Supplementary Material

**The collaborative mode by** ***P******mSVPs* and *PmDAMs* reveals neofunctionalization in the switch of the flower bud development and dormancy for *Prunus mume***

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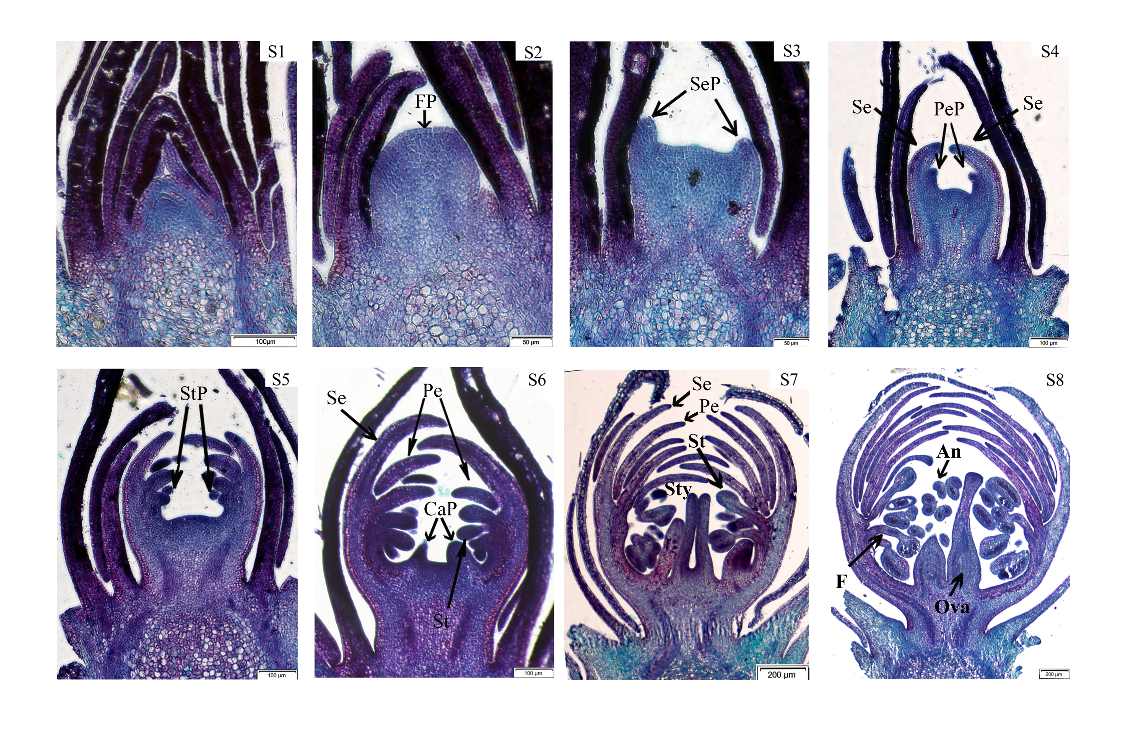
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# 1 Supplementary Figures and Tables

## 1.1 Supplementary Figures

**Supplementary Figure 1.** General flower bud differentiation sections of *P. mume*. The flower bud development was divided into eight stages (S1-8): undifferentiation (S1), flower primordium formation (S2), sepal initiation (S3), petal initiation (S4), stamen initiation (S5), pistil initiation (S6), ovule development (S7), anther development (S8). The letters had different meanings. FP: Flower primordiu; SeP: Sepal primordium; Se: Sepal; PeP: Petal primordium; Pe: Petal; StP: Stamen primordium; St: Stamen; CaP: Carpel primordium; Ca: Carpel; Sty: Style; An: Anther; F: Filament; Ova: Ovary; Ovu: Ovule; Po: Pollen.



## 1.2 Supplementary Tables

**Supplementary Table 1.**Primers used for cloning.

|  |  |  |  |
| --- | --- | --- | --- |
| **Gene** | **Forward primer** | **Reverse primer** | **Annealing temperature** |
| PmSVP1 | 5'AGATCTATGGCGAGGGAGAAGATTCAGA3' | 5'CACGTGTTAACCAGAGTAAGGTAACCCCAAT3' | 61 ℃ |
| PmSVP2 | 5'AGATCTATGACGAGGAGGAAAATCCAGATCAA3' | 5'GGTGACCTCATATCCCGCTAGGAAAAGCT3' | 60 ℃ |
| *PmDAM1* | 5'ATGAAAATGATGAGGGAGAAG3' | 5' TTATGGAAGCCCCAGTTTGAG3' | 52 ℃ |
| *PmDAM2* | 5'ATGGTGAAGACGATGAGGAAG3' | 5' TTAGGGAAGCCCCAGTTTGAG3' | 56 ℃ |
| *PmDAM3* | 5'ATGATGAGGAAGAAGATCAAG3' | 5' TTAAGGAAGCCCCAGTTCGAG3' | 51 ℃ |
| *PmDAM4* | 5'ATGGTGAAAATGATGAGGGAG3' | 5' TTAGGAACGCCCCAGTTTGAG3' | 54 ℃ |
| *PmDAM5* | 5'ATGATGAATAAGATCAAGATC3' | 5' TTAACGCCCCAGTTTGAGAGA3' | 47 ℃ |
| *PmDAM6* | 5'ATGGTGAAAATGATGAGGGAG3' | 5' CTAGGGAAGCCCCAGTTTGAG3' | 59 ℃ |

## Supplementary Table 2. Primers used for real-time quantitative RT-PCR.

|  |  |  |
| --- | --- | --- |
| **Gene** | **Forward primer** | **Reverse primer** |
| *PP2A2* | ATATAGCTGCTCAGTTCAACC | AAAAACAGTCACCACATTCTT |
| *PmSVP1* | CCACTGGAAAACTCTTTGAATACG | CAAGAGATGGTTGTTCTATTTTCG |
| *PmSVP2* | TGTGATGCTGAGATTGCTCTTGTAG | CAGGTGATGCCTTTCAATTACTTG |
| *PmDAM1* | AGTATGAAGGATGTTATTCAA | CTTAAGTTCCTTGCTCAATCT |
| *PmDAM2* | AACCAGCTACGGCAGAGGATG | AGATTCAGATGACATGCCTT |
| *PmDAM3* | TCGGATTGAGCAAGGAACTGG | CATTCTCAGTTCTTCCTTTGT |
| *PmDAM4* | ACCCTTGTCCGTGTGATGGAA | ATCACCATCTGATTGTTGCCT |
| *PmDAM5* | AGGCTGAATAATAATATTGAA | TTAACGCCCCAGTTTGAGAGA |
| *PmDAM6* | AACCAACAACCAGTTAAGGCATA | CAATTACGGCAGATTCAGATGA |

**Supplementary Table 3.** Primer used in PCR reaction for Y2H assays.

|  |  |
| --- | --- |
| **Gene** | **Sequence 5’-3’** |
| BK-PmSVP1-F | CATGGAGGCCGAATTCATGGCGAGGGAGAAGATTCA |
| BK-PmSVP1-R | GCAGGTCGACGGATCCTTAACCAGAGTAAGGTAAC |
| BK-PmSVP2-F | CATGGAGGCCGAATTCATGACGAGGAGGAAAATCCA |
| BK-PmSVP2-R | GCAGGTCGACGGATCCTCATATCCCGCTAGGAAAAG |
| BK-PmDAM1-F | CATGGAGGCCGAATTCATGAAAATGATGAGGGAGAAG |
| BK-PmDAM1-R | GCAGGTCGACGGATCCTTATGGAAGCCCCAGTTTGAG |
| BK-PmDAM5-F | CATGGAGGCCGAATTCATGATGAATAAGATCAAGATC |
| BK-PmDAM5-R | GCAGGTCGACGGATCCTTAACGCCCCAGTTTGAGAGA |
| AD-PmSVP1-F | GGAGGCCAGTGAATTCATGGCGAGGGAGAAGATTCA |
| AD-PmSVP1-R | CGAGCTCGATGGATCCTTAACCAGAGTAAGGTAAC |
| AD-PmSVP2-F | GGAGGCCAGTGAATTCATGACGAGGAGGAAAATCCA |
| AD-PmSVP2-R | CGAGCTCGATGGATCCTCATATCCCGCTAGGAAAAG |
| AD-PmDAM1-F | GGAGGCCAGTGAATTCATGAAAATGATGAGGGAGAAG |
| AD-PmDAM1-R | CGAGCTCGATGGATCCTTATGGAAGCCCCAGTTTGAG |
| AD-PmDAM5-F | GGAGGCCAGTGAATTCATGATGAATAAGATCAAGATC |
| AD-PmDAM5-R | CGAGCTCGATGGATCCTTAACGCCCCAGTTTGAGAGA |

# 2 Supplementary Data

**Supplementary Data1.** The CDS sequences of two *PmSVPs* and six *PmDAMs*.

>PmSVP1

atggcgagggagaagattcagatcaagaagatcgacaacgccacggcgaggcaggtgaccttttccaagcggaggagagggcttttcaagaaggctcaggagctctccgttctctgtgatgcagatattgctcttatcatcttttcttccactggaaaactctttgaatacgccagctccagcacgaaggaaattctagaacgtcacaacttgcacgcaaagaatctctcgaaaatagaacaaccatctcttgagttacagctagtggagaacagcaactactctgcgttgagcaaggaaattacagcacaaagtcaacaacttaggcagataaggggagaagaaatccaaggattaaatttggaagaattgcagcaactggagaagtctcttgaagctggattgggccgcgtaatagagaaaaagggtgaaaagattatgaaagagatcagcgatctcgaaagcaatgcgatgcgattggttgaagagaatgaacggctgagacagcaagtgctggagaaacataatagccagaggccggttcgggccgattcagaaaacatggttatggaggagggtcagtcatcagagtctgtcaccaccaacctctgcaactctaacagcgctccgcaagactatgagagctcagatacatctctcaaattggggttaccttactctggttaa

>PmSVP2

atgacgaggaggaaaatccagatcaagaagatcgacaacacaacggcgaggcaggtgacgttttcgaaaaggaggagagggcttttcaagaaagcccaggagctctctactctctgtgatgctgagattgctcttgtagtcttctccgctactgggaagctctttgaattcaccagctccagcgtgcaacaagtaattgaaaggcatcacctgctttcttccgattttgacaagttgaatcatccatctcttgagctgcagtccttttgtatgtctccgcttgagagcagtacttccgccgcattgagcaaggaaattgcggagaaaacacatgagctgaggaagctaaggggagaagaactccaagaactaaacatgaaagagttgcaggaactagagaaactgctcggatcaggattgaggcgtgttagagatgcaaagtgtgaaattgttctgaaggagatcacctctcttaagtggaagggatcccaacttatgcaagaaaacaagcgattgaagcagatggcaaaccgacaggtccaaacacttgaacttgaacaaggccaatcctccgagccaataggcaatttcatccattcaaacccttcgcaagaccacgacagctctgacacttttctcaagttggggttagcttttcctagcgggatatga

>PmDAM1

atgaaaatgatgagggagaagatcaagatcaagaagattgacaacttgcctgcaaggcaagtgaccttctcaaagaggaggagagggatcttcaagaaagctgcagagttatctgttctgtgtgaatctgaggtggcagttgtcatcttttctgctactggcaagctttttgattattcaagctcaagtatgaaggatgttattgaaaggtaccaagcgcacataaatggtggtgaaaaatttaacgaacggtctattgagttgcagccagagtatgaaaaccacatcagattgagcaaggaacttaaggagaagagccgccagctgaggcagatgaaaggagaggatcttgaagagctgaattttgatgagttgcagaagttagaacaactggtggatgcaagccttggccgtgtgattgaaactaaggacgaacggattatgagtgagattatggcacttgaaagaaagagagctgagcttgtaaaagccaacaaacagctaaggcagaggatgttattcagaggaaatattggacctgagcttatgaagccggagaggttgaataataattttggtggtggaggagaagaagaaggtatgtcatctgaatctgctacctccaccacctgcaacagtgctccgagtctctctcttgaagatgactccgacgacgtcactttatctctcaaactggggcttccataa

>PmDAM2

atggtgaagacgatgaggaagaagatcaagatcaagaagattgactacttgcctgcaaggcaggtgaccttctcaaagaggaggagagggatcttcaaaaaagctgaggagctatctgttctgtgtgaatctgaggtggcagttgtcatcttttctgctactggcaagctttttgattattcaagctcaagtacaaagaatgttgttgaaaggtataaagcgcacacaaatggtgtcgaaaaatcggacgaactgtctgttgagctgcagctagaaattgaaaaccagatcagattgaacaaggaacttgcggagaagagccgccagctgaggcagatgagaggagaggatcttgaagagctgaatattgatgagttgcagaagttagaacaactggtggaggcaagccttggccgtgtgattgaaactaaggaagaactgattatgagtgagattatggcacttgaaagaaagggagctgagctggtagaagccaacaaccagctacggcagaggatggtgatgttatccagaggaaatattggacctgggcttacggagccggagaggttcattaataatattggagatggaggagaagaaggcatgtcatctgaatctgccacaaatgcaaccatcagcagctgcagcagtggtctcagtctctctcttgaagatgactgctcagacgtcactttagctctcaaactggggcttcccTaa

>PmDAM3

atgatgaggaagaagatcaagatcaagaagattgattgcttgcctgcaaggcaggtgactttctcaaagaggagaagagggatcttcaagaaagctgcagagctatctgttctgtgtgaatctaaggtggcagttgtcatattttctgctactggcaagctttttgattattcaagctcaagtatcaaggatgttattgaaagctacaaagcgcacaaaaatggtgtcaaaaaatcggacgaaccgtctgttgagctacagctagagaatgaaaatcacatcggattgagcaaggaactggaggagaagagccatcagctgaggcagatgaaagcagaggatcttgacgagctgaattttgatgagttgcagaagttagaacaactggtggacacaagccttagccgtgtgattgaaacaaaggaagaactgagaatgagtgagattatggcacttgaaagaaagggagctgagctggtagaagccaacaaccagctaaagcagacgatggtgatgttatccggaggaaatactggacctacgcttatggatccggagaggttgaatgataatgtcggaggtggaggagaagaagaaggcatgtcatctgaatctgctatctccaccacctgcaacagtgctctcagtctctccattggagatgactccgacgacgtcactttatctctcgaactggggcttccttaa

>PmDAM4

atgatgaggaagaagatcaagatcaagaagattgactacctgccagcaaggcaggtgacattctcaaagaggagaagagggatcttcaagaaagctgcagagctatctgttctgtgtgaatctgaggtggcagttgtcatcttttctgctactggcaagctttttgattattcaagctcaagtatcaaggatgttattgaaaggtacaaagcgcgcacaaatggtgtcgaaaaatcggatgaacagtctcttgagctgcagctggagaatgaaaaccgcatcaaactcagtacggaactcgaggagaagaaccgccagctgaggcggatgaaaggtgaggatcttgaagagctggatctggatgagttgctgaagttggaacaactggtggaagcaacccttgtccgtgtgatggaaactaaggaagaactgattatgagtgatattgtggcacttgataaaaagggaactgagctggtagaaggcaacaatcagatggtgatgttaagggacaggatggtgatgttatccaaaagaagtaccggacctgcgcttatggagccatctgactctgctacctccaccagctgcaacagtgctctgagtctttctcttgaagatgaatgctccgacgacgccattttatctctcgaactggggcgttcctaa

>PmDAM5

atgatgaataagatcaagatcaagaagattgactacttgcctgcaaggcaggtgaccttctcaaaaaggagaagagggctcttcaagaaagctgcagagctatctgttctgtgtgaatctgaggtggcagttgtcatcttttctgccactggcaagctttttgattattcaagctcaagtaccaaggatgttattgaaaggtacaacgcagacatgaatggtgtcgaaaaatcgaacaatcaagagattgagctgcagctggagaatgaaaaccacatcaaactgagtaaggaactcgagaagacgagccaccagctgaggcagatgaaaggtgaggatcttgaagggctgaatctggatgagttgctgaagttggaacaactggtggaagcaagccttggccgtgtcatggaaactaaggaagagctgattaagagtgagattatggaactcgaaagaaagggagctgagctagttgaagccaacagccagctaaggcagacgatggtgatgttatccggaggaaatactggacctgcgcttatggatccggagaggctgaataataatattgaaggtggaggagaagaagaaggcatgtcagctgaatctgctatctccaccacctgcaacagtgctgtcagtctctctcttgaagatgactcctccgatgaggtcactttgtctctcaaactggggcgttaa

>PmDAM6

Atggtgaaaatgatgagggagaagatcaagatcaagaagattgactacctgccagcaaggcaggttaccttttcaaagagaagaagagggctcttcaagaaagctgcagagctatcggttctgtgtgaatctgaggtggctgtcgtcatcttttctgccactgacaagctctttcattattcaagctcaagtaccgaggatgttattgaaaggtacaaagcgcacacaggtggtgccgaaaaatcagacaaacagtttcttgagctgcaactggagaatgaaaacaacatcaaactgagtaaggaactcgaggagaagagccgccagctgaggcagatgaaaggtgaggatcttgaagggctgaatctggatgagctgctgaagttagaacaagtggtggaagcaagccttggccgtgtgatagaaactaaggaagagctgattatgagtgcgattatggcactggagaaaaagggagctgagctggtagaaaccaacaaccagttaaggcataggatggtgatgttatccggaggaaatactggacctgcgtttgtggagccggagacgttgattactaatgttggaggtggaggacgagaagacgacatgtcatctgaatctgccgtaattgccacctccaccagctgcaacagtgctttcagtctctctcttgaagatgactgctccgatgtcactttatctctcaaactggggcttccctag

**Supplementary Data2.** The GeneBank accession numbers of genes used in alignment.

PmSVP1 (*P. mume*, AML81015.1); PmSVP2 (*P. mume*, AML81016.1); PpSVP1 (*P. persica*,XP\_020422316); PpSVP2 (*P. persica*,XP\_020409383); MdSVP (*M. domestica*, NP 001280915); PySVP (*P. pyrifolia*, AJW29050); PpsSVP (*P. pseudocerasus*, AKM27770); CsSVP1 (*C. sinensis*, XP\_028064640.1); CsSVP2 (*C. sinensis*, XP\_028076077.1); PmDAM1 (*P. mume*, BAK78921); PmDAM2 (*P. mume*, BAK78922); PmDAM3 (*P. mume*, BAK78923); PmDAM4 (*P. mume*, BAK78924); PmDAM5 (*P. mume*, BAK78920); PmDAM6 (*P. mume*, BAH22477); PpDAM1 (*P. persica*, ABJ96361); PpDAM2 (*P. persica*, ABJ96363); PpDAM3 (*P. persica*, ABJ96364); PpDAM4 (*P. persica*, ABJ96358); PpDAM5 (*P. persica*, ABJ96359); PpDAM6 (*P. persica*, ABJ96360); PpsDAM3 (*P. pseudocerasus*, AIU94275.1); PpsDAM4 (*P. pseudocerasus*, AIU94276.1); PpsDAM5 (*P. pseudocerasus*, AIU94277.1); PpsDAM6 (*P. pseudocerasu*s, AIU94278.1); PpyDAM1 (*P. pyrifolia*, BAM74184.1); PpyDAM2 (*P. pyrifolia*, BAM74183.1); PpyDAM3 (*P. pyrifolia*, BAM74167.1); PpyDAM4 (*P. pyrifolia*, BAM74166.1); PpyDAM5 (*P. pyrifolia*, BAI48075.1); PpyDAM6 (*P. pyrifolia*, BAI48074.1); MdDAM1 (*M. domestica*, AJW82923.1); MdDAM2 (*M. domestica*, AJW82922.1); MdDAM3 (*M. domestica*, AJW82921.1); CsDAM1 (*C. sinensis*, AIK35210.1); CsDAM2 (*C. sinensis*, AIK35209.1).

**Supplementary Data3.** The protein sequences of SVP and DAM proteins and other 17 type II MADS-box proteins in *P. mume*.

>PmSVP1

MAREKIQIKKIDNATARQVTFSKRRRGLFKKAQELSVLCDADIALIIFSSTGKLFEYASSSTKEILERHNLHAKNLSKIEQPSLELQLVENSNYSALSKEITAQSQQLRQIRGEEIQGLNLEELQQLEKSLEAGLGRVIEKKGEKIMKEISDLESNAMRLVEENERLRQQVLEKHNSQRPVRADSENMVMEEGQSSESVTTNLCNSNSAPQDYESSDTSLKLGLPYSG\*

>PmSVP2

MTRRKIQIKKIDNTTARQVTFSKRRRGLFKKAQELSTLCDAEIALVVFSATGKLFEFTSS

SVQQVIERHHLLSSDFDKLNHPSLELQSFCMSPLESSTSAALSKEIAEKTHELRKLRGEE

LQELNMKELQELEKLLGSGLRRVRDAKCEIVLKEITSLKWKGSQLMQENKRLKQMANRQVQTLELEQGQSSEPIGNFIHSNPSQDHDSSDTFLKLGLAFPSGI\*

>PmDAM1

MKMMREKIKIKKIDNLPARQVTFSKRRRGIFKKAAELSVLCESEVAVVIFSATGKLFDYS

SSSMKDVIERYQAHINGGEKFNERSIELQPEYENHIRLSKELKEKSRQLRQMKGEDLEEL

NFDELQKLEQLVDASLGRVIETKDERIMSEIMALERKRAELVKANKQLRQRMLFRGNIGP

ELMKPERLNNNFGGGGEEEGMSSESATSTTCNSAPSLSLEDDSDDVTLSLKLGLP\*

>PmDAM2

MVKTMRKKIKIKKIDYLPARQVTFSKRRRGIFKKAEELSVLCESEVAVVIFSATGKLFDY

SSSSTKNVVERYKAHTNGVEKSDELSVELQLEIENQIRLNKELAEKSRQLRQMRGEDLEE

LNIDELQKLEQLVEASLGRVIETKEELIMSEIMALERKGAELVEANNQLRQRMVMLSRGN

IGPGLTEPERFINNIGDGGEEGMSSESATNATISSCSSGLSLSLEDDCSDVTLALKLGLP\*

>PmDAM3

MMRKKIKIKKIDCLPARQVTFSKRRRGIFKKAAELSVLCESKVAVVIFSATGKLFDYSSS

SIKDVIESYKAHKNGVKKSDEPSVELQLENENHIGLSKELEEKSHQLRQMKAEDLDELNF

DELQKLEQLVDTSLSRVIETKEELRMSEIMALERKGAELVEANNQLKQTMVMLSGGNTGP

TLMDPERLNDNVGGGGEEEGMSSESAISTTCNSALSLSIGDDSDDVTLSLELGLP\*

>PmDAM4

MMRKKIKIKKIDYLPARQVTFSKRRRGIFKKAAELSVLCESEVAVVIFSATGKLFDYSSS

SIKDVIERYKARTNGVEKSDEQSLELQLENENRIKLSTELEEKNRQLRRMKGEDLEELDL

DELLKLEQLVEATLVRVMETKEELIMSDIVALDKKGTELVEGNNQMVMLRDRMVMLSKRSTGPALMEPSDSATSTSCNSALSLSLEDECSDDAILSLELGRS\*

>PmDAM5

MMNKIKIKKIDYLPARQVTFSKRRRGLFKKAAELSVLCESEVAVVIFSATGKLFDYSSSS

TKDVIERYNADMNGVEKSNNQEIELQLENENHIKLSKELEKTSHQLRQMKGEDLEGLNLDELLKLEQLVEASLGRVMETKEELIKSEIMELERKGAELVEANSQLRQTMVMLSGGNTGPALMDPERLNNNIEGGGEEEGMSAESAISTTCNSAVSLSLEDDSSDEVTLSLKLGR\*

>PmDAM6

MVKMMREKIKIKKIDYLPARQVTFSKRRRGLFKKAAELSVLCESEVAVVIFSATDKLFHY

SSSSTEDVIERYKAHTGGAEKSDKQFLELQLENENNIKLSKELEEKSRQLRQMKGEDLEG

LNLDELLKLEQVVEASLGRVIETKEELIMSAIMALEKKGAELVETNNQLRHRMVMLSGGN

TGPAFVEPETLITNVGGGGREDDMSSESAVIATSTSCNSAFSLSLEDDCSDVTLSLKLGL

P\*

>PpDAM1

MKMTREKIKIKKIDNLPARQVTFSKRRRGIFKKAAELSVLCESEVAVVIFSATGKLFDYS

SSSMKDVIERYQEHINGAEKFDEPSIELQPEKENHIRLSKELEEKSRQLRQMKGEDLEEL

NFDELQKLEQLVDASLGRVIETKDELIMSEIMALKRKRAELVEANKQLRQRASNYHNHMLSRGNIGPALMEPERLNNNIGGGGEEEGMSSESATSTTCNSAPSLSLEDDSDDVTLSLKLG

LP

>PpDAM2

MVKTMRKKIKIKKIDYLPARQVTFSKRRRGIFKKAEELSVLCESEVAVVIFSATGKLFDY

SSSSTKDVVERYQAHTNGVEKSDEPSVELQLEIENHIRLTKELEEKSRQLRQIKGEDLEE

LNFDELQKLEQLVDASLGRVIETEEELIMSEIMALERKGAELVEANNQLRQRMVMLSRGN

IGPAPTEPERFVNNIGGGGEEGMSSESATNATISSCSSGPSLSLEDDCSDVTLALKLGLP

>PpDAM3

MVKMMRKKIKIKKIDYLPARQVTFSKRRRGIFKKAAELSVLCESKVAVVIFSATGKLFDY

SSSSIKDVIERYKAHTNGVEKSDKPSVELQLENENQIGLSKELKEKSHQLRQMKAEDLEE

LNFDELQKLEQLVDASLGRVIETKEELRMSEIMALERKGAELVEANNQLRQTMMLSGGNTGPTLMEPERLSNNIGGGGEEEGMSSESAISTTCNSALSLSPSLGDDSDDVTLSLKLGLS

>PpDAM4

MVKMMREKIKIKKIDYLPARQVTFSKRRRGIFKKAAELSVLCESEVAVVIFSATGKLFDY

SSSSIKDVIERYEVRTNGVEKSDEQSLELQLENENHTKLSTELEEKNRQLRQMKGEDLEE

LDLDELLKLEQLVEATLVRVMETKEELIMSDIVALEKKGTELVEANNQMVMLRERMVMLSKRNTGPALMEPSESATSTSCNSALSLSLEDDCSDDVVLSLKLGLTVRAGR

>PpDAM5

MMRNKIKIKKIDYLPARQVTFSKRRRGLFKKAAELSVLCESEVAVVIFSATGKLLDYSSS

STKDVIERYNADINGVEKLNNQEIELQLENENHIKLSKELEEKSRQLRQMKGEDLEGLNL

DELLKLEQLVEASLGRVMETKEELIKSEIMALERKGTELVEANNQLRQTMVMLSGGNTGP

ALMDPERLNNNIEGGGEEEGMSAESAISTTCNSAVSLSLEDDSSDEVTLSLKLGR

>PpDAM6

MMREKIKIKKIDYLPARQVTFSKRRRGLFKKAAELSVLCESEVAVIIFSATDKLFDYSSS

STEDVIERYKAHTNDLEKSNKQFLELQLENENHIKLSKELEEKSRQLRQMKGEDLQGLNM

DELLKLEQLVEASLGRVIETKEELIMSEIMALEKKGAELVEANNQLRQKMAMLSGGNTGP

AFVEPETLITNVGGGGEEDGMSSESAIIATSTSCNSAHSLSLEDDCSDVTLSLKLGLP

>PpyDAM1

MVKRMKEKIKIRRIDYLPARQVTFSKRSRGILKKAEELSILCEAEVAVIIFSQTGKLFDY

SSSSTKDVIARYKSHTGGEKWDQITLHQLQLEKENTIRLGKELEDKTRKLRQMKGEDLQD

LDLDQLNKLEKLVKASIGRVIKTKEKKIMSEIMEHANKGAELIKANNQLKQRMVMLSAGGDIGPAGIMELDNLNNVGEEGVTSESATNVTTCSTSAFSLEDDCSDILSLKLGLP

>PpyDAM2

MKIKIRKIDYLPARQVTFSKRRRGIFKKAGELSILCESEVAVIIFSQTGKLFDFSSSSTK

DVIARYNSHVGGEKSDQPTLHQLQLEKENNIRLSKELEDKSCKLRQMKGVDLEDLDLDELQKLEKLVEASLGRVIQTKEEKITSDVMALEKKGAELIEANNQLSQKMVMLPGGDSGPEAILNNIGEESVTSESATNVTTFSNSSLSLEDDCSDTLSLKLGLP

>PpyDAM3

MVKRMNEKIKIRRIDYLPARQVTFSKRRRGIFKKAEELSILCESEVAVIIFSQTGKLFDY

SSSSTKDVIARYKLHTGGEKSDQITLHQLQSEKENTIRLSKELEDKTRKLRQMKGEDLQD

LDLYQLNKLEKLVEASVGRVIKTKEKKIMSEIMALTNKGAELIEANNQLKQRLVMLSARG

DIEPAAIMELENLNNVGEEGMTSESATNVTACSSSALSLEDDCSDILSLKLGLP

>PpyDAM4

MVERMKEKIKIRRIDYLPARQVTFSKRSRGILKKAEELSILCEAEVAVIIFSQTGKLFDY

SSSSTKDVIARYKSHTGGEKWDQITLHQLQLEKENTMRLSKELEDKTRKLRQMKGEDLQDLDLDQLNKLEKLVEASIGRVIKTKKKKIMSEIMAHANKGAELIDANNQLKQRVVMLSAGGDIGPAGIMELDNLNNVGEEGVTSESATNVTTCSSSAFSLEDDCSDILSLKLGLP

>PpyDAM5

MVKRMNEKIKIRRIDYLPARQVTFSKRRRGIFKKAEELSILCESEVAVIIFSQTGKLFDY

SSSSTKDVIARYKLHTGGEKSDQITLHQLQSEKENTIRLSKELEDKTRKLRQMKGEDLQD

LDLYQLNKLEKLVEASVGRVIKTKEKKIMSEIMALTNKGAELIEANNQLKQRLVMLSARG

DIEPAAIMELENLNNVGEEGMTSESATNVTACSSSALSLEDDCSDILSLKLGLP

>PpyDAM6

MKIKIRKIDYLPARQVTFSKRRRGIFKKAGELSILCESEVAVIIFSQTGKLFDFSSSSTK

DVIARYNSHVGGEKSDQPTLHQLLLEKENNIRLSKELEDKSCKLRQMKGVDLEDLDLGEL

QKLEKLVEASLGRVIQTKEEKITSEVMALEKKGAELIEANNQLSQKMVMLPGGDSGPEAI

LELENLNNIGEGSVTSESATNVTTFSNSSLSLEDDCSDTLSLKLGLP

>PpsDAM3

MVKMMRKKIKIKKIDSLPARQVTFSKRRRGIFKKAAELSVLCESKVAVVIFSATGKLFDY

SSSSTKDVIERYKAHTNGVEKSDKPSVELQLENENHIGLSNELEEKSHQLRQMKAEDLEE

LNFDELQQLEQLVDASLGRVIETKEELRMSEIMALERKGAELVEANNQLRQTVSNHHNHMVMLSGGNTGPELMEPERLNNNIGGGGEEEGMSTESAISTTCNSAHSLGDDSGNVILSLKLGLP

>PpsDAM4

MVKMKREKIKIKKIDYLPARQVTFSKRRRGIFKKAAELSVLCESEVAVVIFSPTGKLFDY

SSSSVKDVIKRYKARANGVEKSEESLELQLEHENRIKLSKELEEKNSQLRKMKGEDLEEL

DLDELLKLEKLVEATLVRVMETKEELIMSDIMVLEKKGTALVEANNQMVMLKERMVMLSKRNTGPELMEPSESATSTSCNSALSLSLEDDCSDDVILSLKLGRP

>PpsDAM5

MVRNKIKIKKIDYLPARQVTFSKRRRGLFKKAAELSVLCESEVAVVIFSATGKLFDYSSS

STKDVIERYNVHMNDVDKLNDQEIELQLENENHIKLSKELEEKSRQLRQMKGDDLEGLNLDELLKLEQLVEASLGRVMETKEELIKSEIMELERKGAELVEANNQLRQTMVMLTGGNTGPALMDPERLNNNIGGGGEEEGMSAESAISTTCNSAVSLSLEDDSSDEVTLSLKLGR

>PpsDAM6

MVKMMREKIKIKKIDYLPARQVTFSKRRRGLFKKAAELSVLCESEVAVVIFSATGKLFDY

SSSSIEDVIERYKAHTNGVQKSNKQFLELQLENENHIKLSKELEEKSRQLRQMKGEDLEG

LNLDELLKLEQLVEGSLGRVIETKEELIMSEIIALEKKGAELVETNNQLRQRMAMLSGGN

TGPALVEPETLNTNIGGGGEDGMSSESATMATSTSCNSALSLSLEDDCSDVTLSLKLGLP

>MdDAM1

MAREKIQIKKIDNATARQVTFSKRRRGLFKKAEELSVLCDADIALIIFSSTGKLFEYASS

SMKEILERHNLHSKNLDKLEQPSLELQLVENSNYSRLSKEIAAKSHQLRQMRGEEIQGLS

LEELQQLEKSLEAGLGGVVEKKSEKIMKEINDLQRNMNVQAMQLTEENERLRQQVVEKSNGRRLVHVDSENLITEEGQSSESVTNLCKSNSGPQDYDNSVTSLKLGCA

>MdDAM2

MVKIRKEKIKIRRIDYLPARQVTFSKRRRGIFKKAEELSILCESEVAVIIFSQTGKLFDF

SSSSWKRDIIHVNLIKLWSSPPDNQGELTSFPMFGIGQGHRNTKDVIARYKSHTGEKSNQ

SMLDQLQLEKENTIRLSKELEDKTRKLRHLKGEELQDLDLDELQKLEKLVEASHGRVMET

KGDELVEANNQLKQRMVMLSARGDIGPAAIMELENLNNGGEEGVTSESATNVTTSSNSPL

SLEDDCSDILSLKLGCAALTS

>MdDAM3

MKIKIKKIDYLPARQVTFSKRRRGIFKKAGELSILCESEVAVIIFSQTGKLFDFSSSRLW

SSPPXNQDELVSFPFVDSHAIESDKLIMHVNRRTKDVIARYNSHIGGEKSDQPTIHQLQL

EKENNIRLRKELEDKSCKLRQMKGVDLEDLDLDELQKLEKLVEASLGRVIQTKGAELIEA

NNQLSHRMVMYPRGDIGPEAILELENLNNIGEESXTSESTTNVTTCSNSSLSLEDDCSDI

LSLKLG

>CsDAM1

MVRQRIQIKKIDNVTSRQVTFSKRRKGLFKKAQELSTLCDAEIALIVFSATGKLFEFSSS

SMRQVIERHNLESGNLVNLNQPSLEQQLENSGCTILSKEVNKKIHELRQLRGEELQGLDA

EELKNLEKSLEGGLSRVLKTKGEIMEKEITARERKEARLVEENVWLKQKVPMEIVKIGQT

HDDQQGQSAEFITNNGSSAAPPQDNDSSDTSLKLGLPFPELN

>CsDAM2

MVRQRIQIKKIDNVTARQVTFSKRRRGLFKKAHELSTLCDAEIALIVFSATGRLFEYASS

STRQVIERHNLQPQNLVQLNQPSLELQLENSTRAMLSKEAEERTLELRQLRGEELHELGF

EELKKLEKSLEGGLSRVLKTKDDRVEKEIAALRRKEARLMEENAWSKQQVQMQIVNMGQPQEQGQSSESITNNGSTVAPPQDYDSSDTSLKLGLPYQS

>PmSVP1

MAREKIQIKKIDNATARQVTFSKRRRGLFKKAQELSVLCDADIALIIFSSTGKLFEYASS

STKEILERHNLHAKNLSKIEQPSLELQLVENSNYSALSKEITAQSQQLRQIRGEEIQGLN

LEELQQLEKSLEAGLGRVIEKKGEKIMKEISDLESNAMRLVEENERLRQQVLEKHNSQRP

VRADSENMVMEEGQSSESVTTNLCNSNSAPQDYESSDTSLKLGLPYSG\*

>PmSVP2

MTRRKIQIKKIDNTTARQVTFSKRRRGLFKKAQELSTLCDAEIALVVFSATGKLFEFTSS

SVQQVIERHHLLSSDFDKLNHPSLELQSFCMSPLESSTSAALSKEIAEKTHELRKLRGEE

LQELNMKELQELEKLLGSGLRRVRDAKCEIVLKEITSLKWKGSQLMQENKRLKQMANRQVQTLELEQGQSSEPIGNFIHSNPSQDHDSSDTFLKLGLAFPSGI\*

>PpSVP1

MEIEAAEEAEEAEEAEAEEEDRSMAREKIQIKKIDNATARQVTFSKRRRGLFKKAQELSV

LCDADIALIIFSSTGKLFEYASSSMKEILERHNLHAKNLSKIEQPSLELQLVENSNYSAL

SKEITAQSQQLRQIRGEEIQGLNLEELQQLEKSLEAGLGRVIEKKGEKIMKEISDLESNA

MRLVEENERLRQQVLEKHNSQKPVRADSENIVMEEGQSSESVTTNLCNSNSAPQDYESSD

TSLKLGLPYSG\*

>PpSVP2

MTRRKIQIKKIDNTTARQVTFSKRRRGLFKKAQELSTLCDAEIALVVFSATGKLFEYTSS

SVQQVIERHGLLSSNYDQLNQPSLELQSFGMSQLESSTSAALSKEIAESTHELRKLMGEE

LQELNMKELQELEKLLGSGLRRVRDAKGEFFLKEITSLKWKGSQMMQENKRLKQMANRQVQTLELEQGQSSEPIGDFIHSYPSQDHDSSDTSLKLGQAFPNGI\*

>PpySVP

MAREKIQIKKIDNATARQVTLSKRRRGLFKKAEELSVLCDADIALIIFSSTGKLFEYASA

SMEEILERHNLHSKNLDKLEQPSLELQLVENSNYSRLSKEIAAKSHQLRQMRGEEIQGLS

LEELQQLEKLLEAGLGGVVEKKSEKIMKEINDLQRNAMQLTEENERLRQQVVEKSNGRRLVHVDSENLITEEGQSSESVTNLCKSNSGPQDYDSSVTSLKLGLPYSG\*

>PpsSVP

MTRRKIQIKKIDNTTARQVTFSKRRRGLFKKAQELSTLCDAEIALVVFSATGKLFEYTSS

SVQQVIERHGLLSSTFDKLNQPSLDLQLESSTSAALSKEIAENTHELRKLMGEELQELNM

KELQELEKLLGSGLKRVRDAKGEIVLKEITSLKWKGSLLMQENKQLKQMANQQIQTLELELEQGQSSEPIGDFIHSDPSQDHDSSGTSLKLGLAFPNGI

>MdSVP

MAREKIQIKKIDNATARQVTFSKRRRGLLKKAEELSVLCDADIALIIFSSTGKLFEYASS

SMKEILERHNLHSKNLEKLEQPSLQLQLVENSNYTRLSKEIAAKSHQLRQMRGEEIQGLN

LEELQQLEKSLETGLGRVIEKKSEKIMKEIGDLQRNGMQLMEENERLRQQVAEKSDGRRL

VQVDSENMFTEEGQSSESVTNPCNSNNGPQDYDSSDTSLKLGCV\*

>CsSVP1

MGVFLIAHYYLSIYIYIFEERERLLYIEMAREKIQIKKIDNVTARQVTFSKRRKGLFKKA

EELSVLCDADVALIIFSATGKLFEFSSSSMTEILERRNLHSKNLDKLDQPSLELQLVENS

NFSRLSKEVAEKSHQLRQMRGEELPGLSIEELQQLERSLEAGLSHVIGKKGEKIMKEISN

LQQKEMELMEENERLRQQVKEVSNARKHVAVATDSENMYINEEGQSSESVNICNSTSPPQ

DYDSSVTSLKLGLPYSG

>CsSVP2

MVRQRIQIKKIDNVTARQVTFSKRRRGLFKKAHELSTLCDAEIALIVFSATGRLFEYASS

STRQVIERHNLQPQNLVQLNQPSLELQLENSTRAMLSKEAEERTLELRQLRGEELHELGF

EELKKLEKSLEGGLSRVLKTKDDRVEKEIAALRRKEARLMEENAWLKQQVQMQIVNMGQPQEQGQSSESITNNGSTVAPPQDYDSSDTSLKLGLPYQS

>PmMADS03

MSEGSIEFILLNVGLQIKMGRGKIEIKRIENTTNRQVTFCKRRNGLLKKAYELSILCDAEVALIVFSSRGRLYEYSNNNIRNTIERYKKACSDSSGSTSITEINAQYYQQESAKLRQQIQMLQNSNRHLMGDALSTLSVKELKQLENRLERGINRIRSKKHEMLLAEIEYLQKKEIELENENVCLRTKISEVERLQQANMVGPELNAIQALASRNFFSQTMMEGGATYPQQDKKILHLG\*

>PmMADS15

MAYENKSMSLDSPQRKLGRGKIEIKRIENTTNRQVTFCKRRNGLLKKAYELSVLCDAEVALIVFSNRGRLYEYANNSVKETIERYKKACAESTNTGSVSEASTQYYQQEAAKLRAQIGNLQNSSRHMMGESLSSMNMKDLKNLESKLEKGINRIRSKKNELLFAEIEYMQKREIDLHNNNQLLRAKIAENERSQQNINVMAGGGSYEIMQSQPYDSRNYFQVNALQPNHQYNSRQDPMALQLV\*

>PmMADS12

MGRGKIEIKRIENSSNRQVTYSKRRNGIIKKAKEITVLCDAKVSLVIFASSGKMVEYCSPSVTVTDILDKYHGQAGKKLWDAKHENLSNEVDRVKKDNDSMQVELRHLKGEDITSLTHKELMALEDALENGLASIRDKKSKFVDILRENERALEEEHKRLTYELHKQEMKIEENVRELENGYHQRLGNYNNQIPFAFRVQPIQPNLQERM\*

>PmMADS13

MTRGKIQIKRIENATNRQVTYSKRRNGLFKKAHELTVLCDATVSLIMVSSSGKIHEYISPSTTTKQFFDQFQKTKGVDIWSSHYEVSHSSLLSLSLSLSLSLSIYIYMYIIVWLCVQAMQEHLKKLKEVNRSLQKQIRQRVLGECLNDMSFDELRGVEQEMEGAVDVIRKRKVDARDDTHYRLVENGGEDYESAFGYSSNGGPRIFA\*

>PmMADS14

MGRGRVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCEAEVALIIFSNRGKLYEFCSSSSMLKTLERYQKCNYGAPETNVSAREALELSSQQEYLKLKARYEALQRNQRNLLGEDLGPLSSKELESLERQLDMSLKQIRSTRTQCMLDQLTDLQRKEHMLNEANKTLKQRLFEGYHVNSLQMNPNADEYGRQQAQAHGDGFFHPLDCEPTLQIGYQNDPISVVTAGPSVSNYMAGWLP\*

>PmMADS17

MGRGRVELKRIENKINRQVTFAKRRNGLLKKAYELSILCDAEVALIIFSNRGKLYEFCSSSSSILKTLERYQKCSYGQVEVNKPAKELEQSSYREYLKLKGRFESLQRTQRNLLGEELGPLNTKELEQLERQLESSLKQVRSTKTQYMLDQLSDLQNKEQMLIEANRDLSLKLDDISSRNQIRQSWEGGNQGGMAYGTQHAQSQGFFQPLDCNPTLQIGYSNVGSEQMSATTHAQQVNGFIPGWML\*

>PmMADS18

MGRGKVQLKRIENKISRQVTFSKRRAGLLKKAHEISVLCDADVALIVFSTKGKLFEYSSDSSMESILERYDQYSHAEQQLTTDFDPQGSCWSLEYPKLAARIEVLQRKLRHFTGEDLDSLSLRELQNLELQLETALKRIRTRKNQLMHESISVLHKKQKALQEQNNSLGKKLKEKENMLEVEHDGQVQQVEQHQSNQAAHNSSTLMLMPPPPPQTSSTPALLASLTIGGGIQARGGMEDGDDNDGRTQTRPPPTTNTLMPMWMYRHFNE\*

>PmMADS20

MGRGRVELKRIENKINRQVTFSKRRNGLLKKAYELSVLCDAEVALIIFSSRGKLHEFGSAGFIWILSLPIKTSNEAVASQVLEAPEMKSCSSYLLSSRSMQSWYQEVTKLKAKYESLLRTQRQLLGEDLGPLNVKELQNLEKQLEGALAQARQRKTQLMIEQMEDLRKKERHLGDLNKQLRVKLETEGQNLKAIQNMWSSNAAAGSSSFSFHSSQTNPMDCQPHEPVLQIGYHQYLPVEGPSMSKSMACETNFIQGWVL\*

>PmMADS21

MVRGKTQMRRIENATSRQVTFSKRRSGLLKKAFELSVLCDAEVALIIFSPRGKLYEFASSSMQTTIERYQKHTKDNLTNNKSVSTDQNMQHLKQESSSMMKQIELLEVSKRKLLGEGLGSCSIEELQEIEQQLERSVSNVRARKTQVFKEQIEQLREKGKALAAENEKLIEKCGRIQPRQASNEQRENLAYTESSPSSDVETELFIGLPERRKR\*

>PmMADS22

MVRGKIEMKRIENATSRQVTFSKRRNGLLKKAFELSVLCDAQVSVIIFSQKGRLYEFSSSDMQETIKRYHKHAKAGQTNKIEVEEYVEQLKHESTAMAKKIENLEASQRKLLGHGLDSCSVEELQEITGQLERSVRKIRERKAHLFAEQMEQLRAKERLLLEENAKLSEEFGAQPRLLLQQQQLSVEEKGAVSYWSLSSPSSEVETELFIGPPVTRC\*

>PmMADS23

MGRRKVVLERIENKINRQVTFSKRRNGLLKKAYELSVLCDAQVALIISSSRGKLYEFGSTDYNSVHSLISVNKILERYRQCCYSLQGNVAENETQNLYQEVSKLKVKYESLQLSQRHLLGEDLEKLRLKELVNLENQLDKTLSKARQRKVLVICVM\*

>PmMADS25

MVRGKTQMKRIENAASRQVTFSKRRNGLLKKAFELSVLCDAEVALIIFSTRGKLYEFSSSRRFSIGNTLDRYQKRVKDQGLGSKAVQVDMEHGKDDTSSMAKKIDFIEASKQKLLGNCLESCSIEELQQTENQLERSLSKIRARKTQLLREQIENLKEEEKNLFEQNAKLREKCGMQPLGPPSARKDEENCAVRQPRTPDMEDVETDLVIGPPERRRSSQNP\*

>PmMADS27

MGRGRVQLKRIENKINRQVTFSKRRSGLLKKAQEISVLCDAEVALIVFSTKGKLFEYSTDSCMERILERYERYSYSEKQLLANDNESTGSWTLEHAKLKARVEVLQRNHSHFMGEDLQSLSLKELQNLEQQLDSALKHIRSRKNQVMYESISELQKKDKALQEQNNLLAKKVKEKEKALAPQAQSWEQQVQNQGLDCSSTLLPEALHSGSNYQGIRSDGFGGDHEDENETPTANRPNTLLPPWMLRHLNE\*

>PmMADS28

MGRGRVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSSRGKLYEFCSSMSMLKTLEKYQRCSYGSLEANRPVNDTQKQNSYQEYLKLKARVEVLQQSQRNLLGEDLAPLNTKELEQLEHQLEASLNQIRSTKTQFMLDQLCDLQNKEQMLVEANKALRRKLEETSGQAPPPLAWEAAGHGNNNDQHTRLPHHPHSQGFFHPLGNNSTSQIGYTPLGSDHHEQMNVGNHGQHVNGFIPGWML\*

>PmMADS29

MGRGKIEIKLIENHTNRQVTYSKRRNGIFKKAQELTVLCDAKVSLIMLSNTGKMHETKRMYDDYQKTLGVDLWSSHYQAMKDTLWKLKEINNKLRREIRQRLGHDLNGLTYEQLHSLEDKMASSLEAIRERKYHVLKTQMETYKKKVKNLQERRGNMLHGYFDQEVASEDPQYGYVDNEGDYESAVALANGASNLFTIHLHQDIRDHANLHHHGGSSLGSSITHLHDLRLA\*

>PmMADS31

MGRGRVQLKRIENKINRQVTFSKRRTGLLKKAHEISVLCDAQVALVVFSNKGKLFEYATDSCMDQILDRYERYSYAERQLVEPDFESQCNWTFEYSRLKAKVELLQRNQRHYLGEDLDSLTLKEIQSLEHQLETALKQIRLRKNQLMHESISELQRKERAMQEQNNLLAKKIKEKEKAAAEEVHNWEQQNNGLNMLPQPLPCLNMGGTQQDEFLQVRRNQLDLTLEPLYSCNLGCFAA\*

>PmMADS32

MGRGKVELKRIENKINQQVTFAKRRNGLLKKAYELSVLCDAEVALIVFSTRGKLYEFCSGSSMEKTLERYQRCSYSALEASQPAQDSQSRYQDYVNLKAKVEVLQLTQRNFLGEDLGHLGTKELQQLENQLDMSLRQIRSTKTQVMHGQISDLLRKEQMLLEANNELRRKLEECDAAIERYSWTTEEQNQNVPNSSHHQAAQFEGVLDHSQCNNTLQIGYNPAAVTDHHELQSSTQSHSGLIFPGTWVL\*

**Supplementary Data4.** The genome sequences of SVP1 and SVP2 promoters, 2000 bp up stream fragments.

> Pro-PmSVP1 (Pm002166)

GGACATTCTTCGTTGTTTGCGGGCACAAATCAAACTCGCAACTCACTTTAGCCACATTCTACTATGTGAATGTCAAATACTGTGACCTCAAAAGACGAGAAAGACATTGATGAATGGAGAAAATGCTTTAGAATGATTCTAATTAGGGACATATCGCATATGATAAATTATATATCTTCAAGATGAGATGAGGGAGCGTGGGGACTACCATGACAGAAACACTTGCACATCAACAATTTTAACCATTTTTACCACTTGGTTTAGTTCTATTTGTGTCTATCTAGTTGGAGGAGGTTTTAAGTTTGACTCACATGACATAATTTGTGTGTGTGTGAGAAATCTCATTTCCCTTTAGTTTAGACCATGACTTATACTAAGAAAATATACATCCAAATTGAGCTCAATGCTTCCCCTGCACTGCAAACTCAACATTTCAGTTTTTCACACCATCGGTTAGACCATCTCCAACCCTTGGGGTGGAAACTCAAATTTTGAGTTTAGCCTCCAAAAACCATCTCCAACCCATGTATTTTGGGGGGTGGAAATTTGAGAAATCTCAAATCTTGGGTGGAATTCCAGTCCCATTTTTGCCTGGACTGATAATTTTGTGGGCCCAAAATCTGCTTTTTTTATTATTTTTTTTCTGACTGAAGTCCATGTGCTACACAATGTTTGCTGGGCCCAGTTTTGGTTACACTGTTTGGGCAGCAACTTTGTGCCAAAAATCTGATATTGCTGGTTTGTTTGTTTGTTTTTTTTTTTTGTTTGGTTTTATTTTAAATATTCCAACAACTATATTTGTAATCAATAATCATGATTAATTTTAAGCAATCTCAACGGCAAAATTTAATGATTGTCGTTTATTTAAAAATGCTTAGATAATTTAAACACACTTACATAATTCAATGAAGAGTTCGAATTATTCCGAGCATACGTATAGTATTGTACTTATTTTTATTTTTTAAGTGAAATTCAATTATGTTTTGGAATTTTATTTTTTTTAGGTTAAAATGTTTAGAAAATTAAATCACGAGTGTTGAAACAAAAATAATGTCAAGAAAAATTAACAAGAAACAAAATTTAGGGGTTAATCATTCTTAAACAATTTAATAAAGTTGCGGACTCAAATTATGAGTCTACAAGGTTGGAGGAAAAAAAAATTTGAGTCCTGAAAATACATGAATAGTTGTATTTTGGAGGGTGAAAATTTGAGTTTAGCCCCAACATGGTTGGAGATGGTCTTATACCTTTTTAAAGCAACCAAAGGGCAAAGAAATAGTGACCAAAGGGCGAGGACGTGGAAAACAGCCAGTAGTTTGCTTCACCATAAAAAGGACCTTCCTTTTCCACACTTCCACAAACATTCCCTCTCTCTATAATTTTTTGTCTCTCTCTCCCAATCTCATTGGTGGCCTTGAAGTTTCACAGAACACTAAACCCCAGATTCACTCAGACTGGTGAGTAAATCATTAAATACAAAGCAAATAAAAACTTAAAAAGGCACCAAACAGATCCCCTTTTTACCTAATAATCTAGAAGCCCCTCCCCTAGCTTATCCTGAGAAAATGTTTCTTTTCTCCAATTGGTTGGTTTATTTTTTATTTTCTGAGCCTTGTTGGTGTTGAAAAAGCTCTCTCTGGATCTAAGAATCTAGAGATGGAGATGGGTCTCTTTCTCTCTAAAATTTTGCATTTCATTTCATTGCATATTTAGGGTTTGCCTTTGCCCCCAGAGATTCTTGGCTAAATTTGGCAAAATGCCGCCACTTCTCGCACCAGACCTGTCCCTCTCCAATTAGCCGTCGTTTCCTTTTGCTTCTAATTTCTTTGCCTTTTCTGGTTAGTTTTTTGCTGATTATATTCTCTGACTGAAGATAACTAAACCCTAAAGAAGAAAGCAAAATATTCCATTCCAAACAAAGTTAAGAGTTTTCTTTCTATAATATATCATTCTCCTTTTTTCACAAGCTTGCAGAAGAAGCAGAAGCAGAAGATCGATCG

> Pro-PmSVP (Pm022002)

TTTTTCAAAGTGTTTTGGTCGGTTGTTTATGCTGACTTGATCATAAAGGGTGCGGCTGGTGAGTTAAAACATCGGGTCGATCATCAACTTGGTCAGGTATGATGGGACTAGATGGCGAGGTCTTTGCTGAAGTGTTGTCTATGTGGCATCATGTTAATGGTCAATTGGCTCGGATCAAATTATGTCTCAACAATAGGGGTGAAATTTACAAGTTAATCCAAACTAGGGCCTCTTGTCGGACAATGTGACATAGTTTGAATCACATGTTTAATTAAGAACTTATTTCATTGATTATGTGTGTAGCTTTTTCATGAATTTGTGTATGAGTTTGTAGAGTCTTATAAGTTCGCGTACCAGTTTGAAATGACCTGTAAAATTTAGGAGGGTTTTCATGTAGTAAACTCGTAATAAAAATTACATAATGACCCAAAACATATTGTAAGAAGTTTGACAAAAATAAGAAAAGAATATGTGTAAGAAAAGAAAACCATCCTAATCCCCTCCATTGATGTGACGTATGTTCCCTTTTCCACCCTACCAAATAAAAACTTACATATATATATATATATATTGGAATATTACTGTAGTGATATTTCAAGTCAATGACACATTGTTCTCCATTTTAATTAATTTTTTCATATGATTGTGTTATTGACTTGAGATATTGTTATACTTCTCCGTTGCATTACCTCTATTGAGTGATTGAGTGACTGAGATGATGCCCATTATTTAAGCATTAGCTAATATCCCAATTAAAAACACTAATTTTGAAGGTGAAGATATGAACAGTGAATCCTTCACATCCCGAGAATTTGAACGGTAGGAAGCATGGCATGGTACGAGGGTACAACCATGCCATCATTCTTGCTCTGTCATACGACATGACTCTCTGTACGGGAAAGCAAACCTCACCCACATCAACTATAAAAATAAAATAATAATTTCACTGTATTAGTTAGGCGAAAGACCAACCACACAGAGAGTCCACTACTGTCCATTTTCCATTAAATTCCCTTTACCTCTTTTAAATAAGAAAAAGTAAATAAATATCATCTGAGGGAGATATACCGAAATTGCAGAGATGAGAGAACCTTTTGTTTGGCTTTAAAAGGAATCTTAACTTTTCTTGAACTAGGTCACTCTCTCTCTCTTTCTCTCTCTCTCTCTCTCTCTAGATCATTGGTGACTTTCTTTCTACCTGGCTCTTGTGGGAAGTGTCAACGACACTAAATACGACGTATGTAAAGAAAAGAGGTAAAGAATATTTGAAATGAAATCAGAAGCAAAAATATATAAACGTTTTGTGAGAATCTCACTGGAATTTGCAGACACAATGAGTTAATTGGATTGCTAGGGTTGTTTCTCTCCTTCTGTTTCCCTCTTGGGTTTTCTAAGATTTTCTTCTTTGAATCTAGCTAGGGTTAGTTTTGAAAGGTGCAGCTGGCTCTAACACCAATTGATTCTTTTTTATGTTCTCCTTTTGCTCTTACCCAAAACCTATGATCTTTTTTCTTCTCTCTCCAGATACCATTTCTTCCCACTCTCTAATATTTCCATTTACAGAAGTACCACGCTGTCTCCACTTCGATTGATTTGATTTGCTCTAAATAATATTTTTATATTATTTGTATATTTGTTCGTTTTTTCTTTGTATTTCTGGGTTTAGAGGCAAGTTCTCTTTGATTTTTTTTATTTATGGTTCTTTTGTTTCTTCTATCTCTCTCTTATTTTTCCCATATGTCCAGAAACTCACTTCCTCTTTCTAGTTTTGTTCAAATGGTTTGATTTATATGATGGGGTATCTTTAATTTCCCTTTTTTCATTCCACATTTACTCAGAATAGTTGGATCTGAAACTTCATTAATTTTATTATGCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTATGTATATATATATAGTTTGTGTATGATCGTTTGATAATGATGAAGTGATTTTATGTGAAGGGGTTTCTGCATTTTCCTTGTAATTAA