SUPPLEMENTARY DATA


METHODS

Construction of coexpression constructs

For the co-expression of *MtSEO-F* genes, pBatTL expression cassettes (Müller *et al.,* 2010) containing the double-enhanced CaMV 35*S* promoter (d35S-P), *MtSEO-F* gene and CaMV 35*S* terminator sequence ($T_{35S}$) were amplified using forward primers 5'-AGA <u>CAC GTG</u> ATG GTG GAG CAC GAC ACA C-3' for d35S-P–MtSEO-F1–$T_{35S}$, 5'-AGA <u>CCC GGG</u> ATG GTG GAG CAC GAC ACA C-3' for d35S-P–MtSEO-F2–$T_{35S}$ and d35S-P–MtSEO-F4–$T_{35S}$, in each case combined with the same reverse primer 5'-AGA <u>CCC GGG</u> GGT CAC TGG ATT TTG GTT T-3'. The d35S-P–MtSEO-F1–$T_{35S}$ cassette was digested with *Pml*I/*Sma*I and introduced into the *Sma*I site of pBIN19 (Bevan, 1984) to obtain pBIN19–d35S-P–MtSEO-F1–$T_{35S}$. The other cassettes were digested with *Sma*I and introduced into the *Sma*I site of the pBIN19–d35S-P–MtSEO-F1–$T_{35S}$ vector to yield vectors pBIN19–d35S-P–MtSEO-F1–$T_{35S}$–d35S-P–MtSEO-F2–$T_{35S}$ and pBIN19–d35S-P–MtSEO-F1–$T_{35S}$–d35S-P–MtSEO-F4–$T_{35S}$, respectively. The d35S-P–MtSEO-F4–$T_{35S}$ vector was also amplified using forward primer 5'-AGA <u>CAC GTG</u> ATG GTG GAG CAC GAC ACA C-3' and reverse primer 5'-AGA <u>CCC GGG</u> GGT CAC TGG ATT TTG GTT T-3', and the product was transferred to pBIN19. The d35S-P–MtSEO-F2–$T_{35S}$ cassette was inserted using the same strategy, yielding vector pBIN19–d35S-P–MtSEO-F4–$T_{35S}$–d35S-P–MtSEO-F2–$T_{35S}$. The co-expression of all three *MtSEO* genes and the co-expression of MtSEO-F2 with SEO-F genes from other species were achieved by transferring the d35S-P–MtSEO-F2–$T_{35S}$ cassette into a pBIN19 vector containing an independent mRFP marker as an expression control. The *nos* promoter (NosP) was amplified by PCR using forward primer 5'-AGA <u>GGT ACC</u> GAT CAT GAG CGG AGA ATT AAG-3' and reverse primer 5'-AGA <u>CCA TGG</u> GAA ACG ATC AGA TCC G-3', the mRFP was amplified using forward primer 5'-AGA <u>CCA TGG</u> GAA TGG CCT CCT CCG AG-3' and reverse primer 5'-AGA <u>TCT AGA</u> TGG GCG CCG GTG GAG TGG C-3' and the *nos* terminator (NosT) was amplified using forward primer 5'-AGA <u>TCT AGA</u> TGA GCG GGA CTC TGG GGT TC-3' and reverse primer 5'-CCC GAT CTA GTA ACA TAG ATG-3'. The fragments were digested *Kpn*I/*Nco*I (NosP), *Nco*I/*Xba*I (mRFP)

and *Xba*I (NosT) and were inserted into vector pBluescript II KS+ (Agilent Technologies) linearized with *Kpn*I/*Sma*I. The resulting vector pBS–NosP–mRFP–NosT was digested with *Nhe*I/*Afl*II, resulting in a fragment containing the *mRFP* flanked by parts of the NosP and NosT. The vector pBIN19 was also digested with *Nhe*I/*Afl*II to eliminate the kanamycin-resistance gene also flanked by a NosP and NosT, replacing it with the *mRFP* fragment. The new vector was designated pBIN19–NosP–mRFP–NosT. The d35S-P–MtSEO-F2–T$_{35S}$ cassette was then amplified using forward primer 5'-AGA <u>GAG CTC</u> ATG GTG GAG CAC GAC ACA C-3' and reverse primer 5'-AGA <u>GAG CTC</u> GGT CAC TGG ATT TTG GTT T-3', digested with *Sac*I and inserted into the multiple cloning site of pBIN19–NosP–mRFP–NosT to yield pBIN19–d35S-P–MtSEO-F2–T$_{35S}$–NosP–mRFP–NosT. Restriction sites in the oligonucleotide sequences are underlined. All constructs were verified by sequencing (Sanger *et al.*, 1977) on an ABI PRISM® 3100 Genetic Analyser (Applied Biosystems, Germany).


Construction of pENTR4™ vectors

The full-length *DpSEO-F1* cDNA sequence was amplified using forward primer 5'-AAA <u>CCA TGG</u> CAT CAT TGT CCA ACG GAG CT-3' and reverse primer 5'-AAA <u>GCG GCC GC</u>T TAG CAA ATC TTT TGA CCA TC-3'. The full-length LjSEO-F1 cDNA sequence was amplified using forward primer 5' AGA <u>GTC GAC</u> ATG TCA CAT GTG CCC AAG-3' and reverse primer 5'-AGA <u>GCG GCC GC</u>T CAG ATG CCA AAA CCA TTT G-3'. The sequences were amplified three times with independent cDNAs and consensus sequences were derived. The products were digested with *Nco*I/*Not*I (*DpSEO-F1*) or *Sal*I/*Not*I (*LjSEO-F1*), and inserted into the *Nco*I/*Not*I or *Sal*I/*Not*I sites of pENTR4™ (Invitrogen). Consensus sequences were obtained by side-directed mutagenesis (Agilent Technologies).

Primers for *CgSEOa*, *PsSEO-F1* and *VfSEO-F1* were designed based on published sequences (Noll *et al.,* 2007; Tuteja *et al.*, 2010). Products were amplified from *C. gladiata* cDNA using forward primer 5' AGA <u>CCA TGG</u> CAT CCG ACT CCA AGC CAC-3' and reverse primer 5'-AGA <u>CTC GAG</u> TCA AAC TTT AGC AGT GTC-3'. Products were amplified from *P. sativum* cDNA using forward primer 5'-AGA CCA TGG CAT CCT TTT CTA ACT CAG CTG 3' and reverse primer 5'-AGA <u>CTC GAG</u> TCA AAC ACC AAA ATT ATT TG-3'. Products were amplified from *V. faba* cDNA using forward primer 5'-AGA <u>CCA</u>

TGG CAT CCT TTT CTA ACT CAC CTG CTG CTG CTA CT-3' and reverse primer 5'-AGA CTC GAG TCA AAC ACC AAA GTT ATT TG-3'. Products were digested with *Nco*I/*Xho*I and inserted into the *Nco*I/*Xho*I sites of pENTR4™ (Invitrogen). Restriction sites in the oligonucleotide sequences are underlined. All products were verified by sequencing.

Construction of binary vectors for root transformation

The promoters of the four *MtSEO-F* genes were amplified as follows: The *MtSEO-F1* promoter was amplified from P*MtSEO-F1*–GFP$_{ER}$ (previously named Pmtfor1-GFP$_{ER}$; Noll *et al.*, 2007) using forward primer 5'-AGA GGT ACC AGT CGA CGT CCA TTC GTA CAT GCA GAA A-3' and reverse primer 5'-AGA CTC GAG ACC ATG GTG ATA AAT TCA ACT TTA GGC-3'. The *MtSEO-F2* promoter was amplified from p*BPMtSEO2*–GFP$_{ER}$ (Noll *et al.*, 2009) using forward primer 5'-AGA GGT ACC AGT CGA CAA CAA TGC AAA TGA ACA AAA TTA-3' and reverse primer 5'-AGA CTC GAG ACC ATG GTG ATG ATT TGT TTA TAA ATT AA-3'. The *MtSEO-F3* promoter was amplified from p*BPMtSEO3*–GFP$_{ER}$ (Noll et al. 2009) using forward primer 5'-AGA GGT ACC AGT CGA CAA TCC ATT GCT TGT TAT CGC-3' and reverse primer 5'-AGA CTC GAG ACC ATG GTA GGC CAA GAA AGT TAT TAT ATC-3'. Finally the *MtSEO-F4* promoter was amplified from p*BPMtSEO4*–GFP$_{ER}$ (kindly provided by Dr. Boris Rüping) using forward primer 5'-AGA GGT ACC AGT CGA CAT ACA CAT AAA ATT CTA AAC AG A-3' and reverse primer 5'-AGA CTC GAG ACC ATG GGA TGA CTT AAT ATT AGA GGA G-3'. The *hrGFP* fragment fused to the CaMV T$_{35S}$ was amplified from pBShrGFP (kindly provided by Dr. Boris Rüping) using forward primer 5'-AGA CTC GAG AAT GGT GAG CAA GCA GAT C-3' and reverse primer 5'-AAA GAA TCC CTG CAG GTC ACT GGA TT-3'. The promoter fragments were digested with *Kpn*I/*Xho*I, the *hrGFP*–T$_{35S}$ fragment was digested *Xho*I/*EcoR*I and both were inserted into the corresponding sites of pUC18 (Yanisch-Perron *et al.,* 1985) to yield vectors pUC18–P*MtSEO-FX*–*hrGFP*, where X specifies the promoter. The *MtSEO-F* genes were amplified from the corresponding pENTR4™–*MtSEO-F* constructs (Müller *et al.*, 2010) using forward primer 5'-AGA CCA TGG AAT CAT GTT CCA ATG GAA CTA-3' and reverse primer 5'-AGA CTC GAG AGT ATC TTG CCA TTC TGT GGA G-3' for *MtSEO-F1*, forward primer 5'-AGA CCA TGG

AAT CCA CTG CAT TGT CCT AT-3' and reverse primer 5'-AGA <u>CTC GAG</u> AGA ATG CAG CAA

CTA TCT GGA TC-3' for *MtSEO-F2*, forward primer 5'-AGA <u>TCA TGA</u> AGT CGT CTT CAA TGG

CGC C-3' and reverse primer 5'-AGA <u>CTC GAG</u> AGA GAC CT TTT CTC AAT CTG AAC-3' for

*MtSEO-F3* and forward primer 5'-AGA <u>CCA TGG</u> AAT CCC TTT CCA ACT TAG GA-3' and reverse

primer 5'-AGA A<u>CT CGA G</u>CC AAC ACC AAG ATT GTT TGG TTC-3' for *MtSEO-F4*. The PCR

products were digested *Nco*I/*Xho*I (*MtSEO-F1*, *MtSEO-F2* and *MtSEO-F4*) or *Bsp*HI/*Xho*I (*MtSEO-F3*),

and inserted into the *Nco*I/*Xho*I site of pUC18–P*MtSEO-F–hrGFP* to complete the pUC18–P*MtSEO-F–*

*MtSEO-F–hrGFP* constructs. The expression cassettes were digested with *Sal*I/*Sma*I and inserted into the

corresponding sites of the binary vector pBIN19 (Bevan 1984). As a control, *hrGFP* was expressed under

the control of the P*MtSEO-F1* promoter by inserting the P*MtSEO-F1–hrGFP*–T$_{35S}$ cassette into pBIN19.

Restriction sites in the oligonucleotide sequences are underlined. All constructs were verified by

sequencing.

**FIG. S1.** A phylogram created with FastTree2 based on a MUSCLE (Edgar, 2004) amino acid alignment. SEO proteins previously described by Rüping *et al.*, (2010) as well as DpSEO-F1 and LjSEO-F1 were used to construct the phylogram. The number of amino acid substitutions is related to branch length and bootstrap values are indicated.
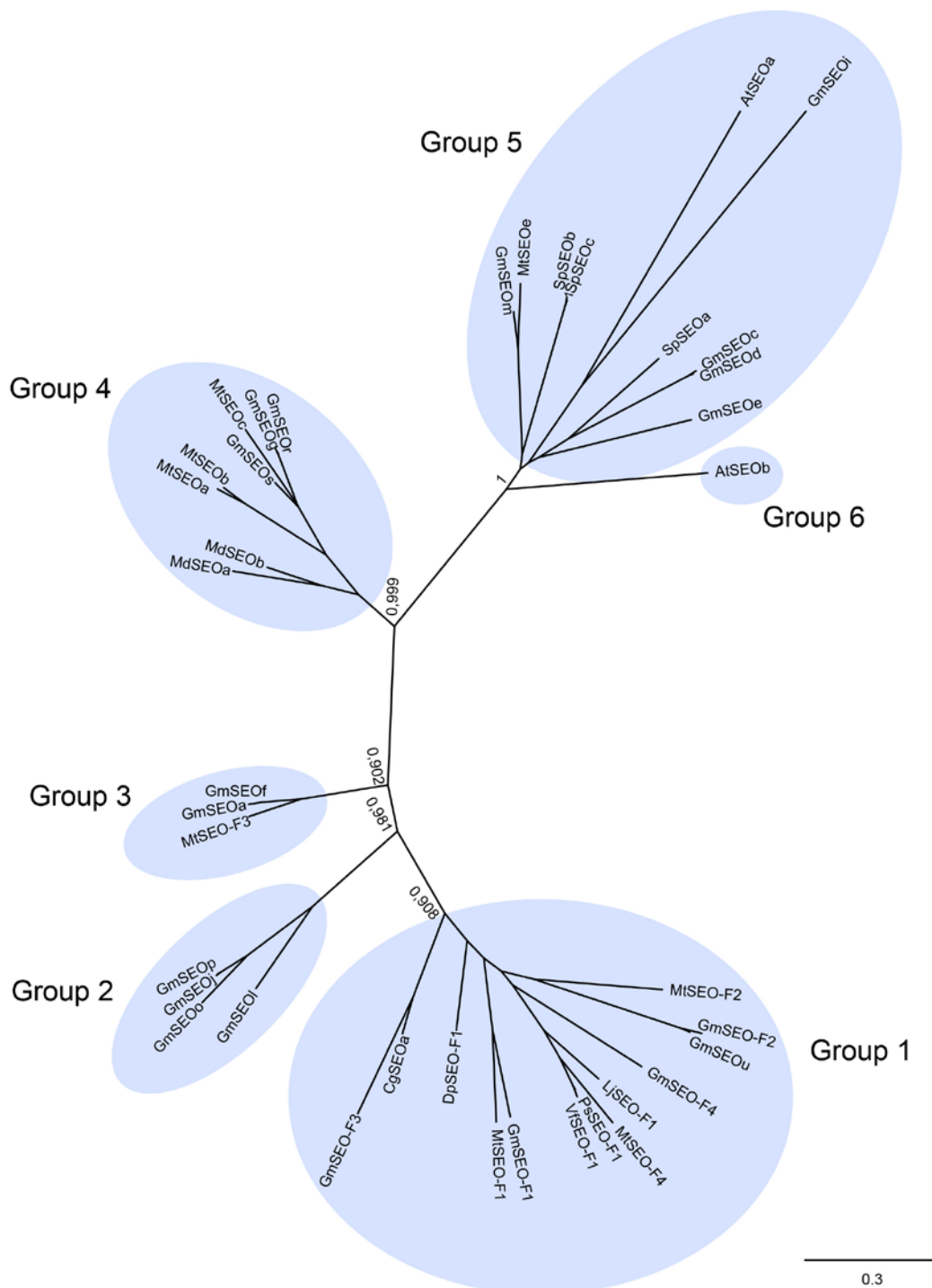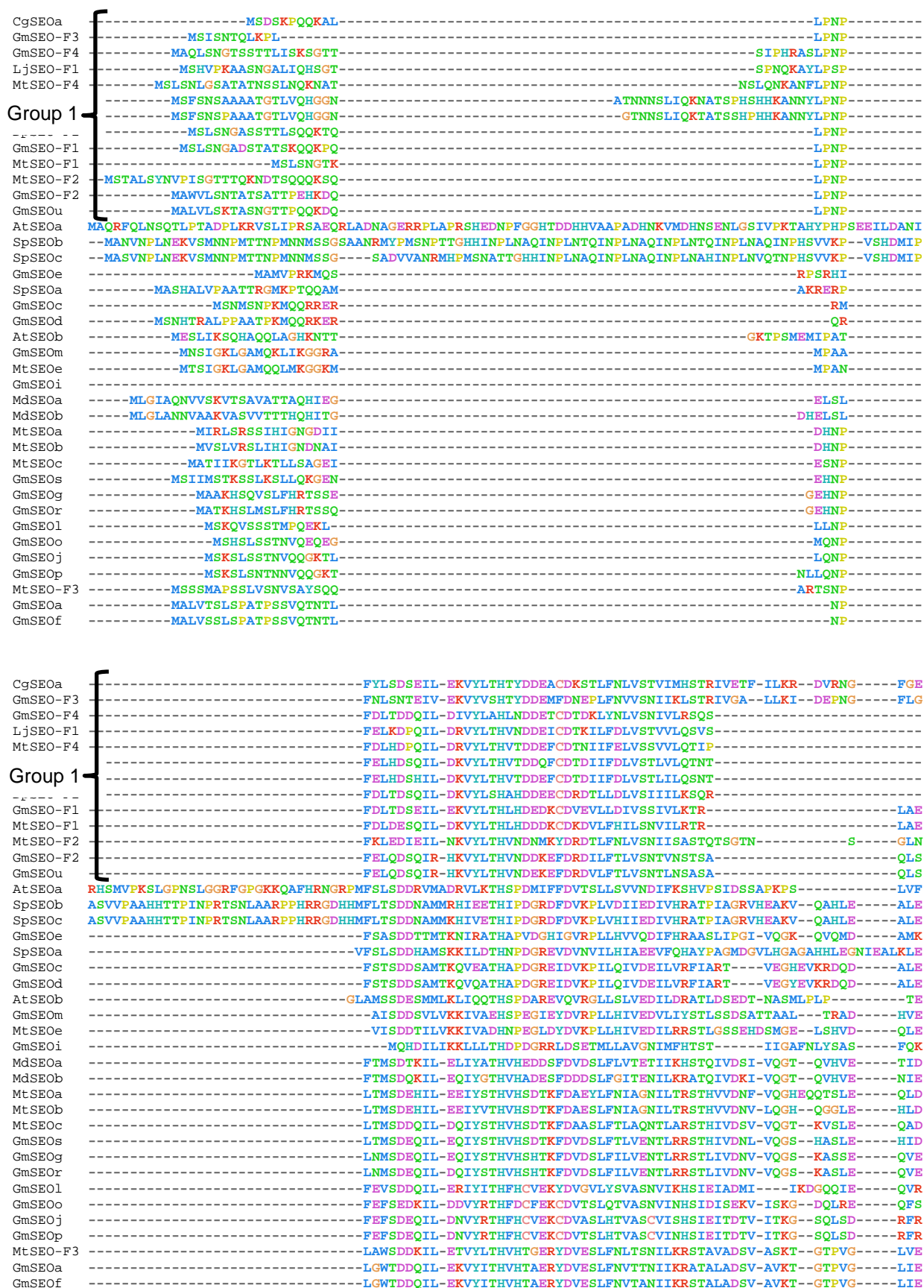
**FIG. S2.** Alignment of the SEO protein family (Rüping *et al.*, 2010) now including DpSEO-F1 and LjSEO-F1. Conspicuous segments containing at least seven neighbouring amino acids that are identical or showing conserved substitutions in all group 1 proteins are indicated with a black box and numbered M5-M9. The previously-described motifs 1 and 2 (Rüping *et al.*, 2010) are also indicated. The alignment was created using MUSCLE (Edgar, 2004).

**Group 1** (block 1)

```
CgSEOa     ---------------MSDSKPQQKAL--------------------------------------------LPNP--------
GmSEO-F3   --------------MSISNTQLKPL---------------------------------------------LPNP--------
GmSEO-F4   ------------MAQLSNGTSSTTLISKSGTT-----------------------------------SIPHRASLPNP-----
LjSEO-F1   -----------MSHVPKAASNGALIQHSGT------------------------------------SPNQKAYLPSP------
MtSEO-F4   ------MSLSNLGSATATNSSLNQKNAT-------------------------------------NSLQNKANFLPNP-----
           -----------MSFSNSAAAATGTLVQHGGN---------------------ATNNNSLIQKNATSPHSHHKANNYLPNP---
           -----------MSFSNSPAAATGTLVQHGGN---------------------GTNNSLIQKTATSSHPHHKANNYLPNP----
           -----------MSLSNGASSTTLSQQKTQ----------------------------------------LPNP--------
GmSEO-F1   -----------MSLSNGADSTATSKQQKPQ---------------------------------------LPNP--------
MtSEO-F1   ---------------MSLSNGTK-----------------------------------------------LPNP--------
MtSEO-F2   -MSTALSYNVPISGTTTQKNDTSQQQKSQ----------------------------------------LPNP--------
GmSEO-F2   ----------MAWVLSNTATSATTPEHKDQ---------------------------------------LPNP--------
GmSEOu     ----------MALVLSKTASNGTTPQQKDQ---------------------------------------LPNP--------
AtSEOa     MAQRFQLNSQTLPTADPLKRVSLIPRSAEQRLADNAGERRPLAPRSHEDNPFGGHTDDHHVAAPADHNKVMDHNSENLGSIVPKTAHYPHPSEEILDANI
SpSEOb     --MANVNPLNEKVSMNNPMTTNPMNNMSSGSAANRMYPMSNPTTGHHINPLNAQINPLNTQINPLNAQINPLNTQINPLNAQINPHSVVKP--VSHDMIP
SpSEOc     --MASVNPLNEKVSMNNPMTTNPMNNMSSG----SADVVANRMHPMSNATTGHHINPLNAQINPLNAQINPLNAHINPLNVQTNPHSVVKP--VSHDMIP
GmSEOe     -----------------MAMVPRKMQS--------------------------------------------RPSRHI----
SpSEOa     --------MASHALVPAATTRGMKPTQQAM----------------------------------------AKRERP-------
GmSEOc     --------------MSNMSNPKMQQRRER------------------------------------------RM--------
GmSEOd     --------MSNHTRALPPAATPKMQQRKER----------------------------------------QR--------
AtSEOb     ---------MESLIKSQHAQQLAGHKNTT--------------------------------------GKTPSMEMIPAT-----
GmSEOm     ----------MNSIGKLGAMQKLIKGGRA---------------------------------------MPAA--------
MtSEOe     ----------MTSIGKLGAMQQLMKGGKM---------------------------------------MPAN--------
GmSEOi     -----------------------------------------------------------------------------------
MdSEOa     -----MLGIAQNVVSKVTSAVATTAQHIEG--------------------------------------ELSL--------
MdSEOb     -----MLGLANNVAAKVASVVTTTHQHITG-------------------------------------DHELSL-------
MtSEOa     ----------MIRLSRSSIHIGNGDII----------------------------------------DHNP--------
MtSEOb     ----------MVSLVRSLIHIGNDNAI----------------------------------------DHNP--------
MtSEOc     ----------MATIIKGTLKTLLSAGEI----------------------------------------ESNP--------
GmSEOs     --------MSIIMSTKSSLKSLLQKGEN----------------------------------------EHNP--------
GmSEOg     ---------MAAKHSQVSLFHRTSSE------------------------------------------GEHNP-------
GmSEOr     ---------MATKHSLMSLFHRTSSQ------------------------------------------GEHNP-------
GmSEOl     ----------MSKQVSSSTMPQEKL------------------------------------------LLNP--------
GmSEOo     ----------MSHSLSSTNVQEQEG------------------------------------------MQNP--------
GmSEOj     ----------MSKSLSSTNVQQGKTL-----------------------------------------LQNP--------
GmSEOp     ----------MSKSLSNTNNVQQGKT-----------------------------------------NLLQNP------
MtSEO-F3   ---------MSSSMAPSSLVSNVSAYSQQ---------------------------------------ARTSNP------
GmSEOa     ---------MALVTSLSPATPSSVQTNTL---------------------------------------NP--------
GmSEOf     ---------MALVSSLSPATPSSVQTNTL---------------------------------------NP--------
```

**Group 1** (block 2)

```
CgSEOa     ------------------------------------------FYLSDSEIL-EKVYLTHTYDDEACDKSTLFNLVSTVIMHSTRIVETF-ILKR--DVRNG-----FGE
GmSEO-F3   ------------------------------------------FNLSNTEIV-EKVYVSHTYDDEMFDNEPLFNVVSNIIKLSTRIVGA--LLKI--DEPNG-----FLG
GmSEO-F4   ------------------------------------------FDLTDDQIL-DIVYLAHLNDDETCDTDKLYNLVSNIVLRSQS---------------------
LjSEO-F1   ------------------------------------------FELKDPQIL-DRVYLTHVNDDEICDTKILFDLVSTVVLQSVS---------------------
MtSEO-F4   ------------------------------------------FDLHDPQIL-DRVYLTHVTDDEFCDTNIIFELVSSVVLQTIP---------------------
           ------------------------------------------FELHDSQIL-DKVYLTHVTDDQFCDTDIIFDLVSTLVLQTNT---------------------
           ------------------------------------------FELHDSHIL-DKVYLTHVTDDEFCDTDIIFDLVSTLILQSNT---------------------
           ------------------------------------------FDLTDSQIL-DKVYLSHAHDDEECDRDTLLDLVSIIILKSQR---------------------
GmSEO-F1   ------------------------------------------FDLTDSEIL-EKVYLTHLHDEDKCDVEVLLDIVSSIVLKTR-------------------LAE
MtSEO-F1   ------------------------------------------FDLDESQIL-DKVYLTHHDDDKCDKDVLFHILSNVILRTR-------------------LAE
MtSEO-F2   ------------------------------------------FKLEDIEIL-NKVYLTHVNDNMKYDRDTLFNLVSNIISASTQTSGTN------------S----GLN
GmSEO-F2   ------------------------------------------FELQDSQIR-HKVYLTHVNDDKEFDRDILFTLVSNTVNSTSA---------------------QLS
GmSEOu     ------------------------------------------FELQDSQIR-HKVYLTHVNDEKEFDRDVLFTLVSNTLNSASA---------------------QLS
AtSEOa     RHSMVPKSLGPNSLGGRFGPGKKQAFHRNGRPMFSLSDDRVMADRVLKTHSPDMIFFDVTSLLSVVNDIFKSHVPSIDSSAPKPS-----------LVF
SpSEOb     ASVVPAAHHTTPINPRTSNLAARPPHRRGDHHMFLTSDDNAMMRHIEETHIPDGRDFDVKPLVDIIEDIVHRATPIAGRVHEAKV--QAHLE-----ALE
SpSEOc     ASVVPAAHHTTPINPRTSNLAARPPHRRGDHHMFLTSDDNAMMKHIVETHIPDGRDFDVKPLVHIIEDIVHRATPIAGRVHEAKV--QAHLE-----ALE
GmSEOe     ------------------------------------FSASDDTTMTKNIRATHAPVDGHIGVRPLLHVVQDIFHRAASLIPGI-VQGK--QVQMD-----AMK
SpSEOa     ------------------------------------VFSLSDDHAMSKKILDTHNPDGREVDVNVILHIAEEVFQHAYPAGMDGVLHGAGAHHLEGNIEALKLE
GmSEOc     ------------------------------------FSTSDDSAMTKQVEATHAPDGREIDVKPILQIVDEILVRFIART----VEGHEVKRDQD-----ALE
GmSEOd     ------------------------------------FSTSDDSAMTKQVQATHAPDGREIDVKPILQIVDEILVRFIART----VEGYEVKRDQD-----ALE
AtSEOb     ------------------------------------GLAMSSDESMMLKLIQQTHSPDAREVQVRGLLSLVEDILDRATLDSEDT-NASMLPLP---------TE
GmSEOm     ------------------------------------AISDDSVLVKKIVAEHSPEGIEYDVRPLLHIVEDVLIYSTLSSDSATTAAL---TRAD-----HVE
MtSEOe     ------------------------------------VISDDTILVKKIVADHNPEGLDYDVKPLLHIVEDILRRSTLGSSEHDSMGE--LSHVD-----QLE
GmSEOi     ------------------------------MQHDILIKKLLLTHDPDGRRLDSETMLLAVGNIMFHTST------IIGAFNLYSAS-----FQK
MdSEOa     ------------------------------------FTMSDTKIL-ELIYATHVHEDDSFDVDSLFLVTETIIKHSTQIVDSI-VQGT--QVHVE-----TID
MdSEOb     ------------------------------------FTMSDQKIL-EQIYGTHVHADESFDDDSLFGITENILKRATQIVDKI-VQGT--QVHVE-----NIE
MtSEOa     ------------------------------------LTMSDEHIL-EEIYSTHVSDTKFDAEYLFNIAGNILTRSTHVVDNF-VQGHEQQTSLE-----QLD
MtSEOb     ------------------------------------LTMSDDHIL-EEIYVTHVHSDTKFDAESLFNIAGNILTDHNVDNV-LQGH--QGGLE-----HLD
MtSEOc     ------------------------------------LTMSDDQIL-DQIYSTHVHSDTKFDAASLFTLAQNTLARSTHIVDSV-VQGT--KVSLE-----QAD
GmSEOs     ------------------------------------LTMSDEQIL-EQIYSTHVHSDTKFDVDSLFTLVENTLRRSTHIVDNL-VQGS--HASLE-----HID
GmSEOg     ------------------------------------LNMSDEQIL-EQIYSTHVHSHTKFDVDSLFILVENTLRRSTLIVDNV-VQGS--KASSE-----QVE
GmSEOr     ------------------------------------LNMSDEQIL-DQIYSTHVHSHTKFDVDSLFILVENTLRRSTLIVDNV-VQGS--KASLE-----QVE
GmSEOl     ------------------------------------FEVSDDQIL-ERIYITHFHCVEKYDVGVLYSVASNVIKHSIEIADMI----IKDGQQIE-----QVR
GmSEOo     ------------------------------------FEFSEDKIL-DDVYRTHFDCFEKCDVTSLQTVASNVINHSIDISEKV-ISKG--DQLRE-----QFS
GmSEOj     ------------------------------------FEFSDEQIL-DNVYRTHFHCVEKCDVASLHTVASCVISHSIEITDTV-ITKG--SQLSD-----RFR
GmSEOp     ------------------------------------FEFSDEQIL-DNVYRTHFHCVEKCDVTSLHTVASCVINHSIEITDTV-ITKG--SQLSD-----RFR
MtSEO-F3   ------------------------------------LAWSDDKIL-ETVYLTHVHTGERYDVESLFNLTSNILKRSTAVADSV-ASKT--GTPVG-----LVE
GmSEOa     ------------------------------------LGWTDDQIL-EKVYITHVHTAERYDVESLFNVTTNIIKRATALADSV-AVKT--GTPVG-----LIE
GmSEOf     ------------------------------------LGWTDDQIL-EKVYITHVHTAERYDVESLFNVTANIIKRSTALADSV-AVKT--GTPVG-----LIE
```

6

## Motif 5        Motif 6

```
Group 1
CgSEOa    GKIL-ITE---FKPEFHKLKLLSCQMITIP-SGLENA-----------HQTTMRILQQLRSFSWGTKALIALAAFALEYGNFWNLYQ-LPPSDQLGNSL
GmSEO-F3  NPIT-ISS---FKPEFSTLKLMSCQMMTLP-WGPENA-----------HQTTLRILQQLRKYSWDAKALIALAAFALEYGNFWNLQQ---ASDPLGNSL
GmSEO-F4  -PIS-AAS---FKPDFLTLKLISCQMISTR-SAAHCV-----------HQTTMWILQHLKCYSWDAKALIAIAALSLEYGSFVHLTQ-FQTNDVLGNSL
LjSEO-F1  -QIP-ATS---FKPEFSTLKLISCQMITTR-NADHCV-----------HQTTMWILQNLRSYSWDAKAIITLAAFTLEYGNYLHLSR-AAVADTLGSSL
MtSEO-F4  -KIS-VTS---FKPEFPTLKLISCQMITTR-NDPHCV-----------HQTTLWILQNLRSYSWDAKALITLAAFTLEYGNYLQLNR-VTTTDTLGNSL
          -?IP-VTG---FKPDFPTLKLISCQMITTR-SAAHCV-----------HQTTLWILQNLRSYSWDAKALITLAAFTLEYGNYLQLNR-VTATDPIGNSL
          IP-VTG---FKPDFPTLKLISCQMITTR-SVAHCV-----------HQTTLWILQNLRSYSWDAKALITLAAFTLEYGNYLQLNR-VTATDPIGNSL
          IP-LAK---YKPEFPTLKLISCQMITTR-GVVHCA-----------HQTTMWILQHLRSFSWDAKALITVAAFSLEYGNFRHLQ--IPTSDQLGNAL
GmSEO-F1  GKAS-QTI---FQPEFRTMKLISCQMITTP-HGERYV-----------HQTTMCILQHLRSYSWEAKALVTLAAFALEYGNLLHLSDVETPENQLTNSL
MtSEO-F1  SRAE-------FEPEFRTLKLMSCQMITTP-RGERYV-----------HQTTMWILQQLRSYSWDAKALIALAAFTLEYGNLLYLTETSTSSDQLVNSL
MtSEO-F2  TDIS-------FKPDFSVLKRISCQMITTR-GTAECA-----------HQTTMWVLHHLRGFSWEAKALITLAAFSLEYGAIMHLHR-IQSSDTLGNSL
GmSEO-F2  AATTSVTS---LKPDFPTLKRLSCQMITTR-GTPECA-----------HQTALRILQQLSGFSWDAKALIAVAGFSLEYGEFWRLDR-VQAADQFGNSL
GmSEOu    ALASSVTS---FKPDFPTLKWLSCQMITTR-GTPECA-----------HQTALRILQQLSGFSWDAKALVAVAASLEYGEFLRLDR-VQAADQFGNSL
AtSEOa    KDYADHTS---FETFADLIDQISCEIDCKCLHGGESHGMMTSGLHLDSRNTTTFSVLSLVSKYRWDAKLVLVLSALAVKYGVFLLLAE-THATNQLTKSL
SpSEOb    EKAPHSGLTELLNYLAYPIHRISMELISKC-ANKEDA-----------HSTTMSLLHSLTTYAWDTKVAITFAAFAQQYGEFGLLVH-QYTTDPLAKSV
SpSEOc    EKAPHSGLTEILNYLAYPIHRISMELISKC-ANKEDA-----------HSTTMSLLHSLTTYAWDTKVAITFAAFAQQYGEFGLLVH-QYTTNPLAKSV
GmSEOe    DSAYQSDLANVIDISYHTINKISCEICCKC-SSGGDV-----------HATTMGILGMLSSYSWDAKVVIALAAFAANFGEFWLVAQ-LYATNRLAKSV
SpSEOa    EKAS-LAFDGILEGLAYIIHKVSCELTCKCSSGGHDT-----------HSTTMSILGMLSGYQWDAKLVISLSAFAVTYGEFWLVAQ-MFATHPLAKSV
GmSEOc    MTAA-LAEFDMLDSLAYIINKISCELSCKC-SGGGDA-----------HSSTMVLLNYMSSYAWHAKVVLTLAAFAVIFGEFWLVAQ-LSAENTLAKSV
GmSEOd    MTAA-LAEFDMLDSLAYIINKISCELSCKC-SGGGDA-----------HSSTMVLLNYISSYAWHAKVVLTLAAFAVIFGEFWLVAQ-LSAENTLAKSV
AtSEOb    DKLMQSSMMSVLDSVSYAIDRVACEIAYKS-LTGSDS-----------HEITMSVFEHLSSFQWDGKLVLTLAAFALNYGEFWLLVQ-FYSKNQLAKSL
GmSEOm    DRSHRPGHTNMLEALSAKIDRISCEISYKT-LNGVDA-----------HSTTIAIFDMLTIYKWDVKIVLALAAFALTYGEFWLLAQ-IHDTNQLAKSM
MtSEOe    DRTHLPSYTSMLEALSVKIDRISCEISYKI-LSGVDA-----------HSTTVAIFEMLTIYKWDVKIVLALAAFALNYGEFWLLAH-IHDTNQLAKSM
GmSEOi    NDITEIETIGCSEPGGFIITKIG-KVLCRC-SGEGDI-----------NSRIILNLFDLIGKYSWDAKVVLVLAAFAVRYGEFWQLKQ-LYRGNALAALI
MdSEOa    EKPP-KAT---FSSPLCTLKSIGCEMSCKP-PGEEIA-----------HKSTLAILNKLSTYSWEAKAVLAFAAFALEYGEFWLLAQ-TQQSDLLAKSV
MdSEOb    ENTP-KAG---FSAPLCTLKSIASEMQCKP-PSEEVA-----------HNTTLAILNKLSSYSWEAKAVLTLAAFAMEYGEFWLLAQ-LQESDRLAKSV
MtSEOa    NINP-PAS---FTSPLCTLKKINSEMACKA-PGEEVA-----------YRTTLAILNKLSNYSWVAKGVLTLSAFALEYGEFWLLSQ-YLPTEPLAKSL
MtSEOb    NINP-PAS---FTSPLCTLKQINSEMSCKA-PGEEIA-----------YKTTLAILKKLSNYSWVAKGVLTLSAFSLEYGEFWLLSQ-NLPTEPLAKSL
MtSEOc    DKSL-IPN---FSSPLCTLKSISSEMSCKP-PSEEIA-----------HKTTLAILNKLSHYDWEAKAVLTLSAFALEFGEFWLLEQ-HLSTDPLAKSV
GmSEOs    DKIP-Q-----FNSPLCTLKQISFEMSCKP-PSEEIG-----------HRTTLAILNKLSNYSWDAKAVLTLAAFALEYSEFWLLAQ-YQPTDPLAKSV
GmSEOg    DKIP-QAN---FNSPLCTLKQIYSEMSCKP-QGEEIA-----------HITTMAILVKLSNYEWDAKAVLTLAAFAMEYGEFWLLAQ-NQPTDPIAKSV
GmSEOr    DKIP-QAN---FNSPLYTLKQIYSEMSCKP-PGEEIA-----------HITTMAILVKLSNYEWDAKAVLTLAAFAMEYGEFWLLAQ-HQPTDPIAKSV
GmSEOl    EETDPLTS---FQR-LPAMKRIACQMMCTA-RGEQYA-----------HQTTMLILEQLRDYSWDAKAVIVLAAFALEFGKFWQLAH--IPRDKLGQSL
GmSEOo    EEIN-ISS----QQLTAKLRRIAYLMICTP-RGEHFG-----------RTTMLILEQLKHYSWDAKVLIVQAAFSLEYGKIMYLPLTTQCQQQIENLF
GmSEOj    EDTT-ITS----QQLTAKLKRIACQMVCTA-RGDHYA-----------HHTTMLILEQLKAYSWDAKALIVQAAFALEYGKFLYLPL-TTQYQMSEKSL
GmSEOp    EDTT-ITS----QQLTAKLKRIACQMVCTA-RGDHYA-----------HHTTMLILEQLKAYSWDAKALIVQAAFALEYGKFLYLPL-TTQYQMSEKSL
MtSEO-F3  DRLP-LSG---YEPPIRKLKHISAQMMSTL-PGEHHA-----------HMTTMSILDQLKSHTWDGKAIFALAAFSLEYGNFWHLVQ-TPSGDTLGRSL
GmSEOa    DKVP-LST---FDPPFLKLKHIASQMMNTP-HGEHHA-----------HNTAMSILDQLRTYTWDGKAIMGLAALALEYGNFWHLVQ-TPTGDHLGRSL
GmSEOf    DKVP-LST---FDPPFLKLKHIASQMMNTP-HGEHHA-----------HSTAMSILDQLRTYTWDGKAILVLAALALEYGNFWHLVQ-TPTGDHLGRSL
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Group 1
CgSEOa    KLLNQI----------QHRQIPIIDINNSVVLVMEVVQKIKNWGIWIA-EGYDTEDVP----ALSDALQEIPLVVYWAVASLVACNSTFVGLSN------
GmSEO-F3  RLLNQI----------QHRQLPVTDINATVKLVMEAVEKIRRWGTLSSDETYETEDVP----ALSDALQLIPLLVWVVASLVACNTNIQGVSN------
GmSEO-F4  RDLNQV----------QNRNA--SAVGELVMYVVQVFQHINEWATYAA-DGYDPEDVP----DLTEAFQAILVVYWSIASTVASTGNLIGVSN------
LjSEO-F1  RDLNQV----------HTRKVP-ADITKLVTFIVHAFQHLKEWATWAD-EGYEPEEVP----SLTEALQHVPVAVYWTIAAIVASTGNLVGVST------
MtSEO-F4  RVLNQV----------QTRKIS-NDVTELKYIVDMLIHLNVWATWSA-DGYDPVDVP----ALTDALQEIPVFVYWTIASIVASTGNLVGVSD------
          -LNQI----------QTRNIS-VSFIVHQLLHLKEWATWSA-EGYDPEDVP----ALTEALQEIPVFVYWTIASIVASTGNLVGVSD------
          -LNQI----------QTRKIS-TDIPELVNFIVHKLLHLKEWAAWSA-EGYDPEDVP----ALTEALQEIPVFVYWTIASIVASTGNLVGVSD------
          -LNQV----------NNGKLS-DDITELATVTVRVLQHLKEWAAWSA-AGYDTEDVP----ALSDALQVIPFVVYWTIASIVASTGNLIGVSD------
GmSEO-F1  KDLNQV----------QARK---NPGTTLVELVMEVLHGIQEWSRLSG-LDYDIVEVP----SLTDAQQEVPVVVYWMIASLVAATANLVALSE------
MtSEO-F1  KILNQI----------QNRKVT-VPATDLVELIMDLHIHEWATRSG-VGYNTLDVP----SLSDALQDIPVAVYWIIASTVAATGNIIGVSD------
MtSEO-F2  KDLSQV----------QFRKVP-ADITELVTFLLQVLQDIKTWAAWSA-FGYDLDDVN----SLPDAMQWIPLVVYWTVATIVACTGNLVGISE------
GmSEO-F2  KDLNQV----------QISRRVP-ADMIDLVTVLGEVLSYINLWAKWSA-MDYDTEAVH----SLQAAMQEIPLVVYWTIASVASIGNLVGISE------
GmSEOu    KDLNQV----------QISRRVP-ADMTDLVTVIGEVLNYINLWAKWSA-MDYDIEAVH----SLQAAMQEIPLVVYWTIASTVASIGNLVGISE------
AtSEOa    ALIKQLPSIFSRQNALHQRL---DKTRILMQDMVDLTTTIIDIYQLPP--NHITAAF----------TDHIPTAVYWIVRCVLICVSHISGASGFKQDQI
SpSEOb    AIIMELPEIMTRQDVLKQKF---DAIHDLIDKMLDVTKCIIEFRDVQT--SHNQHVIITQELEMLINTAHISTAAYWTMRAAVMCAAMILNLIAIGHEQI
SpSEOc    AIIMELPEIMTRQDVLKQKF---DAIHDLIDKMLDVTKCIIEFRDVQT--SHNQQVIT-QELEMLINTAHISTAAYWTMRAAVMCAAMILNLIAIGHEQI
GmSEOe    AKLKHIHETLEQVDDLGPKF---QTVNNLLKAMLDVTNNIVQFHELPS--QYIDPEAP----EMLTASNLIPGAVYWTIRSIVSCASHILGITGLGQGYM
SpSEOa    AILKQLPDIMEHHGSLRSRF---DAINELKAILEVTKIIEVTKIIEFKKLPS--QYISEDQP----PLSVAITHIPTAVYWTIKSIVACASQLTTLLGMSYDMI
GmSEOc    ALLKQLPDIAENFMSLKPHF---EALIRLVKAAMDVTMCIVEFKELPS--EYISEDTP----PMSVASTHIPIASYWVIRSIVACSSQIASLVGMRNESI
GmSEOd    ALLKQLPDIAENFMSMKPHF---EALIRLVKAAMDVTMCIVEFKELPS--EYISEDTP----PMSVASTHIPIASYWVIRSIVACSSQISSFIGMRNESI
AtSEOb    AMLKLVP--VQNRVTLESVS---QGLNDLIREMKSVTACVVELSELPD--RYITPDVP----QLSRILSTIPIAVYWTIRSVIACISQINMITAMGHEMM
GmSEOm    AILKLLPSIMEHGSSLKPRF---DTLNDLVNILEVTKCVIEFPLDQA--QYITQDIS---AYTTAYNIYPIAVYWSWATRSIVACAAQITSLTTLGYEIF
MtSEOe    AILKQLPGIMEHSSSLKPRF---DTLNDLVNVILEVTKCVIEFNDLPI--QYIRQDVS----AYNTVSNHIPVAAYWSIRSIVACAAQITSLTTLGYEIF
GmSEOi    SNIKQL------PNNLKPLKLQIKALSLLVKTMMDVAMCIIKFEYLPLQHVEPGNDIF----LVRDTKSRIYEAAYWITRSCLACFSQVMDFTAKKHDQV
MdSEOa    AILKRVPVLLKPTDLQKRRQAI-VELNVLIKTTLQVIECIFELEKLSA--YDPKDVP----ALAIAMDHIPVDVYWSIITIFSCATKITLLTSDEEKP-
MdSEOb    AILKRVPVLLKPSDLHKRQAI-VELNNLIKATLQVICIDQFDKLSS---YDPKDVP----ALALAMDHIPVDVYWAVATVVCACATKITILTCNEDKE-
MtSEOa    AIMKRVPQLTKPELLKKHRYAV-LEVNNLIKATSQLIDIIIALERLNS--RHDIKEVP----ALAPALEQFPVDVYWVIITIVAIVTQIECLTTDSEER-
MtSEOb    GIIKRVPQLSKPEALKKHRNEI-LELNNLIKATWQVIEIIIALERLNS--RHDIKEVP----ALAPALEQFPVDVYWVIITIVAIVTQFECLTTNSDKR-
MtSEOc    ALLKRVPILAKPAAIQKHRQAI-TELNSLVKITLQVIEFILELDYLND--RYDTKVVP----ALELAYEQIPVDVYWTIITIAAIVTQLDCLITESEHK-
GmSEOs    AIFKRVPLAKPAALQKHRQAI-LEVNNLVKATLQVIEVIFELEKLTT---YDTKDVP----ALGLAIEQIPVDVYWAIITIVAVVTQIDCLTTDSEHK-
GmSEOg    AALKGVPVLTRPAALQKHRQAI-TELNNLVKTTLLVIEFIFELEKLTT---FDTKDVP----ALLPAIEQIPVDVYWAIITIIAAIVTQIDYLTTELGNK-
GmSEOr    AVLKGVPVLTRPAAVQKHRQAI-TELNNLVKTTLLVIEFIFELEKLTT---FDTKDVP----ALLPAIEQIPVDVYWAIITIVAIVTQIDYLTTESGNK-
GmSEOl    AELNGL------QSIMENIQHL-ANFNNLVKKIVQVVKCITDWKKMIT-AEYNVKDVP----SLTDTLHEIPVLAYWTISTLVTCTSHIDFLGDKGYR--
GmSEOo    ADLNGL------LMVPQNTQHL-PYFNSVVKKAMQMIECIIEWKRLIS-LGHDIKDVP----TLAETFHQIPVVVYWAIFTFVSCTGQIDEFTDYKVQR-
GmSEOj    ADLNGL------LMIQHNTQHL-TFFNSVVKKVMQVIECITEWKRLTS-AGYDIKDVP----TLAETLHEIPVVVYWAIFTFVTCTGQIDDFTTDHKIHK
GmSEOp    ADLNGL------LMIQHNTQHL-TFFNSVVKKVMQVIECITEWKRLTS-AGYDIKDVP----TLAETLHEIPVVVYWAIFTFVTCTGQIDDFTTDHKIHK
MtSEO-F3  ATMNRV------QSVDKNRQAI-ADYNSLVKNLLFAVECITELEKLST-KGYEHKDVP----ALSEAMQEIPVAVYWAIITAIICANHLDLLFGDSDDR-
GmSEOa    AQMSRV------HIVERNRQAV-ADYNSLVKNLLIAVECITELERLST-KGYDLKDVP----ALAEAMQETPVAVYWAIVTTVVCANHFDFLLGESDSR-
GmSEOf    AQMSRV------HIVERNRQAV-ADYNSLVKNLLIAVECITELERLST-KGYDLKDVP----ALAEAMQEIPVAVYWAIVTTVVCANHFDFLLGESDSR-
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CgSEOa    -------YTIP-DFSAKLAPALRELNRHLDICKLQIDD---IEDYMSRKRN-----FRKPK-DVVDFLKLLFN---RNGSSDAQVFD--GSAQTKVSV
GmSEO-F3  -------YALS-DFRGKLSTALDEFKHHLEICEQQKAS---IEDYRRRKKA-----FKKPK-DIVDFLKLLI-NQNGYKSQIYD-GNANRNVNV
GmSEO-F4  -------YKLS-EYTFRLSTAVNKLTMHLTKVKEQIAN---VRDYITIRNI-----FDRPK-DIVDLLKALIYPQ-QKGAENPKIFE--GTNLVTKGI
LjSEO-F1  -------YNLQ-GYIDRLDEHVTKLAEQLNSCKLQIGH---VDDYFNRRKI-----FDKPK-DIVDLLKALIH---RNGAQGPQIFE--GGVIVKQGL
MtSEO-F4  -------YKLS-AYKERLSRVVEELVKHLATCERQIRN---VDDLTSRTNN-----YRKPK-DIVDCLKALIH---RNGTDIPQIYQ--GNVQVKSGL
          -------YKLS-EYRERLSGIVQKLVVHLNNCKLQISY---IDDLFNRKKI-----FDKPK-DIVDCLKALIH---RNGTDSPQIYE--GAIHVKTGL
[Group 1] -------YNLS-EYRERLSGIVQKLVVHLNNCKLQISY---IDDLFNRRKI-----FDKPK-DIVDCLKALIH---HNGADSPQIYE--GAIHVKTGL
          -------YKLS-DFKDKLDRVVKTLNDHLDECKKQIDV---IDNYNWRRKA-----FENPK-DIVDLLKLLIH---SKGSPIPQIYD--GRTTTKTDI
GmSEO-F1  -------YKLA-DFLDRLSSAADKFKEHLKSSVVQKGY---ADENYKRRKA-----FSNPK-DIVEFLKLLIQ---HNGSKV-QIYD--GSIKTKTDI
MtSEO-F1  -------YTLS-DFKEKLNFVDSKLKEHLKLSKWQIDS---VEEYLKRRKA-----ISNPK-DIIDFLKLLIQ---RNGDNL-LIYD--GTTKNKTDI
MtSEO-F2  -------HKLS-DYVKSLSDVVKELRRHLKSCELEIGK---IHENENLLKD-----SDNIK-DVVAFLRLLIKG--NGTDQIPPIFI--GNDQVKTGI
GmSEO-F2  -------HKLS-AYKERLEFIFKKLQFHLENCRVEIGR---IQDYHIRFNIR---YPKIK-DVVELLDILIIPGSDNGTSIPKIFE--GGVLIKNGI
GmSEOu    -------HKLS-AYKERLEFIFKKLQFHLENCRVEIGR---IQDYCFRNTIR---YPKLK-DVVELLDILIIPGSDNGTSIPKIFE--GGVLIKNGI
AtSEOa    -MSFM--EVSEIH-ENSERLRKINAYLLEQFKKSKMTIEEGIIEEEYQELIQT-----FTTII-HVDVVPPLL----RLLRPIDFLYHGAGVSKRRVGI
SpSEOb    -SSTS--EAWELS-SLTHKLANILDHLRKVLDLCHQKIEEKRQHDAFEALLRL-----LRTPHIDNMKILSILI---HSRDNQLPLFD--GTHKRRVGL
SpSEOc    -SSTS--EAWELS-SLTHKLANILDHLRKVLDLCHQKIEEKRQHDAFEALLRL-----LRTPHIDNMKILSILI---HSRDDQLPLFD--GTHKRRVSL
GmSEOe    -TSTT--ETWELS-SLAHKLDNINSHLRQLTVCRQHLDDNRQEAFATLRLL-----FETPHQDNSKVLKAMF----CSKDDPLPLFD--GSSKQRVSI
SpSEOa    VASTA--DTWEMS-SSTHKLRNISEHLRAELNRCYQHIQDKMHIEYFQMLVHL-----FEATQFDNMKIMRAMI---YIKDDLLPLEV--GTTHTRASV
GmSEOc    -SSTT--EAWELS-SLAHKVSSIYEHLKNQLVLCYQYIDDKRHIEAFHNLIRL-----FETVHVDNMKILRALI---YAKDDVLPLVD--GTTKSRVSL
GmSEOd    -SSTT--EAWELS-SLAHKVSSIYEHLKNQLVLCYQYIDDKRHIEAFHNLIRL-----FETVHVDNMKILRALI---YAKDDVLPLVD--GTAKSRVSL
AtSEOb    -NTQM--DLWETS-MLANKLKNIHDHLAETLRLCYRHIEKQRSSESLKVLHSL-----FDTTHIDNMKILTALV---HPKPHITPLQD--GLTKRKVHL
GmSEOm    --TST--DAWELS-TLIFKLKNIVDHLRQLLNSCHEHIGKKMDAEAYQMLREL-----FSKPHTDNMKVLKALI---YAQDDILPLYD--GVTKKRVSL
MtSEOe    --TSN--DAWELS-TLAFKLRSIVDHLRKQLDICKIHVEEAMDTEAYGMLREL-----FLTPHTDNMKIIKALI---YSHDDILPLYD--GVSKKRASL
GmSEOi    YSDSAIIAAWELS-SLAYRLSGICCNLRRQVDLCHKELER----NLYDRLLDL-----AREENIDNQKTLTLF-----FPSKNYLPLKD--CSTEVKLRG
MdSEOa    ---------YDLS-QFAQKIHYILNKLKIQLLICKKQIEE---AETYRLRKL-----FQTPA-EVMEVFKALI---FTKDTVQPIID--GSTNKTVSI
MdSEOb    ---------HDLA-PFAQKIHYVLNKLKIQLIVCRKQIEE---AETYRRLRKI-----FRTPT-EIMEVFKALI---FTKENVQPLVD--GSTKQMVKI
MtSEOa    ---------QDLS-QFGQKINIIISKLRKHVSQITIQIDE---AEYNKLLKKL-----FQTPT-EIMEVFKVLIF--WKDTPQTPIYC--GSTKTLVNI
MtSEOb    ---------QDLS-HFGQKINIIISKHVSQCTIQIDE---AEYNKLLKKL-----FQTPT-EIMEVFKVLVF--WKDTPKAPIYD--GSTKTLVNI
MtSEOc    ---------QELS-HYGQKINIILSRLRKQITVCRQQIDT---AKYIQELKKL-----LQTPT-EITVVLSFLI---FPKDVPQLLYD--GATKTTVDI
GmSEOs    ---------QELS-HYGQKINIILSRLRKQITLCRQQIDE---AQYYRLRKF-----FQTPT-EIMEVFKVLI---FNKDAPQPLFD--GATKTKVDI
GmSEOg    ---------QDLS-HYGQKMNIILSRLRKQIMLCRQQIEE---AEYHQRLRKF-----FQTPT-EIMEVFKFLV---YSKDAPQLLFH--GATKTTVEI
GmSEOr    ---------QDLS-HYGQKINIILSRLRKQIMLCRQQIEE---AEYHHRLRKF-----FQTPT-EIMEVFKFLV---YSKDAPQLLFD--GAAKTTVEI
GmSEOl    ---------YDLS-KFDYKLDFILKNFKDHQDKCSTQIGQ---IEDYSRRKDIITSIQTDTQI-DIVKFLEALIIPS-YSQDSRPIVYN--GLTGPQVAL
GmSEOo    ---------HELSKSFEPKLDSILGKFKEFLERCSKEIVR---IEDYTRREKIV----IHTGK-NIVKVLKALIISR-ENRDLRQNVFN--VLTGEQVKI
GmSEOj    ---------HELSKNFENKLDLILRNFKEHLEMCGREIGR---IEDYTRRKNIV----IHTGK-DIVKVLKALIISG-ENRESRQSVFN--VLTGEQIKI
GmSEOp    ---------HELSKNFENKLDLILRNFKEHLEMCGREIGR---IEDYTRRKNIV----IHTGK-DIVKVLKALIISG-ENRESRQSVFN--ILTGEQIKI
MtSEO-F3  ---------YELS-SYDVKLASIVSKLKAHLTRSRKHIGE---LEDYWRRKRV-----LQTPT-EIVEVLKVLVF---HNEIQDPLVFD--GLNRQMVSI
GmSEOa    ---------YEIA-NFDDKLAAVISKLKANLTRSRKKIGD---LEDYWRRKKL-----LQTPT-EIVEVLKVLIY---HNEVHDPHVYD--GITRQMVSI
GmSEOf    ---------YEIA-NFDDKLAAVISKLKANLTRSRKKIGD---LEDYWRRKKL-----LQTPT-EIVEVLKVLIY---HNEVHDPHVYD--GLTRQMVSI
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**Motif 7**

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CgSEOa    F-VFKQKHVLLFIS--TL-DSIADEIRLLNSINDRLVEDPNDK-TG-FKKEEFKILWVPIVDR----WD-DER--KEVL-KSFK-NGIKWYVLEYTS-PL
GmSEO-F3  H-VFKEKYVLLFIS--GL-DRIEDEIRLLNSIYERLVEDPNDK-SG-FKKEEFKILWIPIENK----WG-DAR--RELF-NTLK-SDIKWYVVEYAQVPL
GmSEO-F4  F-VFRQKHVLLFIS--GL-DSIEDEISLLNSIYERLQEDPREA-KG-FKKEDFKILWIPIVVK----WS-QSS--REQF-KALK-SGTKFYAVEYFF-EL
LjSEO-F1  H-VFRQKHVLLFIS--GL-NSIVDEILLLNSIYNRLQDNPTEVIKG-FKKEDFKILWVPMVDR----WD-EAS--REQYLNTWK-RGIKWYIVEYFF-EL
MtSEO-F4  F-IFKQKHVLLFIS--SL-DRIQDEITLLNSIYERLQENPKES-KG-FMKEDFKILWIPIVKK----WD-DIQ--IENF-KALK-SGIKWYVVEYFS-EL
          D-VFRNKHVLVFIS--SL-DSIEDEISLLNSIYERLQENSKESIKG-FKKEDFKILWIPIVNN----WD-DIR--KERF-RALK-SGIKWYAVEYFY-EL
[Group 1] V-VFRHKHVLMFIS--SL-DSIEDEISLLNSIYERLQENSKESIKG-FKKEDFKILWIPIVNN----WD-DIR--KERF-RALK-SGIKWYAVEYFY-EL
          V-VFKQKYVLLFIS--SL-DSIDDERLLNSIYDRLKEDPNEV-KG-FKKEDFKILWIPIVDS----WD-KDS--VEKY-KTLK-TKIKWYAVEFLS-LV
GmSEO-F1  E-VFNQKYVLLFIS--SL-DKIEDEISLLNTIHDRLQENPNEVVKN-YKKGDFKILWIPIVDT----WD-DKQ--KHKF-NILK-NTIKWYAVEFFT-EL
MtSEO-F1  H-VFKDKYVLLFIS--SL-NKVDDEILLLNSIHDRLQDNPQVI-KG-YKKEDFKILWIPI-------WDVDDQ--KIKF-DSLK-NKIRFYAVDYFS-EL
MtSEO-F2  H-VFKKKHVLLFVS--GL-DTLRDEILLLNSIYKRLQDKPQEVLKGSFKKEDFKILWIPIVNK----WD-EDR--KKEF-KNLK-ESMKWYVLEHFS-EL
GmSEO-F2  F-VFQKKYVMLFFS--SL-DSIGDEILLLNSINNGLQENPGEEIKG-FKKGDFKILWIPIVDD----W--KSK--REQF-TNLK-EKIKFYLVEYFE-EL
GmSEOu    F-VFKQKYVMLFFS--SL-DNIGDEISLLNSINNGLQENPGEEIKG-FKKGDFKILWIPIVDI----W--KIT--REQF-NNLK-EKIKFYLVEYFE-KL
AtSEOa    N-VLTQKHVLLLIS--DL-ENIEKELYIILESLYTE------------AWQQSFEILWVPVQDF----WT-EAD--DAKF-EALH-MNMRWYVLGEPR-KL
SpSEOb    D-VLRRKHVLLLIS--DL-DIAPEELFILHHMYAESKTQPN------RPESNYEVVWIPVVDKRLSPWT-EAK--QMKF-EEVQ-ASMPWYSVAHPS-MI
SpSEOc    D-VLRRKHVLLLIS--DL-DIAPEELFVLHHMYDESKTQPN------RPESNYDVVWIPVVDKRLTPWT-EAK--QMKF-EEVQ-ASMPWYSVAHPS-MI
GmSEOe    E-VLRRKIVLLYIT--DVHNVPDQELVIFEQMYQSRQDST------RLESQYELVWIPVVDK-AIPWN-DV---KPKF-EKLQ-SMMSCYSLYDPS-LL
SpSEOa    E-VLRRKTVLLLLS--DL-EASHEEILVLSQIYLESRSRPE------FQ---YEIVWLPIVDR-SKGWN-DAQ--EQKF-KELQ-ALMPWYTLHHPS-LL
GmSEOc    E-VLRRKHVLLLIS--DL-DLSQEEILVLDNLYKDARA---------RGDTHYEMVWIPVVDK-ATWN-ETS--KQKF-EYLQ-SLMAWYSVDPF-II
GmSEOd    E-VLRRKHVLLLIS--DL-DLSQEEILVLDNLYKDARA---------RGDTQYEMVWIPIVDK-ATWN-DMS--KQKF-EYLQ-SLMAWYSVDPF-II
AtSEOb    D-VLRRKTVLLLIS--DL-NILQDELSIFEQIYTESRRNLVGV-DG-KSHMPYEVVWVPVVDP-IEDFE-RSP-ILQKF-EDLR-DPMPWYSVDSPK-LI
GmSEOm    E-PLRRKNVLLLFS--GM-EISTDELLILEQIYNESKAHAP------RMESRYELVWIPIVDP-NSEWI-EPK--QKQF-EILQ-ESMSWYSVVHPS-LI
MtSEOe    E-ALRRKNVLLLFS--GL-EFSTDELLILEQIYNESKAHAP------RQDNRYELVWIPIVDQ-TSEWT-DQK--QMQF-ENLR-ESMPWFSVYHPS-LI
GmSEOi    S-ELKNKTVLLLISKPQLLNPIDIYLLVQQTCDHPLNE--------RLRESYKIVWIPLPSS--DTWT-EAE--ESSF-NFMS-DSLPWNAVRKPR-LL
MdSEOa    D-VLRRKYVLLFIS--TL-DISDDDISIVKPVYEGT-----------KKDDAYKIVWIPIVEQ----WT-DDL--RKKF-EVLR-AKMPWYTVQYFA-PV
MdSEOb    D-ILRRKNVLLFIS--SL-DISDDDISILKPIYDMI-----------KKDNQHKIVWIPIVEVN---WT-DDR--RKKF-ESLR-NKMPWYTVQISA-PV
MtSEOa    D-VLKKKDVFLFIS--TL-DICQEDISTMIRIYDHIQ----------KTGSQHQIVWIPIVEE----WN-DRG--RKKF-DSLK-SKMPWYVLHHFA-TI
MtSEOb    E-VLKKKDVFLFIS--TL-DISQEDISILIPIYDHIK----------KTGSQHKIVWIPIVEE----WN-DKL--RKKF-DSLK-SKMPWYVLHHFA-PI
MtSEOc    N-VVLKKKNVYLFVS--TL-DVTEEEITAVRSVYESI----------KTNEQYKIVWIPIVEG----WN-EQL--RKKF-DILR-SKMPWYVVQNVE-NI
GmSEOs    T-VLKKKNVYLFIS--SL-DITEEEISVLSRKLRKQ-----------KTNDQYKIVWIPIVEE----WT-EQL--HKKF-EVLK-SKMPWYVVQHSG-TI
GmSEOg    T-ELKKKHVYLLIS--TL-DITEEEISVLQPVYDSI-----------KTGDQYKIVWIPIVEE----WN-EML--HKRF-EFLK-SKMPWYVVQHFG-AI
GmSEOr    T-ELKKKHVYLLIS--TL-DITEEEISVLRPVYDSI-----------KANDQYKIVWIPIVEE----WT-EKL--HKKF-EFLK-SKMPWYVVQHSG-PI
GmSEOl    G-EFKNKHVLLFIS--GL-DHIDNEIQLLKSINAKLKEEPNEL-EG-YRKEDFKILWIPIVSV----WD-EQ---KKKL-DV---TKVEWYVVKEFN-FQ
GmSEOo    E-EFK-KYVLLFIS--GL-DKIEDEIRLLKSIHKLKEKPREV-EG-YRSEDFKILWIPIVDD----WN-EER--RKKLESHLQCNKFGWYVVKYFN-FE
GmSEOj    E-EFKKKHVLLFIS--GL-DSIEEETLLLKSIHELKEKPREV-EG-YRKDDFKILWIPIVDE----WN-EER--RKTLETKLQRTKFGWYVVKHFS-FE
GmSEOp    E-EFKKKHVLLFIS--GL-DSIEEETLLLKSIYELKEKPREV-EG-YRKDDFKILWIPIVDE----WN-EER--RKTLETKLQRTKFGWYVVKHFN-FE
MtSEO-F3  E-VFRKKHVLVFIS--GL-DSIRDEIRLLQSIYVGLQEPREL-KG-YRKEDFRILWVPIVDD----WT-LLH--KAEF-DNLK-LEMPWYVVEFY-PL
GmSEOa    E-VFRKKHVLLFIS--GL-DSIRDEVRLLQSIYEGLQEDPREV-KG-YRKEDFRILWVPVVDE----WN-LLH--RAEY-DNLK-LEMPWYVAEYFY-PL
GmSEOf    E-VFRKKHVLLFIS--GL-DSIRDEVRLLQSIYEGLQEDPREV-KG-YRKEDFRILWVPVVDE----WN-LLH--RAEY-DNLK-LEMPWYVTEYFY-PL
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Multiple sequence alignment. Column annotations: **Motif 8** and **Motif 2** (Rüping et al. 2010).

Block 1 (Group 1 bracketed at top):

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                 Motif 8                        Motif 2
                                              (Rüping et al. 2010)

CgSEOa     PGIRLIR--EDLNFQN--KPIVPVVNP-HGIVINDDAMDIIFEWGID AFPFRKSDGDLLAQKW- -KWFWDEV GK-TNLDIQ--VKGDR-YIFIFGGND
GmSEO-F3   PGIRLIE--EDLRFHG--KPILPVVKP-QGVLLNDDALDIIFEWGID AFPFRKSDAYLLAQKW- -KWFWDEV KKTNLHGIQ--VKGDR-YIFIYGGSD
GmSEO-F4   PGLKIIKDTERLNYEI--QPIAPLFSS-KGTLLNGNALEVIFEWGID AFPFRKIDGDELTQKW- -KWLWDLI LK-ATPGLQ--VKENR-YIFIYGGAN
LjSEO-F1   PGRRIITDPERLGYEG--NPIIPVFNP-QGMLTNDNAMDLIFQWGID AFPFRKSDGIDLTLKW- -KWLWDII KK-ATPGLQ--VKVDR-YIFIFGSTN
MtSEO-F4   PGLKIIKDPELIGYID--NPIIPVFNP-KGIITNEDAMDLIFQWGID AFPFRKSDGNDLKLKW- -NWLWDVI KK-ATPGLL--VKVDR-YIFIYGGTN
           PGHIITDPERIGYIG--NPIIPVFNP-QGYITNIDAMDLIFQWGID AFPFRKSDGIDLTLKW- -KWLWDVI KK-ATPGLQ--VKGDR-YIFIYGGTN
           PGHRIITDPERIGYIG-NPIIPVFNP-HGYITNIDAMDLIFEWGVD AFPFRKSDGIDLTFKW- -KWLWDVI KK-ATPGLQ--VKGDR-YIFIYGGTN
-          PGIRLVR--EVLKFET--KPIIPVISP-QGKRINDNAMDIIFEWGVD AFPFRKEDGDQLTQKW- -KWFWDVI KK-VNPAIQ--VEPES-YIFIYGGTD
GmSEO-F1   PGTDLIK--EKFNYLG--KPIAPVLTP-LGDRMNEDAMDLIFQWGID AFPFRKIDGIDLTLKW- -KWFWDAT KK-ANLGIQQ-VTGDR-YIFISGGAD
MtSEO-F1   PGIRLIR--EHLNYSD--KPIVPVLSP-LGEKMNDDAMDLIFEWGID AFPFRKQDGYIDLTLKW -KWFWDVT KR-VNLGIQ--VKGDR-YIFIYGGND
MtSEO-F2   PGRGIIK--KKLNYDIGYPPILAVINP-QGDIINKDAMEIIFQWGID AFPFRISDAEDIFKKW- -EWFWKLN KK-VDVNIEK-MSWDR-YIFIYGGND
GmSEO-F2   PGYDIIM--DKFKYEG--LPIVSVVNP-QGQIMNENALQIIFEWGID AFPFRRSDVYDLNKKW- -KWFWNLI EQ-TDDNAKRLGKDNTSYAFIYGGND
GmSEOu     PGYDIIV--DKFKYEG--LPIVSVVNP-QGQIMNDNAMQIIFEWGID AFPFRRSDVYDLNKKW- -KWFWNLL EK-TDDNAKRLGKDNTSYVFIYGGND
AtSEOa     RRAAIRFVR--EWWGFKN--RPILVALDP-KGQVMSTNAFPMVWIWQPFAHPFTTARERDLWSEQ--EWNLEFLIDGTDPHSLNQLVDGK-YICLYGGED
SpSEOb     DPAVIRCIK--EVWGFKK--KPQLVVVLDP-QGKEANNNAYHMLWIGSLAFPFTKAREEALWKEQ--TWNIELLADSIDQNIFTWISEGK-CICLYGGED
SpSEOc     DPAVIRCIK--EVWGFKK--KPQLVVVLDP-QGKEANNNAYHMLWIGSLAFPFTKARETALWKEQ--TWNIELLADSIDQNVFTWISEGK-CICLYGGED
GmSEOe     EPATIRYIK--EVWLFKT--KPILVVLDP-QGKVVNLNAIPMMWIWGSLAYPFSSSREEALWNAE--TWGLVLLADSIDPSLLEWISEGK-YICLYGGDD
SpSEOa     EPAIVKFVK--EKWHFSK--KMMLVTLDPQQGKVACPNAIHMAWIWGNLAYPFTISKEESLWNME--SWRLELVVDGIDPNLIDWMASGK-FICLYGGED
GmSEOc     EPSAIKYIK--EVWNFSK--TAILVALDP-QGKLSSPNVVHMLWIWGNLAFPFTSEKEESLWKQE--IWSLELLVDGIDPTVLEWMTDGK-LICLYGGED
GmSEOd     EPSAVKYIK--EVWNFSK--KAILVALDP-QGRLSSPNAVHMIWIWGNLAFPFTSEKEESLWKQE--IWSLELLVDGIDPTVLEWMTEGK-LICLYGGED
AtSEOb     ERHVVEFMR--GRWHFMN--KPILVVIDP-QGNEASLNALHMIWIWGTEAFPFTRSREEELWRRE--TFSLNLIVDGIDSVIFNWIKPDN-YIFLYGGDD
GmSEOm     GKPVIWFIQ--REWKYKN--KPILVVLDP-QGRVSCPNAIHMMWIWGSAAYPFTSSREEALWKEE--TWRLELLVDGIDQEILNWVKDGK-YIFLFGGDD
MtSEOe     SKAVVWFIQ--SEWKYKN--KPILVVLDP-QGRVACPNAIHMMWIWGSAAFPFTSFKEETLWKDE--TWRLELLVDGIDSEILNWIKEGK-YIFLYGGDD
GmSEOi     SSAVVKYIR--EQWNYKD--EPIMVALDS-KGKVTNYNALDMINIWGAQAYPFSASKEEELWQDQ--NLTMQLLLDGINPLLAYWVEQGK-NICLYGSEN
MdSEOa     --AGVRFIK--EEWHFKG--KPAVVVMNP-QGKVENTNALHLIRIHGMKAFPFHKGIEDTLTNDK--EWITPIVND-IHPTIQTWIKEEK-YIFFYGGKD
MdSEOb     --AGIRFIK--EEWSFKG--KPTLVVMNP-QGKVEHPNALHMIVRVWGVNAFPFTKATEEELSHGHGDKWIGTVVQG-VSQSVT--IKEDK-YIFFYGGKD
MtSEOa     --KGIRFIK--EELHFKL--NPLVVVLST-QGKILHQNAFHMIHVWGVKGFPFTKTKEESMTQEL--MWVDSVLVG-IDIKIK-W-REDD-IVIICGGKD
MtSEOb     --KGIKYIK--EELHFKQ--KPLFVVLSP-QGKILHHNAFHMIQVWGVKGFPYSKSKEESMTQEL--MWVDSLLAD-IDIKIK-W-KEEK-SVIIYGGKD
MtSEOc     --AGFKFIN--EEWDFKK--KSMFVVFSP-QGKVQHKNAFHLIKSYGIKAFPFTMDDEIRIQKDR--NWIVSVVGN-IDRNISIWTEQNK-HIFFYGGHD
GmSEOs     --AGYKYIK--EEWHFKK--KPMVVVLSP-QGKVQHSNAFHLIQAHGTRAFPFTTLNEEKINSEN--DWVGSVLGS-IHPSISTSIKEQK-YIFFYGGND
GmSEOg     --AGYKYIK--EEWHFKK--MPMVVVLNP-QGKVQHANAFHLIHVYGMKAFPFTIADQERIDREI--HWIGSVVGD-NHPHISTWIREQK-YILIYGGSD
GmSEOr     --AGYKYIK--EEWHFKK--KPMVVVLNP-QGKVQHANAFHLIHVYGMKAFPFTIADQERIDREI--HWIGSVVGD-SHPHISTWIREQK-YILIYGGSD
GmSEOl     --TGIDLIK--EVFNYKG--NPIIMLISP-EGKVENSDAKQIISKWGIDGFPFRTSDHTRLTQQW--NWFWNEMIT-LSPIIRELIKRDS-YIFIYGGTN
GmSEOo     --TGMKLIK--EVFKYKE--KPIIALINP-QGKVENIDTKQIISVWGIDGFPFRTSDHYRLTQQW--NWFWSEMTK-LNQGIESLIEEDC-YLFIYGGMD
GmSEOj     --TGFKLIK--EVFNYKE--RSIIPLISP-EGRVENIDTKQIISVWGIDGFPFRTSDHTRLTQQW--NWFWSEMTK-LNPRIGDLIEEDR-YLFIYGGTD
GmSEOp     --TGIKLIK--EVFNYKE--RSIIPLISP-EGRVENIDTKQIISVWGIDGFPFRTSDHTRLTQQW--NWFWSEMTK-LNPRIGDLIEEDR-YLFIYGGTD
MtSEO-F3   --AGIRLIR--EDLSYKN--KPILPVLNP-LGRIVNHNAMHMIVWGIDAFPFRPTDDESLTQKW--NWFWAEMKK-VYPRLQDLIKGDT-FIFIYGGTD
GmSEOa     --AGIRLIR--EDLNYKN--KPIIPVLNP-QGRVVNYNAMHMIFVWGIDAFPFRPSDDDVLTQKW--NWFWAEMKK-VNPKLQDLIKADS-FIFIYGGSD
GmSEOf     --AGIRLIR--EDLNYKN--KPIIPVLNP-QGRVVNYNAMHMIFVWGIDAFPFRPSDDDVLTQKW--NWFWAEMKK-VNPKLQDLIKADS-FIFIYGGSD
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Block 2 (Group 1 bracketed):

```
CgSEOa     SKWIHDFTLAVDKVKRH--------------------ETIKRADAIIDYYQLGK-----DDPKKVPRFWIGIESKR-QKK-------H-------YEK
GmSEO-F3   K-WTREFTVAVDKIKRH--------------------DTIRRADAIIDYYHLGK-----DDPKIVPRFWIGIERR-QKK-------H-------SEN
GmSEO-F4   NTWVQNFTQELSKIKMN--------------------QSIQRADIIIENYQLGKGKG--ELNNSPSFWIGVERKK-QNKK------H-------QEA
LjSEO-F1   NKWIQDFTIELDKLKRN--------------------ETVKRADVIIEQYQLGK-----DDPNRVPSFWMGVERKK-QNKK------H-------QEA
MtSEO-F4   KKWIQDFTLELEKIKRH--------------------ETIKRADVIIENYQVGK-----DDPNRVPSFWMGIERKK-QNKK------H-------QET
           TIQDFTLELEKIKRH----------------------EIIKRADVIIENYQLGK-----DDPNRVPSFWIGVERKK-QNKK------H-------QEA
           VIQDFTLELEKIKRH----------------------ETLKRADVIIDNYQLGK-----DDPNRVPSFWIGVERKK-QNKK------H-------QEA
           VIQDFTLAVDKVKRH----------------------DTIKRADAIIEHHQLAK------DD-SIVPRFWIGIESKT-HKK-------H-------QEA
GmSEO-F1   KKWIQDFAVAVEKTRGH--------------------AIILNTDTIIDHYQLGK-----DDPTDVRRFWIEIERKR-LKK-------H-------KDA
MtSEO-F1   KKWIQDFTLALEKTKRH--------------------ETILRADAIIEELSLGK-----DDPKIVPRFWIEIERKR-LKK-------H-------QDG
MtSEO-F2   PKWIQDFTRAIGSIKKH--------------------QTIQNVDVNIDYHQLGK-----NNPTEIPYFWMGIDGRKQQNKT------C-------KDS
GmSEO-F2   SSWVQNFKIAIGKIEKH--------------------VINNVDINIEPYQLGE-----SNPDNVPSFWIGLDGKK-KNKG------C-------KDK
GmSEOu     SEWVQNFKIAIGKIEKH--------------------VINNVDINIEPYQLGE-----SNPDNVPSFWIGLDGKK-KNKG------C-------KDK
AtSEOa     MQWIKNFTSLWRNVAKAANIQLEMVYVGK-----RN-PKNGIQPIINTIREENLSHTL---PDLFQIWFFWTRVESMW-ESKQRMLKAHGIKGREGFKEE
SpSEOb     IEWIRSFTSATRAVANAARVPLEMLYVGK-----KN-PKERVRKNSSIIQMENLSHVV---QDQTLIWFFWERLESMW-HSRTQQ----D-------IPG
SpSEOc     IEWIRSFTSATRAVANAARVPLEMLYVGK-----KN-PKERVRKNSSIIQMENLSHVV---QDQTLIWFFWERLESMW-HSRTQQ----D-------IPG
GmSEOe     IEWIRKFTNTAYSLARTLQLPLEMIYVGK-----SN-PGKKVQEINNAVQTEKLSNVL---PDLAISWFFWVRLESMW-HSKSQQ----S-------KTV
SpSEOa     MDWIRNFTKSARSVAQRAGIDLQMLYVGK-----SN-NKERVRRINSMITAENLSYCL---MDLTSVWFYWTRIESMF-YSKMQL----G-------KTI
GmSEOc     LEWIEKFTTTAISVAKAGKFELEMAYVGK-----SN-AKERMQKMIKTFTTRKFSYFW---PNVTSIWFFWTRLESML-YSKLQH----G-------RTV
GmSEOd     LEWIEKFTATAISVAKAGKFELEMAYAGK-----SN-AKERMQKMIKTFTTRKFSYFW---PNVTSIWFFWTRLESML-YSKLLH----G-------RTV
AtSEOb     LDWIRRFTMAAKATAKDSNVNLEMAYVGKR----NHSHREQIRRISEVIRSENLSHSW---AEPALMWFFWTRLESML-YSKIQL----G-------KAD
GmSEOm     PEWVRRFVKEARRVATATQIPLEMVYVGK-----SNKREQVKIIDTIIRDKLNTQYW---SEQSMIWFFWTRLQSML-FSKLQL----K-------QTD
MtSEOe     PEWIKRFVKEARKVAQATRTPLEMVYVGK-----SNKRDQVQKVCDTIIREKLYTHSW---SEQSMIWFFWTRLQSML-FSKIQL----H-------QVD
GmSEOi     LVWIQQFNDKITEIKRA-GLQLETIYVGNSQSGENV-KQIMARGGE------KSLSDP---LSFTNVQHFWVRLETMR-RSKLRL----G-------KTP
MdSEOa     NDWIQQFTKKATTIAND--------------------PFIKELKINIELFCVGKSPKGGEDLGILGRFWNGIESLF-FTKV------N-------KQ-
MdSEOb     NGWIQEFTKKATALAND--------------------PIFKEAKIHIELFCVGKGSKGEDDHLGILGRFWSGIESLF-FTKV------H-------RP-
MtSEOa     KEWIQQFTKYFGALVND--------------------ATIKQTNTSIELICLES-----QQQNVVNTFWKKVESLF-VTKM------H-------EK-
MtSEOb     KEWIQQFTKYAGALAND--------------------AAIKQTKTSIDLFCLES-----QQPNVVNNFWKKVESLF-VTKM------H-------EK-
MtSEOc     KEWIQQFTKYATALAND--------------------ATIKEAKISIELFYVDK-----EDKNLVSRFWSGIESLF-VTKI------H-------KT-
GmSEOs     KDWIQQFTKYVTALAND--------------------AAIKEAKISIELFCVDK-----EDKSLVRRWSGIESLF-VTKV------H-------KQ-
GmSEOg     KEWIHQFTKYATAFAND--------------------AALKDAKIHIELFCVEK-----EDKSFLRRFWSGIESLF-VTKA------H-------NT-
GmSEOr     KEWIHQFTKHATAFAND--------------------AALKDAKIHIELFCVEK-----EDKSFLRRFWSGIESLF-VTKA------H-------NT-
GmSEOl     TKWIQDFTTAVEKLKKN--------------------ETLTLEEETTIESYPLGR-----DSPKIVPRFWITIDNLLASRKLTKK---G-------SEQ
GmSEOo     TKWIQEFATAIETLKRD--------------------VAKLKLNINTTIESYQLGR-----DDPKAIPHFWIADISLL-TRRKQM-----------KKG
GmSEOj     AMWIQEFTTAVEKLKRV--------------------VDSISLQIDITIESYQLGR-----EDPKVVPRFWIAIDSLL-ANRKQQMMKGG------DQG
GmSEOp     IMWIQEFTTAVEKLKRN--------------------VDSISLQIDITIESYQLGR-----EDTKVVPRFWIAIDSLL-ASRKQQMMKGG------DQG
MtSEO-F3   PKWTQDFALAIEKIKRH--------------------EITRKADAVIEHFHFGK-----EDKRIVPRFWIGIESLF-ANMI-----------QKK
GmSEOa     KKWLQDFTQTVEKIKRH--------------------EIIKRADAVIEHYPFGR-----EDHRIVPRFWIGIESLF-ANMI-----------QKT
GmSEOf     KKWLQDFAQAVERIKRH--------------------EIIKRADAVIEHYPFGR-----EDHRIVPRFWIGIESLF-ANMI-----------QKT
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**Motif 9**

```
CgSEOa     LDCEIQEIVKSLLCLKQDIQGWAILSKG---SNVKILGHGEPMYQTLAEFEL-WKENVLVKEGFDIAFKGYYET--KLKDLPATPQPCAFMNV--DNY-T
GmSEO-F3   LDCEIQEIIRSLLCLKQDTQGWAILSKG---SNVRILGHGQPMYQTVADFEK-WKERVLVKEGFDIAFQEYYDT---QRDLPA-PQPCEFNTL-------
GmSEO-F4   VDCEIQKIVKCLFCLKRDPQGWAILSKG---HNIKHLCHGQAVYQTVAEFQN-WKEKVFEREGFDIAFKEYYDA--KEKEISD-TQPCEDY-----TS-A
LjSEO-F1   VDCEIQIVKSLFCLKRDPQGWVILSKG---HNIKLLGHGEAVYQTVVEFPN-WKEKVLEREGFDIAFKEYYDI--KAKEISA-RQPCEIINV--DSY-S
MtSEO-F4   VDCKIQEIVKDLFCLRRDPQGWIILSKG---HSIKLLGHGAEPAYQTLVEFQN-WKDKVLEKEGFDIAFKEYYQM--KAKEISG-REPCEVLNV--DTY-S
           EZIQDIVKSLFCLKRDPQGWIILSKG---QNIKLLGHGEPAYQTLAEFQN-WKDRVLEKEGFDIAFKEYYEM--KAKELSG-REPCEVVNV--DTY-S
           EZIQDIVKSLFCLKRDPQGWVILSKG---QNIKLLGHGEPAYQTLAEFQN-WKDRVLEKEGFDIAFKEYYEM--KAKELSG-REPCEVVNV--DTY-S
           EQIQTIVKSLLCLKRDPQGWAILSKG---NNVKILGHGEPMLQTLTQFES-WKDKVLEKEGFDIALKEFYDG--KVESLSY-RQPCEYLNI--DSQ-S
GmSEO-F1   VDCEIQKVVKTLLCLKQDQQGWAILTKG---SNVRILGHGEPMRQTLAEFDT-WKDKVFQKEGFDVAFDEYYKT--KLDELYA-RQQCAFVKN------N
MtSEO-F1   IDCEIQDIVKSLLCLKQDPSGWVILTKG---YNVKLLGHGEPMYQTLADFDI-WKDRVLQKEGFDIAFKEYYDT--KVKDTYV-KQPCEIINV--DNNIN
MtSEO-F2   VDCEIQTAVKKLLCLKQDPLGWVLLSRG---RHVTVFGHGEPMYQTVADFDK-WKNNVVEKESFDEAFKEYYDT--KLSEISS-SASCAVN--------S
GmSEO-F2   VDCEIQEVVRTLLCLKQDPSGWVVLSRG---RNLKILGHAEPMYQTVLDFEK-WKNKVLEKETFDVAFKEYYDV--VKEKYA--SLPYDH--------T
GmSEOu     VDCEIQEVVRTLLCLKQDPSGWVVLSRG---RNLKILGHAEPMYQTVFDFDK-WKSKVLEKETFDVAFKEYYDV--VKEKYA--SLPYDH--------T
AtSEOa     EKDLVLQEVVAMLGYGGEGDGWGLVSKA---SDMMVRAKGNLFSRGLAEFNE-WEVNIPT-KGFLTALNDHLLM--RLP-----PHHCTRFML--PET-A
SpSEOb     ETDPILQEIVTILSYDGSDLGWAVFSRG---LAEMTRGKGDLIVQVMKGFDR-WRDEVSDVTTFVPALDRQLRD--LHS-----PHHCTRLIL--PST-T
SpSEOc     ETDPILQEIVTILSYDGSDLGWAVFSRG---LAEMTRGKGDLIVQVMKGFDR-WRDEVSDITTFVPALDRQLRD--LHS-----PHHCTRLIL--PST-T
GmSEOe     ENDHIMHEVMRILTYDSGDPGWAVISQG---TGKMAQGKGDTFLKCLNEHEQ-WKDAAKD-KGLLPAMDDYIKE--LQT-----PHHCNRLIL--PGT-S
SpSEOa     QEDKVMQEVLTMLSFDGSDQGWALISRG---SFEMARAKSQIITKTLEDYTI-WEEDARS-KGFVPALIEYFLQ--LHT-----PQHCNRLIL--PGL-D
GmSEOc     ENDDIMSQVMTVLSFDGSDRGWAIFCRG---ATEMARAKGDSALICLQDFDK-WKDRIEE-DGVVQAMNDYLNK--NKP-----PHHCNRLIL--PGS-T
GmSEOd     EKDEIMSEVMTVLSFDGSDRGWAIFCRG---ATEMARAKGDSALRCLQDFDK-WKGRIEE-DGVVHAINDYLNK--NKP-----PHHCNRLIL--PGS-T
AtSEOb     DHDDVMQGIKKILSYDKLG-GWALLSKG---PEIVMIAHG-AIERTMSVYDRTWKTHVPT-KGYTKAMSDHHHDEVLRET----GKPCGHFDFHITAR-S
GmSEOm     DDDHVMQEIKKLLSYDKQG-GWIVLARG---SHIVVNGHATTGLQTLVEYDAVWKE-LADRDGFEPAFKNHYDK--VHSI----VSPCCRFEF--SHS-M
MtSEOe     DNDRVMQEIKKLLSYDKQG-GWIVLAKG---SQIVVNGHASTGLQSLIEYDLMWKEHA-ERDGFETAFKEHYGK--LHAV----DNPCCRFEF--SHS-M
GmSEOi     SSDHVLAELSTLLDMDDREEGWAVIGCGGSSSTDILRLQGMQVMEFLRKCSE-WRENITN-LGLHGALRNFLDPHFV-------EGSCNHSYFVSSRENE
MdSEOa     -TDTVTKEVQKLLSYKNEG-GWAVLTKG---STVVVSGHGFTILKVLDDFDT-WKNFIKE-KGFEFSFKAYYEK--VIQT----MRHCCRLDI--PSV-A
MdSEOb     -ADQVGQEVQKLLSYKNES-GWAVLSKG---HSVVLTGHGVSILRVVEDFDK-WKDHVKE-RGFEFCFKSYHER--VRTV----SRPCCRLDI--PGS-T
MtSEOa     -TNSVTQQVEKLLSYKNES-GWAIVTKG---SIVIAVGHGTTVLKTFAEFGT-WKGDVST-KGFEYSFREYHNT--IASS----VHICSHLEI--PNV-D
MtSEOb     -TNTVTQQVEKLLSYKNET-GWAIVTKG---SIVTSVGHGTSVLKTVSEFDK-WKDVAIN-KGFEFAFREHHHK--VAST----VHICSHLEI--PNV-A
MtSEOc     -TDVVTQEVQKMLSYKNET-GWALLSKG---PSVVLSGHGTTILKTVAEFEK-WKDVVIK-KGFEFAFTEYHTN--VARV----THRCSHLEI--PIV-A
GmSEOs     -ADAVTQEVQKMLSYKNET-GWSLLSKG---PSVVVSGHGTTILKTVAEFEK-WKEVVIK-KGFAVTFKEYHQK--IVGT----THRCSHLEI--PNV-A
GmSEOg     -VDAVTQEVQKMLSYKNET-GWAVLCKG---SSVVMSGHGTTILKTLAEFEK-WKEDVVK-KGFEPSFKEHHER--IRRT----HHRCIHLEI--PNA-A
GmSEOr     -VDAVTQEVQKMLSYKNET-GWAVLCKG---SSVVMSGHGTTILKTVAEFEK-WKEFVVK-KGFEPSFKEHHER--IRRT----HHRCIHLEI--PNA-A
GmSEOl     VQDSTTREIQKLMFLKQDPLGWAILTKG---SHVKLLGHGDAMLRTVTDFES-WKGTMHNEVSFDVAFKNYYDKCKVKSV----PPKCEHREF--ANY-P
GmSEOo     IDFATSEEIKRLLFLKQDPKGWTILSKG---HNVKLLGHGEAMCRTVKDFGM-WHGKLHEEVSFDVAFREYYEE--IMKDNKDCSKKCLNVIS--AGY-A
GmSEOj     VQDFATREIKRLLFLKQDPKGWVILSKG---YNVKLLGQGEAMCRSVRDFGI-WHGKLHEEVSFDVAFKEYYESIKVKDC----PKKCEHSEI--SNY-P
GmSEOp     VQDFATREIKRLLFLKQDPKGWVILSKG---YNVKLLGQGEAMCRSVRDFGI-WYGKLHEEVSFDVAFKEYYESIKVKDC----PKKCEHSEI--SNY-P
MtSEO-F3   HKDPTIDEIKSLLCLKQDPGWVLLSKG---PNVKLLGRGDQMYATAVDFEI-WKEKVLEKAGFDVAFKEYYER--KRREY---PVACANMQL--ANY-P
GmSEOa     QKDPTIEEIKSLLCLKQQPGWVLLSKG---SNVKLLGGGDPMLATAADFEI-WKEKVLEKAGFDVAFKEYYEQ--KRRNY---PQECSHMQL--ANY-P
GmSEOf     HKDPTIEEIKSLLCLKQQQPGWVLLSKG---SNVKLLGSGDPMLATAADFEI-WKEKVLEKAGFDVAFKEYYEQ--KRRNY---PQECSNMQL--ANY-P
```

Group 1 (bracket spanning CgSEOa through GmSEOu)

**Motif 1**
(Rüping et al. 2010)

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CgSEOa     SNVLATITCPNASCGRVMEVTSVNYKCCHRD------ASDTAKV---------------
GmSEO-F3   -DVLATITCPNASCGRVMEVTSVNYKCCHGG--------NVADHAIKSRSTTAT-----
GmSEO-F4   SSVIATIACPNPTCGRVMEVSSVNYKCCHRD-----DALNC---------------
LjSEO-F1   ANVIATITCPNPMCGRVMEVTSVNYKCCHSD------APNGFGI-----------
MtSEO-F4   SNVIGTISCPNPMCGRVMEVSSIHYKCCHRD------EPNNLGV-----------
           VIATIACPNPMCGRVMEVSSAHYKCCHRD------EPNNFGV-----------
           VIATIACPNPMCGRVMEVSSVHYKCCHRD------EPNNFGV-----------
DpSEO-F1   -LVIATITCPNPTCGRVMEVTSVNYRCCHRD------GQKIC----------
GmSEO-F1   ADVLVTITCPNPTCGRVMEVTSVNYKCCHRD------ASNNGNI--------
MtSEO-F1   QNVIATISCPNPTCGRVMEVTSVNYKCCHRDDAA---APQNGKI--------
MtSEO-F2   DVLATITCPNPFCGRVMEVTSVNYKCCHRD------DPDSCCI--------
GmSEO-F2   SSVLATITCPNPLCGRVMEVTSINYRCCHG-------SANSCNL--------
GmSEOu     SSVLATITCPNPLCGRVMEVTSINYRCCHG-------SANSCNL--------
AtSEOa     GGIIPNEVECTE--CRRTMEK-YYLYQCCLE----------------------
SpSEOb     GHIPERVVCAE--CSRPMEK-FIMYRCCIE----------------------
SpSEOc     GHVPERVVCAE--CSRPMEK-FIMYRCCTD----------------------
GmSEOe     GGIPDKVSCAE--CGQTMEK-FYMYRCCNE----------------------
SpSEOa     GDIPEMIVCAE--CGRAMER-FFMYRCCTD----------------------
GmSEOc     GGIPQKVVCAE--CGRQMEK-YFMYRCCVE----------------------
GmSEOd     GGIPQKVVCAE--CGRQMEK-YFMYRCCVE----------------------
AtSEOb     GRIPEKMNCFE--CQRPMEK-YMSFSCCHDEKLH---EDENYNF---------
GmSEOm     GRIPERLTCPE--CRRNMHV-LTTFQCCHDE------KIDEDFFVSTVTPPTI------
MtSEOe     GRIPDRLTCPE--CRRNMHV-LTTFQCCHDD------NVEEDFFVSSVTPPNTN-----
GmSEOi     RPSQGTVMCQV--CKRPMKN-FVVYQP-------------------------
MdSEOa     GKVPETMKCPE--CPRTMET-FVSYKCCHTD------SPINAHH-----------
MdSEOb     GKVPDTMKCPD--CHRSMET-FISYKCCHID------GPTAHH-----------
MtSEOa     GKIPDFIKCPD--CHRTMEV-YISYKCCHNG----------------------
MtSEOb     GKIPDFIECPD--CHRTMEV-FISYKCCHNG------DKVNAEH-----------
MtSEOc     GKLPETIKCPD--CPSTMEI-FISYKCCHNK------TNANGKH-----------
GmSEOs     GKLPETIKCSD--CPRVMEI-FISYKCCHNE------NTANAIH-----------
GmSEOg     GKLPETIRCPE--CGRIMEI-FISYKCNHRD------NTSIAIN-----------
GmSEOr     GKLPETIRCPE--CGRIMEI-FISYKCNHSD------NTSIASN-----------
GmSEOl     TDILAHIPCPNK-CGHEMEVSVKYMCCHGR------EASDIA----------------
GmSEOo     MDILERIVCPKKDCRRPMEVASVSYKCCHDR------KK-------------------
GmSEOj     TDILAHIPCPNMDCGRSMEVTSVNYRCCHGL------EP-------------------
GmSEOp     TDILAHIPCPNMECGRSMEVTSVNYRCCHGL------EP-------------------
MtSEO-F3   SDILDPIYCPDSNCGRSMEIASVSYKCCHGH------THENAEVAPAESGGFVQIEKRS
GmSEOa     ADILHPINCPDAACGRSMEIASVSYKCCHGQTAHHKAEVPESGDVMIEKKLYAS-----
GmSEOf     ADILHPINCPDAACGRSMEIASVSYKCCHGQAAHHKAEVPESGDVMIEKKLYAS-----
```

Group 1 (bracket spanning CgSEOa through GmSEOu)

**Fig. S3.** Incorporation of venus-tagged SEO-proteins into artificial forisomes following expression in *N. benthamiana* epidermal cells. (A) The venus-CgSEOa construct expressed alone does not assemble into a macromolecular protein body, but is distributed in the cytosol. (B, C) The co-expression of CgSEOa with MtSEO-F1 (B) or DpSEO-F1 (C) generates fluorescent artificial forisomes, due to incorporation of venus-CgSEOa. (D) Overlay of fluorescent and bright-field images of the expression of MtSEO-F3-venus, showing that MtSEO-F3-venus does not assemble into a macromolecular protein body, but fluorescent agglomerates can be detected. (E, F) Overlay of fluorescent and bright-field images of the co-expression of MtSEO-F1 + MtSEO-F3-venus (E) or MtSEO-F4 + MtSEO-F3-venus (F) shows that MtSEO-F3 is not incorporated into a protein body. Scale bars: *(*A) 50 µm, (B-F) 10 µm.
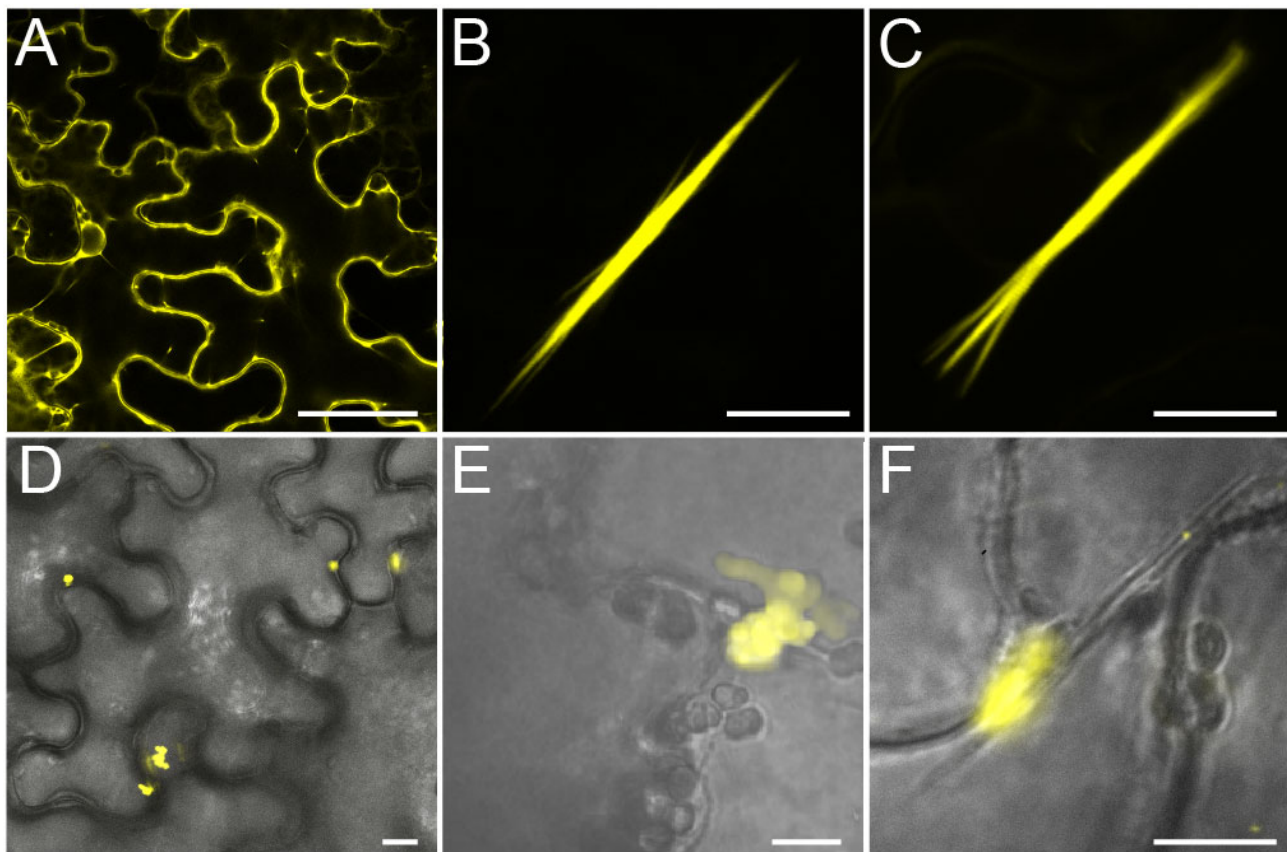
**Table S1.** Geometrical parameters of native and artificial forisomes. Standard deviations are indicated.

|  | *D. panamensis* | *L. japonicus* | *M. truncatula* | *P. sativum* | *V. faba* |
|---|---|---|---|---|---|
| Length (n=15) | 13.7 ± 1.7 µm | 17.2 ± 1.7 µm | 13.7 ± 2.6 µm | 21.5 ± 3.7 µm | 36.3 ± 4.5 µm |
| Width (n=15) | 1.7 ± 0.3 µm | 2.1 ± 2.3 µm | 2.1 ± 0.3 µm | 2.5 ±0.5 µm | 3.4 ± 0.5 µm |

|  | DpSEO-F1 | LjSEO-F1 | MtSEO-F1 | PsSEO-F1 | VfSEO-F1 |
|---|---|---|---|---|---|
| Length (n=15) | 23.7 ± 3.9 µm | 45.7 ± 6.9 µm | 37.4 ± 9.9 µm | 50.1 ± 8.2 µm | 42.2 ± 10.4 µm |
| Width (n=15) | 2.8 ± 0.7 µm | 2.8 ± 0.4 µm | 2.0 ± 0.7 µm | 1.2 ± 0.3 µm | 1.6 ± 0.5 µm |

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