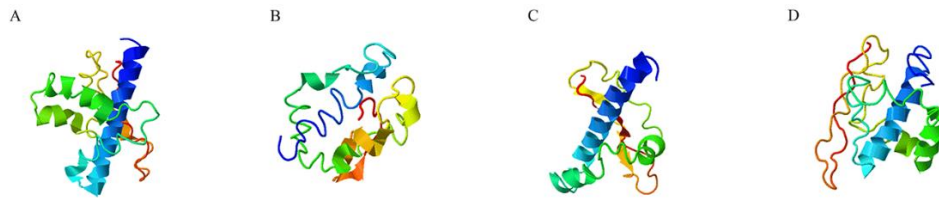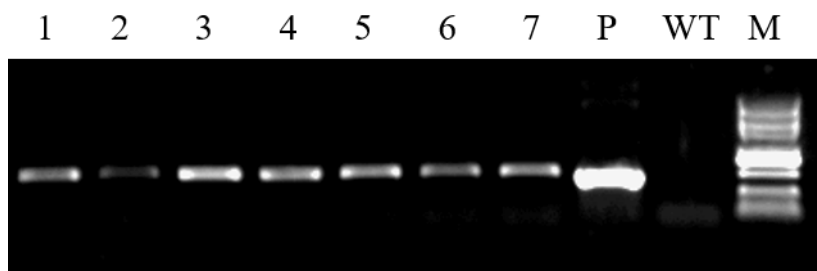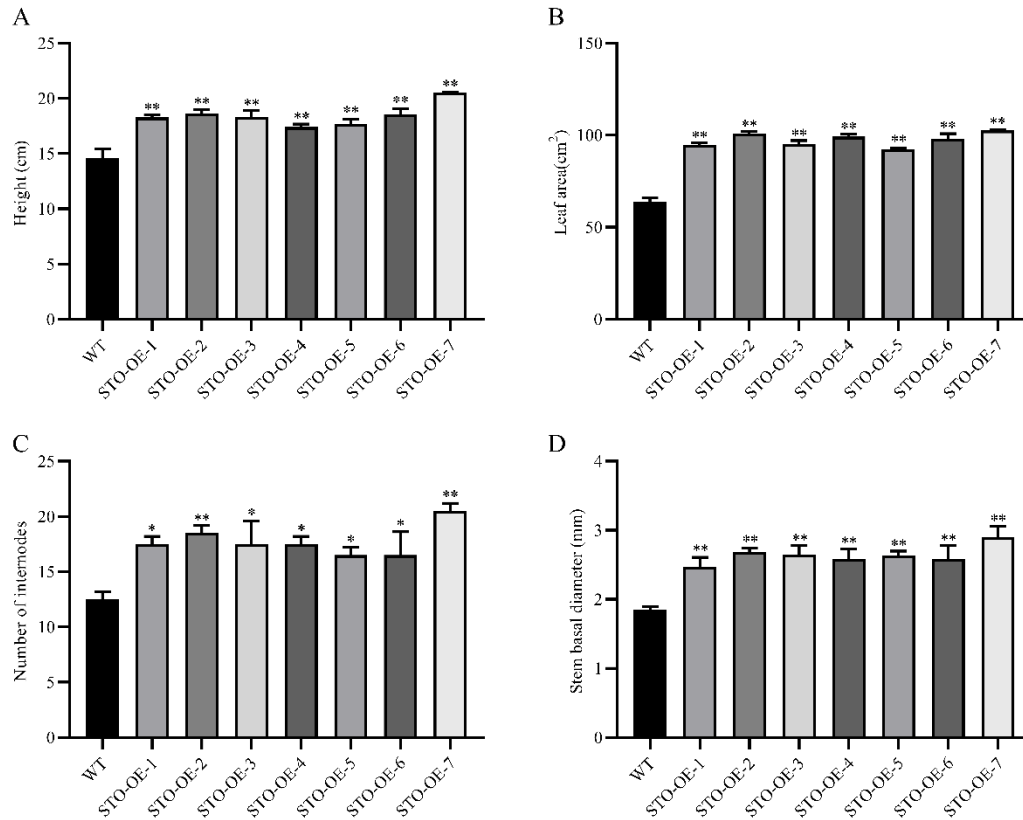**Supplemental Data**

The following supplemental materials are available:

Supplemental Figure S1. 3D structure diagram of *PagSTOMAGEN* (A), *PtrSTOMAGEN* (B), *AtSTOMAGEN* (C), and *OsSTOMAGEN* (D). Prediction of 3D structures was done on the I-TASSER server.
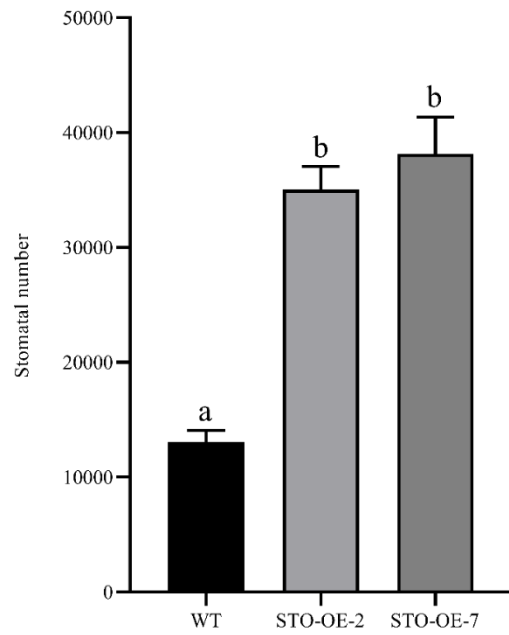

Supplemental Figure S2. Identification of transgenic poplar. P means positive control. WT means wild-type poplar. M means maker.

Supplemental Figure S3. Phenotypic measurements of *PagSTOMAGEN*-overexpressing (STO-OE) and wild-type (WT) lines.

(A) Statistical analysis of plant height of STO-OE and WT lines. (B) Statistical analysis of leaf area of STO-OE and WT lines. (C) Statistical analysis of the number of internodes of STO-OE and WT lines. (D) Statistical analysis of the stem basal diameter of STO-OE and WT lines. Data are presented as the mean ± SD. One-way ANOVA were used to determine variance among the mean values; **, $P < 0.01$; *, $P < 0.05$.

Supplemental Figure S4. Stomatal number of STO-OE and WT lines. Stomatal number = leaf area × stomatal density. Error bars represent the SD for each genotype with five plants. $P < 0.05$ was considered statistically significant and was represented by different letters.

Supplemental Figure S5. Co-expression network centered on STOMAGEN. Blue circle nodes represent photosynthesis and growth-related genes. The node size is positively correlated with the gene degree.

Supplemental Table S1. Primers used for this research.

Primer ID	Primer Sequence (5′->3′)	Purpose
PagSTO-1F	ATGGCAAACACTAGACTATG	Cloning PagSTOMAGEN coding region
PagSTO-378R	TCACCTATGACAAATACATT	Cloning PagSTOMAGEN coding region
PagSTO-Q-13F	AGACTATGCTACTTACTATCCCTTC	qPCR of PagSTOMAGEN
PagSTO-Q-120R	AGAAGATAAGGTGGTCAGCG	qPCR of PagSTOMAGEN
ACTIN-Q-F	AAACTGTAATGGTCCTCCCTCCG	qPCR of ACTIN
ACTIN-Q-R	GCATCATCACAATCACTCTCCGA	qPCR of ACTIN
PBI121-PagSTO-1F	CGGGGGACTCTAATGGCAAACACTAGACTATG	Cloning PagSTOMAGEN coding region into PBI121 vector
PBI121-PagSTO-375R	ACTAGTCAGTCGACTCCTATGACAAATACATT	Cloning PagSTOMAGEN coding region into PBI121 vector
PagSDD1-Q-F	ACATAATTGCAGCCTGGCCT	qPCR of PagSDD1
PagSDD1-Q-R	ATGAGCTGAGCGGATGAGTG	qPCR of PagSDD1
PagTMM-Q-F	AATCCGATGGGGTCTGCTAC	qPCR of PagTMM
PagTMM-Q-R	GCCTAGTGACTCGGGGATTG	qPCR of PagTMM
PagERECTA-Q-F	GGCATTTCGTTTGGAACTTGTCT	qPCR of PagERECTA
PagERECTA-Q-R	AGACGATGGGGAGTCTGTCC	qPCR of PagERECTA
PagEFP1-Q-F	TGTCTTCCGACGGCCATTTC	qPCR of PagEFP1
PagEPF1-Q-R	GCTGGCCATCTCTCCCTGTA	qPCR of PagEFP1
PagEPF2-Q-F	GAAGTTCTTAGTTGGAGCCCACA	qPCR of PagEFP2
PagEPF2-Q-R	CTTGGGGAAATCATGAGCTTCTT	qPCR of PagEFP2
PagSPEECHLESS-Q-F	GGCGGTCAGTGTCACAAAAG	qPCR of PagSPEECHLESS
PagSPEECHLESS-Q-R	AGACATACGTTGCTGCCCAT	qPCR of PagSPEECHLESS
PagMUTE-Q-F	TAGGGCGCCACTGCAATTA	qPCR of PagMUTE
PagMUTE-Q-R	TCGCCGCGATATCACTTTCA	qPCR of PagMUTE
PagFAMA-Q-F	GCCTAGAATCCCAGAAGCGG	qPCR of PagFAMA
PagFAMA-Q-R	CTCAGCGGTTTCTTCACGGA	qPCR of PagFAMA

Supplemental Table S2. Amino acid sequences of the EPF/EPFL family.

>AtEPFL7
MDHVNPTLFHLKSLSIFTLTLLYISSPHFLLFKTLSMYENLRIFLKIIPFNLFGMKSV
SLIAILLLHLFVSSDTFQLDLF

HCKYYLAITWLINRDNECVIYILVGSFICCIVICEVVDKASGSSIPDCSNACGPCKP
CKLVVISSTCSASEACPLVYKCL

CKGKYYHVPSLT

>AtEPFL8
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ATKCRNCKPCLPYLFDIRGAHDDDDS

EPYYPVKWICRCRDRVFEP

>AtEPFL6
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NRNSNSGTLGNFYAKVRKLF

IPLTLLRDLTISDCDGMSRLTGHAEMPCTPKEILSRRIGFSAHEDKDSTQLLVRSP
LVGPCLAYDLDRVEEGKSTVVIKK

TRKIGDRSKEAELRRILRGLGSSPPRCSSKCGRCTPCKPVHVPVPPGTPVTAEYYP
EAWRCKCGNKLYMP

>AtEPFL3
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LNPNENKEEIVKRRRRIGSKPPSC

EKKCYGCEPCEAIQFPTISSIPHLSPHYANYQPEGWRCHCPPP

>AtEPFL5
MGVVLPTLIVYAFLLFFSSSSAASLQRPSGGLGQGKKEIARSGLPGQIVDQKRLG
GPGSVPPMCRLKCGKCEPCKAVHVP

IQPGLIMPLEYYPEAWRCKCGNKLFMP

>AtEPFL9/STOMAGEN
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HMIGSTAPTCTYNECRGCRYKCRAE

QVPVEGNDPINSAYHYRCVCHR

>AtEPFL4
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VPIQPGLSMPLEYYPEAWRCKCGNKLFMP

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NNCHPCMAIQVPTLPTRSRFT

RVNPFSGGFVRPPSSLTTVLDQYSNYKPMGWKCHCNGHFYNP

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GACSPCKRVMISFECSVAESCSVIYRCTCRGRYYHVPSRA

>AtEPF1

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ACPISYKCMCNNKYYPVP*
>PagEPFL10
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MSSKRLMIGSTAPTCTYNECRGCKYKCRAEQVPVEGNDPIHSAYHYKCICHR*

Supplemental Table S3. DEGs in STO-OE and WT poplars.

Supplemental Table S4. The number of DEGs in STO-OE and WT poplars.

Supplemental Table S5. GO terms of DEGs between STO-OE and WT lines in the 1st leaf position.

Supplemental Table S6. GO terms of DEGs between STO-OE and WT lines in the 5th leaf position.

Supplemental Table S7. GO terms of DEGs between STO-OE and WT lines in the 10th leaf position.

Supplemental Table S8. GO terms of DEGs between STO-OE and WT lines in young stem segments.

Supplemental Table S9. DEGs involved in the photosynthesis and growth in the 1st leaf position.

Supplemental Table S10. DEGs involved in the photosynthesis and growth in the 5th leaf position.

Supplemental Table S11. DEGs involved in the photosynthesis and growth in the 10th leaf position.

Supplemental Table S12. DEGs involved in the photosynthesis and growth in

young stem segments.