

A

PGSC0003DMT400078201 1 GAAAGTGCTAAACAGCTCCTATAATGAAGCTATAAATAACT.ACCACCTCTCTTC.CATCAAT...CATCAAAA 70
 PGSC0003DMT400078006 1ACAAGCTATAAATAAATAACCAGGTTCTCTTC.CATCA...ACCATCAAAA 47
 PGSC0003DMT400078007 1G.....TCT...CC...TTCTCTAGAAATCAGTGTAAATCAAA 32

PGSC0003DMT400078201 71 TTGA...AAGCAAGCAAGTAAAAAGTTCTCAAAAAAC.TCACTGAAAATGTCTCTGATCCCAAGAACTTTGGCG 142
 PGSC0003DMT400078006 48 TTGAAAAAACAAGCAAAAAACACAAGTTTTTCAAAAGC.TCACTGAAAATGTCACTGATCCCAAGAACTTTGGCG 121
 PGSC0003DMT400078007 33 ...GAAGAAAGATTGTGAGAACAAACAGTTT...AAGAGCTTAATTGAAAATGTCACTAATTTCTAGAATTTTCGGTG 102

PGSC0003DMT400078201 143 ATCGACGAAGCAGTAGCATGTTGATCCATTCTCAATTGACGTGTTGATTCAATCAGGAATTAGGCTTCCAC 217
 PGSC0003DMT400078006 122 ATCGAAGACGAGCAGCATGTTGATCCATTCTCAATGGACGTGTTGATTTCCTTCAAGGAACTAGGCTTCCAC 196
 PGSC0003DMT400078007 103 ATCGACGAAGCAGCAGTAGCATGTTGATCCATTCTCAATGGACATGTTTGTATTCCTTCAAGGAATTAGGCTTCCAC 177

PGSC0003DMT400078201 218 GTACCAATTTCAGGGGAGACCTCTGCATTTGCTAACACGCGAATAGACTGGAAGGAACTCCAGAGGCTCATGTGT 292
 PGSC0003DMT400078006 159 TTTCCAATTTCAGGAGAGACCTCTGCATTTGCGAACACTCGAGTCGACTGGAAGGAACTCCAGAGGCTCATGTGT 271
 PGSC0003DMT400078007 178 GTTCAAAATTCAGGGGAGATCTCTGCATTTGCCAACACTCGAGTTGATTGGAAGGAACTCCAGAGGCTCATGTGT 252

PGSC0003DMT400078201 293 TCAAGGCCGATCTTCCAGGGCTTAAAGAGGAGGAAGTAAAAGTGGAACTCGAAGAAGATAGGGTTCTTCAAACTCA 367
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 PGSC0003DMT400078007 253 TCAAGGCCGATCTTCCAGGGCTTAAAGAGGAGGAAGTAAAAGTGGAGATCGTGAAGATAGGGTTCTTCAAGATTA 327

PGSC0003DMT400078201 368 CGCGAGAGAGGAAGCTGGAGAAAGAGATAAGAATGATAAGTGGCATCGCGTGGAGCGAAGCAGCGGGAATTTCA 442
 PGSC0003DMT400078006 347 CGCGAGAGAGGAATGTGGAGAAAGAGATAAGAATGATAAGTGGCATCGCGTGGAGCGAAGCAGCATGGGAATTTCA 421
 PGSC0003DMT400078007 328 CGCGAGAGAGGAAGCTGGAGAAAGAGATAAGAATGATAAGTGGCATCGCGTGGAGCGAAGCAGCGGGAATTTCA 402

PGSC0003DMT400078201 443 TGAGGAGATTAGACTTCGGGAGAATGCAAGATGGATCAAGTTAAGGCTTCTATGGAGAATGGAGTGCCTTACTG 517
 PGSC0003DMT400078006 422 TGAGAAATTAGACTTCGGGAGAATGCGAGAGATGGATCAAGTTAAGGCTTCTATGGAGAATGGAGTGCCTTACTG 496
 PGSC0003DMT400078007 403 TGAGGAGATTAGACTTCGGGAGAATGCAAGATGGATCAAGTTAAGGCTTCTATGGAGAATGGAGTGCCTTACTG 477

PGSC0003DMT400078201 518 TAACTGTTCCAAAGGAAGAGCTGAAGAAACCTGAGGTCAAGTCCATTGACATCTCTGGTTAAACG...CTTTGGCT 590
 PGSC0003DMT400078006 569 TGAGAAATTAGACTTCGGGAGAATGCGAGAGATGGATCAAGTTAAGGCTTCTATGGAGAATGGAGTGCCTTACTG 548
 PGSC0003DMT400078007 478 TAACTGTTCCAAAGGAAGAGCTGAAGAAACCTGATGTCAAGTCTATTGAAATCTCTGGTTAAATACATTT...T 549

PGSC0003DMT400078201 591 GGGATTAACTTTGAGTAT...TAAAG...TAAAG...TGTGACTGTTGAAGATTTTCAG 641
 PGSC0003DMT400078006 597 GTGAATTAAGTAGTAT 642
 PGSC0003DMT400078007 550 GTCAATTAAGTAGTAT 618

PGSC0003DMT400078201 642 TTTTCTT...ATTCTTCTGCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 713
 PGSC0003DMT400078006 643 TTTTCTT...ATTCTTCTGCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 709
 PGSC0003DMT400078007 619 TTTTCTT...ATTCTTCTGCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 683

PGSC0003DMT400078201 714 CTTGAGTACTCTATATGTGAAAATGATATTTACTAGTAGTAT...TTCTGGTCCATTCTGCAATCTGTTCAAT 786
 PGSC0003DMT400078006 710 TTCTGA...AATTCATGT.TG...AATATGAAATATAGTCTTTGATTCTGTTCCAAATTC...CTG 767
 PGSC0003DMT400078007 684 TTTCCA...AATTCATGT.TG...AATATGAAATATAGTCTTTTATTAA...TCTGTTGAAGATTTGAAG 726

B

PGSC0003DMT400070986 1CAAGGACCTTCTCTTTATCTATCGCTTTTACAGT 35
 XM_006361313.2 1 TGTGTTGTCTCTACCAAGAGCTCTCTGGAGTTGCCACAATTTTCATGAAACCCCAATACCAAGACAAGGACCTTCTCTTTATCTATCGCTTTTACAGT 101

PGSC0003DMT400070986 36 ATATAATCTCTCAAAACAACAAAATCTTGATCCCTAGACCCCTTGCTAGAAATGTGCTCTTTACCAGTATCCTTTCTCTATATACATCCCTCTCTCACTTGGAC 136
 XM_006361313.2 102 ATATAATCTCTCAAAACAACAAAATCTTGATCCCTAGACCCCTTGCTAGAAATGTGCTCTTTACCAGTATCCTTTCTCTATATACATCCCTCTCTCACTTGGAC 202

PGSC0003DMT400070986 137 AGTTTCTATCAACAACAACAATTTGTCGATCTTCAATATTTCACTCTACACACACTAAACCAAACTATTTTTCAGTAAAAAATGGCTTCTACGACCAACC 237
 XM_006361313.2 203 AGTTTCTATCAACAACAACAATTTGTCGATCTTCAATATTTCACTCTACACACACTAAACCAAACTATTTTTCAGTAAAAAATGGCTTCTACGACCAACC 303

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 XM_006361313.2 304 ACCAAGTGAAAAATCCCATTTTCCGGGCGATAGCTGGATTAACAAAACCCCATTTTGGGAGGGAGAATAGTTTTCGATCAGCGAAGAAATGTTACACGGCAG 404

PGSC0003DMT400070986 339 AAGCGGTGAGGCAAGGTCGAGACCCATGAAGTATGTAAGTGAAGAGGTGGTGGGATAGATTGGGACGACGAATTCAGCGGTGGCAGTAATGGAAG 439
 XM_006361313.2 405 AAGCGGTGAGGCAAGGTCGAGACCCATGAAGTATGTAAGTGAAGAGGTGGTGGGATAGATTGGGACGACGAATTCAGCGGTGGCAGTAATGGAAG 505

PGSC0003DMT400070986 440 TGGGAAACCGACAAATAGTGACAAATCGGAGGGGCAAAAGACGACGCCCTGCTGATGCGGTATACGGAAGATGGGATAGATTAGTTGGGACAGATAGCGA 540
 XM_006361313.2 506 TGGGAAACCGACAAATAGTGACAAATCGGAGGGGCAAAAGACGACGCCCTGCTGATGCGGTATACGGAAGATGGGATAGATTAGTTGGGACAGATAGCGA 606

PGSC0003DMT400070986 541 AAGGCAATCGGTGCTGAATCCGACACACACTTTCTTCTCAGTGAAGAGGTTTATAGGAGGAAAAATGCGCGAGCTTGATGAAGAGTCGAACAGTATTCG 641
 XM_006361313.2 607 AAGGCAATCGGTGCTGAATCCGACACACACTTTCTTCTCAGTGAAGAGGTTTATAGGAGGAAAAATGCGCGAGCTTGATGAAGAGTCGAACAGTATTCG 707

PGSC0003DMT400070986 642 TATAGAGTAATGAAGCATGAGAATGGGAATGTTAAACTTGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 742
 XM_006361313.2 708 TATAGAGTAATGAAGCATGAGAATGGGAATGTTAAACTTGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 808

PGSC0003DMT400070986 743 GCTTGTGATGATGCTCAAAATCTTGAATGATAAAGTGTCTGAAGCAGTGAATACAGTACCCGATACCTCAATGACTCCGACAGCACTGCAACAAAG 843
 XM_006361313.2 809 GCTTGTGATGATGCTCAAAATCTTGAATGATAAAGTGTCTGAAGCAGTGAATACAGTACCCGATACCTCAATGACTCCGACAGCACTGCAACAAAG 909

PGSC0003DMT400070986 844 ATGACGTCGCTATGCGCGATTAGATGTTCTCGGCAATAATCAATGAACCCACTGCTGCTTCTTGGCTTATGGAATTGAGAAGAAGAGTAATGAACCAAT 944
 XM_006361313.2 910 ATGACGTCGCTATGCGCGATTAGATGTTCTCGGCAATAATCAATGAACCCACTGCTGCTTCTTGGCTTATGGAATTGAGAAGAAGAGTAATGAACCAAT 1010

PGSC0003DMT400070986 945 TAGTCTTTGACCTGGAGGTGGTACTTTTATGATATCAG...GTAT 988
 XM_006361313.2 1011 TAGTCTTTGACCTGGAGGTGGTACTTTTATGATATCAGTTCTTCTGAGGTGGAGATGGAGTATTTGAGTACTTTCTAGCTCAGGAGACACACTTAGG 1111

PGSC0003DMT400070986 989 ...CTGA 992
 XM_006361313.2 1112 AGGTGATGATTTTATGAAGAAGATTTGGTACTGGCTTCTGCTGATCTTTAGGAAGAAGAAAGGGATAGAGCTTCTAAAAGACAAACAGCGCTTCAACGTC 1212

PGSC0003DMT400070986 1213 TACTGAAGCTGCTGAAAGGCAACAGATACAATTTGTCATCTTCTGCTCAAACTAATATCAGTTTGCCATTCTACCTGCTACTGCAGATGCTTCGAAACAT 1313
 XM_006361313.2 1213 TACTGAAGCTGCTGAAAGGCAACAGATACAATTTGTCATCTTCTGCTCAAACTAATATCAGTTTGCCATTCTACCTGCTACTGCAGATGCTTCGAAACAT 1313

PGSC0003DMT400070986 993 ...AGACT 997
 XM_006361313.2 1314 ATTGACACACATTTTACAAAGGCGCAAGTTTGAAGGATTTGCTGCACTTATTTGGACAGGCTTAAGACACAGTGTGAAACTGCTTAAAGGATGCCAGCT 1414

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 XM_006361313.2 1415 TCTCTCAAGATATAGATGAAGTACTTCTGTTGCTGGATCAACACGAATACCAAGCTGTTCAAAACCTTGTCCGCAAGATGACTGGTAAAGAGCTTAATG 1515

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 XM_006361313.2 1617 TTTCTGCTCAATCTGATGAAGTGGTTGCTCTTGGAGCTTCAGTTTCAGGCTGGTGTCTTGGCTGGAGATGTTAGTGACATCGTGTATTAGATGTAATCTCA 1717

PGSC0003DMT400070986 1718 AGATGGCGAAACCACTGTTGAGATTAATGCTGCTGCAAGGTGAAGACAGAGTTGTGAAAAGATTAATAGTCTATTGGAAGGTTCCGCGTAGATGGAATCCCTC 1818
 XM_006361313.2 1819 ATCTCCAGGGGTCTTCCAGATTGAAGTGAATTCACATCGATGCCAATGGTATACCTTTCTGCTCAGGCTACTGATAAGGTTACAGGAAAGAGCAAG 1919

PGSC0003DMT400070986 1920 GACATATACCATAAATGCTGCTAGCAGTTTGGCCAAAGATGAGTTGATAGAATGTTCAAGAAAGTGAGAAAGTTGCTAGAGAGGACAGGAGAGAGAGA 2020
 XM_006361313.2 2021 GACATATACCATAAATGCTGCTAGCAGTTTGGCCAAAGATGAGTTGATAGAATGTTCAAGAAAGTGAGAAAGTTGCTAGAGAGGACAGGAGAGAGAGA 2121

PGSC0003DMT400070986 1004 ...GGC 1009
 XM_006361313.2 2122 TGAATCCAAACTGAAAGAGCTCAAGCATGCCATTTCCAGTGATTCTACTCAAACTAAGGAGGAGTGGCTGATTGAACCAACAAAGTAATGCAAGCT 2222

PGSC0003DMT400070986 1010 ...ATCTGG 1015
 XM_006361313.2 2223 GAGCAGTCTCTATACAGCCAGCAGGTGCT 2323

PGSC0003DMT400070986 1016 ...TTCA 1027
 XM_006361313.2 2324 AGATGATGGAGTGAGGAAGTTATCGATGACAGCTTCAGGCAAGAGCAATTAAGATCCATCAATGTATCAAAATTTCTTTAGGAAACACCAACCAAGCTGAA 2424

PGSC0003DMT400070986 1028 ...TACTG 1032
 XM_006361313.2 2425 TATTTCATGTAAATTAATAATGGCAGATGAGAGGATGCTATATGCTGGCTAGTTTACTGGAAGTGAACAAAGTTGAATAATAGCTTTTCCAAACCAATG 2525

PGSC0003DMT400070986 2526 TGTCAACAAAGTACTCTCAAAATCGATTAATAGCGAAATCAATTTGCCAGT 2577
 XM_006361313.2 2526 TGTCAACAAAGTACTCTCAAAATCGATTAATAGCGAAATCAATTTGCCAGT 2577

Figure S1. The alignments of (A) *StHSP17.6* and (B) *StHSP70-2* nucleotide sequences.