



Transcriptome Analysis Reveals the Molecular Regularity Mechanism Underlying Stem Bulblet Formation in Oriental Lily ‘Siberia’; Functional Characterization of the *LoLOB18* Gene

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Table S1. Summary of sample sequencing data quality.

| sample | raw_reads | clean_reads | clean_bases | error_rate | Q20 | Q30 | GC_pct |
|--------|-----------|-------------|-------------|------------|-------|-------|--------|
| AI_1 | 23940635 | 23023593 | 6.91G | 0.03 | 97.05 | 92.49 | 45.76 |
| AI_2 | 26335661 | 24931990 | 7.48G | 0.03 | 97.19 | 92.68 | 46.53 |
| AI_3 | 23631994 | 22749394 | 6.82G | 0.03 | 97.79 | 93.81 | 49.74 |
| AII_1 | 23333055 | 22242572 | 6.67G | 0.03 | 97.46 | 93.18 | 46.98 |
| AII_2 | 22998623 | 22007557 | 6.6G | 0.03 | 97.6 | 93.43 | 47.13 |
| AII_3 | 22686930 | 21628791 | 6.49G | 0.03 | 97.65 | 93.47 | 49.03 |
| AIII_1 | 23382409 | 22517722 | 6.76G | 0.03 | 97.55 | 93.25 | 47.63 |
| AIII_2 | 23922151 | 22604843 | 6.78G | 0.03 | 97.6 | 93.26 | 49.09 |
| AIII_3 | 23025309 | 21890514 | 6.57G | 0.03 | 97.52 | 93.21 | 48.23 |
| BI_1 | 22760794 | 22291418 | 6.69G | 0.02 | 98.55 | 95.48 | 47.45 |
| BI_2 | 25263161 | 24507882 | 7.35G | 0.03 | 97.6 | 93.36 | 49.84 |
| BI_3 | 23510572 | 22740522 | 6.82G | 0.03 | 97.63 | 93.42 | 50.67 |
| BII_1 | 23099381 | 22342918 | 6.7G | 0.03 | 97.73 | 93.61 | 50.29 |
| BII_2 | 23503526 | 22691422 | 6.81G | 0.03 | 97.63 | 93.41 | 50.27 |
| BII_3 | 23393160 | 22605723 | 6.78G | 0.03 | 97.75 | 93.65 | 50.1 |
| BIII_1 | 23694202 | 22980909 | 6.89G | 0.03 | 97.71 | 93.51 | 49.54 |
| BIII_2 | 23625022 | 22302139 | 6.88G | 0.03 | 97.89 | 93.76 | 49.58 |
| BIII_3 | 23767045 | 23075120 | 6.92G | 0.03 | 97.7 | 93.51 | 49.85 |

AI – vertical (control) group after 20 days of planting; AII – horizontal group after 20 days of planting; AIII – slant group after 20 days of planting; BI – vertical (control) group after 50 days of planting; BII – horizontal group after 50 days of planting; BIII – slant group after 50 days of planting.

Table S2. The primer pairs used in study.

| Gene | Primer sequence (5'–3') | Temperature (°C) | Amplification Size |
|---------------------|--|------------------|--------------------|
| <i>LoLOB18</i> | F:ATGAGCTGCAGTACGAGCAGCG | 56 | 687 bp |
| | R:TCACCTAGAGACTGGAGGAGTAT | | |
| <i>TRV-LOB18</i> | F:TGAGTAAGGTTACCGGAATTCATCTGCTACGAGG CACAGG | 58 | 340 bp |
| | R:GGGACATGCCCCGGGCTCGAGGTTGTTGTTGCTGCTGG AGGTT | | |
| <i>qPCR-LOB18</i> | F:TTCCAACCTCCACCCTCCTTGTC | 57.5 | 180 bp |
| | R:CTCCACCACCCTGCTGCTA | | |
| <i>coat protein</i> | F:CCTGCTGACTTGATGGACGA | 55.5 | 359 bp |
| | R:CCAGTGTTGCGCTTGGTAGT | | |
| <i>qPCR-SUS</i> | F:TATTCTGAGAGGCTGATGACACT | 55.2 | 122bp |
| | R:CAAGTTACGGTATTTGAGGGCATA | | |
| <i>qPCR-SUAR</i> | F:TCTCATCTCACACCTTGCCAT | 55 | 144bp |
| | R:CCTCCTGCTCATCATACTTCCT | | |
| <i>qPCR-GID</i> | F:GAGAAATGAAACGGCAATCG | 55.8 | 109 |
| | R:CTCAAATACCAGGTCCTCCC | | |
| <i>qPCR-SLR1</i> | F:GTGGTTGAACAAGAAGCAAATC | 55.5 | 84bp |
| | R:CGAACATAGTAGAGTAGTAGTGG | | |
| <i>qPCR-XTH23</i> | F:GACTTCCACACTTACTCCATCGT | 56.2 | 256bp |
| | R:CCATACCAGACACAGGCATCAG | | |
| <i>qPCR-AGPS</i> | F:GCTTCTTGCGTGAATGTGGTAT | 56 | 274bp |
| | R:ATCTTCTGGTCTATCGGCTTCTT | | |
| <i>qPCR-GH3.8</i> | F:GCTGATGGAGTACGCTATT | 56.4 | 195bp |
| | R:ATGCTCTAAGTGGAGAATGG | | |
| <i>qPCR-EF</i> | F:GGCACTAACTCGCTCCTTCTG | 56 | 173bp |
| | R:TTGGTAAGATGCTGGTGATTGGAT | | |
| <i>qPCR-KNOX1</i> | F:CTTCACCTCACACCTTCTACCA | 55.4 | 146bp |
| | R:GCCTTGACGGACTCCACAT | | |

Table S3. Annotation of assembled unigenes against seven public databases.

| Database | Number of Unigenes | Percentage |
|------------------------|--------------------|------------|
| Annotated in NR | 63762 | 43.81 |
| Annotated in NT | 53444 | 36.72 |
| Annotated in KO | 27326 | 18.77 |
| Annotated in SwissProt | 56595 | 38.88 |
| Annotated in PFAM | 54137 | 37.19 |
| Annotated in GO | 54133 | 37.19 |

| | | |
|------------------------------------|--------|-------|
| Annotated in KOG | 24441 | 16.79 |
| Annotated in all Databases | 13913 | 9.56 |
| Annotated in at least one Database | 145530 | 100 |
| Total Unigenes | 145530 | 100 |

Table S4. The sequences of *LoLOB18*.

ATGAGCTGCAGTACGAGCAGCGGAGCTGGCGGTGGCGCCGCCGGTGGCGGCAGTGGTAGCGGAGGCGGC
 GGTCCGTGCGGGGCATGCAAGTTCCTGAGGAGGAAGTGCGTGAGCGGGTGCATTTTTGCTCCTTACTTCGA
 CTCCGAGCAGGGAGCGGCGCATTTGCGCGCCGTGCACAAGGTGTTTGGTGCGAGCAATGTGTCTGAAGCTG
 CTGCTGCATATTCCGGCACACAAGAGGCTGGATGCGGTCATCACTATCTGCTACGAGGCACAGGCGAGGC
 TGCGGGATCCTGTCTATGGATGTGTTGCTCATATATTTGCGCTGCAGCAGCAGGTGGTGAACCTACAGGCC
 GAGCTCTCCTACTTACAAGCCACCTGGCAACCCTAGAGCTACCATCTCCTCCTCCGCCGCCGCCGCCGAAT
 TCCAACCTCCACCCTCCTTGTCCATGTCTGACCTGCCCTCTGCCTCGAACATAACCCACCTACCTGGACCTCTC
 CAGCCTCTTTGATCCCCCTCAGCAGCCCCCGTGGAACCTCCAGCAGCAACAACAACAGGTTCAACTCCGAC
 AGACGCTTGGGTCCGGTAGCAGCAGTGGTGGTGGAGACCTCCATGCACTGGCGAGGGAACCTCCTGGGTCTG
 CCACCGATGCCCCGCCAGGCGATACACTGGATACTCCTCCAGTCTCTAGGTGA

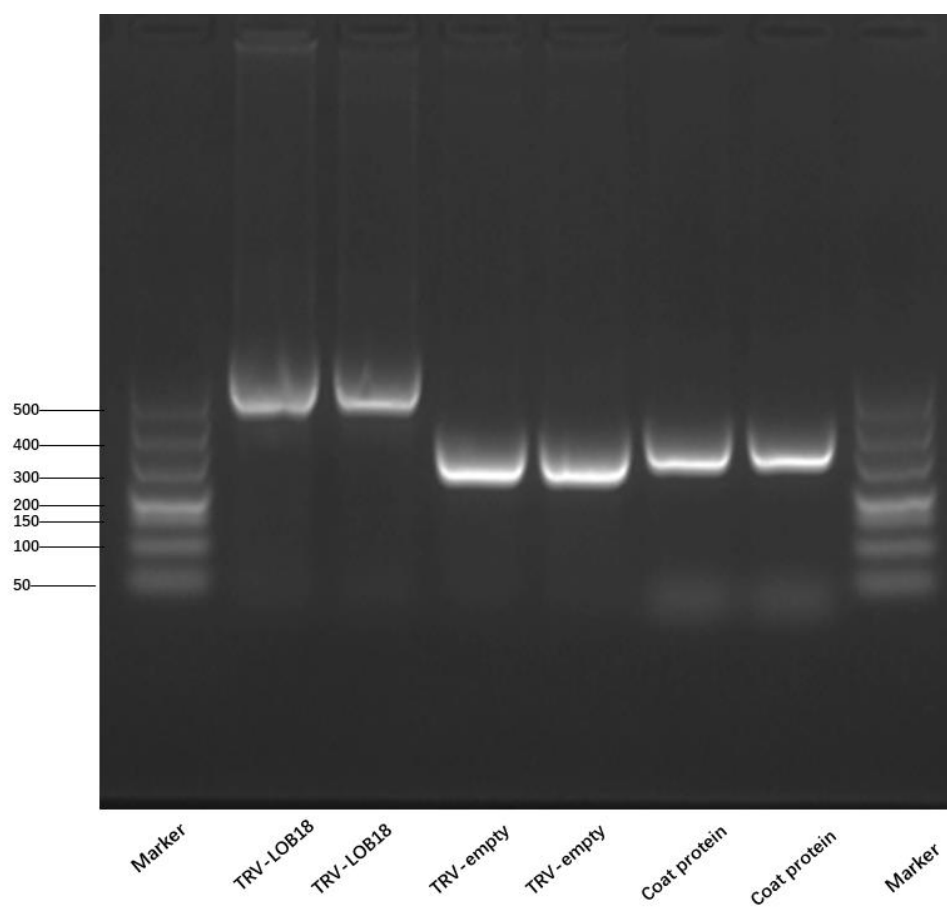


Figure S1. The figure showing successful insertion and expression of TRV2 and TRV2-LOB18 in the genome of lilium.

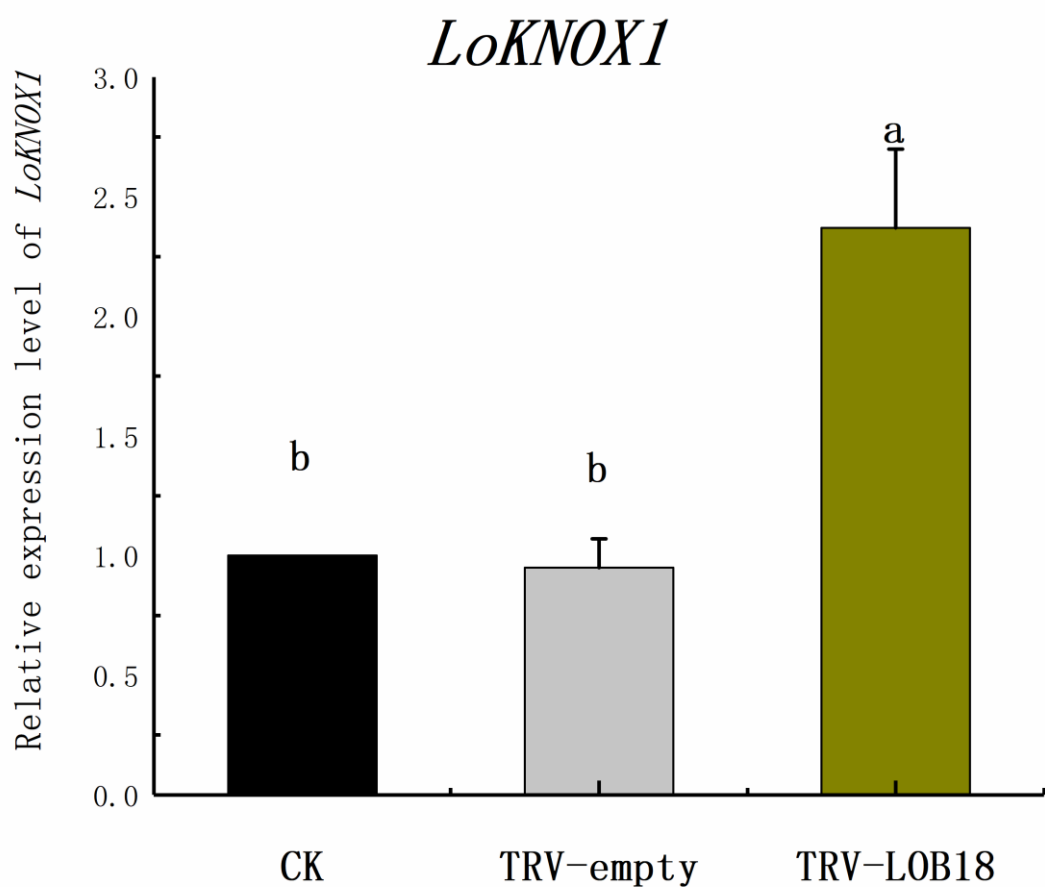


Figure S2. Relative expression of *LoKNOX1* after successful insertion of TRV2 and TRV2-LOB18. Lowercase letters indicate significance among treatment groups according to Duncan's multiple range test at $p < 0.05$.

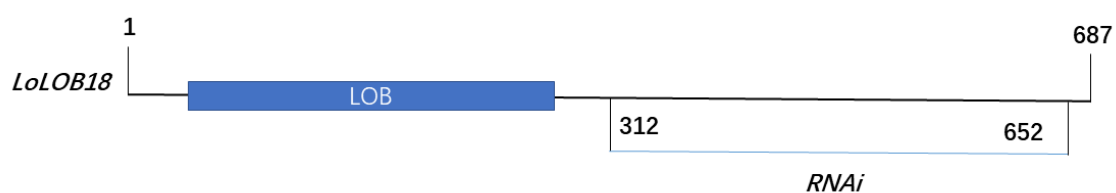


Figure S3. A model showing restriction sites during VIGS experiment.