Figure S1 The predicted transmembrane domains of nine SlUGlcAE proteins

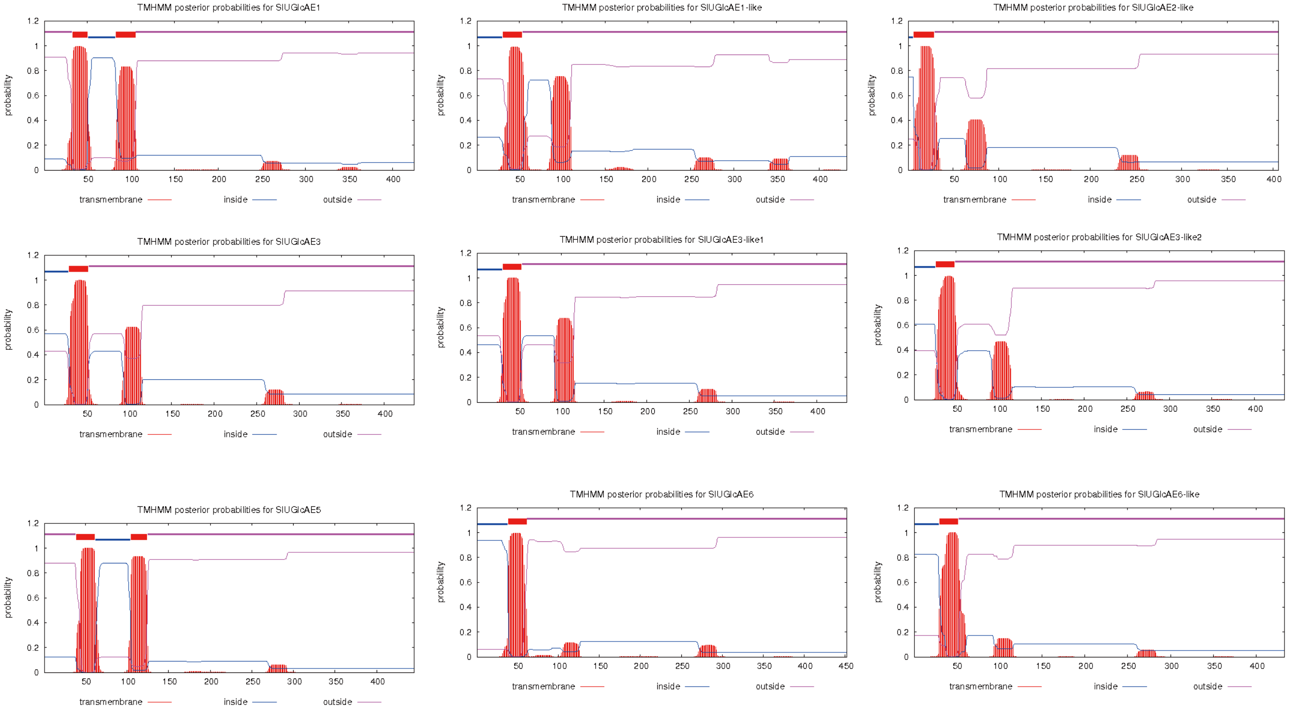


Figure S2 Selective pressure analyses of the other 8 SlUGlcAE proteins

SlUGlcAE1

Selecton Results

1 MPSLEEELFP 11 STPGKFKDRN 21 RHFHRCFAST 31 SNMFLWALFL 41 IALTASYLCF

51 QSFMDSGNRY 61 FTSTWGGHHW 71 ERNVINSAQI 81 RRSHGGMSVL 91 VTGAAGFVGS

101 HVSLALKKRG 111 DGVVGIDNFN 121 NYYDPSLKKA 131 RKNLLTQNSI 141 FIVDGDINDS

151 KLLVKLFDIA 161 RFTHVMHLAA 171 QAGVRYAMEN 181 PGSYIHSNIA 191 GLVSLLEVCK

201 NSNPQPAIVW 211 ASSSSVYGLN 221 EKVPFSESDR 231 TDQPASLYAA 241 TKKAGEEITH

251 TYNHIYGLSI 261 TGLRFFTVYG 271 PWGRPDMAYF 281 SFTRNILQGK 291 PITVYRGKNR

301 VDLARDFTYI 311 DDVVKGCIGS 321 LDTSGKSTGS 331 GGKKRGPAPY 341 RIFNLGNTSP

351 VTVPMMVAML 361 EKHLKVKAKK 371 NFVVMPGNGD 381 VPFTHANISS 391 ARKEFGYKPT

401 TDLQTGLKKF 411 VKWYLSYYGY 421 DQGKL

Legend:

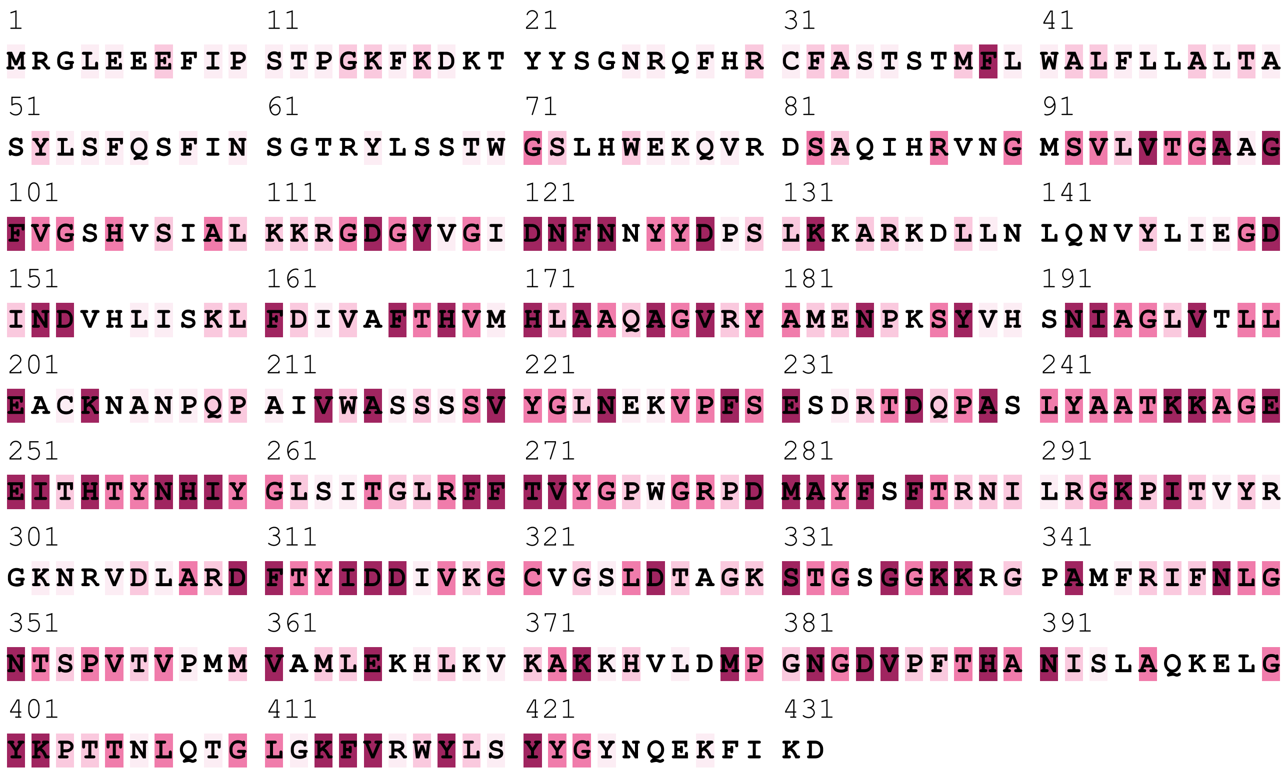
The selection scale:

1 2 3 4 5 6 7

Positive selection Purifying selection

SlUGlcAE1-like

Selecton Results



1 11 21 31 41
MRGLEEEFIP STPGKFKDKT YYSGNRQFHR CFASTSTMFL WALFLLALTA
51 61 71 81 91
SYLSFQSFIN SGTRYLSSTW GSLHWEKQVR DSAQIHRVNG MSVLVTGAAG
101 111 121 131 141
FVGSHVSIAL KKRGDGVVGI DNFNNYYDPS LKKARKDLLN LQNVYLIEGD
151 161 171 181 191
INDVHLISKL FDIVAFTHVM HLAAQAGVRY AMENPKSYVH SNIAGLVTLL
201 211 221 231 241
EACKNANPQP AIVWASSSSV YGLNEKVPFS ESDRTDQPAS LYAATKKAGE
251 261 271 281 291
EITHTYNHIY GLSITGLRFF TVYGPWGRPD MAYFSFTRNI LRGKPITVYR
301 311 321 331 341
GKNRVDLARD FTYIDDIVKG CVGSLDTAGK STGSGGKKRG PAMFRIFNLG
351 361 371 381 391
NTSPVTVPMM VAMLEKHLKV KAKKHVLDMP GNGDVPFTHA NISLAQKELG
401 411 421 431
YKPTTNLQTG LGKFVRWYLS YYGYNQEKFI KD

Legend:

The selection scale:

1 2 3 4 5 6 7

Positive selection Purifying selection

SlUGlcAE2-like

Selecton Results

```
1          11         21         31         41
MDKHRRWTYS ITKLVFWATI FAGAFLFFCF RSSPPSHSTT MKWGSSSNTP
51         61         71         81         91
QWEKRVRLSA RSRSGHLSVL VTGAAGFVGS HVSAALKRRG DGVVGLDNFN
101        111        121        131        141
SYYDPSLKRA RQKLLEQKGV FVMEGDINDE KLLKKLFDIV EFTHVMHLAA
151        161        171        181        191
QAGVRYAMKN PGSYIHSNIA GLVTLFEACK SANPQPSIVW ASSSSVYGLN
201        211        221        231        241
SKVPFSEKDQ TDQPASLYAA TKKAGEEIAH TYNHIYGLSI TGLRFFTVYG
251        261        271        281        291
PWGRPDMAYF FFTKNILKGK PISVFQGSNN KSVARDFTYI DDIVKGCLGA
301        311        321        331        341
LDTAEKSTGS GGKKKKNAQL RVFNLGNTSP VPVTKLVSIL EKLLKVKAKR
351        361        371        381        391
NVLPLPTNGD VMFTHANISY AHKEFGYKPT TDLQTGLHKF VNWYLDYYSV
401
SEKKIY
```

Legend:

The selection scale:

1	2	3	4	5	6	7

Positive selection		Purifying selection

SlUGlcAE3

Selecton Results

```
1          11         21         31         41
MSQMMHIDNI PSTPGKFKME KSPYNRLRMH FSLAKLTFWS FVFLGLIFVF
51         61         71         81         91
FYRSPASSSP VSSDLSRRSL RTSSYGGPAW EKRIKASAKV RSRNGISVLV
101        111        121        131        141
TGAAGFVGTH VSVALKRRGD GVLGLDNFND YYDPSLKRAR QALLERTGVY
151        161        171        181        191
VVEGDINDAT LLKKLFDIVP FTHVMHLAAQ AGVRYAMENP GSYVHSNIAG
201        211        221        231        241
LVNVLEICKS VNPQPAIVWA SSSSVYGLNT KVPFSEKDRT DQPASLYAAT
251        261        271        281        291
KKAGEEIAHT YNHIYGLSLT GLRFFTVYGP WGRPDMAYFF FTRDILKGKS
301        311        321        331        341
IPIFEAANHG TVARDFTYID DIVKGCLAAL DTAEKSTGSG GKKKGAAQLR
351        361        371        381        391
VFNLGNTSPV PVSDLVGILE RLLKVKAKRL VMKLPRNGDV PFTHANISSA
401        411        421        431
HKELGYKPTT DLQTGLKKFV RWYLNYYGNG KKSAQ
```

Legend:

The selection scale:

1	2	3	4	5	6	7

Positive selection — Purifying selection

SlUGlcAE3-like2

Selecton Results

1 11 21 31 41

MSSMKHVDNI PSTPGKFKEK SHYNRLRLHF SVAKLTFWSF VFLGLIFICF

51 61 71 81 91

FKSTSSSSSP VSSDLSRRSL RTSSYDGPAW EKRIKASAKI RSTNGISVLV

101 111 121 131 141

TGAAGFVGTH VSSALKRRGD GVVGLDNFND YYDPSLKRAR QTLLESAGVY

151 161 171 181 191

IVEGDINDVA LLKKLFDIVQ FSHVMHLAAQ AGVRYAMENP SSYVHSNIAG

201 211 221 231 241

LVNLLEFCKN ANPQPAIVWA SSSSVYGLNT KVPFSESDRT DQPASLYAAT

251 261 271 281 291

KKAGEEIAHT YNHIYGLSLT GLRFFTVYGP WGRPDMAYFF FTRDMLKGKS

301 311 321 331 341

ISIFEGADHG TVARDFTYID DIVKGCLGAL DTAEKSTGSG GKKKGPAQLR

351 361 371 381 391

VFNLGNTSPV PVSDLVTILE RLLKVKAKRA VMKLPRNGDV QFTHANISLA

401 411 421 431

QRELGYKPTT DLQTGLKKFV RWYLSYYGEG KKSAQ

Legend:

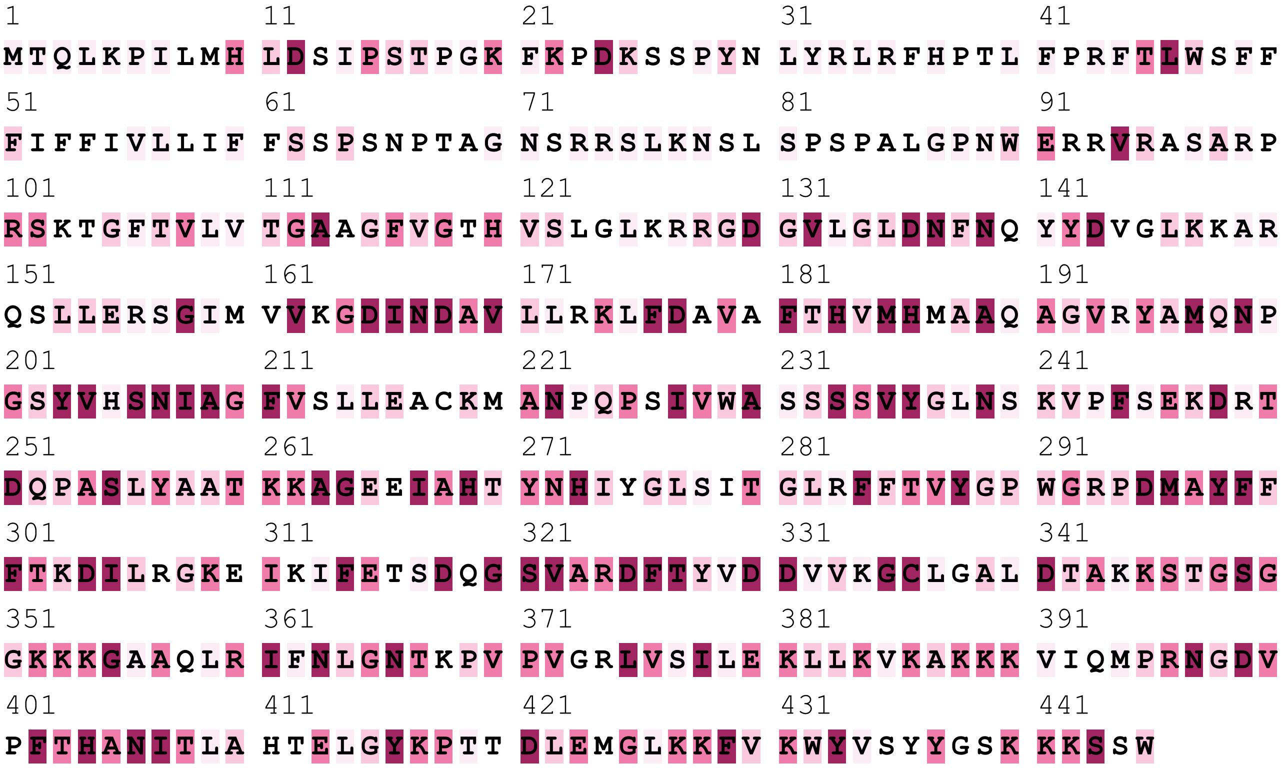
The selection scale:

1 2 3 4 5 6 7

Positive selection Purifying selection

SlUGlcAE5

Selecton Results



```
1          11         21         31         41
MTQLKPILMH LDSIPSTPGK FKPDKSSPYN LYRLRFHPTL FPRFTLWSFF
51         61         71         81         91
FIFFIVLLIF FSSPSNPTAG NSRRSLKNSL SPSPALGPNW ERRVRASARP
101        111        121        131        141
RSKTGFTVLV TGAAGFVGTH VSLGLKRRGD GVLGLDNFNQ YYDVGLKKAR
151        161        171        181        191
QSLLERSGIM VVKGDINDAV LLRKLFDAVA FTHVMHMAAQ AGVRYAMQNP
201        211        221        231        241
GSYVHSNIAG FVSLLEACKM ANPQPSIVWA SSSSVYGLNS KVPFSEKDRT
251        261        271        281        291
DQPASLYAAT KKAGEEIAHT YNHIYGLSIT GLRFFTVYGP WGRPDMAYFF
301        311        321        331        341
FTKDILRGKE IKIFETSDQG SVARDFTYVD DVVKGCLGAL DTAKKSTGSG
351        361        371        381        391
GKKKGAAQLR IFNLGNTKPV PVGRLVSILE KLLKVKAKKK VIQMPRNGDV
401        411        421        431        441
PFTHANITLA HTELGYKPTT DLEMGLKKFV KWYVSYYGSK KKSSW
```

Legend:

The selection scale:

1	2	3	4	5	6	7

Positive selection Purifying selection

SlUGlcAE6

Selecton Results

```
1          11         21         31         41
MKTIMASPPD TSKTTKLERY NSYIRRVNST KLIAASSKLL FRVTLLVALL
51         61         71         81         91
LIFFFTINYP PLTSEKSFNN NIHTTTHNLL SSAIYGGGAS WEKQVRHSST
101        111        121        131        141
PHRPNGLSVL VTGAAGFVGS HCSLALKKRG DGVLGLDNFN SYYDPSLKRA
151        161        171        181        191
RQDQLSKHQI FIVEGDINDT ELLKKLFDIV PFTHILHLAA QAGVRYAMQN
201        211        221        231        241
PLSYVNSNVA GFVNLLEIAK AADPQPAIVW ASSSSVYGLN TKVPFSEDHR
251        261        271        281        291
TDQPASLYAA TKKAGEAIAH TYNHIYGLSL TGLRFFTVYG PWGRPDMAYF
301        311        321        331        341
FFTKDMIQGK SINVYVTQDD KEVARDFTYI DDIVKGCVGA LDTAEKSTGS
351        361        371        381        391
GGKKRGPAQL RVYNLGNTSP VSVKKLVAIL ENLLNLKAKK FFIKMPRNGD
401        411        421        431        441
VPFTHANVSL ALRDFGYKPT TDLSSGLRKF VKWYVSYYGI QSRVKKESEG
451
EK
```

Legend:

The selection scale:

1	2	3	4	5	6	7

Positive selection Purifying selection

SlUGlcAE6-like

Selecton Results

```
1          11         21         31         41
MASLFSIDTK KSIKLDRNTY IHKVNSSTKL IVAFIKLFYC IAILISALLI
51         61         71         81         91
GLFILNHILF ISTDSNQHGR RLFSFGGGAG WEKKVRHSSI PKKINGKVVL
101        111        121        131        141
VTGAAGFVGS HCGLALKKRG DGVIGIDNFN SYYDPSLKRA RQELMSKHEI
151        161        171        181        191
FIVDGDINDI DLVNKLFDIV RFTHVLHLAA QAGVRYAMEN PLSYVHSNVN
201        211        221        231        241
GFVNLLEIAK SANPQPAIVW ASSSSVYGLN TKVPFSENDR TDQPASLYAA
251        261        271        281        291
TKKAGEEIAH TYNHIYGLSL TGLRFFTVYG PWGRPDMAYF FFTKDMIQGK
301        311        321        331        341
PIKVYVSDKE VARDFTYIDD VVKGCLGAID TAEKSTGSGG KKRGPAQLRV
351        361        371        381        391
YNLGNTSPVS VKKLVAILEN LLNIKAKKNL IRMPRNGDVP FTHANVSLAY
401        411        421        431
RDFGYKPTTN LSSGLRKFVK WYLSYYGIQA RIK
```

Legend:

The selection scale:

1 2 3 4 5 6 7

Positive selection Purifying selection

Figure S3 Selective pressure in promoter regions of *SlUGlcAE* genes

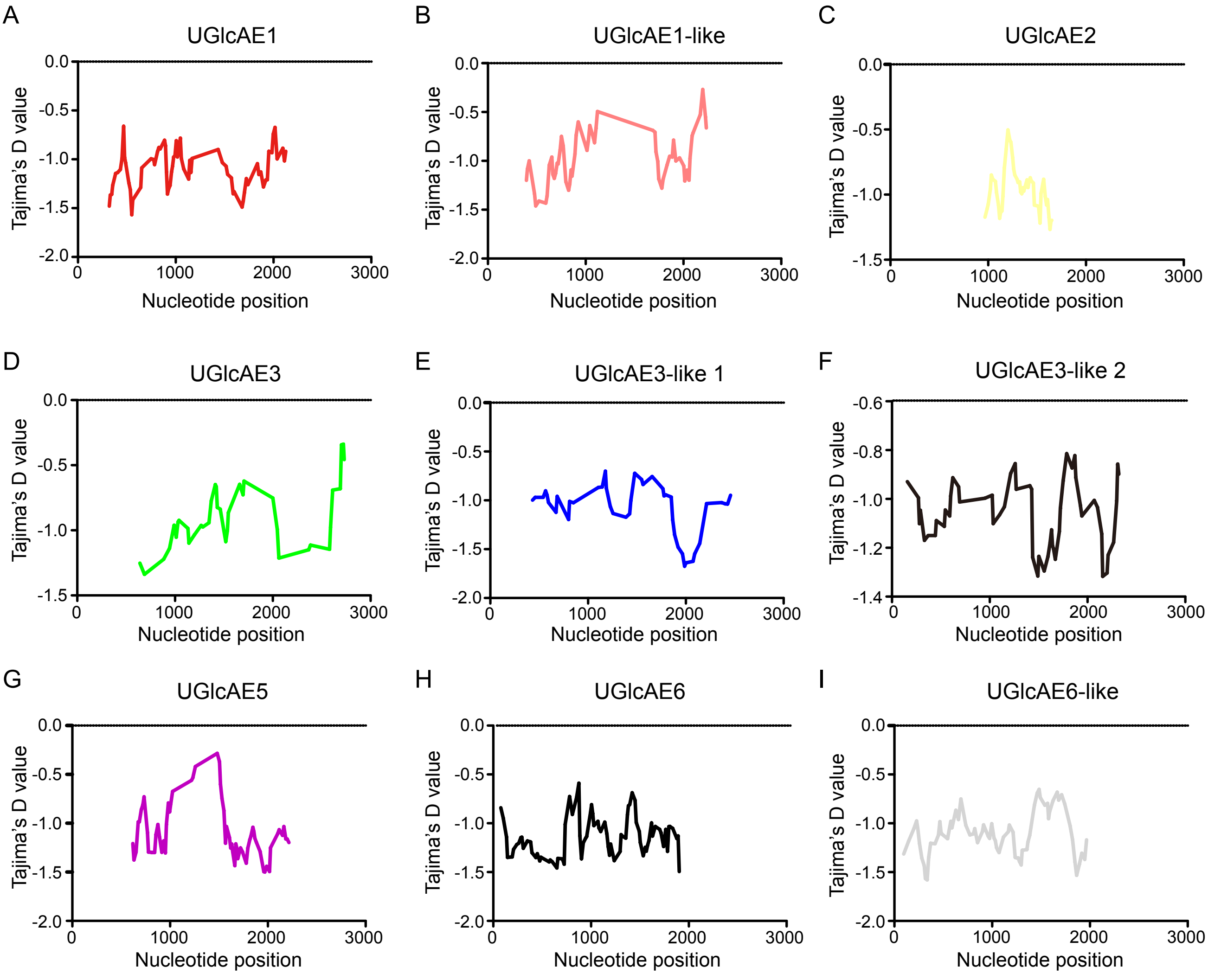


Table S1 Kinds and numbers of *cis*-acting elements in the 0.5 kb upstream regions of 9 *SlUGlcAE* genes

Gene sample	**HSE**	**MBS**	**Skn-1_motif**	**TGA-element**	**HD-Zip 1**	**HD-Zip 2**	**TC-rich repeats**	**circadian**	**CAT-box**	**TATC-box**	**W box**	**WUN-motif**	**LTR**	**TCA-element**	**ELI-box3**
SlUGlcAE1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
SlUGlcAE1-like	0	0	0	0	1	1	1	1	0	0	0	0	0	0	0
SlUGlcAE2-like	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0
SlUGlcAE3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SlUGlcAE3-like1	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0
SlUGlcAE3-like2	0	0	0	0	0	0	1	2	0	0	0	1	0	0	0
SlUGlcAE5	1	0	0	0	0	0	1	0	0	0	0	0	1	2	0
SlUGlcAE6	2	0	1	0	0	0	0	0	0	0	0	0	0	0	1
SlUGlcAE6-like	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table S2 Kinds and numbers of cis-acting elements in the 1.5 kb upstream regions of 9 *SlUGlcAE* genes

Gene sample	**ABRE**	**ARE**	**HSE**	**MBS**	**TGA-element**	**TGACG-motif**	**CGTCA-motif**	**TC-rich repeats**	**circadian**	**AuxRR-core**	**GARE-motif**	**LTR**	**TATC-box**	**P-box**	**ERE**	**WUN-motif**	**MRE**	**TCA-element**	**HD-Zip 1**	**HD-Zip 2**	**Skn-1_motif**	**GCN4_motif**	**O2-site**	**as-2-box**	**W box**	**CAT-box**	**GC-motif**	**CCGTCC-box**	**ELI-box3**
SlUGlcAE1	2	1	1	1	1	2	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0
SlUGlcAE1-like	0	0	0	0	0	1	1	1	1	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	0	0	0	0	0
SlUGlcAE2-like	0	0	0	0	0	1	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	2	0	0	1	2	1	0	0
SlUGlcAE3	0	0	1	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SlUGlcAE3-like1	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
SlUGlcAE3-like2	0	0	2	1	0	0	0	2	2	0	0	0	0	0	1	1	0	0	0	0	0	0	0	1	1	0	0	1	0
SlUGlcAE5	0	0	1	0	0	0	0	3	2	0	0	1	0	0	1	0	1	2	0	0	0	0	0	0	0	0	0	0	0
SlUGlcAE6	0	2	2	1	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	2	1	0	0	1	0	0	0	1
SlUGlcAE6-like	0	0	2	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0