

Supplementary materials

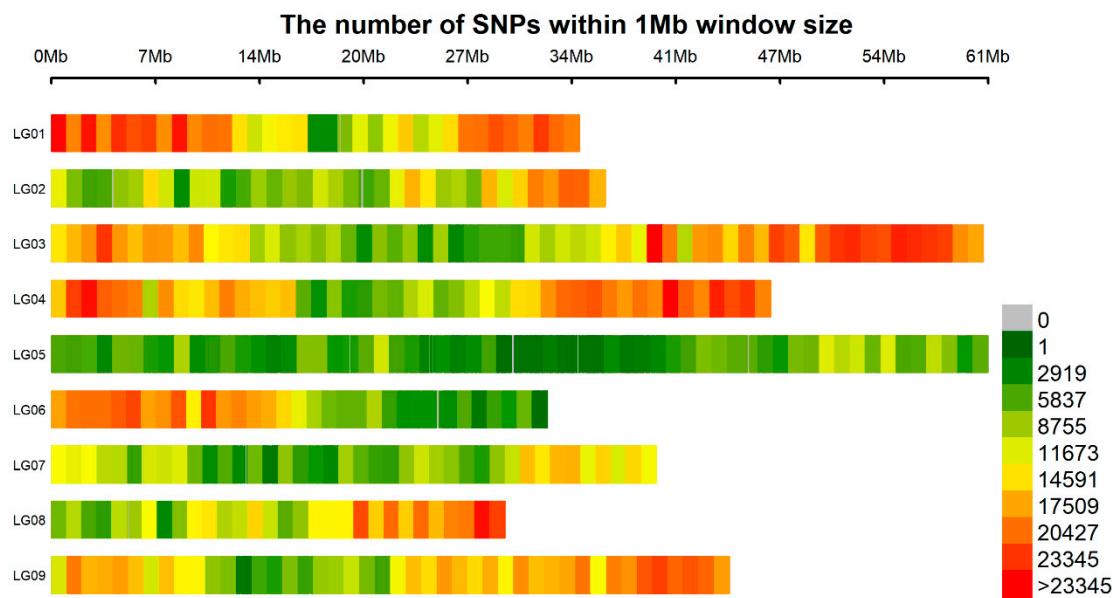


Figure S1. The number of SNPs in chromosomes within 1Mb window size.

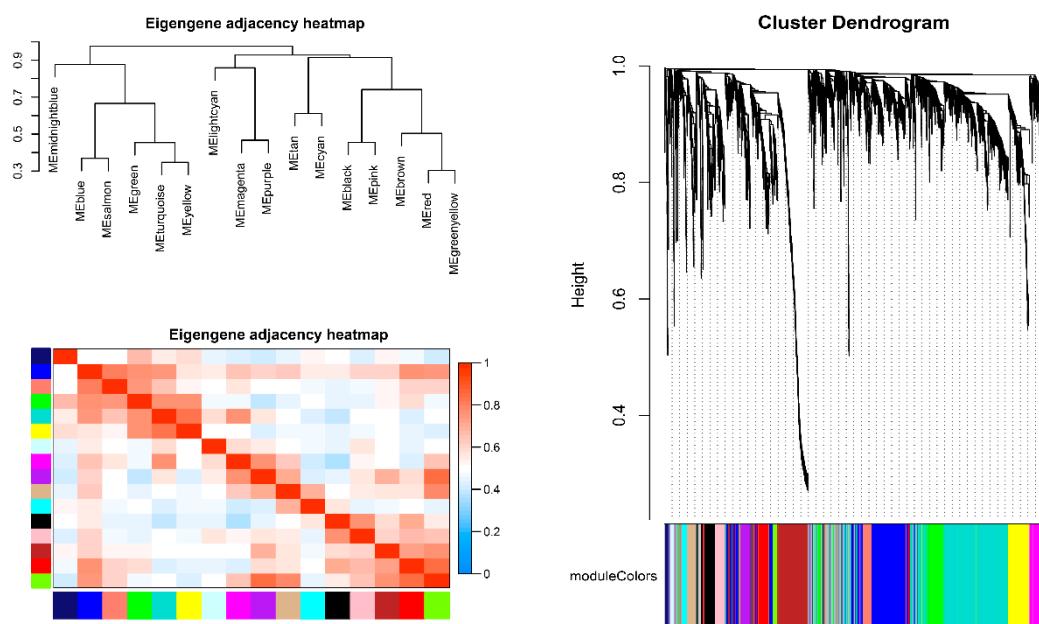


Figure S2. The topological matrix and hierarchical clustering tree of WGCNA.

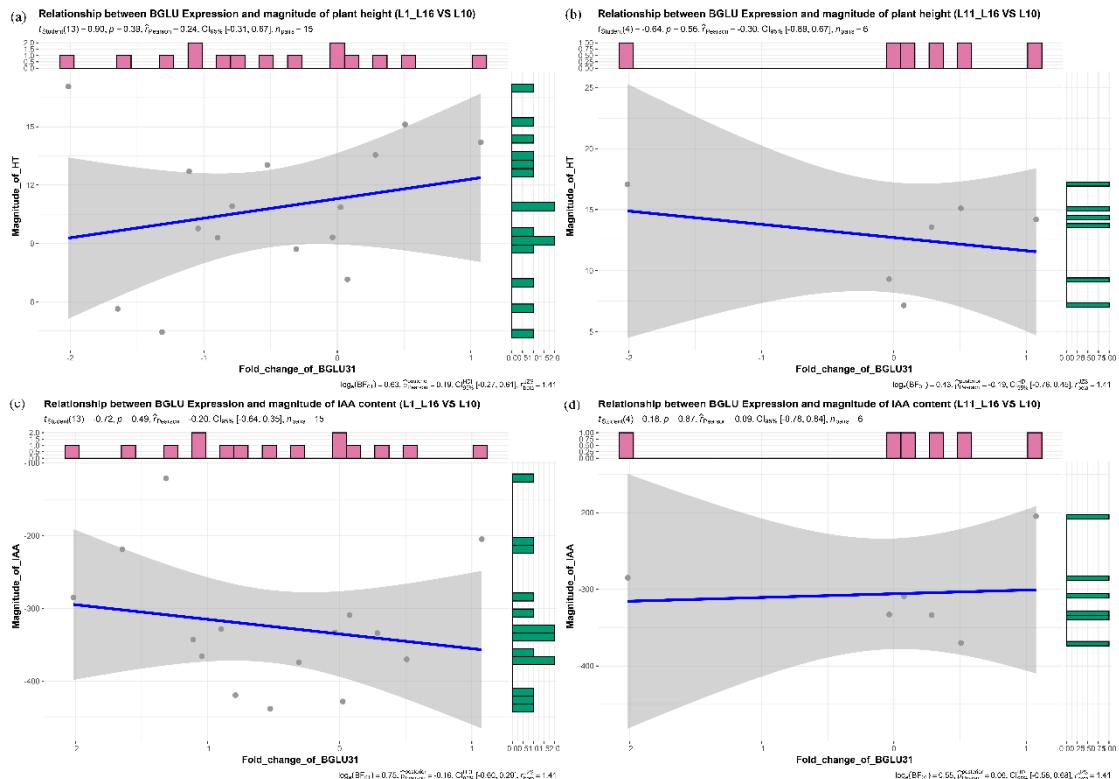


Figure S3. Correlation coefficient analysis between plant traits and BGLU31 expression. (a) Relationship between BGLU Expression and magnitude of plant height (L1_L16 VS L10). (b) Relationship between BGLU Expression and magnitude of plant height (L11_L16 VS L10). (c) Relationship between BGLU Expression and magnitude of IAA content (L1_L16 VS L10). (d) Relationship between BGLU Expression and magnitude of IAA content (L11_L16 VS L10).

CLUSTAL 0(1, 2, 4) multiple sequence alignment

| | |
|-------------------------------|---|
| Cd GCU* this | IAPWRLPDGRGEINPKGLLEYNNNLDL1H6HIEPHATIYHFPLQPVQLQEYSGLSLPR 17 |
| BAH00605.1 0 sBGL31 | ISWSRLLPDRGVAINPKGLLEYNNNLDL1H6HIEPHATIYHFPLQPVQLQEYSGLSLPR 17 |
| QJ0QJC1 | IAPWRLPDGRGEINPKGLLEYNNNLDL1H6HIEPHATIYHFPLQPVQLQEYSGLSLPR 17 |
| QJ0QJC2 | IAPWRLPDGRGEINPKGLLEYNNNLDL1H6HIEPHATIYHFPLQPVQLQEYSGLSLPR 17 |
| XP_015612589.1 0 sBGL32-like | IAPWRLPDGRGEINPKGLLEYNNNLDL1H6HIEPHATIYHFPLQPVQLQEYSGLSLPR 17 |
| NP_001183742.1 2 mBGL31-like | IAPWRLPDGRGEINPKGLLEYNNNLDL1H6HIEPHATIYHFPLQPVQLQEYSGLSLPR 17 |
| PW51718.1 1 ZmBGL31 | IAPWRLPDGRGEINPKGLLEYNNNLDL1H6HIEPHATIYHFPLQPVQLQEYSGLSLPR 17 |
| P14228 | G1PQHVT1YHFDFPLQALQEYSGLSLPR 18 |
| | G1PQHVT1YHFDFPLQALQEYSGLSLPR 14 |
| | ISWSRLLPDRGVAINPKGLQLEYNNNLDL1H6HIEPHATIYHFPLQPVQLQEYSGLSLPR 16 |
| | ***: * * : ***: * * : ***: * * : ***: * * : |

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| CdBGLU* this | SSTEPEVIAAHILLLAHAHAAAVSLSYRDKYKG | 26 |
| BAI00605.1 0sBGL31 | SSTEPEVIAAHILLLAHASAASVSLYRQEYQAT | QQGGQIGL 26 |
| QJ0QJC1 | SSTEPEVIAAHILLLAHASAASVSLYRQEYQAT | QQGGQIGL 26 |
| QJ0QJC2 | SSTEPEVIAAHILLLAHASAASVSLYRQEYQAT | QQGGQIGL 26 |
| XP_015612589.1 0sBGLU32-like | SSTEPEVIAAHILLLAHASAASVSLYRQEYQAT | QQGGQIGL 26 |
| NP_001183741.1 2mBGL31-like | SSTEPEVIAAHILLLAHASAASVSLYRQEYQAT | QQGGQIGL 26 |
| PWZ1718.1 ZmBGL31 | SSTEPEVIAAHILLLAHASAASVSLYRQEYQAT | QQGGQIGL 26 |
| P14228 | SSLEPEVIAVINNMLAHASATILYKQVGVLLSASLSPSS1CIALCYLF1TOYKQHGSV1 28 | QQGRIGL 24 |
| | : *; *; *; *; *; *; : *; *; : | |

| CdBLGU* this | | | | |
|-------------------------------|---|----|--|--|
| BAH00605. 1 0sBGL31 | TLLGGWWYEPGTQDPEDVAAAARMNDFIHGWMPLVYGDYPVPMRKVGWSRLPSFTAAEES | 32 | | |
| QJ0QG1 | TLMVRWHEPYTIDKTDADAAAAA1RMNEPHIIGWPFLHPLVLHGDDYPVPMRSRVGVRSLPSITASD5 | 32 | | |
| QJ0QG2 | TLLGGWWYEPYTDADAAAAA1RMNEPHIIGWPFLHPLVLHGDDYPVPMRSRVGVRSLPSITASD5 | 32 | | |
| XP_015612589. 1 0sBGLU32-like | TLLGGWWYEPYTDADAAAAA1RMNEPHIIGWPFLHPLVLHGDDYPVPMRSRVGVRSLPSITASD5 | 32 | | |
| NP_001183742. 1 ZmBGLU31-like | TLLGGWWYEPGTQTPDVTAAAARMNDFIHGWMPLVYGDYPVPMRKVGWSRLPSFTTDEA33 | 33 | | |
| PWZ1518. 1 ZmBGLU31 | TLLGGWWYEPGTQTPDVTAAAARMNDFIHGWMPLVYGDYPVPMRKVGWSRLPSFTTDEA33 | 33 | | |
| P41298 | SVTVTYGA(P)TNSVK(D)QATARVNED(G)W1 IALP1 VFGC(Y)PCTMKT(W)SGSLR(P)AFTTDEA34 | 34 | | |

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| CdBLGU* this | | | |
| BAI00605.1 0sBGL31 | KRVLYESDFVGFIHHYIAFIVPVLADLSKLQSLDQYMGDAAVKYKDPFLKSNSNEFPLG-LTS | 38 | |
| QQJOG1 | EKIRGSDFPIGILNHYVFIVFVQSDANIDQQLRDLYYDAGVQENG | DDT | 36 |
| QQJOG2 | EKIRGSDFPIGILNHYVFIVFVQSDANIDQQLRDLYYDAGVQENG | GGCFDK | 37 |
| XP_015612589.1 0sBGLU32-like | EKIRGSDFPIGILNHYVFIVFVQSDANIDQQLRDLYYDAGVQENG | GGGFDK | 37 |
| NP_001183742.1 ZmBGLU31-like | ARVRGSDFPIGVFNHYIVVVYQKGLDRLLQDGRYMDQVDAAVKYKDPFLKSNSNEFPLG-LTS | 39 | |
| PWZ1518.1 ZmBGLU31 | ARVYQGSDFPIGVFNHYIVVVYQKGLDRLLQDGRYMDQVDAAVKYKDPFLKSNSNEFPLG-LTS | 36 | |
| P14228 | EQVKYQGSDFPIGVFNHYIVVVYQKGLDRLLQDGRYMDQVDAAVKYKDPFLKSNSNEFPLG-LTS | GNTSIE | 36 |

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| CdBLGU* this | -E1E8PPWALGKLLDILKLKYENPLVYIHEANGAEAPDPPGAIYVDDDEFRSEMLQDYLEV | 31 |
| BAH00605_1 OsBGL31 | DFTM1STPWLALKMLNHLQKCYKPVNPMIHEANGAQGPPDSQCGNTYDDEFRSQRQLQYQLEA | 44 |
| QJ0061 | EN1QCHSWLSGKVLNHLKLEYKGPNPVWYHENGYSDPSLFLIGKNNYNDERSFAFLQGYLEA | 43 |
| QJ0062 | BHQYLPHWALGKMLNHLKLYKGPNPVWYHENGDADSPETPGKIDYDDERFSRDFLQSYLEV | 43 |
| XP_0516212589_1 OsBGLU32-like | BHQYLPHWALGKMLNHLKLYKGPNPVWYHENGDADSPETPGKIDYDDERFSRDFLQSYLEV | 43 |
| NP_001183742_1 ZmBGLU31-like | DFTM1STPWLALKMLNHLRHTVYKPNPAVMIHEANGAQGPPDSQCVNSYDDEFRSQRQLQYQLEA | 45 |
| PWZ15178_1 ZmBGLU31 | DFTM1STPWLALKMLNHLRHTVYKPNPAVMIHEANGAQGPPDSQCVNSYDDEFRSQRQLQYQLEA | 45 |
| P41228 | NEYANTPLSLQQLLWYKETKNGPVPWYHENGDADSPETPGKIDYDDERFSRDFLQSYLEV | 44 |

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|---------------|------------------|--|-----|
| CdBGLU* | this | LHMSTRNGSNARGFYVWSFLDVFEFLFAYRVRFLGCGVDIMNAARTRYVRSSARWYAGFL | 374 |
| BAI00605. | 1 OsBGLU31 | TLSQSTRNGSNVGQFYVWSFLDVFEYLFGYFLRGLGYLGVDASPERTYQRGRISAWYAGFL | 401 |
| QJ0JG1 | | LTLVSRSNGNTFRGVFWSMDFEFLFGYLRGLFGCLVDTAFAARTTRYVLKRSNWSYGF | 483 |
| QJ0JG2 | | LHLSTRNGNTGRGVFWSLIDGFFELSGYGNRFGLCCVDTAPARTTRYVRSSARWYSDFL | 491 |
| XP_051662589. | 1 OsBGLU32-like | LHLSTRNGNTGRGVFWSLIDGFFELSGYGNRFGLCCVDTAPARTTRYVRSSARWYSDFL | 491 |
| NN_001183742. | 1 ZmBGLU31-like | TLSQSTRNGSNVGQFYVWSFLDVFEYLFGYFLRGLGYVGVYVFENNSTARRYQRHSKASYAFSL | 514 |
| PW#15178.1 | 1 ZmBGLU31 | NGSNVGQFYVWSFLDVFEYLFGYFLRGLGYVGVYVFENNSTARRYQRHSKASYAFSL | 561 |
| P41228 | | VLSHLSRKGSDDVGKVQSYLMDVPELFGYERSSPLGGLYVDDFKDPSLKRSPKLSAHWSYGF | 566 |

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|------------------------------|-------------------------|-----|
| CdBGLU* this | RCGELRPPAIFPRPDNRSYVADE | 399 |
| BAH00605.1 0sBGL31 | RGGELRPAAAALACCGAYSQ- | 523 |
| QJ0JG1 | RGGELRPEKSYATL----- | 503 |
| QJ0JG2 | NGGELRPVVKPFVAL----- | 508 |
| XP_015612589.1 0sBLGU32-like | NGGELRPVVKPFVAL----- | 508 |
| NP_001183742.1 ZmBGLU31-like | RGGELRPVVALP---DGAYSQ- | 533 |
| PWZ15718.1 ZmBGLU31 | RGGELRPVVALP---DGAYSQ- | 486 |
| P14228 | KGTLLHIPSYASS----- | 520 |

Figure S4. Alignment

analysis of BGLU gene from different plants.

Table S1. Geographical locations, plant height and IAA content of diverse bermudagrass

| Region | Latitude | Sample | HT | IAA |
|------------------|-----------------|---------------|-----------|------------|
| Subtropical zone | 22°35'40" | L1 | 20.43 | 266.92438 |
| | 22°51'48" | L2 | 17.49 | 244.04445 |
| | 24°10'31" | L3 | 20.76 | 171.6514 |
| | 25°05'29" | L4 | 18.64 | 190.29881 |
| | 26°03'49" | L5 | 18.58 | 181.54994 |
| | 27°00'59" | L6 | 17.01 | 281.34448 |
| | 28°09'14" | L7 | 16.42 | 235.61128 |
| | 29°28'32" | L8 | 13.36 | 390.85805 |
| | 30°25'48" | L9 | 12.16 | 488.7188 |
| | 31°18'59" | L10 | 7.72 | 609.71927 |
| Mesotherm zone | 32°08'38" | L11 | 14.87 | 300.4336 |
| | 33°09'47" | L12 | 17.03 | 276.79077 |
| | 34°00'30" | L13 | 21.27 | 275.84688 |
| | 34°54'04" | L14 | 22.84 | 239.66685 |
| | 35°29'26" | L15 | 21.92 | 405.10552 |
| | 36°18'40" | L16 | 24.79 | 324.74452 |
| Coefficient | Total region | L1-L16 | 0.156 | 0.410 |
| | Subtropics | L1-L10 | -0.890 | 0.792 |
| | Mesotherm | L11-L16 | 0.957 | 0.387 |

Table S2. Detailed data of GO analysis result of DEGs.

| GO ID | Description | DEGs | All Gene | pvalue | p.adjust |
|------------|--|------|----------|-----------|-----------|
| GO:0044710 | single-organism metabolic process | 390 | 2070 | 1.07E-07 | 0.0001002 |
| GO:0055114 | oxidation-reduction process | 221 | 1167 | 0.0001239 | 0.0165487 |
| GO:1901615 | organic hydroxy compound metabolic process | 8 | 12 | 8.04E-05 | 0.0150624 |
| GO:0006082 | organic acid metabolic process | 70 | 307 | 0.0002416 | 0.0208166 |
| GO:0043436 | oxoacid metabolic process | 70 | 306 | 0.000218 | 0.0208166 |
| GO:0019752 | carboxylic acid metabolic process | 70 | 300 | 0.0001155 | 0.0165487 |
| GO:0044281 | small molecule metabolic process | 106 | 452 | 1.55E-06 | 0.0007257 |
| GO:0006520 | cellular amino acid metabolic process | 43 | 153 | 2.97E-05 | 0.0092672 |
| GO:0043038 | amino acid activation | 21 | 66 | 0.000546 | 0.0283608 |
| GO:0006334 | nucleosome assembly | 10 | 20 | 0.0002822 | 0.0208166 |
| GO:0006323 | DNA packaging | 10 | 21 | 0.0004655 | 0.0272037 |
| GO:0071824 | protein-DNA complex subunit organization | 11 | 23 | 0.0002299 | 0.0208166 |
| GO:0031497 | chromatin assembly | 10 | 20 | 0.0002822 | 0.0208166 |
| GO:0006334 | nucleosome assembly | 10 | 20 | 0.0002822 | 0.0208166 |
| GO:0034728 | nucleosome organization | 11 | 21 | 8.05E-05 | 0.0150624 |
| GO:0006066 | alcohol metabolic process | 7 | 11 | 0.0003562 | 0.023791 |
| GO:1901615 | organic hydroxy compound metabolic process | 8 | 12 | 8.04E-05 | 0.0150624 |
| GO:0003824 | catalytic activity | 1005 | 6224 | 1.70E-06 | 0.0009385 |
| GO:0048037 | cofactor binding | 78 | 339 | 2.52E-05 | 0.0057297 |
| GO:0050662 | coenzyme binding | 61 | 250 | 3.11E-05 | 0.0057297 |

Table S3. Phenotypic characterizations of *bglu11* mutant and wild type of Arabidopsis

| | WT | M1 | M2 |
|---------------------|------------|-----------|-----------|
| Height of rosette | 1.99±0.09 | 1.81±0.05 | 1.63±0.04 |
| Diameter of rosette | 5.26±0.03 | 4.73±0.05 | 3.12±0.07 |
| Plant Height | 16.38±0.55 | 7.57±0.24 | 9.75±0.12 |