Fig. S1. Function classification of all unigenes (A) KOG function classification of all unigenes. (B) GO function classification results of the annotated unigenes in *Polygonatum cyrtonema*.

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CCGGAGATTGGAATATCCAAAATACAGTACACATCATCAAGGGTAATGGT  50
CATCTCACCAAAAGGTAAATGGAATGTATTAGTCTCCGGCTGCCACCTCT  100
CAACAAATGCTGAGACTACTACCTTATTGGCATACCTATAGGAACAATCA  150
ATAAGGCTCATCAAACCGGATCTCTGAATATAACCCTTCCAGATGAGGTT  200
GTCTGCAATTGGACTATTTGAATCCAATGACCATTCTGTGAGTTGGTATG  250
CATGATTAAGGCATTTAAGCAATTCCCGTTCCTGGAAAATTAATACAACA  300
TAAAGTGAATTACAAATTAAATTTAATTAAGCAAATAATAATTTAATTAT  350
AATATTGACCAAAATAAATGAAAATCATAATACGTACACTCCCATTCCAA  400
ATCTCTGAGGCAATATGTGTCTTGAAACTTCGTAAAATCCTAGGGTCCTG  450
TGGCCCACCGGGAAATGGTCCTGTCAACTCCTCATGCTCAGATTCAACAG  500
CCTGCGCTTCTACATTCGCTTCTACATTCAGATGCTCCTCTTCTTGAACG  550
TTTGGTTGTATAACTGGTTCATCCTGTACAACTTGTTCTGTCTCTAACTC  600
TGATATATGAACTCGTCTTGCTGCATCTGCTGCACGTCGGGCTGATGCAG  650
TCGTTCTCTTTGTCCTTCGAGATGTGCCAGCCTCATCTACAAATTAAATT  700
AAGATAGTACTGTCAAAAAAATATGATAAATGACTATACAAAATAAGCAT  750
ACCATGACTTCATATATTATAATTTTAGTAAACAAAAACAAATATTGTAC  800
AGTAGAACAAGAAAAAAAAATACACATTGAATATTGTGAAAACTATTTAT  850
GTAGTAAGAAAAGGGAATAGAAGGAAATGAGTTGGGAGTTCATTAGAAAT  900
TGATAGAGAAAGTTCAGTATCTCTACAGAACGAGAGAGAGTATGAGAAGC  950
TAGCAATGATCATGTGTGACACTGATCATTGCATCATTCAAAAACACAAC  1000
TGATCAATGTATATATAGCATAGAGAGAGAGAGAGAAAACAAAGTGGTAA  1050
TGTAATGTGAATGTGACTGTGCTAGTAAGAGTATAGTGATGAGCTCAAGT  1100
CAGCTAGCAGCAATATACAAGCAGTCAGTCGTCGGCCTAAAGAAACCGAC  1150
CAAATAGTCTTTCGTCGGCCTATTTAGGCCGACAGATTAATATTTGGTCG  1200
GTCTTAACAGGCCGACCAAATAGTAATCTGTCGGCCTAAATAGACCGACA  1250
AAAATTAGCCAAGTCGGGTTCTCGGGGCCGACCGACTGTCGCATGAACAA  1300
ACGTTACAGAAAGTTCAAAAAACTTTAATTTTATGATTTATAATCTTAAA  1350
ACAATACCTTGATTGGTTCGAGAAGACATCTAAAGCGTTTGATAGATTCT  1400
CAAAATGAATATATCCTGAATCAAATTAAAAAAACAATCAGTTTAACCCA  1450
AATTTTTTTCTCCAACTAAATAAAAATGAAAGAAATCGAATTAGGGTTTT  1500
CTATTAGGTACAAAGCTATAAAAACTTACCTAAATCCTTGTCTTCTTCTC  1550
TACTCCTCCTACTCTTCTTCACGATCGGCTCCTCCTCCTCTTCTTCGCGA  1600
TGGTTGTTCCTCTTCTTCTTCGCGTTTTTTTTTTTTTTTTACAGTCA  1650
AGTTAATTTTTTCTACTTGGTTGACTGGGTTTACTGAGCAAATCAAATGG  1700
GTATTTTTGGTATAGATAAAGGGTAAACTGAGCAAAATGTTGGGTTTGTT  1750
TTGGTTATGGGTTTACTGAGCAAAAAATTGGGTGCCAATAGAATTCCCCA  1800
ATGAGTTTTGAATGGGGCTACTGAGCAATTTTGGGGGTTCAAATAGAATT  1850
ACCCTATG                                            1855
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Translation Start Codon

Fig. S2. The sequence and cis elements analysis of *PcgalE1* promoter. The position of nucleotide in the promoter is opposite to the translational start site (ATG) that was marked as +1. W-box cis elements are highlighted as red color.