**Figure legends**

**Fig. S1** Isolation and detection of the *LbgAGPS*, *LbgGBSS*, *LbgSSIII* gene. Columns 1-2 represent the 3’ and 5’ intermediate, respectively. Column 3 are the open reading frame.

**Fig. S2**  Nucleotide and deduced amino acid sequences of the *LbgAGPS* gene. The initiation and stop codons are underlined in red. The putative conserved regions are boxed, ATP-binding site[66] in red, catalytic site in deep blue, Glc-1-phosphate binding site[67] in lake blue, and activator site[68] in orange. The orange shaded one is the predicted transit peptide cleavage site.

**Fig. S3**  Nucleotide and deduced amino acid sequences of the *LbgGBSS* gene. The initiation and stop codons are underlined in red.

**Fig. S4**  Nucleotide and deduced amino acid sequences of the *LbgSSIII* gene. The initiation and stop codons are underlined in red.

**Fig. S5** Multiple sequence alignment of CDS in *Lilium*. GenBank accessions: LohAGPS, AQZ41944.1; LbvAGPS, QFV20493.1; LbgAGPS, MT740689; LbAGPS, MT740692; LohGBSSI, AVZ24769.2; LduGBSS, AJG44453.1; LbgGBSS, MT740690; LbGBSS, MT740693; LohSSIII, AVZ24768.2; LbgSSIII, MT740691; LbSSIII, MT740694.

**Table S1 List of primers used in RACE**

|  |  |
| --- | --- |
| Items | Primer sequence (5’ to 3’) |
| 3’ RACE CDS Primer A | AAGCAGTGGTATCAACGCAGAGTAC(T)30 V N, (N = A, C, G, or T; V = A, G, or C) |
| 5’ RACE CDS Primer A | (T)25V N, (N = A, C, G, or T; V = A, G, or C) |
| 10X Universal Primer A Mix (UPM) | CTAATACGACTCACTATAGGGCAAGCAGTGGTATCAACGCAGAGT |
| Universal Primer Short | CTAATACGACTCACTATAGGGC |
| 3’ RACE GSP (*LbgAPS*) | GTGATTTTCTGAAGGAACTTGGTGACA |
| 3’ RACE NGSP (*LbgAPS*) | TGGCTATTTCATCAAGAGCGGTATTG |
| 3’ RACE GSP (*LbgGBSS*) | ATGATGATGGCTGGAGGTGATCTTATC |
| 3’ RACE NGSP (*LbgGBSS*) | TGGGATGCCGGTCATTTGTTCGA |
| 3’ RACE GSP (*LbgSSIII*) | TTGTTTTGCTCGGTTCAGCCCCA |
| 3’ RACE NGSP (*LbgSSIII*) | CGGAGCTGATTCGGGTGGTGTTG |
| 5’ RACE GSP (*LbgAPS*) | CCTCCAAGTATAATCCCCAAAACACTC |
| 5’ RACE NGSP (*LbgAPS*) | GGAGATGTGGGCGGAGGAGGAGA |
| 5’ RACE GSP (*LbgGBSS*) | TTCCACCAGTTTTCCCCCATACC |
| 5’ RACE NGSP (*LbgGBSS*) | TCCCCGACTTTGAACTCAGCCAC |
| 5’ RACE GSP (*LbgSSIII*) | AATCCCCTTTAAGGTCAGTTTTGTGC |
| 5’ RACE NGSP (*LbgSSIII*) | TTGGTCCCTCTTGAAAAGTTCTCCTC |
| *LbgAPS* complete cDNA Forward primer | ATGGCGATGGCTGCGATCGG |
| *LbgAPS* complete cDNA Reverse primer | TTATATCACAGTCCCACTAGGGATCAAAGCGTCT |
| *LbgGBSS* complete cDNA Forward primer | ATGGCTGCGTCGGCGACT |
| *LbgGBSS* complete cDNA Reverse primer | GATCACGGAGTTGCCACATTTTC |
| *LbgSSIII* complete cDNA Forward primer | ATGCCTCAAATGAATGCAGCAAGTTCA |
| *LbgSSIII* complete cDNA Reverse primer | TCATATCTTCCTTGCTGCATGGTAGAGCT |

**Table S2 List of primers used in qRT-PCR**

|  |  |  |  |
| --- | --- | --- | --- |
| Gene name | Forward primer sequence (5’ to 3’) | Reverse primer sequence (5’ to 3’) | Amplicon length (bp) |
| *LbgAGPS* | CCGAGCTCCGCTCATAGTTT | CCCAAAACACTCTTGCTGGC | 93 |
| *LbgGBSS* | CGACAACGGTAATGGAGGCT | GGTCTACAGGCAAGCCAACT | 72 |
| *LbgSSIII* | GGCTCTGCGTGAAAAGGTTG | TGTAACTAAGCGTCCAGCCC | 139 |
| *LbgGAPDH* | TCTCTGCCCCTAGCAAGGAT | TGAGTAGCAGTGATGGCGTG | 193 |