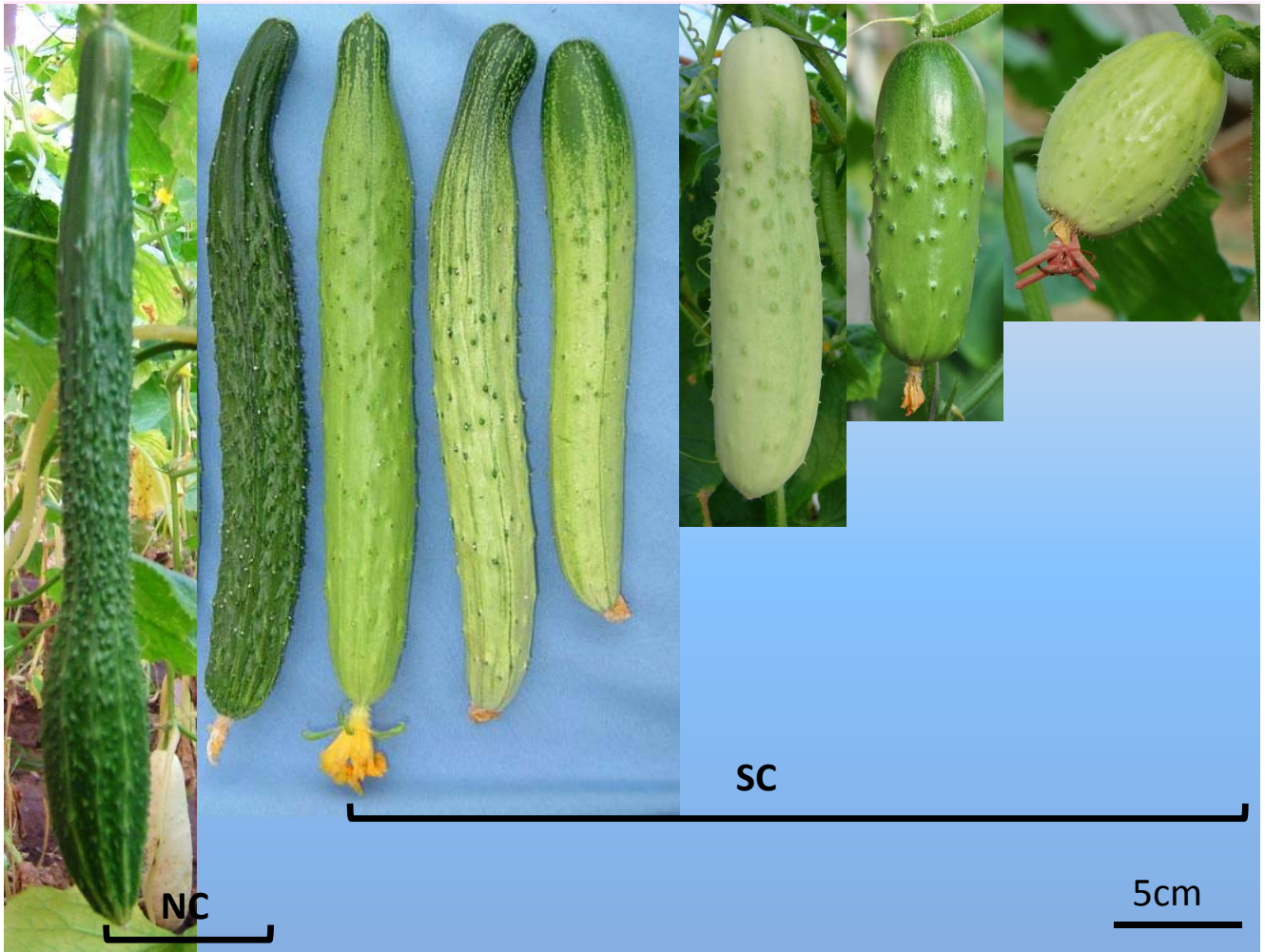# Supplementary information for following article

Comparative transcriptomic analysis reveals the roles of microtubule-related genes and transcription factors in fruit length regulation in cucumber (*Cucumis sativus L.*)

Li Jiang[1,*], Shuangshuang Yan[1,*], Wencai Yang[1], Yanqiang Li[2], Mengxue Xia[1], Zijing Chen[1], Qian Wang[1], Liying Yan[3], Xiaofei Song[4], Renyi Liu[2] and Xiaolan Zhang[1,#]

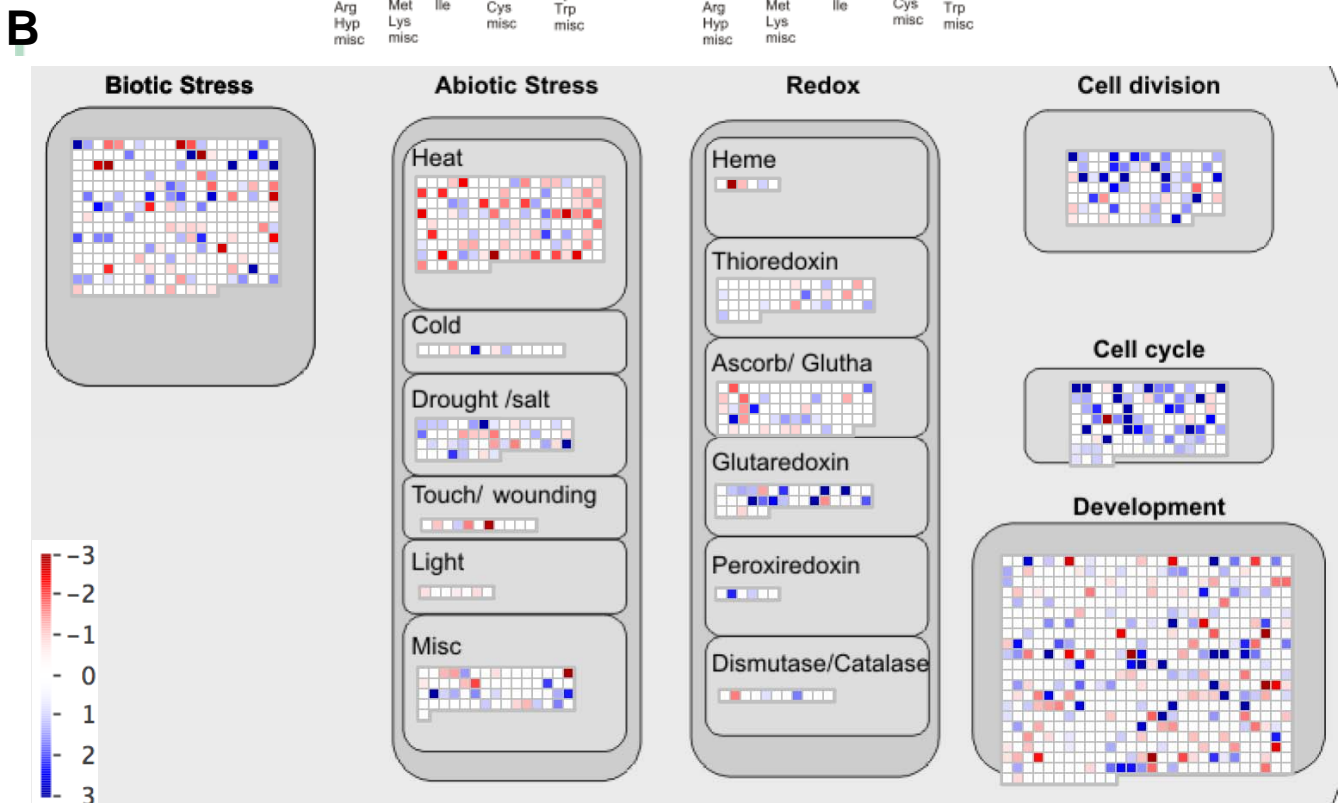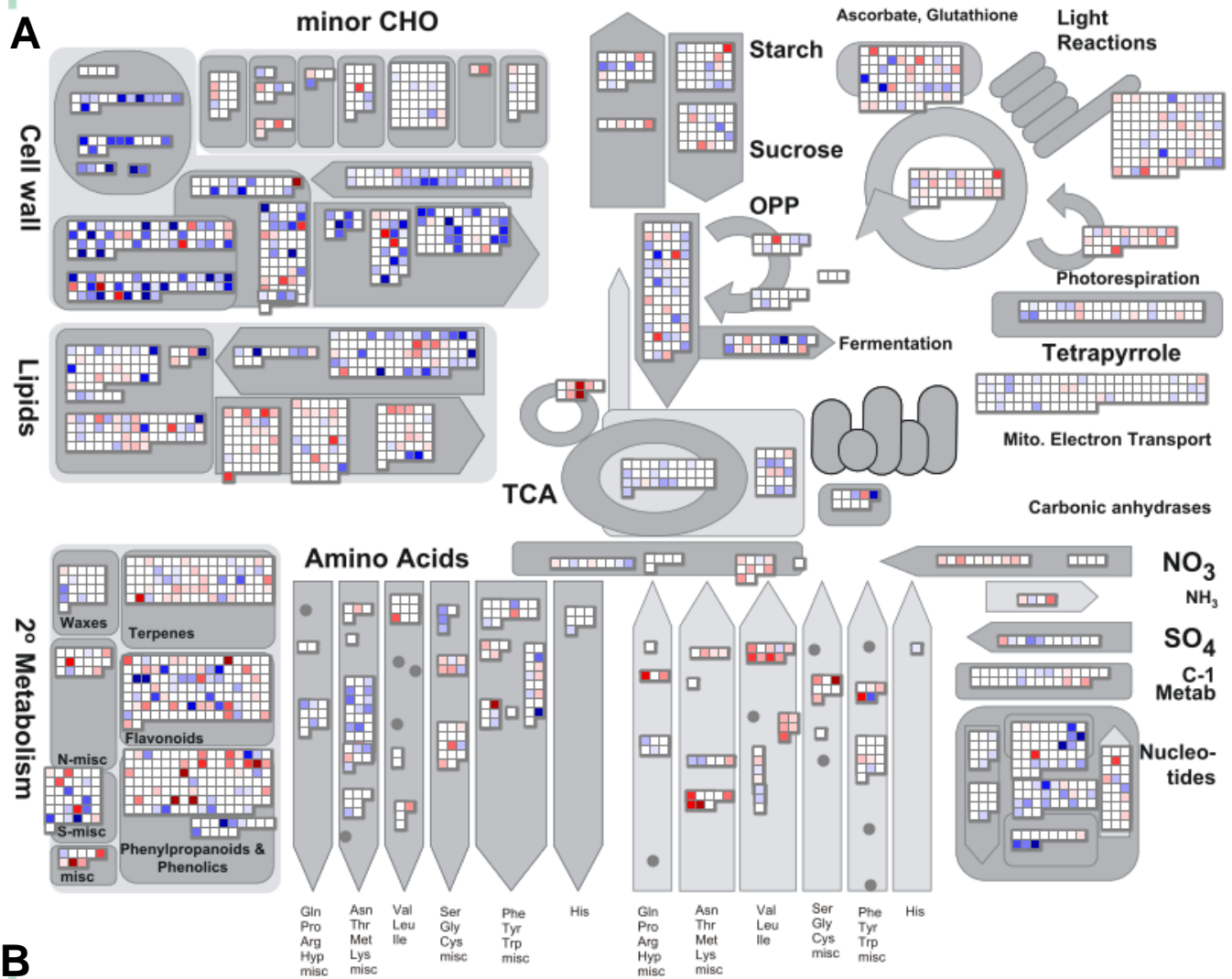**Supplemental Figure S1. Fruit length variation of major cucumber varieties in China.**

NC: examples of cucumber varieties from northern China. SC: examples of cucumber varieties from southern China.

Supplemental Figure S2

Supplemental Figure S2. Functional categorization of the differentially expressed genes between the fruit of 408 and 409 using the MapMan software. Each colored dot represented one gene. The color indicates the log2 fold changes, red indicates a decrease (lower expression in 408) whereas blue indicates an increase (higher expression in 408). (A) Metabolism overview of the differentially expressed genes between 408 and 409; (B) Cellular response overview of the related genes.

Supplemental Figure S3
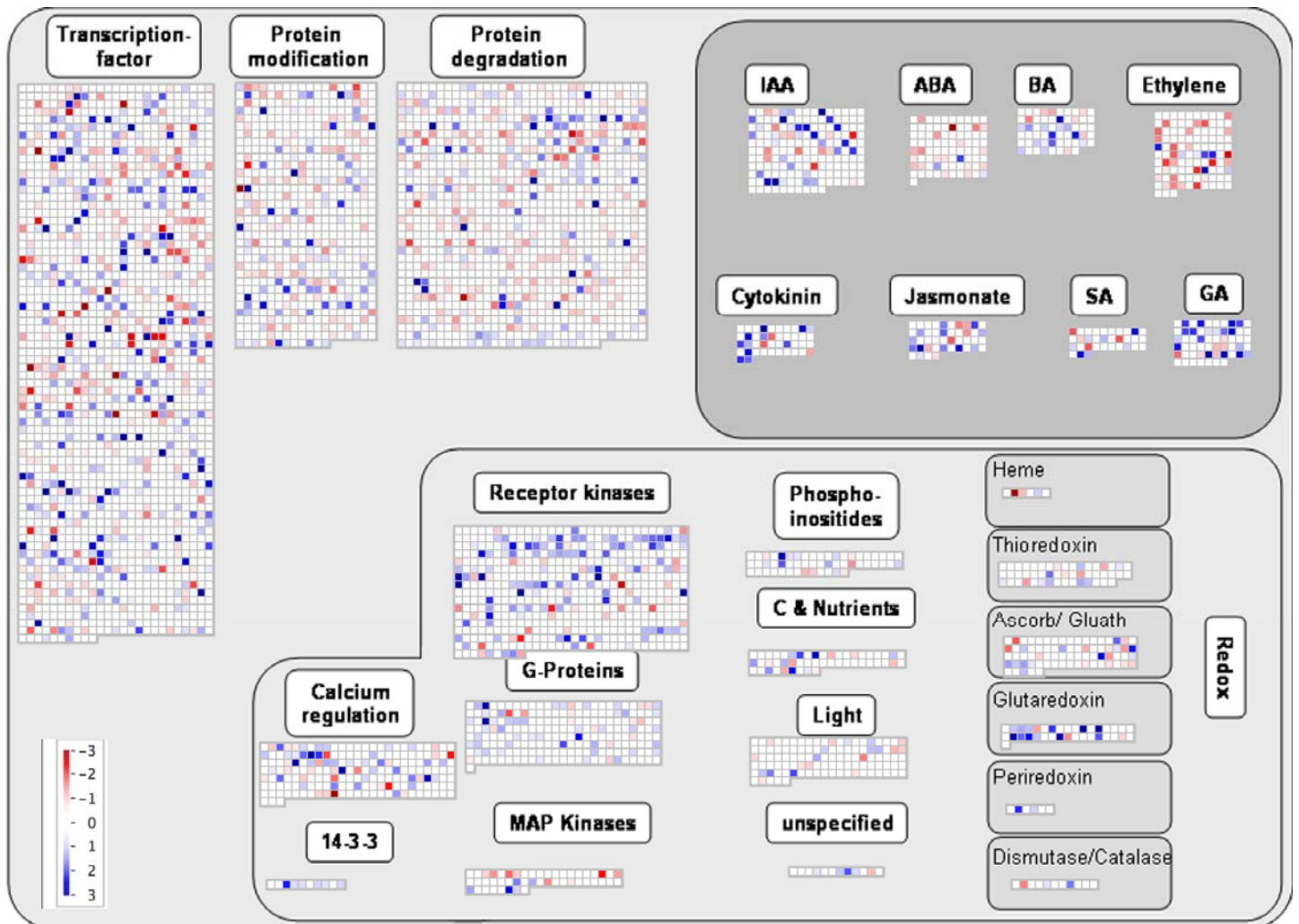
Supplemental Figure S3. Regulation overview of the differentially expressed genes between line 408 and 409 using the MapMan software. Each colored dot represented one gene. The color indicates the log2 fold change, red indicates a decrease (lower expression in 408) whereas blue indicates an increase (higher expression in 408).

Table S4.   Primers used for qRT-PCR assays in this study

Primers for qRT-PCR	
Csa3G000690-F	5'-TCAAGGGTTACGGTCGTCAAA-3'
Csa3G000690-R	5'-GAAATGATAAAGAGGATCCGGC-3'
IAA29b-F	5'-GATTGGCACACTCAACCTCC-3'
IAA29b -R	5'-TTTCCTTGCTATTGCTACCCCT-3'
EXPA16-F	5'-AGTATTGATAACCAACGTGGGAGGC-3'
EXPA16-R	5'-TTTGATTGCCAGTTTTGACCCC-3'
IAA29a-F	5'-GTGGGAATTGCTAGGAAGGTTG-3'
IAA29a-R	5'-CGTTCTCAGCAAGTAACCATTCA-3'
Csa2G031190-F	5'-CCTCCAGGATATCAGAACGGTT-3'
Csa2G031190-R	5'-ATCCACCATTGGTTGTCTTCGT-3'
Csa7G446860-F	5'-CTGTTGCAGGAAGAGGAAGATC-3'
Csa7G446860-R	5'-ATAGATTGCTGCAGCCTTTTG-3'
Csa3G062600-F	5'-CATCAGTTGCAGAGGAGAGTTTTA-3'
Csa3G062600-R	5'-TCGTCATGATACAGTGGTTCAAG-3'
Csa1G495290-F	5'-GAATACACGGTTGATGAACCATC-3'
Csa1G495290-R	5'-CCAGCTAAATGCTTTACATCTCC-3'
Csa4G293320-F	5'-GATTATCTGGTCGATCAGCATTC-3'
Csa4G293320-R	5'-GAACTTTTCCTTCTATCAAACCCC-3'
HIK-F	5'-TCGCTCGTCAAGCATGAG-3'
HIK-R	5'-GGATTCGTCCAGAGCTTGTTTA-3'
CYCB1;2-F	5'-GAGAACGAGAGCAGACCTCA-3'
CYCB1;2-R	5'-CAATCTTTGTCGCAAGGAAA-3'
Csa6G382370-F	5'-GATTTGTTCGTGCTGCTCAA-3'
Csa6G382370-R	5'-TAATTCGGCAAGGAAGTTGG-3'
CYCD3;1-F	5'-CATGTGGAGGAGAAAGCAGA-3'
CYCD3;1-R	5'-TTGATGCTGACACAATCGTC-3'
CDKB1;2-F	5'-CAATCCCTCTATGTCGTTCG-3'
CDKB1;2-R	5'-GCTTGAGATCACGGTGAAGA-3'
EXPA5-F	5'-GCACGGCGCTTTTCGAT-3'
EXPA5-R	5'-TGACACAGCGTAGCTCAAAACA-3'
CDKB2;2-F	5'-ATATGTGGTCTGTTGCCTGCAT-3'
CDKB2;2-R	5'-TCCAGGAAAGAGAGGCTGCTT-3'
EXPA4-F	5'-GAGTACCATGCCGTAAGCAA-3'
EXPA4-R	5'-CCTGCCACGTTCGTTATTAG-3'
CUC3-F	5'-GGAGTCGGCTTTGTCATCG-3'
CUC3-R	5'-TTGTTGGCAGCATTCGTAAT-3'
HAN-F	5'-GGCAACAGGGCACTTACTTC-3'
HAN-R	5'-GTTCTTCACGGCGTTTCTCG-3'
SPT-F	5'-TCGGATTGTAATGTTAGGGATGTG-3'
SPT-R	5'-CAGCGCCGGAGGAAGAAAA-3'
UBI-ep-F	5'-CACCAAGCCCAAGAAGATC -3'
UBI-ep-R	5'-TAAACCTAATCACCACCAGC-3'