

SUPPLEMENTARY MATERIALS

Heavy Metal Transporters-Associated Proteins in *S. tuberosum* : Genome-wide Identification, Comprehensive Gene Feature, Evolution and Expression Analysis

Guandi He ¹, Lijun Qin ¹, Weijun Tian ², Lulu Meng ², Tengbing He ^{2,3,*} and Degang Zhao ^{1,4,*}

¹ The Key Laboratory of Plant Resources Conservation and Germplasm Innovation in Mountainous Region (Ministry of Education), Institute of Agro-Bioengineering and College of Life Sciences, Guizhou University, Guiyang 550025, China; gs.gthe15@gzu.edu.cn (G.H.); lj Qin@gzu.edu.cn (L.Q.)

² Agricultural College, Guizhou University, Guiyang 550025, China; gs.tianwj18@gzu.edu.cn (W.T.); gs.llmeng18@gzu.edu.cn (L.M.)

³ Institute of New Rural Development of Guizhou University, Guiyang 550025, China

⁴ Guizhou Academy of Agricultural Science, Guiyang 550025, China

* Correspondence: tbhe@gzu.edu.cn (T.H.); dgzhao@gzu.edu.cn (D.Z.)

Supplementary table legends

Table S1: qRT-PCR primers for expression analysis of *StHMA* gene family in *Solanum tuberosum*;

Table S2: The IDs of 36 HMA genes as well as their properties in *S. tuberosum*;

Table S3: Subcellular localization prediction of *StHMA* gene family in potato;

Table S4: Ka/Ks ratios of homologous gene pairs between potato and different species;

Table S5: Motif sequences of heavy-metal associated proteins in *S. tuberosum*, *A. thaliana*, *O. sativa* and *S. lycopersicum*;

Table S6: Abiotic stress-related cis-acting elements in the promoter region of *StHMA* genes;

Table S7: RNA-seq data of potato *StHMA* genes in different tissues.

Table S1. qRT-PCR primers for expression analysis of *StHMA* gene family in *Solanum tuberosum*.

| Gene | Transcripts ID | Primer name | Primer sequence |
|----------------|----------------------|------------------|------------------------|
| <i>EF-1a</i> | - | <i>EF1a-F</i> | TCCTTACCTGAACGCCTGTCA |
| | | <i>EF1a-R</i> | ATTGGAAACGGATATGCTCCA |
| <i>StHMA1</i> | PGSC0003DMT400043033 | <i>StHMA1-F</i> | CCCATTTTGCTCACCTTCC |
| | | <i>StHMA1-R</i> | CCGTTTATGCGACTCACAG |
| <i>StHMA2</i> | PGSC0003DMT400045359 | <i>StHMA2-F</i> | ACATCTGATTGCTGCTTGG |
| | | <i>StHMA2-R</i> | ACATGGTGTGAGATTTGGCG |
| <i>StHMA4</i> | PGSC0003DMT400009920 | <i>StHMA4-F</i> | GCCCTCCTTGTTGCATACTG |
| | | <i>StHMA4-R</i> | AACAGGGGAAAGGAGGGAAC |
| <i>StHMA8</i> | PGSC0003DMT400069249 | <i>StHMA8-F</i> | GCCTTCTTACCTGTGCGATG |
| | | <i>StHMA8-R</i> | CTGTGAAGGCTGTGAGAGGA |
| <i>StHMA11</i> | PGSC0003DMT400018392 | <i>StHMA11-F</i> | ACACTCTCGCTGGATCAACA |
| | | <i>StHMA11-R</i> | CGACGTACCAAAGGAGACC |
| <i>StHMA16</i> | PGSC0003DMT400016647 | <i>StHMA16-F</i> | CACCTGAAGTTTGGAGTCCG |
| | | <i>StHMA16-R</i> | GGCTCACCTCGATGTTTAGTG |
| <i>StHMA17</i> | PGSC0003DMT400029503 | <i>StHMA17-F</i> | TGTTTCCTAGGTCCGTCGTT |
| | | <i>StHMA17-R</i> | CCTTGCCAAAACCACCAGA |
| <i>StHMA19</i> | PGSC0003DMT400060398 | <i>StHMA19-F</i> | CAGTGGATTGTGCTGCCTTC |
| | | <i>StHMA19-R</i> | ATGGACTGTGAAGTTGTGC |
| <i>StHMA22</i> | PGSC0003DMT400001032 | <i>StHMA22-F</i> | ACCCAACACTAACAGTACCCT |
| | | <i>StHMA22-R</i> | TCTATGTCAGTTTGACACGAG |
| <i>StHMA25</i> | PGSC0003DMT400021739 | <i>StHMA25-F</i> | GGTTCTGCATTCTCCACACC |
| | | <i>StHMA25-R</i> | CTCCAATCCCAAACCACCG |
| <i>StHMA31</i> | PGSC0003DMT400024481 | <i>StHMA31-F</i> | CGTCACAATGCTGCTGAACT |
| | | <i>StHMA31-R</i> | ACTAAGAAGAAGGTGGCGCT |
| <i>StHMA33</i> | PGSC0003DMT400015784 | <i>StHMA33-F</i> | CACGGACTTTGTTTCGGGTT |
| | | <i>StHMA33-R</i> | TGGGCAAAATGGAAGGTGTT |
| <i>StHMA34</i> | PGSC0003DMT400083194 | <i>StHMA34-F</i> | CTCCTTTTCCTTTGCCGTCC |
| | | <i>StHMA34-R</i> | AGAAAGTTACGTGCGATGCC |
| <i>StHMA35</i> | PGSC0003DMT400040203 | <i>StHMA35-F</i> | AGGACGAAGAAGCTGTTGGA |
| | | <i>StHMA35-R</i> | ATCAACTCGTTCATGCCCTG |
| <i>StHMA36</i> | PGSC0003DMT400073578 | <i>StHMA36-F</i> | TGGAAAGCTAGAGTTGGAGGT |
| | | <i>StHMA36-R</i> | TGGCGTTGTAGAAATGAGGAAG |

Gene-specific primers for real-time reverse transcription quantitative PCR (RT-qPCR) were designed by the Primer 6. F, forward; R, reverse.

Table S2. The IDs of 36 HMA genes as well as their properties in *S. tuberosum*.

| Gene name | Transcripts ID | Positive or negative chains | Amino acid | Molecular weight | Isoelectric point | Formula | Chromosome location |
|-----------|----------------------|-----------------------------|------------|------------------|-------------------|---|---------------------|
| StHMA1 | PGSC0003DMT400015954 | + | 380 | 43356.31 | 5.78 | C ₁₈₉₇ H ₂₈₂₃ N ₅₄₇ O ₆₀₅ S ₁₂ | 3991348-3993998 |
| StHMA2 | PGSC0003DMT400029503 | + | 291 | 32740.54 | 6.9 | C ₁₄₃₄ H ₂₂₂₀ N ₄₁₀ O ₄₄₉ S ₁₁ | 4674833-4676481 |
| StHMA3 | PGSC0003DMT400083194 | - | 565 | 57889.92 | 8.58 | C ₂₄₂₆ H ₃₈₄₃ N ₇₄₁ O ₇₉₈ S ₅₄ | 39130570-39131689 |
| StHMA4 | PGSC0003DMT400073578 | + | 436 | 46116.6 | 8.61 | C ₁₉₃₉ H ₃₀₃₁ N ₅₈₉ O ₆₃₂ S ₄₄ | 255158-259620 |
| StHMA5 | PGSC0003DMT400063687 | - | 372 | 40439.98 | 6.81 | C ₁₇₆₅ H ₂₇₈₉ N ₄₉₁ O ₅₈₁ S ₈ | 5119621-5121945 |
| StHMA6 | PGSC0003DMT400032792 | - | 70 | 7687.09 | 9.3 | C ₃₃₅ H ₅₅₄ N ₉₆ O ₉₆ S ₇ | 52462897-52464137 |
| StHMA7 | PGSC0003DMT400032707 | - | 234 | 24180.04 | 7.64 | C ₁₀₃₁ H ₁₆₇₁ N ₃₁₃ O ₃₄₀ S ₉ | 47318701-47321428 |
| StHMA8 | PGSC0003DMT400015784 | - | 153 | 17285.76 | 9.16 | C ₇₅₄ H ₁₂₀₆ N ₂₂₂ O ₂₂₆ S ₉ | 81897447-81900463 |
| StHMA9 | PGSC0003DMT400024409 | - | 1002 | 107196.01 | 5.16 | C ₄₈₁₉ H ₇₇₀₄ N ₁₂₄₆ O ₁₄₂₈ S ₃₉ | 49903753-49905385 |
| StHMA10 | PGSC0003DMT400009388 | - | 121 | 138879.87 | 9.15 | C ₆₁₀ H ₉₆₄ N ₁₇₈ O ₁₇₉ S ₇ | 87577228-87580997 |
| StHMA11 | PGSC0003DMT400078635 | + | 148 | 16948.78 | 9.98 | C ₇₄₆ H ₁₂₁₉ N ₂₂₁ O ₂₁₁ S ₉ | 76432065-76434200 |
| StHMA12 | PGSC0003DMT400043033 | + | 158 | 17904.9 | 9.71 | C ₈₀₅ H ₁₂₈₈ N ₂₂₀ O ₂₂₅ S ₈ | 48216723-48218378 |
| StHMA13 | PGSC0003DMT400037204 | - | 139 | 15474.69 | 7 | C ₆₉₆ H ₁₀₇₁ N ₁₈₃ O ₂₀₃ S ₇ | 77329843-77331651 |
| StHMA14 | PGSC0003DMT400068079 | + | 326 | 36878.9 | 6.12 | C ₁₆₁₂ H ₂₆₀₃ N ₄₄₃ O ₅₁₅ S ₁₄ | 52417462-52421546 |
| StHMA15 | PGSC0003DMT400001501 | - | 304 | 33894.57 | 5.11 | C ₁₄₈₁ H ₂₄₀₀ N ₃₉₈ O ₄₇₉ S ₁₄ | 27194995-27203856 |
| StHMA16 | PGSC0003DMT400015350 | + | 147 | 16606.14 | 9.49 | C ₇₃₁ H ₁₁₇₇ N ₂₀₁ O ₂₂₁ S ₉ | 58029029-58030494 |
| StHMA17 | PGSC0003DMT400038828 | - | 273 | 31631.03 | 5.3 | C ₁₃₆₅ H ₂₂₅₇ N ₃₇₇ O ₄₅₂ S ₁₄ | 46312673-46314684 |
| StHMA18 | PGSC0003DMT400056666 | + | 152 | 17169.87 | 9.4 | C ₇₅₉ H ₁₂₁₄ N ₂₀₂ O ₂₂₈ S ₁₁ | 61538313-61541184 |
| StHMA19 | PGSC0003DMT400024479 | + | 150 | 16456.18 | 9.46 | C ₇₂₉ H ₁₁₈₇ N ₁₉₇ O ₂₁₆ S ₉ | 42949396-42951085 |
| StHMA20 | PGSC0003DMT400024481 | + | 150 | 16502.2 | 9.46 | C ₇₃₃ H ₁₁₈₅ N ₁₉₇ O ₂₁₆ S ₉ | 55464451-55465720 |
| StHMA21 | PGSC0003DMT400078487 | - | 414 | 46005.21 | 8.1 | C ₁₉₅₂ H ₃₀₇₀ N ₅₉₈ O ₆₃₅ S ₂₉ | 53411225-53413634 |
| StHMA22 | PGSC0003DMT400056199 | - | 154 | 17393.09 | 9.45 | C ₇₆₇ H ₁₂₃₁ N ₂₁₁ O ₂₂₉ S ₁₀ | 2063369-2064790 |
| StHMA23 | PGSC0003DMT400021739 | - | 363 | 40443.68 | 6.66 | C ₁₇₈₀ H ₂₇₅₀ N ₄₈₈ O ₅₄₇ S ₂₂ | 9201119-9206477 |
| StHMA24 | PGSC0003DMT400060398 | + | 77 | 8105.27 | 5.31 | C ₃₄₉ H ₅₇₆ N ₉₄ O ₁₁₆ S ₅ | 5557033-5561866 |
| StHMA25 | PGSC0003DMT400069249 | - | 336 | 38003.29 | 5.91 | C ₁₆₆₈ H ₂₇₀₈ N ₄₆₂ O ₅₂₆ S ₁₁ | 45208003-45209479 |
| StHMA26 | PGSC0003DMT400018392 | + | 253 | 28277.42 | 8.88 | C ₁₂₂₀ H ₂₀₃₅ N ₃₅₁ O ₃₉₂ S ₁₂ | 41760071-41760891 |
| StHMA27 | PGSC0003DMT400079324 | + | 180 | 20955.88 | 9.1 | C ₉₂₆ H ₁₄₂₈ N ₂₆₈ O ₂₆₆ S ₁₂ | 55143456-55145580 |
| StHMA28 | PGSC0003DMT400009920 | + | 367 | 39867.1 | 8.52 | C ₁₇₃₄ H ₂₇₉₈ N ₄₈₄ O ₅₆₀ S ₁₅ | 62455552-62456793 |
| StHMA29 | PGSC0003DMT400016647 | + | 221 | 25708.87 | 9.23 | C ₁₁₅₃ H ₁₈₆₉ N ₃₀₉ O ₃₃₇ S ₈ | 40987375-40990668 |
| StHMA30 | PGSC0003DMT400045359 | - | 300 | 32396.97 | 9.57 | C ₁₃₉₁ H ₂₃₁₆ N ₄₀₄ O ₄₅₃ S ₁₄ | 62479681-62480683 |
| StHMA31 | PGSC0003DMT400072448 | + | 166 | 18145.94 | 9.38 | C ₇₉₉ H ₁₃₂₇ N ₂₂₇ O ₂₄₄ S ₄ | 5176268-5179031 |

| | | | | | | | |
|---------|----------------------|---|-----|----------|------|---|-------------------|
| StHMA32 | PGSC0003DMT400034599 | - | 140 | 16163.83 | 6.36 | C ₆₉₇ H ₁₁₇₁ N ₁₉₉ O ₂₁₇ S ₁₁ | 47049115-47050456 |
| StHMA33 | PGSC0003DMT400050141 | + | 106 | 11370.89 | 4.72 | C ₄₉₇ H ₈₀₂ N ₁₂₈ O ₁₆₅ S ₅ | 11452548-11454378 |
| StHMA34 | PGSC0003DMT400020973 | + | 341 | 36542.76 | 9.21 | C ₁₅₇₁ H ₂₅₈₇ N ₄₅₃ O ₅₀₅ S ₂₀ | 81766806-81768151 |
| StHMA35 | PGSC0003DMT400040203 | + | 260 | 28825.83 | 9.76 | C ₁₂₅₁ H ₂₀₂₇ N ₃₆₃ O ₃₉₁ S ₁₃ | 50982683-50987786 |
| StHMA36 | PGSC0003DMT400001032 | - | 149 | 16708.3 | 5.78 | C ₇₃₂ H ₁₁₈₃ N ₁₉₉ O ₂₂₄ S ₁₁ | 20055033-20059032 |

Table S3. Subcellular localization prediction of StHMA gene family in potato.

| Gene | Cytoplasmic | Nucleus | Peroxisome | Plasma membrane | Mitochondrion | Chloroplast | Extracellular matrix | Vacuole | Endoplasmic reticulum |
|----------------|-------------|---------|------------|-----------------|---------------|-------------|----------------------|---------|-----------------------|
| <i>StHMA1</i> | — | 10 | 2 | — | — | 1 | — | — | — |
| <i>StHMA2</i> | 1 | 10 | — | — | — | 2 | — | — | — |
| <i>StHMA3</i> | 6 | 7 | — | — | — | — | — | — | — |
| <i>StHMA4</i> | 1 | 8 | 2 | 2 | — | — | — | — | — |
| <i>StHMA5</i> | — | 13 | — | — | — | — | — | — | — |
| <i>StHMA6</i> | 2 | 6 | — | — | 1 | 4 | — | — | — |
| <i>StHMA7</i> | — | — | — | — | 3 | 11 | — | — | — |
| <i>StHMA8</i> | — | 2 | — | — | — | 11 | — | — | — |
| <i>StHMA9</i> | 4 | — | — | 6 | — | 4 | — | — | 1 |
| <i>StHMA10</i> | 4 | — | — | — | 2 | 7 | — | — | — |
| <i>StHMA11</i> | — | 3 | — | 2 | 2 | 4 | — | — | — |
| <i>StHMA12</i> | 11 | — | — | — | — | 1 | 1 | — | — |
| <i>StHMA13</i> | 14 | — | — | — | — | — | — | — | — |
| <i>StHMA14</i> | 1 | 1 | — | — | — | 11 | — | — | — |
| <i>StHMA15</i> | 3 | — | — | — | — | 8 | 3 | — | — |
| <i>StHMA16</i> | 4 | 2 | — | — | — | 5 | 2 | — | — |
| <i>StHMA17</i> | 3 | 7 | — | 1 | — | — | 2 | — | — |
| <i>StHMA18</i> | 2 | 1 | — | — | — | 10 | — | — | — |
| <i>StHMA19</i> | — | — | — | — | — | 14 | — | — | — |
| <i>StHMA20</i> | — | — | — | — | — | 14 | — | — | — |
| <i>StHMA21</i> | 1 | 4 | — | 1 | 7 | — | — | — | — |
| <i>StHMA22</i> | 10 | — | — | — | — | 30 | — | — | — |
| <i>StHMA23</i> | 2 | 3 | — | 2 | 1 | 2 | 1 | 2 | — |

| | | | | | | | | | |
|----------------|----|---|---|---|---|----|---|---|---|
| <i>StHMA24</i> | 2 | — | — | — | — | 11 | — | — | — |
| <i>StHMA25</i> | 2 | 5 | — | — | — | 7 | — | — | — |
| <i>StHMA26</i> | — | — | — | — | — | — | — | — | — |
| <i>StHMA27</i> | — | — | — | — | — | 13 | — | — | — |
| <i>StHMA28</i> | 7 | 7 | — | — | — | — | — | — | — |
| <i>StHMA29</i> | 11 | 1 | — | — | 1 | — | — | — | — |
| <i>StHMA30</i> | 2 | 1 | — | — | — | 3 | 6 | 1 | — |
| <i>StHMA31</i> | 7 | 6 | — | — | — | — | — | — | — |
| <i>StHMA32</i> | 4 | — | — | — | 1 | 7 | 1 | — | — |
| <i>StHMA33</i> | — | — | — | — | 1 | 11 | 1 | — | — |
| <i>StHMA34</i> | 2 | 4 | — | — | — | 7 | — | — | — |
| <i>StHMA35</i> | 1 | 2 | — | — | — | 10 | — | — | — |
| <i>StHMA36</i> | 1 | 2 | — | 1 | 2 | 6 | 1 | — | — |

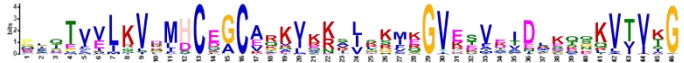








Table S4. Ka/Ks ratios of homologous gene pairs between potato and different species.

| Homologous gene pairs | Ka | Ks | Ka/Ks | P-Value(Fisher) | Length | Divergence-Time | ML-Score |
|---|-----------|----------|-----------|-----------------|--------|-----------------|----------|
| <i>itb12g00660&PGSC0003DMT400056666</i> | 0.0810865 | 4.38347 | 0.0184982 | 1.55E-84 | 441 | 1 | -844.906 |
| <i>itb01g02040&PGSC0003DMT400032707</i> | 0.236192 | 1.08547 | 0.217594 | 2.60E-38 | 675 | 0.469979 | -1478.75 |
| <i>itb01g10210&PGSC0003DMT400038828</i> | 0.185293 | 3.2623 | 0.0567982 | 7.47E-108 | 786 | 1 | -1551.19 |
| <i>itb03g24840&PGSC0003DMT400001501</i> | 0.186874 | 1.80372 | 0.103605 | 1.07E-88 | 867 | 0.593468 | -1759.45 |
| <i>itb06g23970&PGSC0003DMT400024479</i> | 0.109118 | 1.2642 | 0.0863138 | 1.91E-41 | 447 | 0.376053 | -866.649 |
| <i>itb07g13670&PGSC0003DMT400018392</i> | 0.684371 | 0.354983 | 1.9279 | 6.34E-07 | 672 | 0.583759 | -1529.54 |
| <i>itb08g07490&PGSC0003DMT400024409</i> | 0.0930473 | 0.887601 | 0.10483 | 4.34E-186 | 2976 | 0.287233 | -5629.53 |
| <i>itb12g00660&PGSC0003DMT400056199</i> | 0.0846441 | 1.71071 | 0.0494789 | 5.20E-50 | 444 | 0.469529 | -842.093 |
| <i>itb12g04120&PGSC0003DMT400078635</i> | 0.132712 | 3.09671 | 0.0428556 | 5.98E-72 | 438 | 0.854718 | -876.914 |
| <i>itb12g19630&PGSC0003DMT400001032</i> | 0.216476 | 1.88086 | 0.115095 | 2.62E-42 | 381 | 0.602011 | -800.57 |
| <i>itb12g21430&PGSC0003DMT400050141</i> | 0.0998264 | 1.86918 | 0.0534066 | 4.94E-28 | 255 | 0.547936 | -488.251 |
| <i>itb12g25750&PGSC0003DMT400037204</i> | 0.158335 | 1.16841 | 0.135513 | 5.51E-31 | 405 | 0.442904 | -832.823 |

| | | | | | | | |
|---|-----------|----------|-----------|------------|------|----------|----------|
| <i>itb13g21880&PGSC0003DMT400015954</i> | 0.604739 | 1.31886 | 0.458531 | 5.70E-28 | 1059 | 0.783719 | -2571.37 |
| <i>itb13g23030&PGSC0003DMT400083194</i> | 0.377839 | 2.82903 | 0.133557 | 0 | 1461 | 0.977852 | -3308.97 |
| <i>itb14g01030&PGSC0003DMT400078487</i> | 0.60093 | 0.626159 | 0.959709 | 0.658806 | 1050 | 0.60713 | -2526.75 |
| <i>itb14g01060&PGSC0003DMT400015350</i> | 0.216279 | 1.7255 | 0.125343 | 2.35E-45 | 435 | 0.521599 | -910.881 |
| <i>itb14g16600&PGSC0003DMT400040203</i> | 0.370787 | 1.58365 | 0.234134 | 3.16E-54 | 714 | 0.707399 | -1613.22 |
| <i>itb15g00310&PGSC0003DMT400009920</i> | 0.228158 | 1.18822 | 0.192016 | 6.78E-56 | 906 | 0.468059 | -1917.03 |
| <i>itb15g11860&PGSC0003DMT400073578</i> | 0.288882 | 1.64023 | 0.176123 | 1.01E-105 | 1221 | 0.586876 | -2691.65 |
| <i>itb15g13030&PGSC0003DMT400063687</i> | 0.57349 | 0.438458 | 1.30797 | 0.0148055 | 885 | 0.539738 | -2044.25 |
| <i>OIS95687&PGSC0003DMT400078487</i> | 0.160064 | 0.613304 | 0.260987 | 6.67E-27 | 1161 | 0.24622 | -2264.05 |
| <i>OIS97914&PGSC0003DMT400009920</i> | 0.468792 | 1.62175 | 0.289066 | 4.23E-40 | 879 | 0.801679 | -1900.19 |
| <i>OIS97914&PGSC0003DMT400072448</i> | 0.41457 | 0.875985 | 0.473261 | 1.20E-08 | 477 | 0.531936 | -1070.96 |
| <i>OIS98725&PGSC0003DMT400056199</i> | 0.0642516 | 0.454818 | 0.141269 | 9.94E-14 | 453 | 0.146316 | -782.362 |
| <i>OIT01620&PGSC0003DMT400001032</i> | 0.134146 | 0.527214 | 0.254442 | 6.08E-11 | 423 | 0.219811 | -797.128 |
| <i>OIT01983&PGSC0003DMT400045359</i> | 0.283793 | 0.992527 | 0.28593 | 6.94E-34 | 840 | 0.44399 | -1853.19 |
| <i>Os01i0507700-01&PGSC0003DMT400078635</i> | 0.29937 | 3.19711 | 0.0936376 | 0 | 441 | 1 | -1023.74 |
| <i>PGSC0003DMT400001032&AT3G24450</i> | 0.292729 | 3.33597 | 0.0877493 | 0 | 399 | 0.88323 | -873.695 |
| <i>PGSC0003DMT400001501&AT5G24580</i> | 0.320564 | 2.21048 | 0.14502 | 3.08E-105 | 858 | 0.800826 | -1894.9 |
| <i>PGSC0003DMT400009920&AT5G03380</i> | 0.478632 | 2.57844 | 0.185629 | 0 | 963 | 1 | -2290.84 |
| <i>PGSC0003DMT400015350&AT1G22990</i> | 0.271817 | 3.45964 | 0.0785682 | 0 | 432 | 1 | -953.168 |
| <i>PGSC0003DMT400018392&AT5G60800</i> | 0.415165 | 2.87861 | 0.144224 | 0 | 732 | 0.99983 | -1646.35 |
| <i>PGSC0003DMT400032707&AT4G33520</i> | 0.514392 | 2.23315 | 0.230343 | 1.11E-72 | 678 | 1 | -1594.31 |
| <i>PGSC0003DMT400037204&AT3G48970</i> | 0.176086 | 3.50565 | 0.0502291 | 0 | 417 | 1 | -876.451 |
| <i>PGSC0003DMT400040203&AT2G28660</i> | 0.673518 | 0.686989 | 0.980391 | 0.851156 | 645 | 0.676691 | -1575.23 |
| <i>PGSC0003DMT400045359&AT2G37390</i> | 0.553018 | 0.752983 | 0.734436 | 0.00409719 | 645 | 0.598933 | -1577.76 |
| <i>PGSC0003DMT400056199&AT4G39700</i> | 0.216057 | 2.82269 | 0.076543 | 0 | 453 | 0.772722 | -950.172 |
| <i>PGSC0003DMT400056666&AT4G39700</i> | 0.141552 | 4.022 | 0.0351945 | 0 | 450 | 1 | -907.438 |
| <i>PGSC0003DMT400063687&AT5G27690</i> | 0.772629 | 1.55993 | 0.495298 | 7.24E-25 | 939 | 1 | -2269.97 |

| | | | | | | | |
|---|----------|----------|-----------|----------|------|----------|----------|
| <i>PGSC0003DMT400068079&AT5G50740</i> | 0.345197 | 3.68181 | 0.0937572 | 0 | 828 | 1 | -1806.92 |
| <i>PGSC0003DMT400072448&AT2G36950</i> | 1.12019 | 0.439755 | 2.54731 | 7.28E-10 | 423 | 0.936167 | -1031.82 |
| <i>PGSC0003DMT400073578&AT3G05220</i> | 0.702438 | 1.69614 | 0.414139 | 1.25E-43 | 1212 | 1 | -2910.51 |
| <i>PGSC0003DMT400078487&AT1G23000</i> | 0.608026 | 2.00073 | 0.303902 | 5.98E-70 | 924 | 0.955702 | -2264.95 |
| <i>PGSC0003DMT400078635&AT1G71050</i> | 0.252213 | 3.54554 | 0.0711352 | 0 | 438 | 1 | -977.164 |
| <i>PGSC0003DMT400083194&AT3G06130</i> | 0.412553 | 1.37449 | 0.30015 | 1.15E-64 | 1284 | 0.696085 | -2982.4 |
| <i>PGSC0003DMT400009920&Zm00001d032873_T001</i> | 0.99499 | 1.0101 | 0.985044 | 0.837601 | 966 | 1 | -2393.73 |
| <i>PGSC0003DMT400078487&Zm00001d008515_T001</i> | 0.719656 | 1.84144 | 0.390811 | 9.26E-54 | 1095 | 1 | -2662.52 |
| <i>PGSC0003DMT400063687&Zm00001d007130_T001</i> | 0.628382 | 1.9469 | 0.322761 | 5.82E-77 | 876 | 1 | -2141.15 |
| <i>PGSC0003DMT400032707&Zm00001d052801_T001</i> | 0.827484 | 0.700359 | 1.18151 | 0.121641 | 561 | 0.794401 | -1394.38 |

Table S5. Motif sequences of heavy-metal associated proteins in *S. tuberosum*, *A. thaliana*, *O. sativa* and *S. lycopersicum*.

| Motif | Consensus sequence | E-value | Sites | Width |
|-------|---|-----------|-------|-------|
| 1 |  Best Possible Match: PLQTVVLKVDMHCEGCARKYKKSLSKMKGVESVEIDLKQQKVTYKG | 1.0e-912 | 50 | 46 |
| 2 |  Best Possible Match: MAIGAGTDIAIEAADIVLMRSNLEDVITAIIDL SRKTF SRIRLNYWAMAYNVIAPIAAGVLPFTRFRLPPWLAGACMAASSVSVCSLLLKRYKPPR | 1.1e-714 | 13 | 100 |
| 3 |  Best Possible Match: VLVYGMTCEGCASSYERILK LKLPGVFSASYDLLTSKVTVKG | 4.5e-605 | 50 | 41 |
| 4 |  Best Possible Match: PGEKVPVDGVVYWGQSHVNESMITGESRPVAKKSTVIGGTINLNGVLHIKATKVGESALSQIVRLVETAQMSKAPYQ | 1.8e-542 | 15 | 80 |
| 5 |  Best Possible Match: IACPCALGLATPTAYMVAIVGASQGVLIKGGDALERAQYDCYIFDKTGTLTQGKPVVTTTK | 1.0e-477 | 15 | 63 |
| 6 |  Best Possible Match: PTEVYPPQMFSDENPNACSIM | 1.2e-358 | 40 | 21 |
| 7 |  Best Possible Match: MGDLLKWLXTPVQFGIGRRFFYYGAYRALRHGSTNMDVLYALGTNAAYFYSVYSLLY | 3.6e-319 | 13 | 57 |
| 8 |  Best Possible Match: DPLKLV ERYQKKTGKQVELV SPLKPP EE | 1.60E-294 | 37 | 29 |
| 9 |  Best Possible Match: FASLP GKGYQC L GKVVGNRLMENGILPEEFELYEL EEA TGLLVAIDFLYGLXLSISDPLKREAAYVYSG | 3.50E-229 | 10 | 80 |





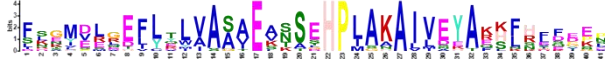

| | | | | | |
|----|---|--|-----------|----|----|
| 10 | Best Possible Match: FSSLPGKGVQCLINGKWILVGNRSLMTENGINPVEAEFLXEESAQTGILVAIDSELIGVLSISDPLKREAAVVYSG |  | 1.30E-298 | 9 | 80 |
| 11 | Best Possible Match: GASTGFWSPPDYFETSAMLIIFYLLGKYLEVLAKGKTSDAIKKLVELAPATAITLLTKDKEGKVVGEREIDALLIQPGDYLK |  | 1.30E-164 | 15 | 21 |
| 12 | Best Possible Match: VVAMVGDGINDSPALAAADV |  | 2.20E-144 | 13 | 29 |
| 13 | Best Possible Match: KFADYIASIFVPTVITLSLLTFLGWFLAG |  | 2.00E-139 | 24 | 21 |
| 14 | Best Possible Match: KVLKVKKTGKKAIEFWPVVY |  | 3.50E-172 | 15 | 41 |
| 15 | Best Possible Match: FSGMDLGEFTLVASAEASSEHPLAKAIVEYAKKFHFEEEP |  | 6.70E-148 | 18 | 29 |
| | Best Possible Match: DPSLVSKEDILEAIEDAGFEAELISSSEQ | | | | |

Table S6. Abiotic stress-related cis-acting elements in the promoter region of StHMA genes.

| Gene | ABRE | | LTR | | MBS | |
|----------------|--------|-------------------------------------|--------|-------------------------|--------|------------------------|
| | Number | Position | Number | Position | Number | Position |
| <i>StHMA1</i> | 3 | +703,+704,-1137 | 0 | | 0 | |
| <i>StHMA2</i> | 2 | +689,-905 | 0 | | 2 | +224,+253 |
| <i>StHMA3</i> | 0 | | 1 | +465 | 0 | |
| <i>StHMA4</i> | 1 | +798 | 1 | -961 | 0 | |
| <i>StHMA5</i> | 1 | -365 | 2 | +1817,+1827 | 0 | |
| <i>StHMA6</i> | 1 | -922 | 0 | | 4 | +1649,+960,-1207,-1682 |
| <i>StHMA7</i> | 6 | +1316,+1319,+1743,+1821,-1318,-1742 | 1 | +407 | 0 | |
| <i>StHMA8</i> | 0 | | 1 | -1013 | 0 | |
| <i>StHMA9</i> | 1 | +60 | 1 | +1271 | 0 | |
| <i>StHMA10</i> | 5 | +1155,+117,+347,-1411,-1413 | 0 | | 2 | -1981,-992 |
| <i>StHMA11</i> | 1 | -135 | 2 | +143,-292 | 0 | |
| <i>StHMA12</i> | 0 | | 0 | | 0 | |
| <i>StHMA13</i> | 2 | +753,+754 | 1 | -1412 | 1 | -1058 |
| <i>StHMA14</i> | 4 | +1758,+1761,-1677,-1760 | 0 | | 1 | -1794 |
| <i>StHMA15</i> | 2 | +648,+649 | 0 | | 0 | |
| <i>StHMA16</i> | 0 | | 0 | | 0 | |
| <i>StHMA17</i> | 0 | | 4 | +1260,+1532,+1634,-1186 | 0 | |
| <i>StHMA18</i> | 4 | +1100,+1349,-1064,-745 | 0 | | 0 | |
| <i>StHMA19</i> | 6 | +590,+591,+627,+629,+630,+653 | 0 | | 0 | |
| <i>StHMA20</i> | 6 | +596,+597,+633,+635,+636,+659 | 0 | | 0 | |
| <i>StHMA21</i> | 2 | +296,+297 | 0 | | 0 | |
| <i>StHMA22</i> | 3 | +179,+181,+182 | 0 | | 0 | |
| <i>StHMA23</i> | 2 | +122,+123 | 0 | | 0 | |
| <i>StHMA24</i> | 2 | +499,-587 | 1 | +1795 | 1 | +1557 |
| <i>StHMA25</i> | 4 | +1266,+1806,+1809,-1808 | 0 | | 1 | +1861 |

| | | | | | |
|----------------|---|----------------|---|-------|---------|
| <i>StHMA26</i> | 2 | +139,+1707 | 0 | | 0 |
| <i>StHMA27</i> | 0 | | 1 | +308 | 0 |
| <i>StHMA28</i> | 1 | -1235 | 1 | +301 | 0 |
| <i>StHMA29</i> | 3 | +326,+327,+339 | 1 | -1258 | 0 |
| <i>StHMA30</i> | 2 | +1007,+460 | 0 | | 1 -738 |
| <i>StHMA31</i> | 2 | +1234,-1235 | 0 | | 1 -275 |
| <i>StHMA32</i> | 1 | -1837 | 0 | | 0 |
| <i>StHMA33</i> | 1 | +1341 | 0 | | 1 -359 |
| <i>StHMA34</i> | 1 | +1843 | 0 | | 0 |
| <i>StHMA35</i> | 2 | +213,+214 | 1 | -825 | 1 -1203 |
| <i>StHMA36</i> | 1 | +1565 | 0 | | 0 |

| Gene | MYB | | MYC | | W-box | |
|----------------|--------|---|--------|---|--------|-------------|
| | Number | Position | Number | Position | Number | Position |
| <i>StHMA1</i> | 5 | +1821,+437,+652,-1521,-1665 | 8 | +1295,+21,+299,+339,+469,+728,-1531,-1655 | 1 | +1342 |
| <i>StHMA2</i> | 5 | +1886,+224,+253,+294,-870 | 4 | +1771,+198,+646,+67 | 0 | |
| <i>StHMA3</i> | 1 | +1084 | 1 | +1809 | 0 | |
| <i>StHMA4</i> | 1 | +1881 | 2 | -153,-710 | 1 | -688 |
| <i>StHMA5</i> | 2 | -1071,-1807 | 6 | +1048,+1286,+1795,+1914,+547,-290 | 0 | |
| <i>StHMA6</i> | 8 | +1045,+1649,+960,-1207,-1499,-1682,-1869,-28 | 7 | +1250,+1373,-1749,-1797,-1851,-236,-409 | 2 | +1234,+1253 |
| <i>StHMA7</i> | 3 | -1281,-1461,-380 | 1 | +142 | 0 | |
| <i>StHMA8</i> | 13 | +1568,+200,+571,+673,-212,-265,-307,-349,-391,-433,-475,-517,-559 | 5 | +1623,+1895,+4,-1164,-1485 | 0 | |
| <i>StHMA9</i> | 3 | +1112,+1436,-1148 | 4 | +1753,+665,+966,-1440 | 1 | +1353 |
| <i>StHMA10</i> | 3 | -1485,-1981,-992 | 7 | +1029,+1218,+1470,+952,-1911,-737,-998 | 1 | +987 |
| <i>StHMA11</i> | 2 | +1884,+789 | 3 | +909,-1549,-1573 | 1 | +483 |
| <i>StHMA12</i> | 1 | +1719 | 3 | +1723,-1273,-305 | 1 | -1116 |
| <i>StHMA13</i> | 3 | +480,-1058,-1783 | 0 | | 0 | |

| | | | | | | |
|----------------|---|---|---|--|---|----------------------|
| <i>StHMA14</i> | 2 | -1794,-1858 | 1 | -514 | 3 | +1419,+1470,+79 |
| <i>StHMA15</i> | 1 | -1706 | 5 | +1172,+1636,+1721,+321,-24 | 1 | -788 |
| <i>StHMA16</i> | 2 | +1546,-699 | 4 | +171,+482,-259,-30 | 2 | +1578,+987 |
| <i>StHMA17</i> | 6 | +1326,+1524,+53,-1346,-148,-1488 | 1 | +653 | 0 | |
| <i>StHMA18</i> | 4 | +241,+329,+622,-1420 | 2 | +1327,+384 | 0 | |
| <i>StHMA19</i> | 2 | +398,-410 | 0 | | 1 | +1073 |
| <i>StHMA20</i> | 2 | +404,-416 | 3 | +1476,-1144,-24 | 0 | |
| <i>StHMA21</i> | 1 | -20 | 6 | +1441,+1688,+1822,+1925,+845,-252 | 0 | |
| <i>StHMA22</i> | 0 | | 2 | +1327,+971 | 0 | |
| <i>StHMA23</i> | 4 | +1004,+1879,-1930,-711 | 3 | +1051,-1008,-372 | 1 | +1623 |
| <i>StHMA24</i> | 1 | +1557 | 1 | -1627 | 1 | -1916 |
| <i>StHMA25</i> | 5 | +1861,+724,-1352,-166,-505 | 2 | +501,+635 | 0 | |
| <i>StHMA26</i> | 4 | +1748,+1948,+83,-1475 | 8 | +127,+1514,+322,+869,-238,-287,-30,-575 | 1 | +1311 |
| <i>StHMA27</i> | 2 | +264,-1281 | 2 | +408,-723 | 1 | -58 |
| <i>StHMA28</i> | 1 | +1798 | 4 | +1924,+686,+713,-1392 | 0 | |
| <i>StHMA29</i> | 4 | +1039,+1459,+1934,-1416 | 3 | +1205,+1467,-351 | 4 | +507,+743,+947,-1413 |
| <i>StHMA30</i> | 4 | +1574,+1825,+519,-738 | 6 | +1666,+1795,+1879,+1956,-116,-744 | 0 | |
| <i>StHMA31</i> | 5 | +1937,+555,-1062,-275,-660 | 4 | +1480,+322,+926,-1043 | 0 | |
| <i>StHMA32</i> | 8 | +1216,+272,+422,+47,+83,-1105,-1219,-1851 | 9 | +185,+612,+782,+828,+901,+970,-1202,-1534,-453 | 0 | |
| <i>StHMA33</i> | 2 | +466,-359 | 4 | +128,+1659,+571,-985 | 2 | +131,+84 |
| <i>StHMA34</i> | 1 | -434 | 5 | +919,-1036,-126,-448,-570 | 1 | -1321 |
| <i>StHMA35</i> | 1 | -1203 | 6 | +462,+626,+928,-293,-419,-542 | 0 | |
| <i>StHMA36</i> | 7 | +1327,+1576,+1812,+864,-577,-651,-685 | 7 | +1243,+1294,-1108,-1309,-1350,-1416,-1457 | 2 | +580,-153 |

Table S7. RNA-seq data of potato *StHMA* genes in different tissues.

| | stolon | young tuber | flower | leaf | shoot apex | petiole | stem | mature tuber | root | stamen | tuber peel | tuber cortex | tuber pith | tuber sprout | whole in vitro plant |
|----------------|--------|-------------|--------|--------|------------|---------|--------|--------------|--------|--------|------------|--------------|------------|--------------|----------------------|
| <i>StHMA1</i> | 5.00 | 4.00 | 9.00 | 15.00 | 1.00 | 13.00 | 10.00 | 3.00 | 20.00 | 18.00 | 0.90 | 5.00 | 2.00 | 9.00 | 14.00 |
| <i>StHMA2</i> | 7.00 | 3.00 | 4.00 | 16.00 | 0.70 | 29.00 | 6.00 | 3.00 | 38.00 | 7.00 | 1.00 | 7.00 | 2.00 | 4.00 | 9.00 |
| <i>StHMA3</i> | 168.00 | 163.00 | 108.00 | 23.00 | 104.00 | 91.00 | 143.00 | 90.00 | 76.00 | 9.00 | 67.00 | 80.00 | 86.00 | 105.00 | 59.00 |
| <i>StHMA4</i> | 231.00 | 192.00 | 151.00 | 55.00 | 48.00 | 478.00 | 323.00 | 57.00 | 259.00 | 30.00 | 237.00 | 164.00 | 133.00 | 725.00 | 328.00 |
| <i>StHMA5</i> | 99.00 | 34.00 | 29.00 | 58.00 | 15.00 | 70.00 | 61.00 | 16.00 | 127.00 | 7.00 | 7.00 | 24.00 | 13.00 | 57.00 | 79.00 |
| <i>StHMA6</i> | 6.00 | 1.00 | 3.00 | 0.80 | 0.50 | 0.00 | 0.50 | 0.00 | 0.00 | 0.30 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| <i>StHMA7</i> | 127.00 | 72.00 | 55.00 | 83.00 | 140.00 | 36.00 | 55.00 | 80.00 | 29.00 | 14.00 | 54.00 | 39.00 | 38.00 | 62.00 | 63.00 |
| <i>StHMA8</i> | 290.00 | 299.00 | 174.00 | 253.00 | 230.00 | 904.00 | 453.00 | 173.00 | 267.00 | 19.00 | 162.00 | 273.00 | 233.00 | 309.00 | 279.00 |
| <i>StHMA9</i> | 34.00 | 34.00 | 45.00 | 27.00 | 25.00 | 115.00 | 76.00 | 48.00 | 91.00 | 61.00 | 53.00 | 52.00 | 44.00 | 66.00 | 109.00 |
| <i>StHMA10</i> | 0.50 | 0.50 | 1.00 | 0.00 | 0.00 | 0.50 | 0.00 | 2.00 | 1.00 | 0.00 | 4.00 | 10.00 | 4.00 | 29.00 | 29.00 |
| <i>StHMA11</i> | 8.00 | 16.00 | 6.00 | 8.00 | 13.00 | 26.00 | 13.00 | 10.00 | 70.00 | 2.00 | 7.00 | 12.00 | 7.00 | 93.00 | 31.00 |
| <i>StHMA12</i> | 1.00 | 8.00 | 3.00 | 9.00 | 2.00 | 11.00 | 10.00 | 0.00 | 9.00 | 1.00 | 1.00 | 2.00 | 0.50 | 8.00 | 7.00 |
| <i>StHMA13</i> | 24.00 | 4.00 | 2.00 | 1.00 | 2.00 | 5.00 | 8.00 | 0.00 | 13.00 | 0.00 | 0.00 | 0.00 | 0.00 | 4.00 | 2.00 |
| <i>StHMA14</i> | 141.00 | 42.00 | 74.00 | 51.00 | 39.00 | 47.00 | 75.00 | 89.00 | 16.00 | 105.00 | 73.00 | 76.00 | 109.00 | 34.00 | 48.00 |
| <i>StHMA15</i> | 13.00 | 156.00 | 99.00 | 3.00 | 80.00 | 34.00 | 144.00 | 194.00 | 108.00 | 12.00 | 104.00 | 123.00 | 151.00 | 40.00 | 13.00 |
| <i>StHMA16</i> | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 15.00 | 0.00 | 1.00 | 0.00 | 0.00 | 23.00 | 43.00 |
| <i>StHMA17</i> | 114.00 | 12.00 | 32.00 | 24.00 | 0.00 | 0.70 | 8.00 | 0.00 | 0.00 | 0.20 | 0.00 | 0.00 | 0.00 | 3.00 | 8.00 |
| <i>StHMA18</i> | 8.00 | 21.00 | 16.00 | 2.00 | 68.00 | 2.00 | 32.00 | 36.00 | 472.00 | 0.50 | 38.00 | 11.00 | 11.00 | 28.00 | 26.00 |
| <i>StHMA19</i> | 0.00 | 0.50 | 1.00 | 0.00 | 0.00 | 0.90 | 0.00 | 0.00 | 0.80 | 0.00 | 0.00 | 0.00 | 0.00 | 4.00 | 0.00 |
| <i>StHMA20</i> | 0.00 | 0.70 | 2.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 2.00 | 0.00 | 0.00 | 0.40 | 0.00 | 2.00 | 0.50 |
| <i>StHMA21</i> | 198.00 | 45.00 | 13.00 | 32.00 | 67.00 | 38.00 | 36.00 | 38.00 | 5.00 | 0.00 | 12.00 | 17.00 | 24.00 | 26.00 | 14.00 |
| <i>StHMA22</i> | 0.00 | 40.00 | 0.00 | 0.00 | 93.00 | 0.00 | 0.00 | 21.00 | 23.00 | 0.00 | 29.00 | 5.00 | 2.00 | 36.00 | 2.00 |
| <i>StHMA23</i> | 0.00 | 0.50 | 0.00 | 0.20 | 1.00 | 0.80 | 0.00 | 0.30 | 0.50 | 1.00 | 0.70 | 0.00 | 0.00 | 0.50 | 0.00 |
| <i>StHMA24</i> | 59.00 | 75.00 | 76.00 | 60.00 | 75.00 | 112.00 | 65.00 | 52.00 | 143.00 | 87.00 | 32.00 | 36.00 | 23.00 | 72.00 | 146.00 |
| <i>StHMA25</i> | 52.00 | 84.00 | 37.00 | 16.00 | 99.00 | 124.00 | 179.00 | 236.00 | 129.00 | 22.00 | 291.00 | 307.00 | 497.00 | 362.00 | 105.00 |

| | | | | | | | | | | | | | | | |
|----------------|-------|-------|--------|-------|-------|--------|--------|-------|--------|--------|-------|-------|--------|--------|--------|
| <i>StHMA26</i> | 7.00 | 0.00 | 0.00 | 0.00 | 0.60 | 0.00 | 0.60 | 0.00 | 0.30 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| <i>StHMA27</i> | 1.00 | 0.00 | 0.00 | 0.70 | 0.90 | 2.00 | 0.40 | 2.00 | 24.00 | 0.20 | 1.00 | 5.00 | 2.00 | 3.00 | 2.00 |
| <i>StHMA28</i> | 30.00 | 11.00 | 120.00 | 30.00 | 26.00 | 28.00 | 71.00 | 45.00 | 306.00 | 318.00 | 73.00 | 96.00 | 133.00 | 106.00 | 113.00 |
| <i>StHMA29</i> | 0.00 | 0.00 | 0.00 | 0.00 | 4.00 | 0.00 | 0.00 | 13.00 | 0.40 | 0.00 | 9.00 | 0.00 | 0.00 | 3.00 | 0.50 |
| <i>StHMA30</i> | 19.00 | 3.00 | 11.00 | 18.00 | 0.40 | 14.00 | 6.00 | 2.00 | 11.00 | 3.00 | 0.90 | 4.00 | 2.00 | 8.00 | 18.00 |
| <i>StHMA31</i> | 3.00 | 2.00 | 10.00 | 5.00 | 0.50 | 2.00 | 0.70 | 0.30 | 1.00 | 13.00 | 2.00 | 0.50 | 0.20 | 3.00 | 2.00 |
| <i>StHMA32</i> | 2.00 | 1.00 | 0.00 | 6.00 | 4.00 | 2.00 | 3.00 | 0.60 | 0.20 | 0.00 | 0.60 | 2.00 | 1.00 | 1.00 | 6.00 |
| <i>StHMA33</i> | 59.00 | 66.00 | 90.00 | 68.00 | 13.00 | 274.00 | 311.00 | 48.00 | 78.00 | 150.00 | 21.00 | 15.00 | 16.00 | 32.00 | 473.00 |
| <i>StHMA34</i> | 35.00 | 70.00 | 14.00 | 15.00 | 55.00 | 9.00 | 15.00 | 30.00 | 18.00 | 2.00 | 10.00 | 19.00 | 15.00 | 19.00 | 8.00 |
| <i>StHMA35</i> | 7.00 | 6.00 | 0.40 | 4.00 | 2.00 | 12.00 | 5.00 | 6.00 | 31.00 | 0.00 | 1.00 | 0.90 | 0.00 | 14.00 | 36.00 |
| <i>StHMA36</i> | 5.00 | 14.00 | 7.00 | 3.00 | 4.00 | 15.00 | 24.00 | 10.00 | 1.00 | 2.00 | 3.00 | 3.00 | 2.00 | 2.00 | 6.00 |
