

|                  |                                                                                   |     |
|------------------|-----------------------------------------------------------------------------------|-----|
| osa_Os08g0434300 | .....GSSELGRNASLRASVAPRIVPRAK                                                     | 24  |
| zma_100193663    | .....MASTVTFNEVSFAALIQKPNLGAISYAGLKMPASVSSGSSSELGWNASLRFAVTPRIVPKTK               | 65  |
| ath_At3g47520    | .....MATATASLIFSIVSSSYSKASSIPHSRLQSVKFNSVPSFTGLKSTSLISGSSSLAKTIRGSVTRAQ           | 68  |
| gmx_100783173    | KAFAPFATFTTIGTSGLQGRNSLIPQIKSSGLKFNSQNLKSCGLKAMSSVRCESSSFLVNKTGAIRASFAASKAKE      | 80  |
| nta_107783258    | KARTSRTTFSVGSATSLGCKGSSVSQSKAFGVKFNSKNLRSFSGLKAFATTVSYSESSSFLGKE SVAVIKQSTITPKAKE | 80  |
| sly_101258932    | KARTSRTTISVGSATSLGCKGSSISQSKAFGVKFNSKNLRSFSGLKAFATTVSCESSSFLGKE SIAAIKQSTITPKAQKG | 80  |
| consensus        | S                                                                                 |     |
| osa_Os08g0434300 | S...GSQISPEASYKVFVLGAAGGICQPIGLILIKMSPIVSLNLYDIANVKGVAADLSHCNTPSOVLDFTCPSELANCL   | 100 |
| zma_100193663    | S...GSQISPCASYKVFVLGAAGGICQPIGLILIKMSPIVSLNLYDIANVKGVAADLSHCNTPSOVLDFTCPSELANCL   | 141 |
| ath_At3g47520    | TSDDKPYGFKINASYKVFVLGAAGGICQPIGLILIKMSPIVSLNLYDIANVKGVAADLSHCNTPSOVLDFTCPSELANCL  | 148 |
| gmx_100783173    | NDQNFNYSQPCASYKVFVLGAAGGICQPIGLILIKMSPIVSLNLYDIANVKGVAADLSHCNTPSOVLDFTCPSELANCL   | 160 |
| nta_107783258    | N.KGYGYFVQPCASYKVFVLGAAGGICQPIGLILIKMSPIVSLNLYDIANVKGVAADLSHCNTPSOVLDFTCPSELANCL  | 159 |
| sly_101258932    | N.RGYVSCVQPCASYKVFVLGAAGGICQPIGLILIKMSPIVSLNLYDIANVKGVAADLSHCNTPSOVLDFTCPSELANCL  | 159 |
| consensus        | asykva lga ggigqpl ll kmsplvs l lydianvkgvaad shcntp v dftg sela cl               |     |
| osa_Os08g0434300 | KGVVVVVIFAGVPRKPGMTRDDLFNINASTIVKTLVEAVADNCPDAFTLISNPVNSTVPIAAEVLKKGVYDPKKLFGVT   | 180 |
| zma_100193663    | KGVVVVVIFAGVPRKPGMTRDDLFNINASTIVKTLVEAVADNCPDAFTLISNPVNSTVPIAAEVLKKGVYDPKKLFGVT   | 221 |
| ath_At3g47520    | KGVVVVVIFAGVPRKPGMTRDDLFNINASTIVKTLVEAVADNCPDAFTLISNPVNSTVPIAAEVLKKGVYDPKKLFGVT   | 228 |
| gmx_100783173    | KGVVVVVIFAGVPRKPGMTRDDLFNINASTIVKTLVEAVADNCPDAFTLISNPVNSTVPIAAEVLKKGVYDPKKLFGVT   | 240 |
| nta_107783258    | KGVVVVVIFAGVPRKPGMTRDDLFNINASTIVKTLVEAVADNCPDAFTLISNPVNSTVPIAAEVLKKGVYDPKKLFGVT   | 239 |
| sly_101258932    | KGVVVVVIFAGVPRKPGMTRDDLFNINASTIVKTLVEAVADNCPDAFTLISNPVNSTVPIAAEVLKKGVYDPKKLFGVT   | 239 |
| consensus        | k v vvvipagvprkpqmttrcdlfnina iv lv ava p afi iisnpvnstvpiaaevlk kgvy pkkllfgvt   |     |
| osa_Os08g0434300 | TLVVVFANTFVQAKKNLRLIDVDPVVGGHAGTITLPLSKTKPSTFTDEETDEELTKRIONAGTEVVFAKAGAGSATLS    | 260 |
| zma_100193663    | TLVVVFANTFVQAKKNLRLIDVDPVVGGHAGTITLPLSKTKPSTFTDEETDEELTKRIONAGTEVVFAKAGAGSATLS    | 301 |
| ath_At3g47520    | TLVVVFANTFVQAKKNLRLIDVDPVVGGHAGTITLPLSKTKPSTFTDEETDEELTKRIONAGTEVVFAKAGAGSATLS    | 308 |
| gmx_100783173    | TLVVVFANTFVQAKKNLRLIDVDPVVGGHAGTITLPLSKTKPSTFTDEETDEELTKRIONAGTEVVFAKAGAGSATLS    | 320 |
| nta_107783258    | TLVVVFANTFVQAKKNLRLIDVDPVVGGHAGTITLPLSKTKPSTFTDEETDEELTKRIONAGTEVVFAKAGAGSATLS    | 319 |
| sly_101258932    | TLVVVFANTFVQAKKNLRLIDVDPVVGGHAGTITLPLSKTKPSTFTDEETDEELTKRIONAGTEVVFAKAGAGSATLS    | 319 |
| consensus        | tlldvvrantfv q knl lid dvpv qghaqitilpllskt ps ftdee lt riqnagtevv akaqagsatls    |     |
| osa_Os08g0434300 | KAYAAARFVESSLRALDGDPLVYECEFTVQSELTLDLFFASRVKLGKNQVEALISSDLOGITEYEKALALALPEIKASTE  | 340 |
| zma_100193663    | KAYAAARFVESSLRALDGDPLVYECEFTVQSELTLDLFFASRVKLGKNQVEALISSDLOGITEYEKALALALPEIKASTE  | 381 |
| ath_At3g47520    | KAYAAARFVESSLRALDGDGLVYECSEFTVQSELTLDLFFASRVKLGKNQVEALISSDLOGITEYEKALALALPEIKASTE | 388 |
| gmx_100783173    | KAYAAARFVESSLRALDGDGLVYECSEFTVQSELTLDLFFASRVKLGKNQVEALISSDLOGITEYEKALALALPEIKASTE | 400 |
| nta_107783258    | KAYAAARFVESSLRALDGDGLVYECSEFTVQSELTLDLFFASRVKLGKNQVEALISSDLOGITEYEKALALALPEIKASTE | 399 |
| sly_101258932    | KAYAAARFVESSLRALDGDGLVYECSEFTVQSELTLDLFFASRVKLGKNQVEALISSDLOGITEYEKALALALPEIKASTE | 399 |
| consensus        | mayaaarfvesslral qd dvyec v s lpffasr k q q e i dl q ye kal lk el si              |     |
| osa_Os08g0434300 | KGIEFVHKQOTFAASV                                                                  | 356 |
| zma_100193663    | KGIAFVHKQOTFAASV                                                                  | 397 |
| ath_At3g47520    | KGVAFVHKQOTFAAN                                                                   | 403 |
| gmx_100783173    | KGIAFVHKQOTFAA...                                                                 | 413 |
| nta_107783258    | KGIRFVHKQOTFAA...                                                                 | 412 |
| sly_101258932    | KGIRFVHKQOTFAA...                                                                 | 412 |
| consensus        | kq f k aa                                                                         |     |

### Supplementary information, Figure S3 Amino acid sequence alignments of SOM410.

Amino acid sequence alignments of SOM410 in *Arabidopsis thaliana* (ath), *Zea mays* (zma), *Solanum lycopersicum* (sly), *Nicotiana tabacum* (nta), *Glycine max* (gmx), and *Oryza sativa* (osa). The red line indicates the malate dehydrogenase domain. Dark blue and cyan shading indicate 100% and > 50% conserved amino acid residues, respectively. The red, blue and green triangles indicate the mutation sites of *som410*, *som430*<sup>+/−</sup> and *som2167*, respectively.