTCAGGGTGCTAGACGCTTGCCAAGTGCCGGAATTGGGGGAGCCTCGACTAACTGAC 600

AMH-3\_13 ATCGTCAGGGTGCTAGACGCTTGCCAAGTGCCGGAATTGGGGGAGCCTCGACTAACTGAC 600

AY198374.1 ATCGTCAGGGTGCTAGACGCTTGCCAAGTGCCGGAATTGGGGGAGCCTCGACTAACAGAC 600

AMH-1\_2 ATCGTCAGGGTGCTAGACGCTTGCCAAGTGCCGGAATTGGGGGAGCCTCGACTAACAGAC 600

AMH-1\_7 ATCGTCAGGGTGCTAGACGCTTGCCAAGTGCCGGAATTGGGGGAGCCTCGACTAACTGAC 600

AMH-1\_11 ATCGTCAGGGTGCTAGACGCTTGCCAAGTGCCGGAATTGGGGGAGCCTCGACTAACTGAC 600

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AMH-3\_16 TGCGTTTACCGAGTGTCAGACGAAGATGGGAGGCTTAGTATCGAGCCCATGACATTCCGC 657

AMH-2\_4 TGCGTTTACCAAGTGTCAGACGAAGATGGGAGGCTTAGTATCGAGCCCATGACATTCCGC 660

AMH-2\_1 TGCGTTTACCAAGTGTCAGACGAAGATGGGAGGCTTAGTATCGAGCCCATGACATTCCGC 660

AMH-2\_5 TGCGTTTACCAAGTGTCAGACGAAGATGGGAGGCTTAGTATCGAGCCCATGACATTCCGC 660

AMH-3\_1 TGCGCTTACCAAGTGTCAGACGAAGATGGGAGGCTTAGTATCGAGCCCATGACATTCCGC 660

AMH-3\_13 TGCGTTTACCAAGTGTCAGACGAAGATGGGAGGCTTAGTATCGAGCCCATGACATTCCGC 660

AY198374.1 TGCGTTTACCAAGTGTCAGACGAAGATGGGAGGCTTAGTATCGAGCCCATGACATTCCGC 660

AMH-1\_2 TGCGTTTACCAAGTGTCAGACGAAGATGGGAGGCTTAGTATCGAGCCCATGACATTCCGC 660

AMH-1\_7 TGCGTTTACCAAGTGTCAGACGAAGATGGGAGGCTTAGTATCGAGCCCATGACATTCCGC 660

AMH-1\_11 TGCGTTTACCAAGTGTCAGACGAAGATGGGAGGCTTAGTATCGAGCCCATGACATTCCGC 660

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AMH-3\_16 CTCACATCAGACCGTGAAGACGTACAGATATTCTATGTGGAGCCAGCTCACATTACTGGT 717

AMH-2\_4 CTCACATCAGACCGTGAAGACGTACAGATATTCTATGTGGAGCCAGCTCACATTACTGGT 720

AMH-2\_1 CTCACATCAGACCGTGAAGACGTACAGATATTCTATGTGGAGCCAGCTCACATTACTGGT 720

AMH-2\_5 CTCACATCAGACCGTGAAGACGTACAGATATTCTATGTGGAGCCAGCTCACATTACTGGT 720

AMH-3\_1 CTCACATCGGACCGTGAAGACGTACAGATATTCTATGTGGAGCCAGCTCACATTACTGGT 720

AMH-3\_13 CTCACATCAGACCGTGAAGACGTACAGATATTCTATGTGGAGCCAGCTCACATTACTGGT 720

AY198374.1 CTCACATCAGACCGTGAAGACGTACAGATATTCTATGTGGAGCCAGCTCACATTACTGGT 720

AMH-1\_2 CTCACATCAGACCGTGAAGACGTACAGATATTCTATGTGGAGCCAGCTCACATTACTGGT 720

AMH-1\_7 CTCACATCAGACCGTGAAGACGTGCAGATATTCTATGTGGAGCCAGCTCACATTACTGGT 720

AMH-1\_11 CTCACATCAGACCGTGAAGACGTACAGATATTCTATGTGGAGCCAGCTCACATTACTGGT 720

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AMH-3\_16 GATTGGTTCAACATGCAAATTACTATCGGTATCCTATCAGCGCTTAACTTCGAAAGCAAC 777

AMH-2\_4 GATTGGTTCAACATGCAAATTACTATCGGTATCCTATCAGCGCTTAACTTCGAAAGCAAC 780

AMH-2\_1 GATTGGTTCAACATGCAAATTACTATCGGTATCCTATCAGCGCTTAACTTCGAAAGCAAC 780

AMH-2\_5 GATTGGTTCAACATGCAAATTACTATCGGTATCCTATCAGCGCTTAACTTCGAAAGCAAC 780

AMH-3\_1 GATTGGTTCAACATGCAAATTACTATCGGTATCCTATCAGCGCTTAACTTCNAAAGCAAC 780

AMH-3\_13 GATTGGTTCAACATGCAAATTACTATCGGTATCCTATCAGCGCTTAACTTCGAAAGCAAC 780

AY198374.1 GATTGGTTCAACATGCAAATTACTATCGGTATCCTATCAGCGCTTAACTTCGAAAGCAAC 780

AMH-1\_2 GATTGGTTCAACATGCAAATTACTATCGGTATCCTATCAGCGCTTAACTTCGAAAGCAAC 780

AMH-1\_7 GATTGGTTCAACATGCAAATTACTATCGGTATCCTATCAGCGCTTAACTTCGAAAGCAAC 780

AMH-1\_11 GATTGGTTCAACATGCAAATTACTATCGGTATCCTATCAGCGCTTAACTTCGAAAGCAAC 780

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AMH-3\_16 CCGCTTCACATCTTTCAAATCACTGCTTTGGACTCCTGGCCCAACAACCATACGGTGACG 837

AMH-2\_4 CCGCTGCACATCTTTCAAATCACTGCTTTGGACTCCTGGCCCAACAACCATACGGTGACG 840

AMH-2\_1 CCGCCGCACATCTTTCAAATCACTGCTTTGGACTCCTGGCCCAACTACCATACGGTGACG 840

AMH-2\_5 CCGCTGCACATCTTTCAAATCACTGCTTTGGACTCCTGGCCCAACAACCATACGGTGACG 840

AMH-3\_1 CCGCTGCACATCTTTCAAATCACTGCTTTGGACTCCTGGCCCNACAACCATACGGNGACG 840

AMH-3\_13 CCGCTGCACATCTTTCAAATCACTGCTTTGGACTCCTGGCCCAACAACCATACGGTGACG 840

AY198374.1 CCGCTGCACATCTTTCAAATCACTGCTTTGGACTCCTGGCCCAACAACCATACGGTGACG 840

AMH-1\_2 CCGCTGCACATCTTTCAAATCACTGCTTTGGACTCCTGGCCCAACAACCATACGGTGACG 840

AMH-1\_7 CCGCTGCACATCTTTCAAATCACTGCTTTGGACTCCTGGCCCAACAACCATACGGTGACG 840

AMH-1\_11 CCGCTGCACATCTTTCAAATCACTGCTTTGGACTCCTGGCCCAACAACCATACGGTGACG 840

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AMH-3\_16 GTGATGGTGCAAGTCCAGAATGTGGAACACCGACCGCCGCGATGGATGGAAATCTTCGCA 897

AMH-2\_4 GTGATGGTGCAAGTCCAGAATGTGGAGCACCGACCGCCGCGATGGATGGAAATCTTCGCA 900

AMH-2\_1 GTGATGGTGCAAGTCCAGAATGTGGAGCACCGACCGCCGCGATGGATGGAAATCTTCGCA 900

AMH-2\_5 GTGATGGTGCGAGTCCAGAATGTGGAGTACCGACCGCCGCGATGGATGGAAATCTTCGCA 900

AMH-3\_1 GTGATGGTGCAAGTCCAGAATGNGGNACACCGACCGCCGCGATGGATGNAAATCTTCGCA 900

AMH-3\_13 GTGATGGTGCAAGTCCAGAATGTGGAACACCGACCGCCGCGATGGATGGAAATCTTCGCA 900

AY198374.1 GTGATGGTGCAAGTTCAGAATGTGGAGCACCGACCGCCGCGATGGATGGAAATCTTCGCA 900

AMH-1\_2 GTGATGGTGCAAGTCCAGAATGTGGAACACCGACCGCCGCGATGGATGGAAATCTTCGCA 900

AMH-1\_7 GTGATGGTGCAAGTCCAGAATGTGGAACACCGACCGCCGCGATGGATGGAAATCTTCGCA 900

AMH-1\_11 GTGATGGTGCAAGTCCAGAATGTGGAACACCGACCGCCGCGATGGATGGAAATCTCCGCA 900

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AMH-3\_16 GTCCAGCAGTTTGACGAGATGACGGAGCAGCAATTCCAGGTGCGCGCCATCGACGGAGAC 957

AMH-2\_4 GCCCAGCAGTTTGACGAGATGACGGAGCAGCAATTCCAGGTGCGCGCCATCGACGGAGAC 960

AMH-2\_1 GTCCAGCAGTTTGACGAGATGACGGAGCAGCAATTCCAGGTGCGCGCTATCGACGGAGAC 960

AMH-2\_5 GTCCAGCAGTTTGACGAGATGACGGAGCAGCAATTCCAGGTGCGCGCCATCGACGGAGAC 960

AMH-3\_1 GTCCANCANTTTGACGAGATGANGGANCAGCAATTCCNGGTGCGCGCCATCGACGGAGAC 960

AMH-3\_13 GTCCAGCAGTTTGACGAGATGACGGAGCAGCAATTCCAGGTGCGCGCCATCGACGGAGAC 960

AY198374.1 GTCCAGCAGTTTGACGAGATGACGGAGCAGCAATTCCAGGTGCGCGCCATCGACGGAGAC 960

AMH-1\_2 GTCCAGCAGTTTGACGAGATGACGGAGCAGCAATTCCAGGTGCGCGCCATCGACGGAGAC 960

AMH-1\_7 GTCCAGCAGTTTGACGAGATGACGGAACAGCAATTCCAGGTGCGCGCCATCGACGGAGAC 960

AMH-1\_11 GTCCAGCAGTTTGACGAGATGACGGAGCAGCAATTCCAGGTGCGCGCCATCGACGGAGAC 960

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AMH-3\_16 ACTGGCATCGGGAAAGCTATACACTATACCCTCGAGACAGATGAGGAAGAAGATTTGTTC 1017

AMH-2\_4 ACTGGCATCGGGAAAGCTATACACTATACCCTCGAGACAGATGAGGAAGAAGATTTGTTC 1020

AMH-2\_1 ACTGGCATCGGGAAAGCTATACACTATACCCTCGAGACAGATGAGGAAGAAGATTTGTTC 1020

AMH-2\_5 ACTGGCATCGGGAAAGCTATACACTATACCCTCGAGACAGATGAGGAAGAAGATTTGTTC 1020

AMH-3\_1 ACTGGCATCGGGAAAGCTATACACTATACCCTCGAGACAGATGAGGAAGAAGATTTGTTC 1020

AMH-3\_13 ACTGGCATCGGGAAAGCTATACACTATACCCTCGAGACAGATGAGGAAGAAGATTTGTTC 1020

AY198374.1 ACTGGCATCGGGAAAGCTATACACTATACCCTCGAGACAGATGAGGAAGAAGATTTGTTC 1020

AMH-1\_2 ACTGGCATCGGGAAAGCTATACACTATACCCTCGAGACAGATGAGGAAGAAGATTTGTTC 1020

AMH-1\_7 ACTGGCATCGGGAAAGCTATACACTATACCCTCGAGACAGATGAGGAAGAAGATTTGTTC 1020

AMH-1\_11 ACTGGCATCGGGAAAGCTATACACTATACCCTCGAGACAGATGAGGAAGAAGATTTGTTC 1020

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AMH-3\_16 TTCATCGAAACACTTCCGGGCGGCCATGACGGAGCCATCTTCAGCACTGCCATGATTGAT 1077

AMH-2\_4 TTCATCGAAACACTTCCGGGCGGCCATGACGGAGCCATCTTCAGCACTGCCATGATTGAT 1080

AMH-2\_1 TTCATCGAAACACTTCCGGGCGGCCATGATGGAGCCATCTTCAGCACTGCCATGATTGAT 1080

AMH-2\_5 TTCATCGAAACACTTCCGGGCGGCCATGACGGAGCCATCTTCGGCACTGCCATGATTGAT 1080

AMH-3\_1 TTCATCGAAACACTTCCGGGCGGCCATGACGGAGCCATCTTCAGCACTGCCATGATTGAT 1080

AMH-3\_13 TTCATCGAAACACTTCCGGGCGGCCATGACGGAGCCATCTTCAGCACTGCCATGATTGAT 1080

AY198374.1 TTCATCGAAACACTTCCGGGCGGCCATGACGGAGCCATCTTCAGCACTGCCATGATTGAT 1080

AMH-1\_2 TTCATCAAAACACTTCCGGGCGGCCATGACGGAGCCATCTTCAGCACTGCCATGATTGAT 1080

AMH-1\_7 TTCATCGAAACACTTCCGGGCGGCCATGACGGAGCCATCTTCAGCACTGCCATGATTGAT 1080

AMH-1\_11 TTCATCGAAACACTTCCGGGCGGCCATGACGGAGCCATCTTCAGCACTGCCATGATTGAT 1080

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AMH-3\_16 GTGGATAGGCTCCGGCGAGATGTCTTCAGACTGTCCCTGGTGGCATACAAGTACGACAAT 1137

AMH-2\_4 GTGGATAGGCTCCGGCGAGATGTCTTCAGACTGTCCCTGGTGGCATACAAGTACGACAAT 1140

AMH-2\_1 GTGGATAGGCTCCGGCGAGATGTCTTCAGACTGTCCCTGGTGGCATACAAGTACGACAAT 1140

AMH-2\_5 GTGGATAGGTTCCGGCGAGATGTCTTCAGACTGTCCCTGGTGGCATACAAGTACGACAAT 1140

AMH-3\_1 GTGGATAGGCTCCGGCGAGATGTCTTCAGACTGTCCCTGGTGGCATACAAGTACGACAAT 1140

AMH-3\_13 GTGGATAGGCTCCGGCGAGATGTCTTCAGACTGTCCCTGGTGGCATACAAGTACGACAAT 1140

AY198374.1 GTGGATAGGCTCCGGCGAGATGTCTTCAGACTGTCCCTGGTGGCATACAAGTACGACAAT 1140

AMH-1\_2 GTGGATAGGCTCCGGCGAGATGTCTTCAGACTGTCCCTGGTGGCATACAAGTACGACAAT 1140

AMH-1\_7 GTGGATAGGCTCCGGCGAGATGTCTTCAGACTGTCCCTGGTGGCATACAAGTACGACAAT 1140

AMH-1\_11 GTGGATAGGCTCCGGCGAGATGTCTTCAGACTGTCCCTGGTGGCATACAAGTACGACAAT 1140

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AMH-3\_16 GTGTCCTTCGCCACCCCGACACCCGTCGTGATCATAGTCAACGACATCAACAACAAGCAA 1197

AMH-2\_4 GTGTCCTTCGCCACCCCAACACCCGTCGTGATCATAGTCAACGACATCAACAACAAGCAA 1200

AMH-2\_1 GTGTCCTTCGCCACCCCGACACCCGTCGTGATCATAGTCAACGACATCAACAACAAGCAA 1200

AMH-2\_5 GTGTCCTTCGCCACCCCGACACCCGTCGTGATCATAGTCAACGACATCAACAACAAGCAA 1200

AMH-3\_1 GTGTCCTTCGCCACCCCGACACCCGTCGTGATCATAGTCAACGACATCAACAACAAGCAA 1200

AMH-3\_13 GTGTCCTTCGCCACCCCGACACCCGTCGTGATCATAGTCAACGACATCAACAACAAGCAA 1200

AY198374.1 GTGTCCTTCGCCACCCCGACACCCGTCGTGATCATAGTCAATGACATCAACAACAAGAAA 1200

AMH-1\_2 GTGTCCTTCGCCACCCCGACACCCGTCGTGATCATAGTCAATGACATCAACAACAAGAAA 1200

AMH-1\_7 GTGTCCTTCGCCACCCCGACACCCGTCGTGATCATAGTCAACGACATCAACAACAAGCAA 1200

AMH-1\_11 GTGTCCTTCGCCACCCCGACACCCGTCGTGATCATAGTCAACGACATCAACAACAAGCAA 1200

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AMH-3\_16 CCCCAACCGCTGCAAGATGAGTACACAATCTCCATAATGGAAGAAACTCCACTGTCGCTG 1257

AMH-2\_4 CCCCAACCGCTGCAAGATGAGTACACAATCTCCATAATGGAAGAAACTCCACTGTCGCTG 1260

AMH-2\_1 CCCCAACCGCTGCAAGATGAGTACACAATCTCCATAATGGAAGAAACTCCACTGTCGCTG 1260

AMH-2\_5 CCCCAACCGCTGCAAGATGAGTACACAATCTCCATAATGGAAGAAACTCCACTGTCGCTG 1260

AMH-3\_1 CCCCAACCGCTGCAAGATGAGTACACAATCTCCATAATGGAAGAAACTCCACTGTCGCTG 1260

AMH-3\_13 CCCCAACCGCCGCAAGATGAGTACACAATCTCCATAATGGAAGAAACTCCACTGTCGCTG 1260

AY198374.1 CCCCAACCGCTGCAAGATGAGTACACAATCTCCATAATGGAAGAAACTCCACTGTCGCTG 1260

AMH-1\_2 CCCCAACCGCTGCAAGATGAGTACACAATCTCCATAATGGAAGAAACTCCACTGTCGCTG 1260

AMH-1\_7 CCCCAACCGCTGCAAGATGAGTACACAATCTCCATAATGGAAGAAACTCCACTGTCGCTG 1260

AMH-1\_11 CCCCAACCGCTGCAAGATGAGTACACAATCTCCATAATGGAAGAAACTCCACTGTCGCTG 1260

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AMH-3\_16 AATTTTGCTGAACTTTTTGGTTTCTATGATGAAGATTTGATCTACGCACAATTCTTGGTG 1317

AMH-2\_4 AATTTTGCTGAACTTTTTGGTTTCTATGATGAAGATTTGATCTACGCGCAATTCTTGGTG 1320

AMH-2\_1 AATTTTGCTGAACTTTTTGGTTTCTATGATGAAGATTTGATCTACGCACAATTCTTGGTG 1320

AMH-2\_5 AATTTTGCTGAACTTTTTGGTTTCTATGTTGAAGATTTGATCTACGCACAATTCTTGGTG 1320

AMH-3\_1 AATTTTGCTGAACTTTTTGGTTTCTATGATGAAGATTTGATCTACGCACAATTCTTGGTG 1320

AMH-3\_13 AATTTTGCTGAACTTTTTGGTTTCTATGATGAAGATTTGATCTACGCACAATTCTTGGTG 1320

AY198374.1 AATTTTGCTGAACTTTTTGGTTTCTATGATGAAGATTTGATCTACGCACAATTCTTGGTG 1320

AMH-1\_2 AATTTTGCTGAACTTTTTGGTTTCTATGATGAAGATTTGATCTACGCACAATTCTTGGTG 1320

AMH-1\_7 AATTTTGCTGAACTTTTTGGTTTCTATGATGAAGATTTGATCTACGCACAATTCTTGGTG 1320

AMH-1\_11 AATTTTGCTGAACTTTTTGGTTTCTATGATGAAGATTTGATCTACGCACAATTCTTGGTG 1320

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AMH-3\_16 GAAATACAAGGCGAGAACCCTCCAGGCGTAGAGCAAGCGTTTTATATTGCGCCCACCGCA 1377

AMH-2\_4 GAAATACAAGGCGAGAACCCTCCAGGCGTAGAGCAAGCGTTTTATATTGCGCCCACCGCA 1380

AMH-2\_1 GAAATACAAGGCGAGAACCCTCCAGGCGTAGAGCAAGCGTTTTATATTGCGCCCACCGCA 1380

AMH-2\_5 GAAATACAAGGCGAGAACCCTCCAGGCGTAGAGCAAGCGTTTTATATTGCGCCCACCGCA 1380

AMH-3\_1 GAAATACAAGGCGAGAACCCTCCAGGCGTAGAGCAAGCGTTTTATATTGCGCCCACCGCA 1380

AMH-3\_13 GGAATACAAGGCGAGAACCCTCCAGGCGTAGAGCAAGCGTTTTATATTGCGCCCACCGCA 1380

AY198374.1 GAAATACAAGGCGAGAACCCTCCAGGCGTAGAGCAAGCGTTTTATATTGCGCCCACCGCA 1380

AMH-1\_2 GAAATACAAGGCGAGAACCCTCCAGGCGTAGAGCAAGCGTTTTATATTGCGCCCACCGCA 1380

AMH-1\_7 GAAATACAAGGCGAGAACCCTCCAGGCGTAGAGCAAGCGTTTTATATTGCGCCCACCGCA 1380

AMH-1\_11 GAAATACAAGGCGAGAACCCTCCAGGCGTAGAGCAAGCGTTTTATATTGCGCCCACCGCA 1380

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AMH-3\_16 GGCTTCCAGAACCAGACATTCGCCATAGGGACTCAAGATCACCGAATGCTGGATTATGAG 1437

AMH-2\_4 GGCTTCCAGAACCAGACATTCGCCATAGGGACTCAAGATCACCGAATGCTGGATTATGAG 1440

AMH-2\_1 GGCTTCCAGAACCAGACATTCGCCATAGGGACTCAAGATCACCGAATGCTGGATTATGAG 1440

AMH-2\_5 GGCTTCCAGAACCAGACATTCGCCATAGGGACTCAAGATCACCGAATGCTGGATTATGAG 1440

AMH-3\_1 GGCTTCCAGAACCAGACATTCGCCATAGGGACTCAAGATCACCGAATGCTGGATTATGAG 1440

AMH-3\_13 GGCTTCCAGAACCAGACATTCGCCATAGGGACTCAAGATCACCGAATGCTGGATTATGAG 1440

AY198374.1 GGCTTCCAGAACCAGACATTCGCCATAGGGACTCAAGATCACCGAATGCTGGATTATGAG 1440

AMH-1\_2 GGCTTCCAGAACCAGACATTCGCCATAGGGACTCAAGATCACCGAATGCTGGATTATGAG 1440

AMH-1\_7 GGCTTCCAGAACCAGACATTCGCCATAGGGACTCAAGATCACCGAATGCTGGATTATGAG 1440

AMH-1\_11 GGCTTCCAGAACCAGACATTCGCCATAGGGACTCAAGATCACCGAATGCTGGATTATGAG 1440

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AMH-3\_16 GATGTTCCTTTCCAAAACATCAAGCTCAAGGTAATAGCAACGGACCGTGACAATACCAAT 1497

AMH-2\_4 GATGTTCCTTTCCAAAACATCAAGCTCAAGGTAATAGCAACGGACCGTGACAATACCAAT 1500

AMH-2\_1 GATGTTCCTTTCCAAAACATCAAGCTCAAGGTAATAGCAACGGACCGTGACAATACCAAT 1500

AMH-2\_5 GATGTTCCCTTCCAAAACATCAAGCTCAAGGTAATAGCAACGGACCGTGACAATACCAAT 1500

AMH-3\_1 GATGTTCCTTTCCAAAACATCAAGCTCAAGGTAATAGCAACGGACCGTGACAATACCAAT 1500

AMH-3\_13 GATGTTCCTTTCCAAAACATCAAGCTCAAGGTAATAGCAACGGACCGTGACAATACCAAT 1500

AY198374.1 GATGTTCCTTTCCAAAACATCAAGCTCAAGGTAATAGCAACGGACCGTGACAATACCAAT 1500

AMH-1\_2 GATGTTCCTTTCCAAAACATCAAGCTCAAGGTAATAGCAACGGACCGTGACAATACCAAT 1500

AMH-1\_7 GATGTTCCTTTCCAAAACATCAAGCTCAAGGTAATAGCAACGGACCGTGACAATACCAAT 1500

AMH-1\_11 GATGTTCCTTTCCAAAACATCAAGCTCAAGGTAATAGCAACGGACCGTGACAATACCAAT 1500

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AMH-3\_16 TTTACTGGAGTCGCGGAAGTCAACGTGAACCTGATTAATTGGAACGACGAGGAGCCGATC 1557

AMH-2\_4 TTCACTGGAGTGGCGGAAGTCAACGTGAATCTGATTAATTGGAACGACGAGGAGCCGATC 1560

AMH-2\_1 TTCACTGGAGTGGCGGAAGTCAACGTGAATCTGATTAATTGGAACGACGAGGAGCCGATC 1560

AMH-2\_5 TTCACTGGAGTGGCGGAAGTCAACGTGAATCTGATTAATTGGAACGACGAGGAGCCGATC 1560

AMH-3\_1 TTTACTGGAGTCGCGGAAGTCAACGTGAACCTGATTAATTGGAACGACGAGGAGCCGATC 1560

AMH-3\_13 TTTACTGGAGTCGCGGAAGTCAACGTGAACCTGATTAATTGGAACGACGAGGAGCCGATC 1560

AY198374.1 TTTACTGGAGTCGCGGAAGTCAACGTGAACCTGATTAATTGGAACGACGAGGAGCCGATC 1560

AMH-1\_2 TTTACTGGAGTCGCGGAAGTCAACGTGAACCTGATTAATTGGAACGACGAGGAGCCGATC 1560

AMH-1\_7 CTTACTGGAGTCGCGGAAGTCAACGTGAACCTGATTAATTGGGACGACGAGGAGCCGATC 1560

AMH-1\_11 TTTACTGGAGTCGCGGAAGTCAACGTGAACCTGATTAATTGGAACGACGAGGAGCCGATC 1560

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AMH-3\_16 TTTGAGGAAGACCAGCTCGTTGTCAAGTTCAAGGAGACTGTACCCAAGGACTATCACGTC 1617

AMH-2\_4 TTTGAGGAGGACCAGCTGGTTGTCAAGTTCAAGGAGACTGTACCCAAGGACTATCACGTC 1620

AMH-2\_1 TTTGAGGAGGACCAGCTGGTTGTCAAGTTCAAGGAGACTGTACCCAAGGACTATCACGTC 1620

AMH-2\_5 TTTGAGGAGGACCAGCTGGTTGTCAAGCTCAAGGAGACTGTACCCAAGGACTATCACGTC 1620

AMH-3\_1 TTTGAGGAAGACCAGCTCGTTGTCAAGTTCAAGGAGACTGTACCCAAGGACTATCACGTC 1620

AMH-3\_13 TTTGAGGAAGACCAGCTCGTTGTCAAGTTCAAGGAGACTGTACCCAAGGACTATCACGTC 1620

AY198374.1 TTTGAGGAAGACCAGCTCGTTGTCAAGTTCAAGGAGACTGTACCCAAGGACTATCACGTC 1620

AMH-1\_2 TTTGAGGAAGACCAGCTCGTTGTCAAGTTCAAGGAGACTGTACCCAAGGACTATCACGTC 1620

AMH-1\_7 TTTGAGGAAGACCAGCTCGTTGTCAAGTTCAAGGAGACTGTACCCAAGGACTATCACGTC 1620

AMH-1\_11 TTTGAGGAAGACCAGCTCGTTGTCAAGTTCAAGGAGACTGTACCTAAGGACTATCACGTC 1620

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AMH-3\_16 GGCAGACTGAGGGCTCACGACCGGGACATANGAGACAGCGTTGTGCATTCCATCTTGGGA 1677

AMH-2\_4 GGCAGACTGAGGGCTCACGACCGGGACATANGAGACAGCGTTGTGCATTCCATCTTGGGA 1680

AMH-2\_1 GGCAGACTGAGGGCTCACGACCGGGACATANGAGACAGCGTTGTGCATTCCATCTTGGGA 1680

AMH-2\_5 GGCAGACTGANGGCTCACGACCGGGACATANGAGACAGCGTTGTGCATTCCATCTTGGGA 1680

AMH-3\_1 GGCAGACTGAGGGCTCACGACCGGGACATAGGAGACAGCGTTGTGCATTCCATCTTGGGA 1680

AMH-3\_13 GGCAGACTGAGGGCTCACGACCGGGACATAGGAGACAGCGTTGTGCATTCCATCTTGGGA 1680

AY198374.1 GGCAGACTGAGGGCTCACGACCGGGACATAGGAGACAGCGTTGTGCATTCCATCTTGGGA 1680

AMH-1\_2 GGCAGACTGAGGGCTCACGACCGGGACATAGGAGACAGCGTTGTGCATTCCATCTTGGGA 1680

AMH-1\_7 GGCAGACTGAGGGCTCACGACCGGGACATANGAGACAGCGTTGTGCATTCCATCTTGGGA 1680

AMH-1\_11 GGCAGACTGAGGGCTCACGACCGGGACATAGGAGACAGCGTTGTGCATTCCATCTTGGGA 1680

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AMH-3\_16 AATGCGAATACATTTTTAAGAATCGACGAANAAACTGGCGACATCTACGTAACTATTGAT 1737

AMH-2\_4 AATGCGAATACATTTTTGAGAATCGACGAAGAAACTGGCGACATCTACGTAGCTATTGAT 1740

AMH-2\_1 AATGCGAATACATTTTTGAGAATCGACGAAGAAACTGGCGACATCTACGTAGCTATTGAT 1740

AMH-2\_5 AATGCGAATACATTTTTGAGAATCGACGAAGAAACTGGCGACATCTACGTAGCTATTGAT 1740

AMH-3\_1 AATGCGAATACATTTTTAAGAATCGACGAAGAAACTGGCGACATCTACGTAACTATTGAT 1740

AMH-3\_13 AATGCGAATACATTTTTAAGAATCGACGAAGAAACTGGCGACATCTACGTAACTATTGAT 1740

AY198374.1 AATGCGAATACATTTTTGAGAATCGACGAAGAAACTGGCGACATATACGTAGCTATTGAT 1740

AMH-1\_2 AATGCGAATACATTTTTGAGAATCGACGAAGAAACTGGCGACATATACGTAGCTATTGAT 1740

AMH-1\_7 AATGCGAATACATTTTTAAGAATCGACGAAGAAACTGGCGACATCTACGTAACTATTGAT 1740

AMH-1\_11 AATGCGAATACATTTTTAAGAATCGACGAAGAAACTGGCGACATCTACGTAACTATTGAT 1740

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AMH-3\_16 GACGCGTTCGATTATCACAGACAGAATGAATTTAACATACAAGTTCGCGCTCAGGACACC 1797

AMH-2\_4 GACGCGTTCGATTATCACAGACAGAATGAATTTAACATACAAGTTCGCGCTCAGGACACC 1800

AMH-2\_1 GACGCGTTCGATTATCACAGACAGAATGAATTTAACATACAAGTTCGCGCTCAGGACACC 1800

AMH-2\_5 GACGCGTTCGATTATCACAGACAGAATGAATTTAACATACAAGTTCGCGCTCAGGACACC 1800

AMH-3\_1 GACGCGTTCGATTATCACAGACAGAATGAATTTAACATACAAGTTCGCGCTCAGGACACC 1800

AMH-3\_13 GACGCGTTCGATTATCACAGACAGAATGAATTTAACATACAAGTTCGCGCTCAGGACACC 1800

AY198374.1 GACGCGTTCGATTATCACAGACAGAATGAATTTAACATACAAGTTCGCGCTCAGGACACC 1800

AMH-1\_2 GACGCGTTCGATTATCACAGACAGAATGAATTTAACATACAAGTTCGCGCTCAGGACACC 1800

AMH-1\_7 GACGCGTTCGATTATCACAGACAGAATGAATTTAACATACAAGTTCGCGNTCAGGACACC 1800

AMH-1\_11 GACGCGTTCGATTATCACAGACAGAATGAATTTAACATACAAGTTCGCGCTCAGGACACC 1800

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AMH-3\_16 ATGTCNGANCCAGANTCCAGGCATACAGCGACTGCTCAGCTGGTCATAGAACTCGAGGAN 1857

AMH-2\_4 ATGTCGGAGCCAGAGTCCAGGCATACAGCGACTGCTCAGCTGGTCATAGAACTCGAGGAC 1860

AMH-2\_1 ATGTCGGAGCCAGAGTCCAGGCATACAGCGACTGNTCAGCTGGTCATAGAACTCGAGGAC 1860

AMH-2\_5 ATGTCGGAGCCAGAGTCCAGGCATACAGCGACTGCTCAGCTGGTCATAGAACTCGAGGAC 1860

AMH-3\_1 ATGTCGGAGCCAGAGTCCAGGCATACAGCGACTGCTCAGCTGGTCATAGAACTCGAGGAC 1860

AMH-3\_13 ATGTCGGAGCCAGAGTCCAGGCATACAGCGACTGCTCAGCTGGTCATAGAACTCGAGGAC 1860

AY198374.1 ATGTCGGAGCCAGAGTCCAGGCATACAGCGACTGCTCAGCTGGTCATAGAACTCGAGGAC 1860

AMH-1\_2 ATGTCGGAGCCAGAGTCCAGGCATACAGCGACTGCTCAGCTGGTCATAGAACTCGAGGAC 1860

AMH-1\_7 ATGTCGGAGCCAGAGTCCAGGCATACAGCGACTGCTCAGCTGGTCATAGAACTCGAGGAC 1860

AMH-1\_11 ATGTCGGAGCCAGAGTCCAGGCATACAGCGACTGCTCAGCTGGTCATAGAACTCGAGGAC 1860

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AMH-3\_16 GTCAACAACACANCTCCTACTCTGAGGCTGCCGCGCGTAANTCCGTCTGTAGAAGAGAAT 1917

AMH-2\_4 GTCAACAACACACNTCCCACTCTGAGGCCGCCTCGCGTAAGTCCGTCTGTAGAAGAGAAT 1920

AMH-2\_1 GTCAACAACACNCCTCCCACTCTGAGGCTGCCTCGCGTAAGTCCGTCTGTAGAAGAGAAT 1920

AMH-2\_5 GTCAACAACACACCTCCCACTCTGAGGCTGCCTCGCGTAAGTCCGTCTGTAGAAGAGAAT 1920

AMH-3\_1 GTCAACAACACACCTCCTACTCTGAGGCTGCCGCGCGTAAGTCCGTCTGTAGAAGAGAAT 1920

AMH-3\_13 GTCAACAACACACCTCCTACTCTGAGGCTGCCGCGCGTAAGTCCGTCTGTAGAAGAGAAT 1920

AY198374.1 GTCAACAACACACCTCCTACTCTGAGGCTGCCTCGCGTAAGTCCGTCTGTAGAAGAGAAT 1920

AMH-1\_2 GTCAACAACACACCTNCTACTCTGAGGCTGCCTCGCGTAAGTCCGTCTGTAGAAGAGAAT 1920

AMH-1\_7 GTCAACAACACACCTCCTACTCTGAGGCTGCCGCGCGTAAGTCCGTCTGTAGAAGAGAAT 1920

AMH-1\_11 GTCAACAACACACCTCCTACTCTGAGGCTGCCGCGCGTAAGTCCGTTTGTAGAAGAGAAT 1920

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AMH-3\_16 GTGCCAGAGGGCTTTGAAATCAACCGGGAGATAACCGCCACGGACCCTGACACCGCAGCA 1977

AMH-2\_4 GTGCCAGAGGGCTTTGAAATCAACCGGGAGATAACCGCCACGGACCCTGACACCACAGCA 1980

AMH-2\_1 GTGCCAGAGGGCTTTGAAATCAACCGGGAGATAACCGCCACGGACCCAGACACCACAGCA 1980

AMH-2\_5 GTGCCAGAGGGCTTTGAAATCAACCGGGAGATAACCGCCACGGACCCTGACACCACAGCA 1980

AMH-3\_1 GTGCCAGAGGGCTTTGAAATCAACCGGGAGATAACCGCCACGGACCCTGACACCACAGCA 1980

AMH-3\_13 GTGCCAGAGGGCTTTGAAATCAACCGGGAGATAACCGCCACGGACCCTGACACCGCAGCA 1980

AY198374.1 GTGCCAGAGGGCTTTGAAATCAACCGGGAGATAACCGCCACGGACCCTGACACCACAGCA 1980

AMH-1\_2 GTGCCAGAGGGCTTTGAAATCAACCGGGAGATAACCGCCACGGACCCTGACACCACAGCA 1980

AMH-1\_7 GTGCCAGAGGGCTTTGAAATCAACCGGGAGATAACCGCCACGGACCCTGACACCACAGCA 1980

AMH-1\_11 GTGCCAGAGGGCTTTGAANTCAACCGGGAGATAACCGCCACGGACCCTGACACCACAGCA 1980

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AMH-3\_16 TACCTGCAGTTTGAAATAGATTGGGACACATCCTTTGCCACTAAACAGGGGCGTGATACC 2037

AMH-2\_4 TACCTGCAGTTTGAAATAGATTGGGACACATCCTTTGCCACTAAACAGGGGCGTGATACC 2040

AMH-2\_1 TACNTGCAGTTTGAAATAGATTGGGACACATCCTTTGCCACTAAACAGGGGCGTGATACC 2040

AMH-2\_5 TACCTGCAGTTTGAAATAGATTGGGACACATCCTTTGCCACTAAACAGGGGCGTGATACC 2040

AMH-3\_1 TACCTGCAGTTTGAAATAGATTGGGACACATCCTTTGCCACTAAACAGGGGCGTGATACC 2040

AMH-3\_13 TACCTGCAGTTTGAAATAGATTGGGACACATCCTTTGCCACTAAACAGGGGCGTGATACC 2040

AY198374.1 TACCTGCAGTTTGAAATAGATTGGGACACATCCTTTGCCACTAAACAGGGGCGTGATACC 2040

AMH-1\_2 TACCTGCAGTTTGAAATAGATTGGGACACATCCTTTGCCACTAAACAGGGGCGTGATACC 2040

AMH-1\_7 TACCTGCAGTTTGAAATAGATTGGGACACATCCTTTGCCACTAAACAGGGGCGTGATACC 2040

AMH-1\_11 TACCTGCAGTTTGAAATAGATTGGGACACATCCTTTGCCACTAAACAGGGGCGTGATACC 2040

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AMH-3\_16 AATCCAATAGAGTTCCACGGATGCGTGGATATAGAAACCATCTTCCCAAACCCAGCCGAC 2097

AMH-2\_4 AATCCAATAGAGTTCCACGGATGCGTGGATATAGAAACCATTTTCCCAAACCCAGCCGAC 2100

AMH-2\_1 AATCCAATAGAGTTCCACGAATGCGTGGATATAGAAACCATCTTCCCAAACCCAGCCGAC 2100

AMH-2\_5 AATCCAATAGAGTTCCACGGATGCGTGGATATAGAAACCATCTTCCCAAACCCAGCCGAC 2100

AMH-3\_1 AATCCAATAGAGTTCCACGGATGCGTGGATATAGAAACCATCTTCCCAAACCCAGCCGAC 2100

AMH-3\_13 AATCCAATAGAGTTCCACGGATGCGTGGATATAGAAACCATCTTCCCAAACCCAGCCGAC 2100

AY198374.1 AATCCAATAGAGTTCCACGGATGCGTGGATATAGAAACCATCTTCCCAAACCCAGCCGAC 2100

AMH-1\_2 AATCCAATAGAGTTCCACGGATGCGTGGATATAGAAACCATCTTCCCAAACCCAGCCGAC 2100

AMH-1\_7 AATCCAGTAGAGTTCCACGGATGCGTGGATATAGAAACCATCTTCCCAAACCCAGCCGAC 2100

AMH-1\_11 AATCCAGTAGAGTTCCACGGATGCGTGGATATAGAAACCATCTTCCCAAACCCAGCCGAC 2100

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AMH-3\_16 ACCGGAGAAGCTGTGGGGCGAGTGGTAGCGAAGGAGATCCGCCATAACGTGACCATCGAT 2157

AMH-2\_4 ACCAGAGAGGCTGTGGGGCGAGTGGTAGCGAAGGAGATCCGCCATAACGTGACCATCGAT 2160

AMH-2\_1 ACCAGAGAGGCTGTGGGGCGAGTGGTAGCGAAGGAGATCCGCCATAACGTGACCATCGAT 2160

AMH-2\_5 ACCAGAGAGGCTGTGGGGCGAGTGGTAGCGAAGGAGATCCGCCATAACGTGACCATCGAT 2160

AMH-3\_1 ACCAGAGAAGCTGTGGGGCGAGTGGTAGCGAAGGAGATCCGCCATAACGTGACCATCGAT 2160

AMH-3\_13 ACCGGAGAAGCTGTGGGGCGAGTGGTAGCGAAGGAGATCCGCCATAACGTGACCATCGAT 2160

AY198374.1 ACCAGAGAGGCTGTGGGGCGAGTGGTAGCGAAGGAGATCCGCCATAACGTGACCATCGAT 2160

AMH-1\_2 ACCAGAGAGGCTGTGGGGCGAGTGGTAGCGAAGGAGATCCGCCATAACGTGACCATCGAT 2160

AMH-1\_7 ACCAGAGAAGCTGTGGGGCGAGTGGTAGCGAAGGAGATCCGCCATAACGTGACCATCGAT 2160

AMH-1\_11 ACCAGAGAAGCTGTGGGGCGAGTGGTAGCGAAGGAGATCCGCCATAACGTGACCATCGAT 2160

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AMH-3\_16 TTTGAAGAGTTTGAATTTCTCTACCTCACAGTGAGAGTTCGAGACTTGCACACAGNNGAT 2217

AMH-2\_4 TTCGAAGAGTTTGAATCTCTCTACCTCACAGTGAGAGTTCGGGACTTGCACACAGATGAC 2220

AMH-2\_1 TTTGAAGAGTTTGAATTTCTCTACCTCACAGTGAGAGTTCGGGACTTGCACACAGATGAC 2220

AMH-2\_5 TTTGAAGAGTTTGAATTTCTCTACCTCACAGTGAGAGTTCGGGACTTGCACACAGATGAC 2220

AMH-3\_1 TTTGAAGAGTTTGAACTTCTCTACCTCACAGTGAGAGTTCGAGACTTGCACACAGAAGAT 2220

AMH-3\_13 TTTGAAGAGTTTGAATTTCTCTACCTCACAGTGAGAGTTCGAGACTTGCACACAGAAGAT 2220

AY198374.1 TTTGAAGAGTTTGAATTTCTCTACCTCACAGTGAGAGTTCGGGACTTGCACACAGATGAC 2220

AMH-1\_2 TTTGAAGAGTTTGAATTTCTCTACCTCACAGTGAGAGTTCGGGACTTGCACACAGATGAC 2220

AMH-1\_7 TTTGAAGAGTTTGAATTTCTGTACCTCACAGTGAGAGTTCGAGACTTGCACACAGAAGAT 2220

AMH-1\_11 TTCGAAGAGTTTGAATTTCTGTACCTCACAGTGAGAGTTCGAGACTTGCACACAGAAGAT 2220

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AMH-3\_16 GGACGAGATTANGANGAATCTACCTTCACGATAATANTAATAGATATGAACGACAACTGG 2277

AMH-2\_4 GGACGAGATTATGATGAATCTACCTTCACGATAATAATAATAGATATGAACGACAACTGG 2280

AMH-2\_1 GGACGAGATTATGATGAATCTACCTTCACGATAATAATAATAGATATGAACGACAACTGG 2280

AMH-2\_5 GGACGAGATTATGATGAATCTACCTTCACGATAATAATAATAGATATGAACGACAACTGG 2280

AMH-3\_1 GGACGAGATTATGATGAATCTACCTTCACGATAATAATAATAGATATGAACGACAACTGG 2280

AMH-3\_13 GGACGAGATTATGATGAATCTACCTTCACGATAATAATAATAGATGCGAACGACAACTGG 2280

AY198374.1 GGACGAGATTATGATGAATCTACCTTCACGATAATAATAATAGATATGAACGACAACTGG 2280

AMH-1\_2 GGACGAGATTATGATGAATCTACTTTCACGATAATAATAATAGATATGAACGACAACTGG 2280

AMH-1\_7 GGACGAGATTATGATGAATCTACCTTCACGATAATAATAATAGATGTGAACGACAACTGG 2280

AMH-1\_11 GGACGAGATTATGATGAATCTACCTTCACGATAATAATAATAGATATGAACGACAACTGG 2280

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AMH-3\_16 CCTATCTGGGCGTCTGGTTTCCTGAACCAGNCNTNCAGTATTCGGGAGCGATCATNTACC 2337

AMH-2\_4 CCTATCTGGGCGTCTGGTTTCCTGAACCAGACCTTCAGTATCCGGGAGCGATCATCTACC 2340

AMH-2\_1 CCTATCTGGGCGTCTGGTTTCCTGAACCAGACCTTCAGTATCCGGGAGCGATCATCTACC 2340

AMH-2\_5 CCTATCTGGGCGTCTGGTTTCCTGAACCAGACCTTCAGTATCCGGGAGCGATCATCTACC 2340

AMH-3\_1 CCTATCTGGGCGTCTGGTTTCCTGAACCAGACCTTCAGTATTCGGGAGCGATCATCTACC 2340

AMH-3\_13 CCTATCTGGGCGTCTGGTTTCCTGAACCAGACCTTCAGTATTCGGGAGCGATCATCTACC 2340

AY198374.1 CCTATCTGGGCGTCTGGTTTCCTGAACCAGACCTTCAGTATTCGGGAGCGATCATCTACC 2340

AMH-1\_2 CCTATCTGGGCGTCTGGTTTCCTGAACCAGACCTTCAGTATCCGGGAGCGATCATCTACC 2340

AMH-1\_7 CCGATCTGGGCGTCTGGTTTCCTGAACCAGACCTTCAGTATTCGGGAGCGATCATCTACC 2340

AMH-1\_11 CCTATCTGGGCGTCTGGTTTCCTGAACCAGACCTTCAGTATTCGGGAGCGATCATCTACC 2340

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AMH-3\_16 GGCGTCGTCATCGGGTCNNTACTCGCTACAGACATTGATGGCCCACTTTACAACCAAGTC 2397

AMH-2\_4 GGCGTCGTCATCGGGTCCGTACTCGCTACAGACATTGATGGCCCACTTTACAACCAAGTC 2400

AMH-2\_1 GGCGTCGTCATCGGGTCCGTACTCGCTACAGACATTGATGGCCCACTTTACAACCAAGTC 2400

AMH-2\_5 GGCGTCGTCATCGGGTCCGTACTCGCTACAGACATTGATGGCCCACTTTACAACCAAGTC 2400

AMH-3\_1 GGCGTCGTCATCGGGTCCGTACTCGCTACAGACATTGATGGCCCACTTTACAACCAAGTC 2400

AMH-3\_13 GGCGTCGTCATCGGGTCCGTACTCGCTACAGACATTGATGGCCCACTTTACAACCAAGTC 2400

AY198374.1 GGCGTCGTCATCGGGTCCGTACTCGCTACAGACATTGATGGCCCACTTTACAACCAAGTC 2400

AMH-1\_2 GGCGTCGTCATCGGGTCCGTACTCGCTACAGACATTGATGGCCCACTTTACAACCAAGTC 2400

AMH-1\_7 GGCGTCGTCATCGGGTCCGTACTCGCTACAGACATTGATGGCCCACTTTACAACCAAGTC 2400

AMH-1\_11 GGCGTCGTCATCGGGTCCGTACTCGCTACAGACATTGATGGCCCACTTTACAACCAAGTC 2400

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AMH-3\_16 CGGTACACCATTATCCCCCAGGAAGATACTCCTGAAGGTCTAGTCCAGATACACTTCGAT 2457

AMH-2\_4 CGGTACACAATTATCCCCCAGGAAGATACTCCTGAAGGTCTAGTCCAGATACATTTCGTT 2460

AMH-2\_1 CGGTACACAATTATCCCCCAGGAAGATACTCCTGAAGGTCTAGTCCAGATACATTTCGTT 2460

AMH-2\_5 CGGTACACAATTATCCCCCAGGAAGATACTCCTGAAGGTCTAGTCCAGATACATTTCGTC 2460

AMH-3\_1 CGGTACACCATTATCCCCCAGGAAGATACTCCTGAAGGTCTAGTCCAGATACACTTCGTT 2460

AMH-3\_13 CGGTACACCATTATCCCCCAGGAAGATACTCCTGAAGGTCTAGTCCAGATACACTTCGTT 2460

AY198374.1 CGGTACACCATTATCCCCCAGGAAGATACTCCTGAAGGTCTAGTCCAGATACACTTCGTT 2460

AMH-1\_2 CGGTACACCATTATCCCCCAGGAAGATACTCCTGAAGGTCCAGTCCAGATACACTTCGTT 2460

AMH-1\_7 CGGTACACCATTATCCCCCAGGAAGATACTCCTGAAGGTCTAGTCCAGATACACTTCGTT 2460

AMH-1\_11 CGGTACACCATTATCCCCCAGGAAGATACTCCTGAAGGCCTAGTCCAGATACACTTCGTT 2460

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AMH-3\_16 ACGGGTCAGATTACAGTTGATGAGAATGGTGCAATCGACGCTGATATTCCACCTCGTTGG 2517

AMH-2\_4 ACGGGTCAGATTACAGTTGATGAGAATGGTGCAATCGACGCTGATATTCCACCTCGTTGG 2520

AMH-2\_1 ACGGGTCAGATTACAGTTGATGAGAATGGTGCAATCGACGCTGATATTCCACCTCGTTGG 2520

AMH-2\_5 ACGGGTCAGATTACAGTTGATGAGAATGGTGCAATCGACGCTGATATTCCACCTCGTTGG 2520

AMH-3\_1 ACGGGTCAGATTACAGTTGATGAGAATGGTGCAATCGACGCTGATATTCCACCTCGTTGG 2520

AMH-3\_13 ACGGGTCAGATTACAGTTGATGAGAATGGTGCAATCGACGCTGATATTCCACCTCGTTGG 2520

AY198374.1 ACGGGTCAGATTACAGTTGATGAGAATGGTGCAATCGACGCTGATATTCCACCTCGTTGG 2520

AMH-1\_2 ACGGGTCAGATTACAGTTGATGAGAATGGTGCAATCGACGCTGATATTCCACCTCGTTGG 2520

AMH-1\_7 ACGGGTCAGATTACAGTTGATGAGAATGGTGCAATCGACGCTGATATTCCACCTCGTTGG 2520

AMH-1\_11 ACGGGTCAGATTACAGTTGATGAGAATGGTGCAATCGACGCTGATATTCCACCTCGTTGG 2520

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AMH-3\_16 CACCTCAACTACGCGGTTATAGCCAGCGACAAATGTTCTGAAGAAAATGAAGAGAACTGT 2577

AMH-2\_4 CACCTCAACTACACGGTTATAGCCAGCGACAAATGCTCTGAAGAAAATGAAGAGAACTGT 2580

AMH-2\_1 CACCTCAACTACACGGTTATAGCCAGCGACAAATGTTCTGAAGAAAATGAAGAGAACTGT 2580

AMH-2\_5 CACCTCAACTACACGGTTATAGCCAGCGACAAATGTTCTGAAGAAAATGAAGAGAACTGT 2580

AMH-3\_1 CACCTCAACTACACGGTTATAGCCAGCGACAAATGTTCCGAAGAAAATGAAGAGAACTGT 2580

AMH-3\_13 CACCTCAACTACACGGTTATAGCCAGCGACAAATGTTCCGAAGAAAATGAAGAGAACCGT 2580

AY198374.1 CACCTCAACTACACGGTTATAGCCAGCGACAAATGTTCCGAAGAAAATGAAGAGAACTGT 2580

AMH-1\_2 CACCTCAACTACACGGTTATAGCCAGCGACAAATGTTCCGAAGAAAATGAAGAGAACTGT 2580

AMH-1\_7 CACCTCAACTACACAGTTATAGCCAGCGACAAATGTTCCGAAGAAAATGAAGAGAACTGT 2580

AMH-1\_11 CACCTCAACTACACAGTTATAGCCAGCGACAAATGTTCCGAAGAAAATGAAGAGAACTGT 2580

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AMH-3\_16 CCCCCGGATCCAGTATTCTGGGATACTCTGCGCGACAACGTAATTAACATCGTGGACATA 2637

AMH-2\_4 CCCCCGGATCCAGTGTTCTGGGATACTCTGCGCGACAATGTAATTAACATCGTGGACATA 2640

AMH-2\_1 CCCCCGGATCCAGTGTTCTGGGATACTCTGCGCGACAATGTAATTAACATCGTGGACATA 2640

AMH-2\_5 CCCCCGGATCCAGTGTTCTGGGATACTCTGCGCGACAATGTAATTAACATCGTGGACATA 2640

AMH-3\_1 CCCCCGGATCCAGTGTTCTGGGATACTCTGGGTGACAATGTAATTAACATCGTGGACATA 2640

AMH-3\_13 CCCCCGGATCCAGTGTCCTGGGATACTCTGGGTGACAATGTAATTAACATCGTGGACATA 2640

AY198374.1 CCCCCGGATCCAGTGTTCTGGGATACTCTGGGCGACAATGTAATTAACATCGTGGACATA 2640

AMH-1\_2 CCCCCGGATCCAGTGTTCTGGGATACTCTGGGCGACAATGTAATTAACATCGTGGACATA 2640

AMH-1\_7 CCCCCGGATCCAGTGTTCTGGGATACTCTGGGCGACAATGTAATTAACATCGTGGACATA 2640

AMH-1\_11 CCCCCGGATCCAGTGTTCTGGGATACTCTGGGCGACAATGTAATTAACATCGTGGACATA 2640

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AMH-3\_16 AACAACAAGGTCCCGGCAGCAGACCTCAGTAGACTCAACGAAACGGTGTACATTCATGAA 2697

AMH-2\_4 AACAACAAGGTCCCGGCAGCAGACCTCAGTCGATTCAACGAAACGGTGTACATTTACGAA 2700

AMH-2\_1 AACAACAAGGTCCCGGCAGCAGACCTCAGTCGATTCAACGAAACGGTGTACATTTATGAA 2700

AMH-2\_5 AACAACAAGGTCCCGGCAGCAGACCTCAGTCGATTCAACGAAACGGTGTACATTTATGAA 2700

AMH-3\_1 AACAACAAGGTCCCGGCAGCAGACCTCAGTCGATTCAACGAAACGGTGTACATTTATGAA 2700

AMH-3\_13 AACAACAAGGTCCCGGCAGCAGACCTCAGTCGATTCAACGAANCGGTGTACATTTATGAA 2700

AY198374.1 AACAACAAGGTCCCGGCAGCAGACCTCAGTCGATTCAACGAAACGGTGTACATTTATGAA 2700

AMH-1\_2 AACAACAAGGTCCCGGCAGCAGACCTCAGTCGATTCAACGAAACGGTGTACATTTATGAA 2700

AMH-1\_7 AACAACAAGGTCCCGGCAGCAGACCTCAGTAGATTCAACGAAACGGTGTACATTTATGAA 2700

AMH-1\_11 AACAACAAGGTCCCGGCAGCAGACCTCAGTAGATTCAACGAAACGGTGTACATTTATGAA 2700

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AMH-3\_16 AATGCACCCGATTTCACAAACGTGGTCAAGATATACTCCATCGACGAAGACAGAGACGAA 2757

AMH-2\_4 AATGCACCCGATTTCACAAACGTGGTCAAGATATACTCCATCGACGAAGACAGAGACGAA 2760

AMH-2\_1 AATGCACCCGATTTCACAAACGTGGTCAAGATATACTCCATCGACGAAGACAGAGACGAA 2760

AMH-2\_5 AATGCACCCGATTTCACAAACGTGGTCAAGATATACTCCATCGACGAAGACAGAGACGAA 2760

AMH-3\_1 AATGCACCCGATTTCACAAACGTGGTCAAGATATACTCCATCGACGAAGACAGAGACGAA 2760

AMH-3\_13 AATGCACCCGATTTCACNNACGTGGTCAAGATATACTCCATCGACGAAGACAGAGACGAA 2760

AY198374.1 AATGCACCCGATTTCACAAACGTGGTCAAGATATACTCCATCGACGAAGACAGAGACGAA 2760

AMH-1\_2 AATGCACCCGATTTCACAAACGTGGTCAAGATATACTCCATCGACGAAGACAGAGACGAA 2760

AMH-1\_7 AATGCACCCGATTTCACAAACGTGGTCAAGATATACTCCATCGACGAAGACAGAGACGAA 2760

AMH-1\_11 AATGCACCCGATTTCACAAACGTGGTCAAGATATACTCCATCGACGAAGACAGAGACGAA 2760

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AMH-3\_16 ATATATCACACGGTGCGGTACCAGATCAATTATGCTGTGAACCAGCGGCTGCGAGGTTTC 2817

AMH-2\_4 ATATATCACACGGTGCGGTACCAGATCAATTATGCTGTGAACCAGCGGCTGCGAGACTTC 2820

AMH-2\_1 ATATATCACACGGTGCGGTACCAGATCAATTATGCTGTGAACCAGCGGCTGCGAGACTTC 2820

AMH-2\_5 ATATATCACACGGTGCGGTACCAGATCAATTATGCTGTGAACCAGCGGCTGCGAGACTTC 2820

AMH-3\_1 ATATATCACACGGTGCGGTACCAGATCAATTGTGCTGTGAACCAGCGGCTGCGAGACTTC 2820

AMH-3\_13 ATATATCACACGGTGCGGTACCAGATCNNTTATGCTGTGAACCAGCGGCTGCGAGACTTC 2820

AY198374.1 ATATATCACACGGTGCGGTACCAGATCAATTATGCTGTGAACCAGCGGCTGCGAGACTTC 2820

AMH-1\_2 ATATATCACACGGTGCGGTACCAGATCAATTATGCTGTGAACCAGCGGCTGCGAGACTTC 2820

AMH-1\_7 ATATATCACACGGTGCGGTACCAGATCAATTATGCTGTGAACCAGCGGCTGCGAGACTTC 2820

AMH-1\_11 ATATATCACACGGTGCGGTACCAGATCAATTATGCTGTGAACCAGCGGCTGCGAGACTTC 2820

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AMH-3\_16 TTCGCCATAGACCTGGATTCAGGCCAGGTGTACGTGGAGAACACCAACAATGAGCTCCTG 2877

AMH-2\_4 TTCGCCATAGACCTGGATTCAGGCCAGGTGTACGTGGAGAACACCAACAATGAGCTCCTG 2880

AMH-2\_1 TTCGCCATAGACCTGGATTCAGGCCAGGTGTACGTGGAGAACACCAACAATGAGCTCCTG 2880

AMH-2\_5 TTCGCCATAGACCTGGATTCAGGCCAGGTGTACGTGGAGAACACCAACAATGAGCTCCTG 2880

AMH-3\_1 TTCGCCATAGACCTGGATTCAGGCCAGGTGTACGTGGAGAACACCAACAATGAGCTCCTG 2880

AMH-3\_13 TTCGCCATAGACCTGGATTCAGGCCAGGTGTACGTGGAGAACGCCAACAATGAGCTCCTG 2880

AY198374.1 TTCGCCATAGACCTGGATTCAGGCCAGGTGTACGTGGAGAACACCAACAATGAGCTCCTG 2880

AMH-1\_2 TTCGCCATAGACCTGGATTCAGGCCAGGTGTACGTGGAGAACACCAACAATGAGCTCCTG 2880

AMH-1\_7 TTCGCCATAGACCTGGATTCAGGCCAGGTGTACGTGGAGAACACCAACAATGAGCTCCTG 2880

AMH-1\_11 TTCGCCATAGACCTGGATTCAGGCCAGGTGTACGTGGAGAACACCAACAATGAGCTCCTG 2880

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AMH-3\_16 GATCGGGACAGAGGCGAAGACCAACACAGGATATTCATTAACCTCATTGACAACTTTTAT 2937

AMH-2\_4 GATCGGGACAGAGGCGAAGACCAACACAGGATATTCATTAACCTCATTGACAACTTTTAT 2940

AMH-2\_1 GATCGGGGCAGAGGCGAAGACCAACACAGGATATTCATTAACTTCATTGACAACTTTTAT 2940

AMH-2\_5 GATCGGGACAGAGGCGAAGACCAACACAGGATATTCATTAACCTCATTGACAACTTTTAT 2940

AMH-3\_1 GATCGGGGCAGAGGCGAAGACCAACACAGGATATTCATTAACCACATTGACAACTTTTAT 2940

AMH-3\_13 GATCGGGACAGAGGCGAAGACCAACACAGGATATTCATTAACCTCATTGACAACTTTTAT 2940

AY198374.1 GATCGGGACAGAGGCGAAGACCAACACAGGATATTCATTAACCTCATTGACAACTTTTAT 2940

AMH-1\_2 GATCGGGACAGAGGCGAGGACCAACACAGGATATTCATTAACCTCATTGACAACTTTTAT 2940

AMH-1\_7 GATCGGGACAGAGGCGAAGACCAACACAGGATATTCATTAACCTCATTGACAACTTTTAT 2940

AMH-1\_11 GATCGGGACAGAGGCGAAGACCAACACAGGATATTCATTAACCTCATTGACAACTTTTAT 2940

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AMH-3\_16 AGCGAAGGAGATGGAAATAGAAATGTAAACACTACAGAGGTGCTGGTGATACTATTAGAT 2997

AMH-2\_4 AGCGAAGGAGATGGAAATAGAAATGTAAACACTACAGAGGTGCTGGTGATACTATTAGAT 3000

AMH-2\_1 AGCGAAGGAGATGGAAATAGAAATGTAAACACTACAGAGGTGCTGGTGATACTATTAGAT 3000

AMH-2\_5 AGCGAAGGAGATGGAAATAGAAATGTAAACACTACAGAGGTGCTGGTGATACTATTAGAT 3000

AMH-3\_1 AGCGAAGGAGATGGAAATAGAAATGTAAACACTACAGAGGTGCTGGTGATACTATTAGAT 3000

AMH-3\_13 AGCGAAGGAGATGGAAATAGAAATGTAAACACCACAGAGGTGCTGGTGATACTATTAGAT 3000

AY198374.1 AGCGAAGGAGATGGAAATAGAAATGTAAACACTACAGAGGTGCTGGTGATACTATTAGAT 3000

AMH-1\_2 AGCGAAGGAGATGGAAATAGAAATGTAAACACTACAGAGGTGCTGGTGATACTATTAGAT 3000

AMH-1\_7 AGCGAAGGAGATGGAAATAGAAATGTAAACACTACAGAGGTGCTGGTGATACTATTAGAT 3000

AMH-1\_11 AGCGAAGGAGATGGAAATAGAAATGTAAACACTACAGAGGTGCTGGTGATACTATTAGAT 3000

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AMH-3\_16 GAGAATGACAACGCTCCTGAATTGCCGACTCCAGAAGAGCTGAGTTGGAGCATTTCCGAG 3057

AMH-2\_4 GAGAATGACAACGCTCCTGAATTGCCGACTCCAGAAGAGCTGAGTTGGAGCATTTCCGAG 3060

AMH-2\_1 GAGAATGACAACGCTCCTGAATTGCCGACTCCAGAAGAGCTGAGTTGGAGCATTTCCGAG 3060

AMH-2\_5 GAGAATGACAACGCTCCTGAATTGCCGACTCCAGAAGAGCTGAGTTGGAGCATTTCCGAG 3060

AMH-3\_1 GAAAATGACAACGCTCCTGAATTGCCGACTCCAGAAGAGCTGAGTTGGAGCATTTCCGAG 3060

AMH-3\_13 GAAAATGACAACGCTCCTGAATTGCCGACTCCAGAAGAGCTGAGTTGGAGCATTTCCGAG 3060

AY198374.1 GAGAATGACAACGCTCCTGAATTGCCGACTCCAGAAGAGCTGAGTTGGAGCATTTCCGAG 3060

AMH-1\_2 GAAAATGACAACGCTCCTGAATTGCCGACTCCAGAAGAGCTGAGTTGGAGCATTTCCGAG 3060

AMH-1\_7 GAGAATGACAACGCTCCTGAATTGTCGACTCCAGAAGAGCTGAGTTGGAGCATTTCCGAG 3060

AMH-1\_11 GAGAATGACAACGCTCCTGAATTGCCGACTCCAGAAGAGCTGAGTTGGAGCATTTCCGAG 3060

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AMH-3\_16 AATTTACAAGAGGGTATAACACTCGATGGCGAAAGCGATGTGATATACGCACCGGATATA 3117

AMH-2\_4 AATTTACAAGAGGGTATAACACTCGATGGCGAAAGCGATGTGATATACGCACCGGATATA 3120

AMH-2\_1 AATTTACAAGAGGGTATAACACTCGATGGCGAAAGCGATGTGGTATACGCACCGGATATA 3120

AMH-2\_5 AATTTACAAGAGGGTATAACACTCGATGGCGAAAGCGATGTGATATACGCACCGGATATA 3120

AMH-3\_1 AATTTACAAGAGGGTATAACACTCGATGGCGAACGCGATGTAATATACGCACCGGATATA 3120

AMH-3\_13 AATTTACAAGAGGGTATAACGCTCGATGGCGAACGCGATGTAATATACGCACCGGATATA 3120

AY198374.1 AATTTACAAGAGGGTATAACACTCGATGGCGAAAGCGATGTGATATACGCACCGGATATA 3120

AMH-1\_2 AATTTACAAGAGGGTATAACACTCGATGGCGAACGCGATGTAATATACGCACCGGATATA 3120

AMH-1\_7 AATTTACAAGAGGGTATAACACTCGATGGCGAAAGCGATGTGATATACGCACCGGATATA 3120

AMH-1\_11 AATTTACAAGAGGGTATAACACTCGATGGCGAAAGCGATGTGATATACGCACCGGATATA 3120

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AMH-3\_16 GACGAAGAGGACACGCCAAACTCTCACGTTGGCTACGCAATCCTGGCCATGACAGTCACC 3177

AMH-2\_4 GACGAAGAGGACACGCCAAACTCTCACGTTGGCTACGCAATCCTGGCCATGACAGTCACC 3180

AMH-2\_1 GACGAAGAGGACACGCCAAACTCTCACGTTGGCTACGCAATCCTGGCCATGACAGTCACC 3180

AMH-2\_5 GACGAAGAGGACACGCCAAACTCTCACGTTGGCTACGCAATCCTGGCCATGACAGTCACC 3180

AMH-3\_1 GACGAAGAGGACACGCCAAACTCTCACGTTGGCTACGCAATCCTGGCCATGACAGTCACC 3180

AMH-3\_13 GACGAAGAGGACACGCCAAACTCTCACGTTGGCTACGCAATCCTGGCCATGACAGTCACC 3180

AY198374.1 GACGAAGAGGACACGCCAAACTCTCACGTTGGCTACGCAATCCTGGCCATGACAGTCACC 3180

AMH-1\_2 GACGAAGAGGACACGCCAAACTCTCACGTTGGCTACGCAATCCTGGCCATGACAGTCACC 3180

AMH-1\_7 GACGAAGAGGACACGCCAAACTCTCACGTTGGCTACGCAATCCTGGCCATGACAGTCACC 3180

AMH-1\_11 GACGAAGAGGACACGCCAAACTCTCACGTTGGCTACGCAATCCTGGCCATGACAGTCACC 3180

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AMH-3\_16 AATAGAGACCTGGACACTGTTCCGAGACTTCTCAACATGCTGTCGCCTAACAACGTAACC 3237

AMH-2\_4 AATAGAGACCTGGACACTGTTCCGAGACTTCTCAACATGCTGTCGCCTAACAACGTAACC 3240

AMH-2\_1 AATAGAGACCTGGACACTGTTCCGAGACTTCTCAACATGCTGTCGCCTAACAACGTAACC 3240

AMH-2\_5 AATAGAGACCTGGACACTGTTCCGAGACTTCTCAACATGCTGTCGCCTAACAACGTAACC 3240

AMH-3\_1 AATAGAGACCTGGACACTGTTCCGAGACTTTTCAACATGCTGTCGCCTAACAACGTAACC 3240

AMH-3\_13 AATAGAGACCTGGACACTGTTCCGAGACTTCTCAACATGCTGTCGCCTAACAACGTAACC 3240

AY198374.1 AATAGAGACCTGGACACTGTTCCGAGACTTCTCAACATGCTGTCGCCTAACAACGTAACC 3240

AMH-1\_2 AATAGAGACCTGGACACTGTTCCGAGACTTCTCAACATGCTGTCGCCTAACAACGTAACC 3240

AMH-1\_7 AATAGAGACCTGGACACTGTTCCGAGACTTCTCAACATGCTGTCGCCTAACAACGTAACC 3240

AMH-1\_11 AATAGAGACCTGGACACTGTTCCGAGACTTCTCAACATGCTGTCGCCTAACAACGTAACC 3240

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AMH-3\_16 GGATTCCTCCAGACAGCAATGCCTTTGAGAGGATATTGGGGGACTTACGATATAAGTGTA 3297

AMH-2\_4 GGATTCCTCCAGACAGCAATGCCTTTGAGAGGATATTGGGGGACTTACGATATAAGTGTA 3300

AMH-2\_1 GGATTCCTCCAGACAGCAATGCCTTTGAGAGGATATTGGGGGACTTACGATATAAGTGTA 3300

AMH-2\_5 GGATTCCTCCAGACAGCAATGCCTTTGAGAGGATATTGGGGGACTTACGATATAAGTGTA 3300

AMH-3\_1 GGATTCCTCCAGACAGCAATGCCTTTAAGAGGATATTGGGGGACTTACGATATAAGTATA 3300

AMH-3\_13 GGATTCCTCCAGACAGCAATGCCTTTAAGAGGATATTGGGGGACTTACGATATAAGTATA 3300

AY198374.1 GGATTCCTCCAGACAGCAATGCCTTTGAGAGGATATTGGGGGACTTACGATATAAGTATA 3300

AMH-1\_2 GGATTCCTCCAGACAGCAATGCCTTTAAGAGGATATTGTGGGACTTACGATATAAGTATA 3300

AMH-1\_7 GGATTCCTTCAGACAGCAATGCCTTTGAGAGGATATTGGGGTACTTACGATATAAGTATA 3300

AMH-1\_11 GGATTCCTTCAGACAGCAATGCCTTTGAGAGGATATTGGGGTACTTACGATATAAGTATA 3300

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AMH-3\_16 CTGGCGTTCGACCACGGTATCCCTCAGCAGATATCTCATGAGGTGTATGAATTGGAAATT 3357

AMH-2\_4 CTGGCGTTCGACCACGGTATTCCTCAGCAGATATCTCATGAGGTGTATGAATTGGAAATT 3360

AMH-2\_1 CTGGCGTTCGACCACGGTATTCCTCAGCAGATATCTCATGAGGTGTATGAATTGGAAATT 3360

AMH-2\_5 CTGGCGTTCGACCACGGTATTCCTCAGCAGATATCTCATGAGGTGTATGAATTGGAAATT 3360

AMH-3\_1 CTGGCGTTCGACCACGGTATTCCTCAGCAGATATCTCATGAGGTGTATGAATTGGAAATT 3360

AMH-3\_13 CTGGCGTTCGACCACGGTATTCCTCAGCAGATATCTCATGAGGTGTATGAATTGGAAATT 3360

AY198374.1 CTGGCGTTCGACCACGGTATTCCTCAGCAGATATCTCATGAGGTGTATGAATTGGAAATT 3360

AMH-1\_2 CTGGCGTTCGACCACGGTATTCCTCAGCAGATATCTCATGAGGTGTATGAATTGGAAATT 3360

AMH-1\_7 CTGGCGTTCGACCACGGTATTCCTCAGCAGATATCTCATGAGGTGTATGAATTGGAAATT 3360

AMH-1\_11 CTGGCGTTCGACCACGGTATTCCTCAGCAGATATCTCATGAGGTGTATGAATTGGAAATT 3360

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AMH-3\_16 CGACCTTACAATTACAATCCTCCCCAGTTCGTTTTTCCCGAATCCGGGACGATTCTACGA 3417

AMH-2\_4 CGACCTTTCAATTACAATCCTCCCCAGTTCGTTTTTCCTGAATCCGGGACGATTCTACGA 3420

AMH-2\_1 CGACCTTACAATTACAATCCTCCCCAGTTCGTTTTTCCTGAATCCGGGACGATTCTACGA 3420

AMH-2\_5 CGACCTTACAATTACAATCCTCCCCAGTTCGTTTTTCCTGAATCCGGGACGATTCTACGA 3420

AMH-3\_1 CGACCCTACAATTACAATCCTCCTCAGTTCGTTTTTCCTGAATCCGGGACGATTCTACGA 3420

AMH-3\_13 CGACCTTACAATTACAATCCTCCTCAGTTCGTTTTTCCTGAATCCGGGACGATTCTACGA 3420

AY198374.1 CGACCTTACAATTACAATCCTCCCCAGTTCGTTTTTCCTGAATCCGGGACGATTCTACGA 3420

AMH-1\_2 CGACCTTACAATTACAATCCTCCCCAGTTCGTTTTTCCTGAATCCGGGACGATTCTACGA 3420

AMH-1\_7 CGACCTTACAATTACAATCCTCCCCAGTTCGTTTTTCCTGAATCCGGGACGATTCTACGA 3420

AMH-1\_11 CGACCTTACAATTACAATCCTCCCCAGTTCGTTTTTCCTGAATCCGGGACGATTCTACGA 3420

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AMH-3\_16 CTGGCTTTGGAACGCGCTGTGGTAAATAATGTATTGTCACTTGTAAACGGTGACCCGTTA 3477

AMH-2\_4 CTGGCTTTGGAACGCGCTGTGGTAAATAATGTATTGTCACTTGTAAACGGTGACCTGTTA 3480

AMH-2\_1 CTGGCTTTGGAACGCGCTGTGGTAAATAATGTATTGTCACTTGTAAACGGTGACCTGTTA 3480

AMH-2\_5 CTGGCTTTGGAACGCGCTGTGGTAAATAATGTATTGTCACTTGTAAACGGTGACCTGTTA 3480

AMH-3\_1 CTGGCTTTGGAACGCGCAGTGGTAAATAATGTTTTGTCACTTGTAAACGGTGACCCGTTA 3480

AMH-3\_13 CTGGCTTTGGAACGCGCAGTGGTAAATAATGTTTTGTCACTTGTAAACGGTGACCCGTTA 3480

AY198374.1 CTGGCTTTGGAACGCGCAGTGGTAAATAATGTTTTGTCACTTGTAAACGGTGACCCGTTA 3480

AMH-1\_2 CTGGCTTTGGAACGCGCAGTGGTAAATAATGTTTTGTCACTTGTAAACGGTGACCCGTTA 3480

AMH-1\_7 CTGGCTTTGGAACGCGCAGTGGTAAATAATGTTTTGTCACTTGTAAACGGTGACCCGTTA 3480

AMH-1\_11 CTGGCTTTGGAACGCGCAGTGGTAAATAATGTTTTGTCACTTGTAAACGGTGACCCGTTA 3480

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AMH-3\_16 GACAGGATACAAGCAGTTGACGACGATGGTCTCGATGCTGGCGTGGTGACTTTCGATATT 3537

AMH-2\_4 GACAGGATACAAGCAATTGACGACGATGGTCTCGATGCTGGCGTGGTGACTTTCGATATT 3540

AMH-2\_1 GACAGGATACAAGCAATTGACGACGATGGTCTCGATGCTGGCGTGGTGACTTTCGATATT 3540

AMH-2\_5 GACAGGATACAAGCAATTGACGACGATGGTCTCGATGCTGGCGTGGTGACTTTCGATATT 3540

AMH-3\_1 GACAGGATACAAGCAATTGACGACGATGGTCTTGATGCTGGCGTGGTGACTTTCGATATT 3540

AMH-3\_13 GACAGGATACAAGCAATTGACGACGATGGTCTTGATGCTGGCGTGGTGACTTTCGATATT 3540

AY198374.1 GACAGGATACAAGCAATTGACGACGATGGTCTTGATGCTGGCGTGGTGACTTTCGATATT 3540

AMH-1\_2 GACAGGATACAAGCAATTGACGACGATGGTCTTGATGCTGGCGTGGCGACTTTCGATATT 3540

AMH-1\_7 GACAGGATACAAGCAATTGACGACGATGGTCTTGATGCTGGCGTGGTGACTTTCGATATT 3540

AMH-1\_11 GACAGGATGCAAGCAATTGACGACGATGGTCTTGATGCTGGCGTGGTGACTTTCGATATT 3540

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AMH-3\_16 GTTGGAGATGCTGATGCATCAAACTACTTCAGAGTAAATAATGATGGCGACAATTTTGGA 3597

AMH-2\_4 GTTGGAGATGCTGATGCATCAAACTACTTCAGAGTAAATAATGATGGCGACAACTTTGGA 3600

AMH-2\_1 GTTGGAGATGCTGATGCATCAAACTACTTCAGAGTAAATAATGATGGCGACAACTTTGGA 3600

AMH-2\_5 GTTGGAGATGCTGATGCATCAAACTACTTCAGAGTAAATAATGATGGCGACAACTTTGGA 3600

AMH-3\_1 GTTGGAGATGCTGATGCATCAAACTACTTCAGAGTAAATAATGATGGCGACAACTTTGGA 3600

AMH-3\_13 GTTGGAGATGCTGATGCATCAAACTACTTCAGAGTAAATAATGATGGCGACAACTTTGGA 3600

AY198374.1 GTTGGAGATGCTGATGCATCAAACTACTTCAGAGTAAATAATGATGGCGACAACTTTGGA 3600

AMH-1\_2 GTTGGAGATGCTGATGCATCAAACTACTTCAGAGTAAATAATGATGGCGACAACTTTGGA 3600

AMH-1\_7 GTTGGAGATGCTGATGCATCAAACTACTTCAGAGTAAATAATGATGGCGACAACTTTGGA 3600

AMH-1\_11 GTTGGAGATGCTGATGCATCAAACTACTTCAGAGTAAATAATGATGGCGACAACTTTGGA 3600

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AMH-3\_16 ACCTTGTTGCTGACACAGGCGCTTCCTGAGGAAGGCAAGGAATTTGAGGTTACCATCCGG 3657

AMH-2\_4 ACCTTGTTGCTGACACAGGCGCTTCCTGAGGAAGGCAAGGAATTTGAGGTTACCATCCGG 3660

AMH-2\_1 ACCTTGTTGCTGACACAGGCGCTTCCTGAGGAAGGCAAGGAATTTGAGGTTACCATCCGG 3660

AMH-2\_5 ACCTTGTTGCTGACACAGGCGCTTCCTGAGGAAGGCAAGGAATTTGAGGTTACCATCCGG 3660

AMH-3\_1 ACCTTGTTGCTGACACAGGCGCTTCCTGAGGAAGGCAAGGAATTTGAGGTTACCATCCGG 3660

AMH-3\_13 ACCTTGTTGCTGACACAGGCGCTTCCTGAGGAAGGCAAGGAATTTGAGGTTACCATCCGG 3660

AY198374.1 ACCTTGTTGCTGACACAGGCGCTTCCTGAGGAAGGCAAGGAATTTGAGGTTACCATCCGG 3660

AMH-1\_2 ACCTTGTTGCTGACACAGGCGCTTCCTGAGGAAGGCAAGGAATTTGAGGTTACCATCCGG 3660

AMH-1\_7 ACCTTGTTGCTGACACAGGCGCTTCCTGAGGAAGGCAAGGAATTTGAGGTTACCATCCGG 3660

AMH-1\_11 ACCTTGTTGCTGACACAGGCGCTTCCCGAGGAAGGCAAGGAATTTGAGGTTACCATCCGG 3660

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AMH-3\_16 GCTACAGACGGCGGAACGGAACCTCGATCATATTCAACAGACTCTACTATAACAGTCCTC 3717

AMH-2\_4 GCTACAGACGGCGGAACAGAACCTCGATCATATTCAACAGACTCCACTATAACAGTCCTC 3720

AMH-2\_1 GCTACAGACGGCGGAACAGAACCTCGATCATATTCAACAGACTCCACTATAACAGTCCTC 3720

AMH-2\_5 GCTACAGACGGCGGAACAGAACCTCGATCATATTCAACAGACTCCACTATAACAGTCCTC 3720

AMH-3\_1 GCTACAGGCGGCGGAACGGAACCTCGATCATATTCAACAGACTCCACTATAACAGTGCTC 3720

AMH-3\_13 GCTACAGGCGGCGGAACGGAACCTCGATCATATTCAACAGACTCCACTATAACAGTGCTC 3720

AY198374.1 GCTACAGACGGCGGAACAGAACCTCGATCATATTCAACAGACTCCACTATAACAGTGCTC 3720

AMH-1\_2 GCTACAGACGGCGGAACGGAACCTCGATCATATTCAACAGACTCCACTATAACAGTGCTC 3720

AMH-1\_7 GCTACAGACGGCGGAACAGAACCTCGATCATATTCAACAGACTCCACTATAACAGTGCTC 3720

AMH-1\_11 GCTACAGACGGCGGAACAGAACCTCGATCATATTCAACAGACTCCACTATAACAGTGCTC 3720

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AMH-3\_16 TTCGTTCCGACTTTGGGTGATCCGATCTTTCAAGATAACACTTACTCAGTAGCATTCTTT 3777

AMH-2\_4 TTCGTTCCGACTTTGGGTGATCCGATCTTTCAAGATAACACTTACTCAGTAGCATTCTTT 3780

AMH-2\_1 TTCGTTCCGACTTTGGGTGATCCGATCTTTCAAGATAACACTTACTCAGTAGCATTCTNT 3780

AMH-2\_5 TTCGTTCCGACTTTGGGTGATCCGATCTTTCAAGATAACACTTACTCAGTAGCATTCTTT 3780

AMH-3\_1 TTCGTTCCGACTTTGGGTGATCCGATATTTCAAGATAACACTTACTCAGTAGCATTCTTT 3780

AMH-3\_13 TTCGTTCCGACTTTGGGTGATCCGATATTTCAAGATAACACTTACTCAGTAGCATTCTTT 3780

AY198374.1 TTCGTTCCGACTTTGGGTGATCCGATCTTTCAAGATAACACTTACTCAGTAGCATTCTTT 3780

AMH-1\_2 TTCGTTCCGACTTTGGGTGATCCGATCTTTCAAGATAACACTTACTCAGTAGCATTCTTT 3780

AMH-1\_7 TTCGTTCCGACTTTGGGTGATCCGATCTTTCAAGATAACACTTACTCGGTAGCATTCTTT 3780

AMH-1\_11 TTCGTTCCGACTTTGGGTGATCCGATCTTTCAAGATAACACTTACTCAGTAGCATTCTTT 3780

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AMH-3\_16 GAAAAAGAGGTTGGCTTGACTGAGAGGTTCACGCTCCCACTAGCAGAGGACCCTAAGAAC 3837

AMH-2\_4 GAAAAAGAGGTTGGCTTGACTGAGAGGTTCTCGCTCCCACATGCAGAGGACCCTAAGAAC 3840

AMH-2\_1 GAAAAAGAGGTTGGCTTGACTGAGAGGTTCTCGCTCCCACATGCAGAGGACCCTAAGAAC 3840

AMH-2\_5 GAAAAAGAGGTTGGCTTGACTGAGAGGTTCTCGCTCCCACATGCAGAGGACCCTAAGAAC 3840

AMH-3\_1 GAAAAAGAGGTTGGCTTGACTGAGAGGTTCTCGCTCCCACTAGCAGAGGACCCTAAGAAC 3840

AMH-3\_13 GAAAAAGAGGTTGGCTTGACTGAGAGGTTCTCGCTCCCACTAGCAGAGGACCCTAAGAAC 3840

AY198374.1 GAAAAAGAGGTTGGCTTGACTGAGAGGTTCTCGCTCCCACATGCAGAGGACCCTAAGAAC 3840

AMH-1\_2 GAAAAAGAGGTTGGCTTGACTGAGAGGTTCTCGCTCCCACATGCAGAGGACCCTAAGAAC 3840

AMH-1\_7 GAAAAAGAGGTTGGCTTGACTGAGAGGTTCTCGCTCCCACATGCAGAGGACCCTAAGAAC 3840

AMH-1\_11 GAAAAAGAGGTTGGCTTGACTGAGAGGTTCTCGCTCCCACATGCAGAGGACCCTAAGAAC 3840

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AMH-3\_16 AAACTTTGCACTGACGACTGTCACGATATTTACTACAGGATCTTTGGTGGTGTGGATTAC 3897

AMH-2\_4 AAACTCTGCACTGACGACTGTCACGATATTTACTACAGGATCTTTGGTGGTGTGGATTAC 3900

AMH-2\_1 AAACTCTGCACTGACGACTGTCACGATATTTACTACAGGATCTTTGGTGGTGTGGATTAC 3900

AMH-2\_5 AAACTCTGCACTGACGACTGTCACGATATTTACTACAGGATCTTTGGTGGTGTGGATTAC 3900

AMH-3\_1 AAACTCTGCACTGACGACTGTCACGATATTTACTACAGGATCTTTGGTGGTGTGGATTAC 3900

AMH-3\_13 AAACTCTGCACTGACGACTGTCACGATATTTACTACAGGATCTTTGGTGGTGCGGATTAC 3900

AY198374.1 AAACTCTGCACTGACGACTGTCACGATATTTACTACAGGATCTTTGGTGGTGTGGATTAC 3900

AMH-1\_2 AAACTCTGCACTGACGACTGTCACGATATTTACTACAGGATCTTTGGTGGTGTGGATTAC 3900

AMH-1\_7 AAACTCTGCACTGACGACTGTCACGATATTTACTACAGGATCTTTGGTAGTGTGGATTAC 3900

AMH-1\_11 AAACTCTGCACTGACGACTGTCACGATATTTACTACAGGATCTTTGGTGGTGTGGATTAC 3900

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AMH-3\_16 GAGCCATTTGACCTGGACCCGGTGACGAACGTGATCTTCCTGAAATCAGAACTAGACCGG 3957

AMH-2\_4 GAGCCATTTGACCTGGACCCGGTGACGAACGTGATCTTCCTGAAATCAGAACTGGACCGA 3960

AMH-2\_1 GAGCCATTTGACCTGGACCCGGTGACGAACGTGATCTTCCTGAAATCAGAACTGGACCGA 3960

AMH-2\_5 GAGCCATTTGACCTGGACCCGGTGACGAACGTGATCTTCCTGAAATCAGAACTGGACCGA 3960

AMH-3\_1 GAGCCATTTGACCTGGACCCGGTGACGAACGTGATCTTCCTGAAATCAGAACTAGACCGG 3960

AMH-3\_13 GAGCCATTTGACCTGGACCCGGTGACGAACGTGATCTTCCTGAAATCAGAACTAGACCGG 3960

AY198374.1 GAGCCATTTGACCTGGACCCGGTGACGAACGTGATCTTCCTGAAATCAGAACTAGACCGG 3960

AMH-1\_2 GAGCCATTTGACCTGGACCCGGTGACGAACGTGATCTTCCTGAAATCAGAACTAGACCGG 3960

AMH-1\_7 GAGCCATTTGACCTGGACCCGGTGACGAACGTGATCTTCCTGAAATCAGAACTAGACCGG 3960

AMH-1\_11 GAGCCATTTGACCTGGACCCGGTGACGAACGTGATCTTCCTGAAATCAGAACTAGACCGG 3960

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AMH-3\_16 GATACCACTGCCACGCATGTGGTGCAAGTGGCAGCCAGTAATTCGCCCACAGGAGGCGGA 4017

AMH-2\_4 GAGACCACTGCCACGCAGGTGGTTCAAGTGGCTGCCAGTAATTCGCCCACAGGAGGCGGA 4020

AMH-2\_1 GAGACCACTGCCACGCATGTGGTTCAAGTGGCTGCCAGTAATTCGCCCACAGGAGGCGGA 4020

AMH-2\_5 GAGACCACTGCCACGCATGTGGTTCAAGTGGCTGCCAGTAATTCGCCCACAGGAGGCGGA 4020

AMH-3\_1 GAGACCACTGCCACGCATGTGGTGCAAGTGGCAGCCAGTAATTCGCCCACAGGAGGCGGA 4020

AMH-3\_13 GAGACCACTGCCACGCATGTGGTGCAAGTGGCAGCCAGTAATTCGCCCACAGGAGGCGGA 4020

AY198374.1 GAGACCACTGCTACGCATGTGGTGCAAGTGGCAGCCAGTAATTCGCCCACAGGAGGCGGA 4020

AMH-1\_2 GAGACCACTGCTACGCATGTGGTGCAAGTGGCAGCCAGTAATTCGCCCACAGGAGGCGGA 4020

AMH-1\_7 GAGACCACTGCTACGCATGTGGTGCAAGTGGCAGCCAGTAATTCGCCCACAGGAGGCGGA 4020

AMH-1\_11 GAGACCACTGCTACGCATGTGGTGCAAGTGGCAGCCAGTAATTCGCCCACAGGAGGCGGA 4020

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AMH-3\_16 ATACCACTCCCTGGGTCTCTTCTCACCGTCACTGTCACTGTACGAGAAGCGGATCCACGG 4077

AMH-2\_4 ATACCACTCCCTGGGTCTCTTCTCACCGTCACTGTCACTGTACGAGAAGCGGATCCACGG 4080

AMH-2\_1 ATACCACTCCCTGGGTCTCTTCTCACCGTCACTGTCACTGTACGAGAAGCGGATCCACGG 4080

AMH-2\_5 ATACCACTCCCTGGGTCTCTTCTCACCGTCACTGTCACTGTACGAGAAGCGGATCCACGG 4080

AMH-3\_1 ATACCACTCCCTGGGTCTCTTCTCACCGTCACTGTCACTGTACGAGAAGCGGATCCACGG 4080

AMH-3\_13 ATACCACTCCCTGGGTCTCTTCTCACCGTCACTGTCACTGTACGAGAAGCGGATCCACGG 4080

AY198374.1 ATACCACTCCCTGGGTCTCTTCTCACCGTCACTGTCACTGTACGAGAAGCGGATCCACGG 4080

AMH-1\_2 ATACCACTCCCTGGGTCTCTTCTCACCGTCACTGTCACTGTACGAGAAGCGGATCCACGG 4080

AMH-1\_7 ATACCACTCCCTGGGTCTCTTCTCACCGTCACTGTCACTGTACGAGAAGCGGATCCACGG 4080

AMH-1\_11 ATACCACTCCCTGGGTCTCTTCTCACCGTCACTGTCACTGTACGAGAAGCGGATCCACGG 4080

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AMH-3\_16 CCTGTGTTCGAGCAGCGTCTGTACACGGCTGGCATTTCCACTTCCGATAACATCAACAGG 4137

AMH-2\_4 CCTGTGTTCGAGCAGCGTCTGTACACGGCTGGCATTTCCACTTCCGATAACATCAACAGA 4140

AMH-2\_1 CCTGTGTTCGAGCAGCGTCTGTACACGGCTGGCATTTCCACTTCCGATAACATCAACAGA 4140

AMH-2\_5 CCTGTGTTCGAGCAGCGTCTGTACACGGCTGGCATTTCCACTTCCGATAACATCAACAGA 4140

AMH-3\_1 CCTGTGTTCGAGCAGCGTCTGTACACGGCTGGCATTTCCACTTCCGATAACATCAACAGG 4140

AMH-3\_13 CCTGTGTTCGAGCAGCGTCTGTACACGGCTGGCATTTCCACTTCCGATAACATCAACAGG 4140

AY198374.1 CCTGTGTTCGAGCAGCGTCTGTACACGGCTGGCATTTCCACTTCCGATAACATCAACAGG 4140

AMH-1\_2 CCTGTGTTCGAGCAGCGTCTGTACACGGCTGGCATTTCCACTTCCGATAACATCAACAGG 4140

AMH-1\_7 CCTGTGTTCGAGCAGCGTCTGTACACGGCTGACATTTCCACTTCCGATAACATCAACAGG 4140

AMH-1\_11 CCTGTGTTCGAGCAGCGTCTGTACACGGCTGGCATTTCCACTTCCGATAACATCAACAGG 4140

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AMH-3\_16 GAACTACTCACCGTTCGTGCAACTCATTCCGAAAACGCACAATTGACATATACTATCGAA 4197

AMH-2\_4 GAACTACTCACCGTTCGTGCAACTCATTCCGAAAACGCACAATTGACATATACCATCGAA 4200

AMH-2\_1 GAACTACTCACCGTTCGTGCAACTCATTCCGAAAACGCACAATTGACATATACCATCGAA 4200

AMH-2\_5 GAACTACTCACCGTTCGTGCGACTCATTCCGAAAACGCACAATTGACATATACCATCGAA 4200

AMH-3\_1 GAACTACTCACCGTTCGTGCAACTCATTCCGAAAACGCACAATTGACATATACCATCGAA 4200

AMH-3\_13 GAACTACTCACCGTTCGTGCAACTCATTCCGAAAACGCACAATTGACATATACCATCGAA 4200

AY198374.1 GAACTACTCACCGTTCGTGCAACTCATTCCGAAAACGCACAATTGACATATACCATCGAA 4200

AMH-1\_2 GAACTACTCACCGTTCGTGCAACTCATTCCGAAAACGCACAATTGACATATACCATCGAA 4200

AMH-1\_7 GGACTACTCACCGTTCGTGCAACTCATTCCGAAAACGCACAATTGACATATACCATCGAA 4200

AMH-1\_11 GAACTACTCACCGTTCGTGCAACTCATTCCGAAAACGCACAATTGACATATACCATCGAA 4200

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AMH-3\_16 GACGGTTCTATGGTGGTGGACTCCACTCTGGAAGCCGTCAAGGACTCGGCGTTCCATCTG 4257

AMH-2\_4 GATGGTTCTATGGTGGTGGACTCCACTCTGGAAGCCGTCAAGGACTCGGCGTTCCATCTG 4260

AMH-2\_1 GATGGTTCTATGGTGGTGGACTCCACTCTGGAAGCCGTCAAGGACTCGGCGTTCCATCTG 4260

AMH-2\_5 GATGGTTCTATGGTGGTGGACTCCACTCTGGAAGCCGTCAAGGACTCGGCGTTCCATCTG 4260

AMH-3\_1 GATGGTTCTATGGTGGTGGACTCCACTCTGGAAGCCGTCAAGGACTCGGCGTTCCATCTG 4260

AMH-3\_13 GATGGTTCTATGGTGGTGGACTCCACTCTGGAAGCCGTCAAGGACTCGGCGTTCCATCTG 4260

AY198374.1 GACGGTTCTATGGCGGTGGACTCCACTCTGGAAGCCGTCAAGGACTCGGCGTTCCATCTG 4260

AMH-1\_2 GACGGTTCTATGGCGGTGGACTCCACTCTGGAAGCCGTCAAGGACTCGGCGTTCCATCTG 4260

AMH-1\_7 GACGGTTCTATGGCGGTGGACTCCACTCTGGAAGCCGTCAAGGACTCGGCGTTCCATCTG 4260

AMH-1\_11 GACGGTTCTATGGCGGTGGACTCCACTCTGGAAGCCGTCAAGGACTCGGCGCTCCATCTG 4260

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AMH-3\_16 AACGCGCAGACCGGCGTCCTCATACTGAGGATACAACCTACTGCCAGCATGCAGGGCATG 4317

AMH-2\_4 AACGCGCAGACCGGCGTCCTCATACTGAGGATACAACCTACTGCCAGCATGCAGGGCATG 4320

AMH-2\_1 AACGCGCAGACCGGCGTCCTCATACTGAGGATACAACCTACTGCCAGCATGCAGGGCATG 4320

AMH-2\_5 AACGCGCAGACCGGCGTCCTCATACTGAGGATACAACCTACTGCCAGCATGCAGGGCATG 4320

AMH-3\_1 AACGCGCAGACCGGCGTCCTCATACTGAGGATACAACCTACTGCCAGCATGCAGGGCATG 4320

AMH-3\_13 AACGCGCAGACCGGCGTCCTCATACTGAGGATACAACCTACTGCCAGCATGCAGGGCATG 4320

AY198374.1 AACGCGCAGACCGGCGTCCTCATACTGAGGATACAACCTACTGCCAGCATGCAGGGCATG 4320

AMH-1\_2 AACGCGCAGACCGGCGTCCTCATACTGAGGATACAACCTACTGCCAGCATGCAGGGCATG 4320

AMH-1\_7 AACGCGCAGACCGGCGTCCTCATACTGAGGATACAACCTACTGCCAGCATGCAGGGCATG 4320

AMH-1\_11 AACGCGCAGACCGGCGTCCTCATACTGAGGATACAACCTACTGCCAGCATGCAGGGCATG 4320

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AMH-3\_16 TTCGAGTTCAACGTCATCGCTACTGACCCAGATGAGAAGACAGATACGGCAGAGGTGAAA 4377

AMH-2\_4 TTTGAGTTCAACGTCATCGCTACTGACCCAGATGAGAGGACAGATACGGCAGAGGTGAAA 4380

AMH-2\_1 TTTGAGTTCAACGTCATCGCTACTGACCCAGATGAGAAGACAGATACGGCAGAGGTGAAA 4380

AMH-2\_5 TTTGAGTTCAACGTCATCGCTACTGACCCAGATGAGAAGACAGATACGGCAGAGGTGAAA 4380

AMH-3\_1 TTTGAGTTCAACGTCATCGCTACTGACCCAGATGAGAAGACAGATACGGCAGAGGTGAAA 4380

AMH-3\_13 TTTGAGTTCAACGTCATCGCTACTGACCCAGATGAGAAGACAGATACGGCAGAGGTGAAA 4380

AY198374.1 TTCGAGTTCAACGTCATCGCTACTGATCCAGATGAGAAGACAGATACGGCAGAGGTGAAA 4380

AMH-1\_2 TTTGAGTTCAACGTCATCGCTACTGACCCAGATGAGAAGACAGATACGGCAGAGGTGAAA 4380

AMH-1\_7 TTCGAGTTCAACGTCATCGCTACTGATCCAGATGAGAAGACAGATGCGGCAGAGGTGAAA 4380

AMH-1\_11 TTCGAGTTCAACGTCGTCGCTACTGATCCAGATGAGAAGACAGATACGGCAGAGGTGAAA 4380

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AMH-3\_16 GTCTACCTCATTTCATCCCAAAATAGGGTGTCCTTCATATTCCTGAACGATGTGGAGACG 4437

AMH-2\_4 GTCTACCTCATTTCATCCCAAAATAGGGTGTCCTTCATATTCCTGAACGATGTGGAGACT 4440

AMH-2\_1 GTCTACCTCATTTCATCCCAAAATAGGGTGTCCTTCATATTCCTGAACGATGTGGAGACT 4440

AMH-2\_5 GTCTACCTCATTTCATCCCAAAATAGGGTGTCCTTCATATTCCTGAACGATGTGGAGACT 4440

AMH-3\_1 GTCTACCTCATTTCATCCCAAAATAGGGTGTCCTTCATATTCCTGAACGATGTGGAGACG 4440

AMH-3\_13 GTCTACCTCATTTCGTCCCAAAATAGGGTGTCCTTCATATTCCTGAACGATGTGGAGACG 4440

AY198374.1 GTCTACCTCATTTCATCCCAAAATAGGGTGTCCTTCATATTCCTGAACGATGTGGAGACG 4440

AMH-1\_2 GTCTACCTCATTTCATCCCAAAATGGGGTGTCCTTCATATTCCTGAACGATGTGGAGACG 4440

AMH-1\_7 GTCTACCTCATTTCATCCCAAAATAGGGTGTCCTTCATATTCCTGAACGATGTGGAGACG 4440

AMH-1\_11 GTCTACCTCATTTCATCCCAAAATAGGGTGTCCTTCATATTCCTGAACGATGTGGAGACG 4440

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AMH-3\_16 GTTGAGAGTAACAGAGACTTTATCGCAGAAACGTTCAGCGTTGGCTTCAACATGACCTGC 4497

AMH-2\_4 GTTGAGAGTAACAGAGACTTTATCGCAGAAACGATCAGCGTTGGCTTCAACATGACCTGC 4500

AMH-2\_1 GTTGAGAGTAACGGAGACTTTATCGCAGAAGCGTTCAGCGTTGGCTTCAACATGACCTGC 4500

AMH-2\_5 GTTGAGAGTAACAGAGACTTTATCGCAGAAACGTTCAGCGTTGGCTTCAACATGACCTGC 4500

AMH-3\_1 GTTGAGAGTAACAGAGACTTTATCGCAGAAACGTTCAGCGTTGGCTTCAACATGACCTGC 4500

AMH-3\_13 GTTGAGAGTAACAGAGACTTTATCGCAGAAACGTTCAGCGTTGGCTTCAACATGACCTGC 4500

AY198374.1 GTTGAGAGTAACAGAGACTTTATCGCAGAAACGTTCAGCGTTGGCTTCAACATGACCTGC 4500

AMH-1\_2 GTTGAGAGTAACAGAGACTTTATCGCAGAAACGTTCAGCGTTGGCTTCAACATGACCTGC 4500

AMH-1\_7 GTTGAGAGTAACAGAGACTTTATCGCAGAAACGTTCAGCGTTGGCTTCAACATGACCTGC 4500

AMH-1\_11 GTTGAGAGTAACAGAGACTTTATCGCAGAAACGTTCAGCGTTGGCTTCAACATGACCTGC 4500

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AMH-3\_16 AATATAGATCAGGTGCTGCCGGGCACCAACGACGCCGGGGTGATTCAGGAGGCCATGGCG 4557

AMH-2\_4 AATATAGATCAGGTGCTGCCGGGCACCAACGACGCCGGGGTGATTCAGGAGGCCATGGCG 4560

AMH-2\_1 AATATAGATCAGGTGCTGCCGGGCACCAACGACGCCGGGGTGATTCAGGAGGCCATGGCG 4560

AMH-2\_5 AATATAGATCAGGTGCTGCCGGGCACCAACGACGCCGGGGTGATTCAGGAGGCCATGGCG 4560

AMH-3\_1 AATATAGATCAGGTGCTGCCGGGCACCAACGACGCCGGGGTGATTCAGGAGGCCATGGCG 4560

AMH-3\_13 AATATAGATCAGGTGCTGCCGGGCACCAACGACGCCGGGGTGATTCAGGAGGCCATGGCG 4560

AY198374.1 AATATAGATCAGGTGCTGCCGGGCACCAACGACGCCGGGGTGATTCAGGAGGCCATGGCG 4560

AMH-1\_2 AATATAGATCAGGTGCTGCCGGGCACCAACGACGCCGGGGTGATTCAGGAGGCCATGGCG 4560

AMH-1\_7 AATATAGATCAGGTGCTGCCGGGCACCAACGACGCCGGGGTGATTCAGGAGGCCATGGCG 4560

AMH-1\_11 AATATAGATCAGGTGCTGCCGGGCACCAACGACGCCGGGGTGATTCAGGAGGCCATGGCG 4560

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AMH-3\_16 GAAGTCCATGCTCACTTCATACAGGATAACATCCCTGTGAGCGCCGACAGTATTGAAGAG 4617

AMH-2\_4 GAAGTCCATGCTCACTTCATACAGGATAACATCCCTGTGAGCGCCGACAGTATTGAAGAG 4620

AMH-2\_1 GAAGTCCATGCTCACTTCATACAGGATAACATCCCTGTGAGCGCCGACAGTATTGAAGAG 4620

AMH-2\_5 GAAGTCCATGCTCACTTCATACAGGATAACATCCCTGTGAGCGCCGACGGTATTGAAGAG 4620

AMH-3\_1 GAAGTCCACGCTCACTTCATACAGGATAACATCCCTGTGAGCGCCGACAGTATTGAAGAG 4620

AMH-3\_13 GAAGTCCACGCTCACTTCATACAGGATAACATCCCTGTGAGCGCCGACAGTACTGAAGAG 4620

AY198374.1 GAAGTCCATGCTCACTTCATACAGGATAACATCCCTGTGAGCGCCGACAGTATTGAAGAG 4620

AMH-1\_2 GAAGTCCATGCTCACTTCATACAGGATAACATCCCTGTGAGCGCCGACAGTATTGAAGAG 4620

AMH-1\_7 GAAGTCCATGCTCACTTCATGCAGGATAACATCCCTGTGAGCGCCGACAGTATTGAAGAG 4620

AMH-1\_11 GAAGTCCATGCTCACTTCATACAGGATAACATCCCTGTGAGCGCCGACAGTATTGAAGAG 4620

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AMH-3\_16 CTTCGCAGTGACACTCAGCTGCTGCGCTCCGTCCAAGGTGTGTTGAATCAACGGCTACTG 4677

AMH-2\_4 CTTCGCAGTGACACTCAGCTGCTGCGCTCCGTCCAAGGTGTGTTGAATCAACGGCTGTTG 4680

AMH-2\_1 CTTCGCAGTGACACTCAGCTGCTGCGCTCCGTCCAAGGTGTGTTGAACCAACGGCTGTTG 4680

AMH-2\_5 CTTCGCAGTGACACTCAGCTGCTGCGCTCCGTCCAAGGTGCGTTGAACCAACGGCTGTTG 4680

AMH-3\_1 CTTCGCGGTGACACTCAGCTGCTGCGCTCCGTCCAAGGTGTGTTGAACCAACGGCTGTTG 4680

AMH-3\_13 CTTCGCAGTGACACTCAGCTGCTGCGCTCCGTCCAAGGTGTGTTGAACCAACGGCTGTTG 4680

AY198374.1 CTTCGCAGTGACACTCAGCTGCTGCGCTCCGTCCAAGGTGTGTTGAACCAACGGCTGTTG 4680

AMH-1\_2 CTTCGCAGTGACACTCAGCTGCTGCGCTCCGTCCAAGGTGTGTTGAACCGACGGCTGTTG 4680

AMH-1\_7 CTTCGCAGTGACACTCAGCTGCTGCGCTCCGTCCAAGGTGTGTTGAACCAACGGCTGTTG 4680

AMH-1\_11 CTTCGCAGTGACACTCAGCTGCTGCGCTCCGTCCAAGGTGTGTTGAACCAACGGCTGTTG 4680

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AMH-3\_16 GTCCTGAACGACCTGGTGACCGGGGTCAGCCCTGATCTCGGCACTGCCGGCGTGCAGATC 4737

AMH-2\_4 GTCCTGAACGACCTGGTGACCGGGGTCAGCCCTGATCTCGGCACTGCCGGCGTGCAGATC 4740

AMH-2\_1 GTCCTGAACGACCTGGTGACCGGGGTCAGCCCTGATCTCGGCACTGCCGGCGTGCAGATC 4740

AMH-2\_5 GTCCTGAACGACCTGGTGACCGGGGTCAGCCCTGATCTCGGCACTGCCGGCGTGCAGATC 4740

AMH-3\_1 GTCCTGAACGACCTGGTGACGGGGGTCAGCCCTGATCTCGGCACTGCCGGCGTGCAGATC 4740

AMH-3\_13 GTCCTGAACGACCTGGTGACGGGGGTCAGCCCTGATCTCGGCACTGCCGGCGTGCAGATC 4740

AY198374.1 GTCCTGAACGACCTGGTGACGGGGGTCAGCCCTGATCTCGGCACTGCCGGCGTGCAGATC 4740

AMH-1\_2 GTCCTGAACGACCTGGTGACGGGGGTCAGCCCTGATCTCGGCACTGCCGGCGTGCAGATC 4740

AMH-1\_7 GTCCTGGACGACCTGGTGACGGGGGTCAGCCCTGATCTCGGCACTGCCGGCGTGCAGATC 4740

AMH-1\_11 GTCCTGAACGACCTGGTGACGGGGGTCAGCCCTGATCTCGGCACTGCCGGCGTGCAGATC 4740

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AMH-3\_16 ACCATCTATGTGCTAGCCGGGTTGTCAGCCATCCTTGCCTTCCTGTGCCTTATTCTGCTC 4797

AMH-2\_4 ACCATCTATGTGCTAGCCGGGTTGTCAGCCATCCTTGCCTTCCTGTGCCTTATTCTGCTC 4800

AMH-2\_1 ACCATCTATGTGCTAGCCGGGTTGTCAGCCATCCTTGCCTTCCTGTGCCTTATTCTGCTC 4800

AMH-2\_5 ACCATCTATGTGCTAGCCGGGTTGTCAGCCATCCTTGCCTTCCTGTGCCTTATTCTGCTC 4800

AMH-3\_1 ACCATCTATGTGCTAGCCGGGTTGTCAGCCATCCTTGCCTTCCTGTGCCTTATTCTGCTC 4800

AMH-3\_13 ACCATCTATGTGCTAGCCGGGTTGTCAGCCATCCTTGCCTTCCTGTGCCTTATTCTGCTC 4800

AY198374.1 ACCATCTATGTGCTAGCCGGGTTGTCAGCCATCCTTGCCTTCCTGTGCCTTATTCTGCTC 4800

AMH-1\_2 ACCATCTATGTGCTAGCCGGGTTGTCAGCCATCCTTGCCTTCCTGTGCCTTATTCTGCTC 4800

AMH-1\_7 ACCATCTATGTGCTAGCCGGGTTGTCAGCCATCCTTGCCTTCCTGTGCCTTATTCTGCTC 4800

AMH-1\_11 ACCATCTATGTGCTAGCCGGGTTGTCAGCCATCCTTGCCTTCCTGTGCCTTATTCTGCTC 4800

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AMH-3\_16 ATCACATTCATCGTGAGGACCCGAGCTCTGAACCGCCGTTTGGAAGCACTGTCGATGACG 4857

AMH-2\_4 ATCACATTCATCGTGAGGACCCGAGCTCTGAACCGCCGTTTGGAAGCACTGTCGATGACG 4860

AMH-2\_1 ATCACATTCATCGTGAGGACCCGAGCTCTGAACCGCCGTTTGGAAGCACTGTCGATGACG 4860

AMH-2\_5 ATCACATTCATCGTGAGGACCCGAGCTCTGAACCGCCGTTTGGAAGCACTGTCGATGACG 4860

AMH-3\_1 ATCACATTCATCGTGAGGACCCGAGCTCTGAACCGCCGTTTGGAAGCACTGTCGATGACG 4860

AMH-3\_13 ATCACATTCATCGTGAGGACCCGAGCTCTGAACCGCCGTTTGGAAGCACTGTCGATGACG 4860

AY198374.1 ATCACATTCATCGTGAGGACCCGAGCTCTGAACCGCCGTTTGGAAGCACTGTCGATGACG 4860

AMH-1\_2 ATCACATTCATCGTGAGGACCCGAGCTCTGAACCGCCGTTTGGAAGCACTGTCGGTGACG 4860

AMH-1\_7 ATCACATTCATCGTGAGGACCCGAGCTCTGAACCGCCGTTTGGAAGCACTGTCGATGACG 4860

AMH-1\_11 ATCACATTCATCGTGAGGACCCGAGCTCTGAACCGCCGTTTGGAAGCACTGTCGATGACG 4860

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AMH-3\_16 AAATACGGCTCGGTGGATTCGGGGCTGAACCGAGTGGGGATAGCGGCCCCAGGAACCAAC 4917

AMH-2\_4 AAATACGGCTCGGTGGATTCGGGGCTGAACCGAGTGGGGATAGCGGCCCCAGGAACCAAC 4920

AMH-2\_1 AAATACGGCTCGGTGGATTCGGGGCTGAACCGAGTGGGGATAGCGGCCCCAGGAACCAAC 4920

AMH-2\_5 AAATACGGCTCGGTGGATTCGGGGCTGAACCGAGTGGGGATAGCGGCCCCAGGAACCAAC 4920

AMH-3\_1 AAATACGGCTCGGTGGATTCAGGGCTGAACCGAGTGGGGATAGCGGCCCCAGGAACCAAC 4920

AMH-3\_13 AAATACGGCTCGGTGGATTCAGGGCTGAGCCGAGTGGGGATAGCGGCCCCAGGAACCAAC 4920

AY198374.1 AAATACGGCTCGGTGGATTCGGGGCTGAACCGAGTGGGGATAGCGGCCCCAGGAACCAAC 4920

AMH-1\_2 AAGTACGGCTCGGTGGATTCGGGGCTGAACCGAGTGGGGATAGCGGCCCCAGGAACCAAC 4920

AMH-1\_7 AAATACGGCTCGGTGGATTCGGGGCTGAACCGAGTGGGGATAGCGGCCCCAGGAACCAAC 4920

AMH-1\_11 AAATACGGCTCGGTGGATTCGGGGCTGAACCGAGTGGGGATAGCGGCCCCAGGAACCAAC 4920

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AMH-3\_16 AAACACGCCATCGAAGGCTCCAACCCCATCTGGAACGAGCAGATCAAGGCCCCGGACTTC 4977

AMH-2\_4 AAACACGCCATCGAAGGCTCCAACCCCATCTGGAACGAGCAGATCAAGGCCCCGGACTTC 4980

AMH-2\_1 AAACACGCCATCGAAGGCTCCAACCCCATCTGGAACGAGCAGATCAAGGCCCCGGACTTC 4980

AMH-2\_5 AAACACGCCATCGAAGGCTCCAACCCCATCTGGAACGAGCAGATCAAGGCCCCGGACTTC 4980

AMH-3\_1 AAACACGCCATCGAAGGCTCCAACCCCATCTGGAACGAGCAGATCAAGGCCCCGGACTTC 4980

AMH-3\_13 AAACACGCCATCGAAGGCTCCAACCCCATCTGGAACGAGCAGATCAAGGCCCCGGACTTC 4980

AY198374.1 AAACACGCCATCGAAGGCTCCAACCCCATCTGGAACGAGCAGATCAAGGCCCCGGACTTC 4980

AMH-1\_2 AAACACGCCATCGAAGGCTCCAACCCCATCTGGAACGAGCAGATCAAGGCCCCGGACTTC 4980

AMH-1\_7 AAACACGCCATCGAAGGCTCCCACCCCATCTGGAACGAGCAGATCAAGGCCCCGGACTTC 4980

AMH-1\_11 AAACACGCCATCGAAGGCTCCAACCCCATCTGGAACGAGCAGATCAAGGCCCCGGACTTC 4980

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AMH-3\_16 GATGCCATCAGTGACACATCTGACGAGTCTGATCTGATCGGCATCGAGGATCTACCACAA 5037

AMH-2\_4 GATGCCATCAGTGACACATCTGACGAGTCTGATCTGATCGGCATCGAGGATCTACCACAA 5040

AMH-2\_1 GATGCCATCAGTGACACATCTGACGAGTCTGATCTGATCGGCATCGAGGATCTACCACAA 5040

AMH-2\_5 GATGCCATCAGTGACACATCTGACGAGTCTGATCTGATCGGCATCGAGGATCTACCACAA 5040

AMH-3\_1 GATGCCATCAGTGACACATCTGACGAGTCTGATCTGATCGGCATCGAGGATCTACCACAA 5040

AMH-3\_13 GATGCCATCAGTGACACATCTGACGAGTCTGATCTGATCGGCATCGAGGATCTACCACAA 5040

AY198374.1 GATGCCATCAGTGACACATCTGACGAGTCTGATCTGATCGGCATCGAGGATCTACCACAA 5040

AMH-1\_2 GATGCCATCAGTGACACATCTGACGAGTCTGATCTGATCGGCATCGAGGATCTACCACAA 5040

AMH-1\_7 GATGCCATCAGTGACACATCTGACGAGTCTGATCTGATCGGCATCGAGGATCTACCACAA 5040

AMH-1\_11 GATGCCATCAGTGACACATCTGACGAGTCTGATCTGATCGGCATCGAGGATCTACCACAA 5040

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AMH-3\_16 TTCAGGAGCGACTATTTCCCGCCTGAGGACTCGGAATCCGCTCACGCCTCCTTTAGCGAC 5097

AMH-2\_4 TTCAAGAGCGACTATTTCCCGCCTGAGGACTCGGAATCCGCTCACGCCGCCTTTAGCGAC 5100

AMH-2\_1 TTCAAGAGCGACTATTTCCCGCCTGAGGACTCGGAATCCGCTCACGCCGCCTTTAGCGAC 5100

AMH-2\_5 TTCAAGAGCGACTATTTCCCGCCTGAGGACTCGGAATCCGCTCACGCCGCCTTTAGCGAC 5100

AMH-3\_1 TTCAAGAGCGACTATTTCCCGCCTGAGGACTCGGAATCCGCTCACGCCGCCTTTAGCGAC 5100

AMH-3\_13 TTCAAGAGCGACTATTTCCCGCCTGAGGACTCGGAATCCGCTCACGCCGCCTTTAGCGAC 5100

AY198374.1 TTCAAGAGCGACTATTTCCCGCCTGAGGACTCGGAATCCGCTCACGCCGCCTTTAGCGAC 5100

AMH-1\_2 TTCAAGAGCGGCTATTTCCCGCCTGAGGACTCGGAATCCGCTCACGCCGCCTTTAGCGAC 5100

AMH-1\_7 TTCAAGAGCGACTATTTCCCGCCTGAGGACTCGGAATCCGCTCACGCCGCCTTTAGCGAC 5100

AMH-1\_11 TTCAAGAGCGACTATTTCCCGCCTGAGGACTCGGAATCCGCTCACGCCGCCTTTAGCGAC 5100

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AMH-3\_16 CGCACGCCACGCGGGAACGATGCGCCTATTGCACACAGTAGCAACAACTTCGGTTTCAAC 5157

AMH-2\_4 CGCACGCCACGCGGGAACGATGCGCCTATTGCACACAGTAGCAACAACTTCGGTTTCAAC 5160

AMH-2\_1 CGCACGCCACGCGGGAACGATGCGCCTATTGCACACAGTAGCAACAACTTCGGTTTCAAC 5160

AMH-2\_5 CGCACGCCACGCGGGAACGATGCGCCTATTGCACACAGTAGCAACAACTTCGGTTTCAAC 5160

AMH-3\_1 CGCACGCCACGCGGGAACGATGCGCCTATTGCACACAGTAGCAACAACTTCGGTTTCAAC 5160

AMH-3\_13 CGCACGCCACGCGGGAACGATGCGCCTATTGCACACAGTAGCAACAACTTCGGTTTCAAC 5160

AY198374.1 CGCACGCCACGCGGGAACGATGCGCCTATTGCACACAGTAGCAACAACTTCGGTTTCAAC 5160

AMH-1\_2 CGCACGCCACGCGGGAACGATGCGCCTATTGCACACAGTAGCAACAACTTCGGTTTCAAC 5160

AMH-1\_7 CGCACGCCACGCGGGAACGATGCGCCTATTGCACACAGTAGCAACAACTTCGGTTTCAAC 5160

AMH-1\_11 CGCACGCCACGCGGGAACGATGCGCCTATTGCACACAGTAGCAACAACTTCGGTTTCAAC 5160

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AMH-3\_16 ACCAGCCCTTTTAGCGCGGAGTTCACTAACAGGCGCATGCGACCATAG 5205

AMH-2\_4 ACCAGCCCTTTTAGCGCGGAGTTCACTAACAGGCGCATGCGACCATAG 5208

AMH-2\_1 ACCAGCCCTTTTAGCGCGGAGTTCACTAACAGGCGCATGCGACCATAG 5208

AMH-2\_5 ACCAGCCCTTTTAGCGCGGGGTTCACTAACAGGCGCATGCGACCATAG 5208

AMH-3\_1 ACCAGCCCTTTTAGCGCGGAGTTCACTAACAGGCGCATGCGACCATAG 5208

AMH-3\_13 ACCAGCCCTTTTAGCGCGGAGTTCACTAACAGGCGCATGCGACCATAG 5208

AY198374.1 ACCAGTCCTTTTAGCGCGGAGTTCACTAACAGGCGCATGCGACCATAG 5208

AMH-1\_2 ACCAGCCCTTTTAGCGCGGAGTTCACTAACAGGCGCATGCGACCATAG 5208

AMH-1\_7 ACCAGTCCTTTTAGCGCGGAGTTCACTAACAGGCGCATGCGACCATAG 5208

AMH-1\_11 ACCAGTCCTTTTAGCGCGGAGTTCACTAACAGGCGCATGCGACCATAG 5208

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