

Supplementary materials

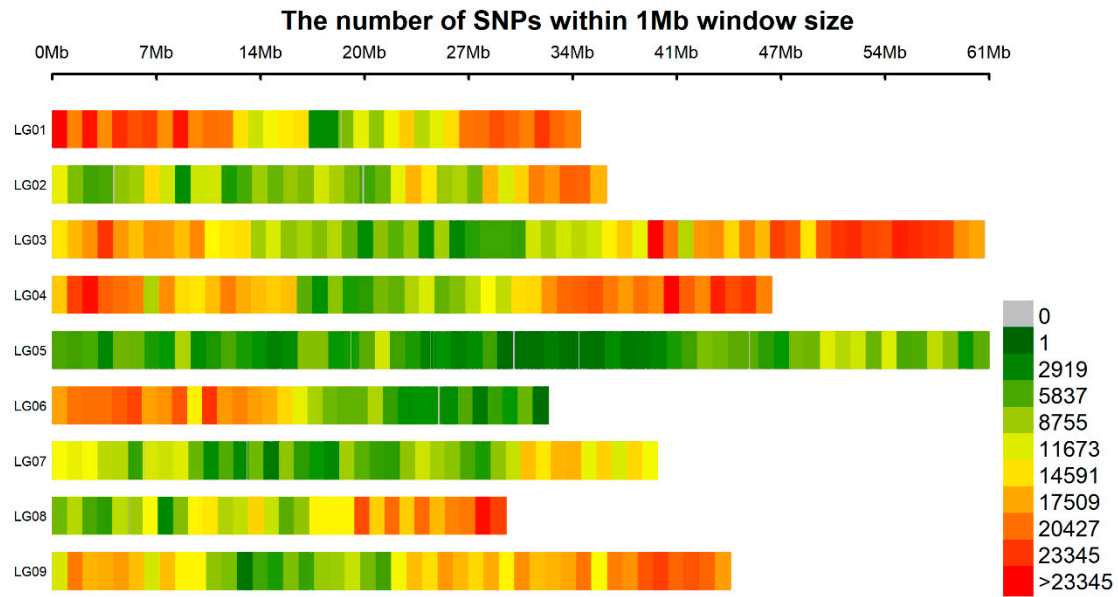


Figure S1. The number of SNPs in chromosomes within 1Mb window size.

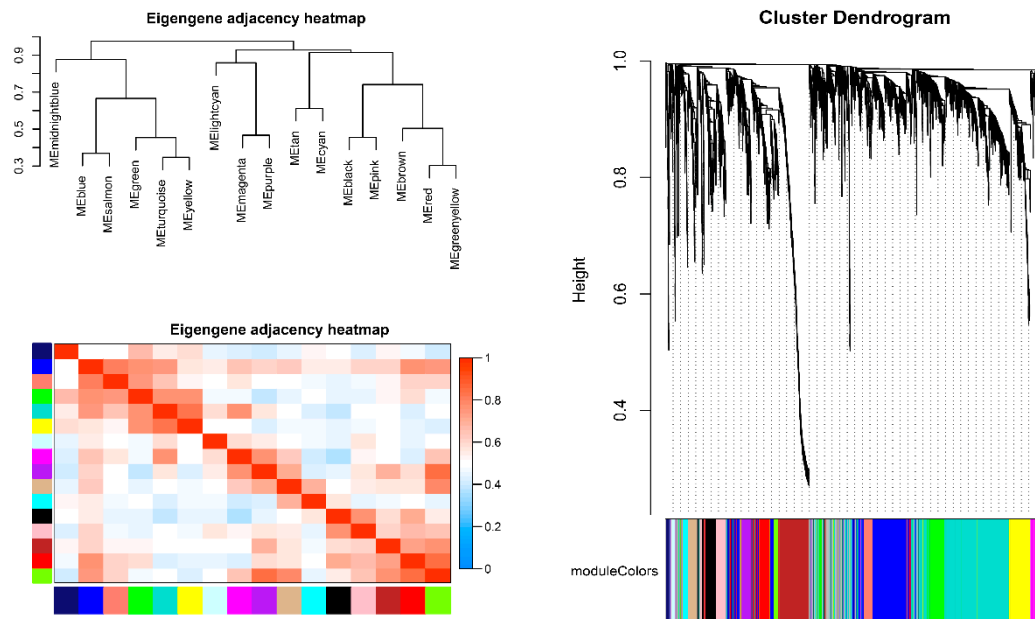


Figure S2. The topological matrix and hierarchical clustering tree of WGCNA.

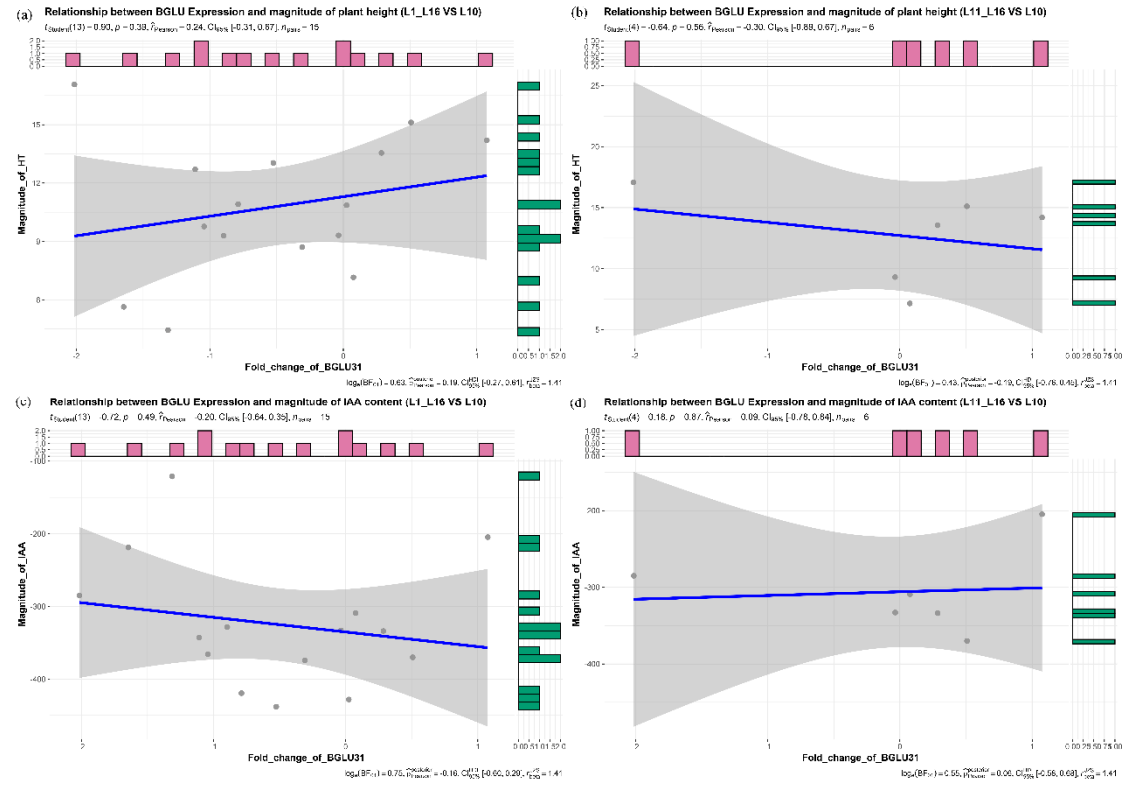


Figure S3. Correlation coefficient analysis between plant traits and BGLU31 expression. (a) Relationship between BGLU Expression and magnitude of plant height (L1_L16 VS L10). (b) Relationship between BGLU Expression and magnitude of plant height (L11_L16 VS L10). (c) Relationship between BGLU Expression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

[illegible]

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