**SUPPLEMENTARY TABLES**

Table S1. Accession numbers of the polyamine metabolic pathway genes from Arabidopsis, rice and maize, used for phylogenetic analysis of polyamine metabolic pathway genes in barley.

|  |  |  |
| --- | --- | --- |
| **Class** | **Gene name** | **Accesion number** |
| ADC | *OsADC1* | Os04g01690.3 |
| *OsADC2* | Os06g04070.1 |
| *ZmADC* | NM001323076 |
| *AtADC1* | AT2G16500 |
| *AtADC2* | AT4G34710 |
| ODC | *OsODC1* | Os02g28110.1 |
| *OsODC2* | Os04g04980 |
| *OsODC3* | Os09g37120 |
| *ZmODC* | NM 001148682 |
| CuAO | *OsCuAO1* | EEC82302.1 |
| *OsCuAO2* | EEC80539.1 |
| *OsCuAO3* | CAD39884.2 |
| *OsCuAO7* | EAZ31082.1 |
| *ZmCuAO1* | NP\_001145964.1 |
| *ATAO1* | At4g14940 |
| *AtCuAO1* | At1g62810 |
| *AtCuAO2* | At1g31710 |
| *AtCuAO3* | At2g42490 |
| *AtCuAO8* | At1g31670 |
| SPDS/SPMS | *OsSPDS1* | Os07g22600.1 |
| *OsSPDS2* | Os06g33710.4.1 |
| *OsSPDS3* | ACD87085.1 |
| *ZmSPDS* | NM 001155838 |
| *AtSPDS1* | At1G23820 |
| *AtSPDS2* | NP\_973900.2 |
| *AtSPDS3* | BAB08415.1 |
| *AtSPDS4* | AAM64782.1 |
| *OsSPMS1* | Os06g33710.2 |
| *OsSPMS2* | Os02g15550.2 |
| *ZmSPMS* | AY730048 |
| *AtSPMS* | At5G53120 |
| SAMDC | *OsSAMDC1* | Os04g42095 |
| *OsSAMDC2* | Os02g39795 |
| *OsSAMDC3* | Os05g04990 |
| *OsSAMDC4* | Os09g25625 |
| *OsSAMDC5* | Os09g24600 |
| *OsSAMDC6* | Os05g13480 |
| *ZmSAMDC* | NM 001112243 |
| *AtSAMDC1* | At3G02470.1 |
| *AtSAMDC2* | At5G15950.1 |
| *AtSAMDC3* | At3G25570.1 |
| *AtSAMDC4* | At5G18930.1 |
| PAO | *AtPAO1* | NP196874.1; AT5G13700 |
| *AtPAO2* | AAL75899; ABI93934.1; At2g43020 |
| *AtPAO3* | NP191464.1; AT3G59050 |
| *AtPAO4* | NP176759.1; AT1G65840 |
| *AtPAO5* | NP194701.1; AT4G29720 |
| *OsPAO1* | XP015630114.1 |
| *OsPAO2* | BAF11161.2 |
| *OsPAO3* | XP015636130.1 |
| *OsPAO4* | XP015637015.1 |
| *OsPAO5* | XP015636452.1 |
| *OsPAO6* | BAF24924.2 |
| *OsPAO7* | BAF24925.1 |
| *ZmPAO1* | NP\_001105106.2 |

Table S2. Details of MEME motifs identified in the SAMDC genes of barley, Arabidopsis, rice and maize.

|  |  |  |  |
| --- | --- | --- | --- |
| Motif Number | Mtif Sequnece | Pfam database | |
| Family | Description |
| 1 | IIPEMEICDFDFEPCGYSMNAIHGSAFSTIHVTPEDGFSYA | SAM\_decarbox | Adenosylmethionine decarboxylase |
| 2 | QJDSVLDLARCTIVSELSNKQFDSYVLSESSLFVYPYKIVIKTCGTTKLL | SAM\_decarbox | Adenosylmethionine decarboxylase |
| 3 | LSLPLAAVKYSRGSFJFPGAQPFPHRSFSEEVAVLBRYFGG | SAM\_decarbox | Adenosylmethionine decarboxylase |
| 4 | GNAYVIGDPAKPGQKWHVYYATZHPEQPMVTLEMCMTGLDK | SAM\_decarbox | Adenosylmethionine decarboxylase |
| 5 | SYEVMGFDPSSLAYGDLVKRVLRCFGPSEFSVAVTIFGGHG | SAM\_decarbox | Adenosylmethionine decarboxylase |
| 6 | AIGFEGYEKRLEITFSEAPVF | SAM\_decarbox | Adenosylmethionine decarboxylase |
| 7 | KKASVFFKTSADGHTSCAKEMTKLSGISD | Na | Na |
| 8 | YDCBNMVEQELPGGGLLIYQSFTA | Na | Na |
| 9 | LSIPRJLELAE | Na | Na |
| 10 | DPNGRGLRALS | Na | Na |

Table S3. Details of MEME motifs identified in the PAO genes of barley, Arabidopsis, rice and maize.

|  |  |  |  |
| --- | --- | --- | --- |
| Motif number | Motif sequence | Pfam database | |
| Family | Description |
| 1 | EARDRIGGRVHTDYFFGVPVEMGASWVHG | Amino\_oxidase | Flavin containing amine oxidoreductase |
| 2 | PSWKIEAIYQLGVGVYNKIFLKFPKVFWP | Amino\_oxidase | Flavin containing amine oxidoreductase |
| 3 | DATDILVSRWGSDRFFLGSYS | Amino\_oxidase | Flavin containing amine oxidoreductase |
| 4 | HEVLQWYLCRMEAWFAADADEISLKNWDQEHVLPGGHGLMVRGYRPVINT | Na | Na |
| 5 | VYFTGEATSEKYNGYVHGAYLAGIDAAE | Amino\_oxidase | Flavin containing amine oxidoreductase |
| 6 | FEHKYPGSNVLLVTVAGREARRIEKQSDE | Na | Na |
| 7 | PVDMVVDYYKYDYEFAEPPRVTSLQNTVPLPTFSDFGDDVYFVADQRGYE | Na | Na |
| 8 | EDGSTYVADYVIVSVSLGVLKABJIKFEP | Amino\_oxidase | Flavin containing amine oxidoreductase |
| 9 | VCNENPLAPLIGRLGLPLYRTSGDNSVLYDHDLESYALFDKDGNQVPQEL | Na | Na |
| 10 | PSVIVIGAGISGISAAKRLSEASFEVLLJ | NAD\_binding\_8 | NAD(P)-binding Rossmann-like domain |

Table S4. Details of MEME motifs identified in the CuAO genes of barley, Arabidopsis, rice and maize.

|  |  |  |  |
| --- | --- | --- | --- |
| Motif number | Motif sequence | Pfam database | |
| Family | Description |
| 1 | EMFVPYMDPTEEWYYKTFLDAGEYGLGLNAFPLQPGADCPAN | Cu\_amine\_oxid | Copper amine oxidase, enzyme domain |
| 2 | WSKRBRSIEEEDIVLWYTVGLHHVPYQEDFPVMPTLSGGFELRPSNFFER | Cu\_amine\_oxid | Copper amine oxidase, enzyme domain |
| 3 | TLITEVRPDVSLVVRMVVTVGNYDYILDWEFKTDGSIKIEVSLTGILEVK | Cu\_amine\_oxid | Copper amine oxidase, enzyme domain |
| 4 | DDYPQRRAAFTKKNVWVTPYNKSEKWAGGLYABQSPGDDEL | Cu\_amine\_oxid | Copper amine oxidase, enzyme domain |
| 5 | YLDGHFAGQDGKPVKIENMICVFERYAGD | Cu\_amine\_oxid | Copper amine oxidase, enzyme domain |
| 6 | DGHFVRWANWEFHVGFDPRAGLVISLASVVD | Cu\_amine\_oxid | Copper amine oxidase, enzyme domain |
| 7 | ENTIAVVHDHFVTYRLDLDVDGTPNSFVK | Cu\_amine\_oxid | Copper amine oxidase, enzyme domain |
| 8 | TANFYARPIEGITVVVDLDNMAVIEFEDRK | Cu\_amine\_oxidN3 | Copper amine oxidase, N3 domain |
| 9 | PAELLVVNPNKKTRTGNPVGYRLVPGGAA | Cu\_amine\_oxid | Copper amine oxidase, enzyme domain |
| 10 | TAEEQAAAEALVKKYPPFIESVRRRGVDD | Na | Na |

Table S5. Details of MEME motifs identified in the SPDS/SPMS genes of barley, Arabidopsis, rice and maize.

|  |  |  |  |
| --- | --- | --- | --- |
| Motif number | Motif sequence | Pfam database | |
| Family | Description |
| 1 | FQGKSPYQEVLVFESSTYGKVLVLDGIVQLTEKDECAYQEMITHLPLCSI | Spermine\_synt\_N | Spermidine synthase tetramerisation domain |
| 2 | YDAIIVDSSDPIGPAQELVEKPFFZTIARALRPGGVLCNQAESMWLHTHL | Spermine\_synth | Spermine/spermidine synthase domain |
| 3 | GDGGVLREIARHSSVESIDICEIDQLVIDVSKDFFPDLAVGFKDPRVQLH | Spermine\_synth | Spermine/spermidine synthase domain |
| 4 | GSVHYAWTSVPTYPSGVIGFLLCAKEGPPVBFLTPINPIEK | Spermine\_synth | Spermine/spermidine synthase domain |
| 5 | PLPPCCVKARAAAPESEAKCHATVVSGWFTEPRSRSGKTS | Na | Na |
| 6 | AMKAGREJRFYNSEMHRAAFVLPTFARRE | Na | Na |
| 7 | NPMWPGEAHSLKVEKIL | Spermine\_synt\_N | Spermidine synthase tetramerisation domain |
| 8 | VGDAVEFLRNAPEGK | Na | Na |
| 9 | ZDMLSICRZTF | Na | Na |
| 10 | PSPKKVLVIGG | Na | Na |

Table S6. Details of MEME motifs identified in the ODC and ADC genes of barley, Arabidopsis, rice and maize.

|  |  |  |  |
| --- | --- | --- | --- |
| Motif number | Motif Sequence | Pfam database | |
| Family | Description |
| 1 | DPVYTYHINLSVFTSIPDFWGIGQLFPIIPIHRLBERPAVDGVLSDLTCD | Na | Na |
| 2 | LQLPLIVRFPDVLKHRLESLHAAFDYAIKSTGYGSRYQGVYPVKCNQDRY | PSY3 | Shu complex component Psy3, DNA-binding description |
| 3 | LLLALAARGAGLBCAIVLEMEEELDJVVEPSRILYVNPVKG | Orn\_Arg\_deC\_N | Pyridoxal-dependent decarboxylase, pyridoxal binding domain |
| 4 | KLRTKHPGHFGSTSGEKGKFGLTAAQILEVVRKLKQJGMLDCLQLLHFHI | Orn\_Arg\_deC\_N | Pyridoxal-dependent decarboxylase, pyridoxal binding domain |
| 5 | STVFGPTCDSLDTVVTGYQLPEMSVGDWLVFDDMGAYTTASGSNFNGFAT | Orn\_DAP\_Arg\_deC | Pyridoxal-dependent decarboxylase, C-terminal sheet domain |
| 6 | RYFAETAFTLAARVIGKRTRGEVREYWIDDGLYGSLNCILMDHYVPRPRP | Orn\_DAP\_Arg\_deC | Pyridoxal-dependent decarboxylase, C-terminal sheet domain |
| 7 | AHMKVIDVGGGLGIDYDGSKSGESDMSVAYSLEEYAAAVVAAVRLVCDRK | Orn\_Arg\_deC\_N | Pyridoxal-dependent decarboxylase, pyridoxal binding domain |
| 8 | WSPDLSSALYNIDGWGAPYFIVNSDGNIAVRPHGAETLPGQDIDLAKVV | Na | Na |
| 9 | HLEYAAEVGVNLTTYDSEEEVAKVKRCHPGCELLLRIKAPD | Orn\_Arg\_deC\_N | Pyridoxal-dependent decarboxylase, pyridoxal binding domain |
| 10 | HNLFGGPSVVRVSQSDGPHCFAVTRAVAGPSSADVLRAMQHEPELMFZVL | Na | Na |

Table S7. Ka and Ks values and estimated divergence time for tandemly duplicated barley polyamine metabolic pathway genes.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Gene pair** | **Ka** | **Ks** | **Ka/Ks** | **T(MYA)** | **Mode of duplication** |
| *HvPAO6*/ *HvPAO3* | 0.026915 | 0.25214 | 0.106745 | 19.39539 | Tandem |
| *HvPAO7/ HvPAO8* | 0.18683 | 1.892623 | 0.098715 | 145.5864 | Tandem |
| Average | 0.1068725 | 1.0723815 | 0.102730 | 82.49088 |  |

Table S8. Ka and Ks values and estimated divergence time for segmentally duplicated barley polyamine metabolic pathway genes.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Gene pair** | **Ka** | **Ks** | **Ka/Ks** | **T(MYA)** | **Mode of duplication** |
| *HvPAO2/ HvPAO1* | 0.192744 | 0.4279 | 0.450443 | 32.91536 | Segmental |
| *HvSPMS1/ HvSPMS2* | 0.227914 | 1.118458 | 0.203775 | 86.03525 | Segmental |
| *HvODC1/ HvODC2* | 0.167863 | 0.232121 | 0.723168 | 17.85549 | Segmental |
| *HvSAMDC2/ HvSAMDC3* | 0.163407 | 0.958405 | 0.170499 | 73.72343 | Segmental |
| *HvCuAO6/ HvCuAO7* | 0.075179 | 1.080265 | 0.069593 | 83.09732 | Segmental |
| *HvCuAO2/ HvCuAO3* | 0.025881 | 0.198433 | 0.130429 | 15.2641 | Segmental |
| Average | 0.142165 | 0.669264 | 0.29132 | 51.4818 |  |

Table S9. Ka, Ks and Ka/Ks values for each paralogous gene pair of the duplicated polyamine metabolic pathway genes in barley.

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Seq\_1 | Seq\_2 | Ka | Ks | Ka\_Ks | EffectiveLen | AverageS-sites | AverageN-sites | cN | cS | pN | pS |
| HvPAO6 | HvPAO3 | 0.026914752 | 0.252140075 | 0.106745 | 1485 | 350.25 | 1134.75 | 30 | 75 | 0.026438 | 0.214133 |
| HvPAO2 | HvPAO1 | 0.192744478 | 0.427899647 | 0.450443 | 1479 | 356.25 | 1122.75 | 190.8333 | 116.1666667 | 0.16997 | 0.326082 |
| HvPAO7 | HvPAO8 | 0.186830014 | 1.892623063 | 0.098715 | 1464 | 354.4167 | 1109.583 | 183.5 | 244.5 | 0.165377 | 0.689866 |
| HvSPMS1 | HvSPMS2 | 0.227913581 | 1.118458274 | 0.203775 | 1155 | 278.1667 | 876.8333 | 172.3333 | 161.6666667 | 0.196541 | 0.581186 |
| HvODC1 | HvODC2 | 0.167862806 | 0.232121392 | 0.723168 | 540 | 137.75 | 402.25 | 60.5 | 27.5 | 0.150404 | 0.199637 |
| HvSAMDC2 | HvSAMDC3 | 0.163406946 | 0.958404533 | 0.170499 | 1149 | 277.25 | 871.75 | 128 | 150 | 0.146831 | 0.541028 |
| HvCuAO6 | HvCuAO7 | 0.075178784 | 1.080265105 | 0.069593 | 1683 | 380.5833 | 1302.417 | 93.16667 | 217.8333333 | 0.071534 | 0.572367 |
| HvCuAO2 | HvCuAO3 | 0.025881369 | 0.198433278 | 0.130429 | 525 | 131.9167 | 393.0833 | 10 | 23 | 0.02544 | 0.174352 |

Table S10. The kmeans clustering of protein-interaction analysis of polyamine metabolic pathway genes in barley.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| #clustering method | cluster number | cluster color | gene count | protein name | protein identifier | protein description |
| kmeans | 1 | Red | 18 | HvCuAO3 | 4513.MLOC\_70980.2 | Uncharacterized protein; Amine oxidase; Belongs to the copper/topaquinone oxidase family |
| kmeans | 1 | Red | 18 | MLOC\_12946.1 | 4513.MLOC\_12946.1 | Uncharacterized protein; Aldehyde dehydrogenase; Belongs to the aldehyde dehydrogenase family |
| kmeans | 1 | Red | 18 | MLOC\_17787.2 | 4513.MLOC\_17787.2 | Aldedh domain-containing protein; Uncharacterized protein |
| kmeans | 1 | Red | 18 | MLOC\_18180.1 | 4513.MLOC\_18180.1 | Uncharacterized protein |
| kmeans | 1 | Red | 18 | MLOC\_19387.1 | 4513.MLOC\_19387.1 | Uncharacterized protein |
| kmeans | 1 | Red | 18 | MLOC\_34526.1 | 4513.MLOC\_34526.1 | Predicted protein; uncharacterized protein; Predicted protein; Belongs to the aldehyde dehydrogenase family |
| kmeans | 1 | Red | 18 | MLOC\_60513.1 | 4513.MLOC\_60513.1 | Aminotran\_1\_2 domain-containing protein; Uncharacterized protein |
| kmeans | 1 | Red | 18 | MLOC\_76303.1 | 4513.MLOC\_76303.1 | Predicted protein; uncharacterized protein; Uncharacterized protein |
| kmeans | 1 | Red | 18 | MLOC\_77509.4 | 4513.MLOC\_77509.4 | Uncharacterized protein |
| kmeans | 2 | Green | 9 | MLOC\_15403.1 | 4513.MLOC\_15403.1 | Uncharacterized protein |
| kmeans | 2 | Green | 9 | MLOC\_24740.1 | 4513.MLOC\_24740.1 | Uncharacterized protein |
| kmeans | 2 | Green | 9 | MLOC\_35821.1 | 4513.MLOC\_35821.1 | Ornithine aminotransferase; Uncharacterized protein; Belongs to the class-III pyridoxal-phosphate-dependent aminotransferase family |
| kmeans | 2 | Green | 9 | MLOC\_61790.1 | 4513.MLOC\_61790.1 | Cn hydrolase domain-containing protein; Uncharacterized protein |
| kmeans | 2 | Green | 9 | MLOC\_63263.1 | 4513.MLOC\_63263.1 | Predicted protein; uncharacterized protein; Uncharacterized protein |
| kmeans | 2 | Green | 9 | MLOC\_65968.1 | 4513.MLOC\_65968.1 | Uncharacterized protein; Belongs to the arginase family |
| kmeans | 2 | Green | 9 | MLOC\_7062.1 | 4513.MLOC\_7062.1 | Uncharacterized protein |
| kmeans | 3 | Blue | 11 | MLOC\_15895.1 | 4513.MLOC\_15895.1 | PNP\_UDP\_1 domain-containing protein; Uncharacterized protein |
| kmeans | 3 | Blue | 11 | MLOC\_5973.1 | 4513.MLOC\_5973.1 | Predicted protein; uncharacterized protein; Uncharacterized protein |
| kmeans | 3 | Blue | 11 | MLOC\_64689.1 | 4513.MLOC\_64689.1 | Aminotran\_1\_2 domain-containing protein; Uncharacterized protein; ACC synthase |
| kmeans | 3 | Blue | 11 | MLOC\_65908.2 | 4513.MLOC\_65908.2 | Aminotran\_1\_2 domain-containing protein; Uncharacterized protein |
| kmeans | 3 | Blue | 11 | MLOC\_80387.3 | 4513.MLOC\_80387.3 | S-adenosylmethionine synthase 4; Catalyzes the formation of S-adenosylmethionine from methionine and ATP |

Table S11. Details of primers used for PCR amplification of the identified polyamine metabolic pathway gene in barley.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Name of gene** | **gDNA (bp)** | **Primer \_Frw** | **Primer \_Rev** | **Position \_Start** | **Position \_Stop** | **Product size** |
| *HvSAMDC1* | 1329 | ATTGGGTTTGAGGGCTACGAGAAG | AAGATGGTGACGGCGACTGAGAAG | 495 | 1337 | 866 |
| *HvSAMDC2* | 1421 | GTTTGACTCGTATGTCCTTTCTGA | CTCCTCATCTTCTTACCATCCCC | 567 | 1550 | 984 |
| *HvSAMDC3* | 1353 | CCTGTGGGACTACCATGCTT | TTGATGGCGTTCATGGAGTA | 664 | 1135 | 472 |
| *HvODC1* | 1756 | GGTGAAGGACAAGAAGGTGCTGG | AGGTGGAGAAGCCATTGAAGTTG | 348 | 1495 | 1148 |
| *HvODC2* | 721 | GGCAGTACTTCGCCGAGA | GAGTAGGCCAAGTGCGTCTT | 463 | 844 | 382 |
| *HvADC1* | 2022 | CTACCTTACCAAAGCCAAGCCCG | CTTCTCCCACACCTCCTTCTCC | 951 | 2304 | 1354 |
| *HvCuAO2* | 2112 | GTTCGTGTCGGAGGTATTCGTG | CCTGGTAGGGTATGTGGTGGATG | 12497 | 13925 | 1429 |
| *HvCuAO3* | 558 | GTCATCTCACTAGCTTCGATCCAC | CTCCAGGAGACCAGTAAGAGACAC | 52 | 719 | 668 |
| *HvCuAO4* | 1879 | ATCCATGACCACTATGTCACCTTC | ACGCAGACGGGGAGATCCTTCT | 2536 | 3416 | 881 |
| *HvCuAO6* | 2133 | AATATGGCACAACTATTGCTCCT | AGACTTGTATTTAGGAACGGAGG | 3208 | 4573 | 1366 |
| *HvCuAO7* | 1760 | CTCTAATCTTTTGCCGAACCGAG | CTTCTCATCGCTCTTGTATGGTGT | 574 | 2664 | 2091 |
| *HvPAO6* | 1823 | CGACTACTACCAGCACGACTTC | CACATTTTCTTCTTGGCACAGTTG | 3785 | 4886 | 1102 |
| *HvPAO3* | 1688 | GTCCCAGAGTCATCATCGTCGG | TGCTTTCCCTTGACATCGTATTTG | 1120 | 4235 | 3116 |
| *HvPAO2* | 1912 | ATGGTCAACTCCACCCTCAAGC | CATCCCGTAGTAGCCTCTCCTG | 470 | 3433 | 2964 |
| *HvPAO1* | 1988 | TTTATAGATGTAGCATTACTCCTTTG | CACATTCTCTTCTGAGCACACTTG | 41 | 2540 | 2500 |
| *HvPAO9* | 1496 | CTACTGAACACGCAGCCACTCG | CGGTGAAATAAACCCTCCCAACGG | 2236 | 3069 | 834 |
| *HvPAO4* | 2389 | ATGACACTAATGGCTCTCAAGTCC | CCTCATCCGACATCTTTTCAATG | 3391 | 4472 | 1082 |
| *HvPAO7* | 2327 | CATCGAGGACGGCACACAAT | GCCTTTCCTCATCAGCAACC | 2304 | 3008 | 705 |
| *HvPAO8* | 2258 | TGTATGCGTGGAAGACGGGACA | ACAGGTCAGAGATACCGAGCTGC | 4019 | 4778 | 760 |
| *HvPAO5* | 3535 | CTGAGTTTGCCGACCATCGTCTC | GCTCCTCTTGATTCTCTTCACCC | 1960 | 3107 | 1148 |
| *HvSPDS1* | 1696 | GATGATTACCCACCTTCCTCTCTG | TAGTTCACCGAGCCCTTGAAAAC | 461 | 922 | 462 |
| *HvSPMS1* | 1692 | GTTTTGGTTATTGGAGGTGGAGAT | GATTTATGGGTGCCAGGAAGTTGA | 2685 | 5301 | 2617 |
| *HvSPMS2* | 5130 | CTGACTGACAAGGATGAATGTGC | ACCTCCCGACAGATAGAAAGCAT | 2607 | 3677 | 1071 |

Table S12. Details of primers used for gene expression analysis using qPCR for the identified polyamine metabolic pathway gene in barley.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Gene name** | **Transcript ID** | Primer\_for | Primer\_rev | Product size |
| *HvSAMDC1* | HORVU5Hr1G064040.8 | TACTCGATGAACGGCGTCTG | CTGTAAACCAGGGAGCCAGG | 119 |
| *HvSAMDC2* | HORVU6Hr1G056110.3 | GGCGAGAGGCTGAATGTTGG | ATCTTGGCGACCCACTGGA | 127 |
| *HvSAMDC3* | HORVU2Hr1G086140.5 | ACCAGAGCTTTACCGCGAAT | CCTTCCTTGACCAGAGGGTG | 115 |
| *HvPAO1* | HORVU4Hr1G071450.1 | TACTACGGAGTGTGGCAGGA | GAACATGCTCCTCAGCACCT | 150 |
| *HvPAO2* | HORVU7Hr1G090410.1 | TCCAGGAGAGGCTACTACGG | CGTAGATATCGGTGGCGTCG | 199 |
| *HvPAO3* | HORVU7Hr1G118260.1 | AGCTCTGGTGCTCGTTGTAGC | CGAACTTGGTCTTGTGGATGC | 191 |
| *HvPAO4* | HORVU2Hr1G103220.3 | TCTGGCCTAACGTGGAGTTC | CGGCCTCATCCGACATCTTT | 156 |
| *HvPAO5* | HORVU3Hr1G066920.1 | TCGGCAAACTCAGACGTGAA | CGGATTGTCATAGTGGGCG | 143 |
| *HvPAO6* | HORVU7Hr1G118240.1 | GTTTCCTGGGAAGGAGGTGC | TGCTCCCCGGTGAAGTAAAC | 165 |
| *HvPAO7* | HORVU2Hr1G121060.1 | GTGCCTACTCGTCTGGGATG | TAGGTGCGGCAAATCTGGAG | 145 |
| *HvPAO8* | HORVU2Hr1G121050.1 | CTCGTGTGACTTGGTCGGAA | GGTCAGAGATACCGAGCTGC | 191 |
| *HvPAO9* | HORVU6Hr1G091060.1 | AGCAACAATCAGACAAGCAGAC | CCGATAGGCCAGTTGGAGAAG | 154 |
| *HvSPMS1* | HORVU5Hr1G052890.2 | AGGGTTCTGTCCACTATGCC | GTGCCAGGAAGTTGACTGGT | 105 |
| *HvSPMS2* | HORVU7Hr1G079430.2 | GCCCAGGAACTTGTGGAGAA | GCCCTTGAATACCTCCCGAC | 150 |
| *HvSPDS1* | HORVU7Hr1G055560.1 | AAGCCTTTCTTCCAGTCCGT | GAGCAGAGCATGAAACCTTACG | 200 |
| *HvCuAO2* | HORVU4Hr1G074530.5 | AAGGCCAAGGGGACGGATTA | GTCGATTTGAAAGCCCCTGC | 111 |
| *HvCuAO3* | HORVU0Hr1G009050.1 | GGCACGGTCATCTCACTAGC | CATGTACGGCACGAAGACCT | 102 |
| *HvCuAO4* | HORVU2Hr1G012710.2 | ACACGCTGGCTACTTGGAC | ACGTAAATCAGACGGCTCACAT | 111 |
| *HvCuAO6* | HORVU6Hr1G053060.9 | CGTATGGACATGGCAGTGGA | ACAATCACGCATGGCCTGTA | 162 |
| *HvCuAO7* | HORVU2Hr1G082420.5 | GCCTCCTCTAAAGGGATACCCA | TCAGGAGATTTTCCAGCGGC | 122 |
| *HvADC1* | HORVU1Hr1G002090.11 | CTCAACGAGAAGCCGACTCA | TAGTAGCCGTCGCTCTCAGG | 134 |
| *HvODC1* | HORVU5Hr1G084750.1 | CTTCCATGCGTGGAGGTGAT | CGTAGTGGTCCATGGGGATG | 166 |
| *HvODC2* | HORVU7Hr1G032100.1 | GAGATGAACGTGGGGGAGTG | GAGTAGGCCAAGTGCGTCTT | 116 |
| *ACTB* (actin) | AY145451 | AGCAACTGGGATGACATGGAG | CGTACATGGCAGGAACATTG | 172 |