

1 **Supplementary File 7**

2 BLASTN alignment of the *P. marinus* Hmx homeobox containing gene model  
3 (PMZ\_0038761-RA, Query) on scaffold\_00813 with the *P. marinus* Hmx locus (Sbjct)  
4 of scaffold\_00015. See Materials and Methods for more details.

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6 Identity= 2448/2455 (99.71%) , Positive= 2448/2455 (99.71%)  
7 Query Matches 1 to 2448 Hit Matches = 7402804 to 7400350

8  
9 Query: 1 ATGACGGACAAGCAGTCCCCGCCGTGTAGCGCGGCGCCCAAGTTCAGCATCCAGCGCATC 60  
10 |  
11 Sbjct: 7402804 ATGACGGACAAGCAGTCCCCGCCGTGTAGCGCGGCGCCCAAGTTCAGCATCCAGCGCATC 7402745  
12  
13 Query: 61 CTGGGCACGGACCTGGCCGACTCGTGCAGGAGACCAGGCCAAGGGCCATCAAGGGCGAC 120  
14 |  
15 Sbjct: 7402744 CTGGGCACGGACCTGGCCGACTCGTGCAGGAGACCAGGCCAAGGGCCATCAAGGGCGAC 7402685  
16  
17 Query: 121 GCGTGGAGAGGCTTCCCCTGTCCGCGGCCGCGTCCGACCTGTCCCTGTTCTCGTCGAGC 180  
18 |  
19 Sbjct: 7402684 GCGTGGAGAGGCTTCCCCTGTCCGCGGCCGCGTCCGACCTGTCCCTGTTCTCGTCGAGC 7402625  
20  
21 Query: 181 AACGGCCCCACTACGCGGGCGGCGGAGGGAGGGCTCTGCGGGTGTAGAAGAAGAAG 240  
22 |  
23 Sbjct: 7402624 AACGGCCCCACTACGCGGGCGGCGGAGGGAGGGCTCTGCGGGTGTAGAAGAAGAAG 7402565  
24  
25 Query: 241 CGGCTCCAGGGAGCGACAGCCCCGGACGGTGCCGCCCGGGCAGGCGGGGACATCGAG 300  
26 |  
27 Sbjct: 7402564 CGGCTCCAGGGAGCGACAGCCCCGGACGGTGCCGCCCGGGCAGGCGGGGACATCGAG 7402505  
28  
29 Query: 301 GCGCTCGTGTGCGCCCGCTCAAGCGTCTCGTCTGACGGTAAGGTGGGGGGGGG-CAGAGC 360  
30 |  
31 Sbjct: 7402504 GCGCTCGTGTGCGCCCGCTCAAGCGTCTCGTCTGACGGTAAGGTGGGGGGGGGCAGAGC 7402445  
32  
33 Query: 361 AGAGCGCCAGGCTGGTTTGTGTGATGCTGCTGCTGCTGCTGCTGATGTCGGCTACAACA 420  
34 |  
35 Sbjct: 7402444 AGAGCGCCAGGCTGGTTTGTGTGATGCTGCTGCTGCTGCTGATGTCGGCTACAACA 7402385  
36  
37 Query: 421 ATAGTAACGGTAGCAGCGGCTGCGTTGAGCAAAGCTGAAGGATCCAGCAATGACCACCAA 480  
38 |  
39 Sbjct: 7402384 ATAGTAACGGTAGCAGCGGCTGCGTTGAGCAAAGCTGAAGGATCCAGCAATGACCACCAA 7402325  
40  
41 Query: 481 CAGCCACCACCACCACCAATGCGAATAAGACCCCCCCCC-TACCCACCCTCTTAACAAT 540  
42 |  
43 Sbjct: 7402324 CAGCCACCACCACCACCAATGCGAATAAGACCCCCCCCCCTACCCACCCTCTTAACAAT 7402265  
44  
45 Query: 541 AGCTATCAGCAACTAATACTACCGGCATTGACATTATCAACACCACCCTAGCGCCACCA 600  
46 |  
47 Sbjct: 7402264 AGCTATCAGCAACTAATACTACCGGCATTGACATTATCAACACCACCCTAGCGCCACCA 7402205  
48  
49 Query: 601 CCAACGGCCAACCAAAACACCACCAACAACACTACAACAAAACACCAATACTGTAACAAGAA 660  
50 |  
51 Sbjct: 7402204 CCAACGGCCAACCAAAACACCACCAACAACACTACAACAAAACACCAATACTGTAACAAGAA 7402145  
52  
53 Query: 661 CCATCATCACCATTAAATAAACAATAGCCACCGCCACCAACAATAATATCAAAAACCAC 720  
54 |  
55 Sbjct: 7402144 CCATCATCACCATTAAATAAACAATAGCCACCGCCACCAACAATAATATCAAAAACCAC 7402085  
56  
57 Query: 721 CAACAGCCATCAACAACAATAACCAGCAGCAGTAGCAACACCCTACAACCATCACCACC 780  
58 |  
59 Sbjct: 7402084 CAACAGCCATCAACAACAATAACCAGCAGCAGTAGCAACACCCTACAACCATCACCACC 7402025  
60  
61 Query: 781 AAGGCTCTCGGGATCGCCCGGTTGTAGTAACAGCAGTAGCGGACCCGTGTCAAGTAGATT 840  
62 |  
63 Sbjct: 7402024 AAGGCTCTCGGGATCGCCCGGTTGTAGTAACAGCAGTAGCGGACCCGTGTCAAGTAGATT 7401965  
64  
65 Query: 841 GACCATTGCTCCACACCCAAGTCTAGTTTATGGTCAGTATAATTGCATTGCCACGTGGA 900  
66 |  
67 Sbjct: 7401964 GACCATTGCTCCACACCCAAGTCTAGTTTATGGTCAGTATAATTGCATTGCCACGTGGA 7401905  
68  
69 Query: 901 TAACTCGATGTAGCCACTCGCAGTGTGATTTGACAGGTGTGCCAATAATTAACCAACAC 960  
70 |  
71 Sbjct: 7401904 TAACTCGATGTAGCCACTCGCAGTGTGATTTGACAGGTGTGCCAATAATTAACCAACAC 7401845  
72  
73 Query: 961 GGTCCGCCAGTTAAGCGTCTGCCGGTTAAGAGTGAACAGGTTTATGGAGCAAATAGATAG 1020  
74 |

75 Sbjct: 7401844 GGTCGGCCAGTTAAGCGTCTGCCGGTTAAGAGTGAACAGGTTTATGGAGCAAATAGATAG 7401785  
76  
77 Query: 1021 AAGTGATGTTATAAACGAGTGAATAAACACAATGTCATGGGTGTAAGTTTGTAGTTAAG 1080  
78 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
79 Sbjct: 7401784 AAGTGATGTTATAAACGAGTGAATAAACACAATGTCATGGGTGTAAGTTTGTAGTTAAG 7401725  
80  
81 Query: 1081 TATTGCCACATACATGTGTGTGTGT--ATTACAGTTGCTTTGATATAGATTTGCGTTGTT 1140  
82 ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||  
83 Sbjct: 7401724 TATTGCCACATACATGTGTGTGTGTATTACAGTTGCTTTGATATAGATTTGCGTTGTT 7401665  
84  
85 Query: 1141 GGAGTATGCCCGTATATTTGGGTTGTTTATTCGCAACAACATGAATATATTCGCTTGTTA 1200  
86 ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||  
87 Sbjct: 7401664 GGAGTATGCCCGTATATTTGGGTTGTTTATTCGCAACAACATGAATATATTCGCTTGTTA 7401605  
88  
89 Query: 1201 CCGAACGAAATATATTTAACGGCGACCTTTCCCCGTAAATATTTAATTGCTAGATCGA 1260  
90 ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||  
91 Sbjct: 7401604 CCGAACGAAATATATTTAACGGCGACCTTTCCCCGTAAATATTTAATTGCTAGATCGA 7401545  
92  
93 Query: 1261 AGTAATTAATAATTTGTGTTGTTTTAAAAATACATTGTCAGGCTTATAAGCTTATCGGAG 1320  
94 ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||  
95 Sbjct: 7401544 AGTAATTAATAATTTGTGTTGTTTTAAAAATACATTGTCAGGCTTATAAGCTTATCGGAG 7401485  
96  
97 Query: 1321 AGGACGTAAAATATGCCTCGGGAAAGTTTGAATTGAATAATTTCTGCCACTTTCAGTGC 1380  
98 ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||  
99 Sbjct: 7401484 AGGACGTAAAATATGCCTCGGGAAAGTTTGAATTGAATAATTTCTGCCACTTTCAGTGC 7401425  
100  
101 Query: 1381 TAACGTACTCGTTTGTTTAATCAGAGATCTACGTCCGAACACGTTCCGTAACAAGATGAC 1440  
102 ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||  
103 Sbjct: 7401424 TAACGTACTCGTTTGTTTAATCAGAGATCTACGTCCGAACACGTTCCGTAACAAGATGAC 7401365  
104  
105 Query: 1441 GAAGATAATTCTGACGCGTGAAACACAACCGTTATTAGTGTTCGGGGGAAGGAGAC 1500  
106 ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||  
107 Sbjct: 7401364 GAAGATAATTCTGACGCGTGAAACACAACCGTTATTAGTGTTCGGGGGAAGGAGAC 7401305  
108  
109 Query: 1501 AACCGGAAAAACATATTGTATGCGCGCTTCGCTATGAACGAGACGGCCGAAGTTCGATT 1560  
110 ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||  
111 Sbjct: 7401304 AACCGGAAAAACATATTGTATGCGCGCTTCGCTATGAACGAGACGGCCGAAGTTCGATT 7401245  
112  
113 Query: 1561 CCGACCACGGCTAACATCGGTAGCGAGTGGTGTCTGATCCGCGGTCCTGTGTGCGACTAC 1620  
114 ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||  
115 Sbjct: 7401244 CCGACCACGGCTAACATCGGTAGCGAGTGGTGTCTGATCCGCGGTCCTGTGTGCGACTAC 7401185  
116  
117 Query: 1621 GACTAACAACTCTAAATCATGGACGATATTAATGTCGCCTGTCCGAAAGTTTAACTGTA 1680  
118 ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||  
119 Sbjct: 7401184 GACTAACAACTCTAAATCATGGACGATATTAATGTCGCCTGTCCGAAAGTTTAACTGTA 7401125  
120  
121 Query: 1681 CAGAGGTGTAATGCGATTACCAATATATATAACGGCGAGAATTGGTGAATTGCATATA 1740  
122 ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||  
123 Sbjct: 7401124 CAGAGGTGTAATGCGATTACCAATATATATAACGGCGAGAATTGGTGAATTGCATATA 7401065  
124  
125 Query: 1741 AAGATATAATCGAATAACTCGTCAATAACTTACAATCTCGAATAGTTGCTTCATATATGC 1800  
126 ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||  
127 Sbjct: 7401064 AAGATATAATCGAATAACTCGTCAATAACTTACAATCTCGAATAGTTGCTTCATATATGC 7401005  
128  
129 Query: 1801 CTAACGAATGAAGACTGGCTGACCAGTGTGGTGAAGTATGGTACAAGAAAACCCCTCTA 1860  
130 ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||  
131 Sbjct: 7401004 CTAACGAATGAAGACTGGCTGACCAGTGTGGTGAAGTATGGTACAAGAAAACCCCTCTA 7400945  
132  
133 Query: 1861 TGCCCGGCACTGCGTGGCGGGGAGGCGTTTCGTCAATTGGTGAGAACTGAGACTCTCTCTC 1920  
134 ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||  
135 Sbjct: 7400944 TGCCCGGCACTGCGTGGCGGGGAGGCGTTTCGTCAATTGGTGAGAACTGAGACTCTCTCTC 7400885  
136  
137 Query: 1921 CAGTACATTGTTTATTTTTTCGCAATTAACGCCCGTATTGTTTACGCCTATTTTTTTTTT 1980  
138 ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||  
139 Sbjct: 7400884 CAGTACATTGTTTATTTTTTCGCAATTAACGCCCGTATTGTTTACGCCTATTTTTTTTTT 7400825  
140  
141 Query: 1981 GCACCGCAGCCACCAAAGAGACGTCCTTAGATTTATCAAACCCGGACGACGTCGCCGAAA 2040  
142 ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||  
143 Sbjct: 7400824 GCACCGCAGCCACCAAAGAGACGTCCTTAGATTTATCAAACCCGGACGACGTCGCCGAAA 7400765  
144  
145 Query: 2041 GGGTCTCGCCGACTTCAAGGCCCGCCGAGAAAGCGCTCGGCGAGTCCGGGTACGGCGG 2100  
146 ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||  
147 Sbjct: 7400764 GGGTCTCGCCGACTTCAAGGCCCGCCGAGAAAGCGCTCGGCGAGTCCGGGTACGGCGG 7400705  
148  
149 Query: 2101 ACGACAGAGACTCCAGACGGAGGAGGGACGCGGAGAGCGCCGCGTGTCCGGCCGGGG 2160  
150 ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||  
151 Sbjct: 7400704 ACGACAGAGACTCCAGACGGAGGAGGGACGCGGAGAGCGCCGCGTGTCCGGCCGGGG 7400645

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Query:      2161 ACAGGGCCTGCGAGAGCCCCCTCAGCACGGCAGCCCGCGTGCGCCCCCAAGAAGAAGA 2220
            |||
Sbjct:     7400644 ACAGGGCCTGCGAGAGCCCCCTCAGCACGGCAGCCCGCGTGCGCCCCCAAGAAGAAGA 7400585

Query:      2221 CGCGGACCGTGTTCACCGAGC-AAGTGTTCAGCTGGAGTCGACGTTGACATGAAGC 2280
            |||
Sbjct:     7400584 CGCGGACCGTGTTCACCGAGCCAAGTGTTCAGCTGGAGTCGACGTTGACATGAAGC 7400525

Query:      2281 GCTACCTGAGCAGCGCGGAGCGCGGGGCTCGCCGCGTGCCTGCACCTCACCGAGACGC 2340
            |||
Sbjct:     7400524 GCTACCTGAGCAGCGCGGAGCGCGGGGCTCGCCGCGTGCCTGCACCTCACCGAGACGC 7400465

Query:      2341 AGGTGAAGATCTGGTTCAGAACCGGCGCAACAAGTGGAAGCGCCAGCTCGCCGCCGAGC 2400
            |||
Sbjct:     7400464 AGGTGAAGATCTGGTTCAGAACCGGCGCAACAAGTGGAAGCGCCAGCTCGCCGCCGAGC 7400405

Query:      2401 TCGAGGCCGCAAAC-TGGCGCA-GTGTGCGGCGGCACAGACTCGTGCGTGTGCC 2448
            |||
Sbjct:     7400404 TCGAGGCCGCAAACCTGGCGCAGGTGTGCGGCGGCACAGACTCGTGCGTGTGCC 7400350
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