Table S1. RNA-seq data statistics

Sample	Raw Reads	Clean Reads	Clean Base (G)	Q20 (%)	Q30 (%)	Reads mapped	Unique mapped	Multi mapped
BTx623-1	53982606	52470048	7.87	97.83	93.76	51563975 (98.27%)	49801187 (94.91%)	1762788 (3.36%)
BTx623-2	53375036	52152596	7.82	98.02	94.14	51336136 (98.43%)	49486214 (94.89%)	1849922 (3.55%)
BTx623-3	51890268	50930700	7.64	97.86	93.81	50065505 (98.30%)	48048639 (94.34%)	2016866 (3.96%)
sbgpgl1-1	51048612	49827532	7.47	98.19	94.60	49076033 (98.49%)	47128929 (94.58%)	1947104 (3.91%)
sbgpgl1-2	54403578	53638352	8.05	98.09	94.33	52848713 (98.53%)	50800996 (94.71%)	2047717 (3.82%)
sbgpgl1-3	51281782	50031486	7.50	97.99	94.10	49217836 (98.37%)	47009111 (93.96%)	2208725 (4.41%)

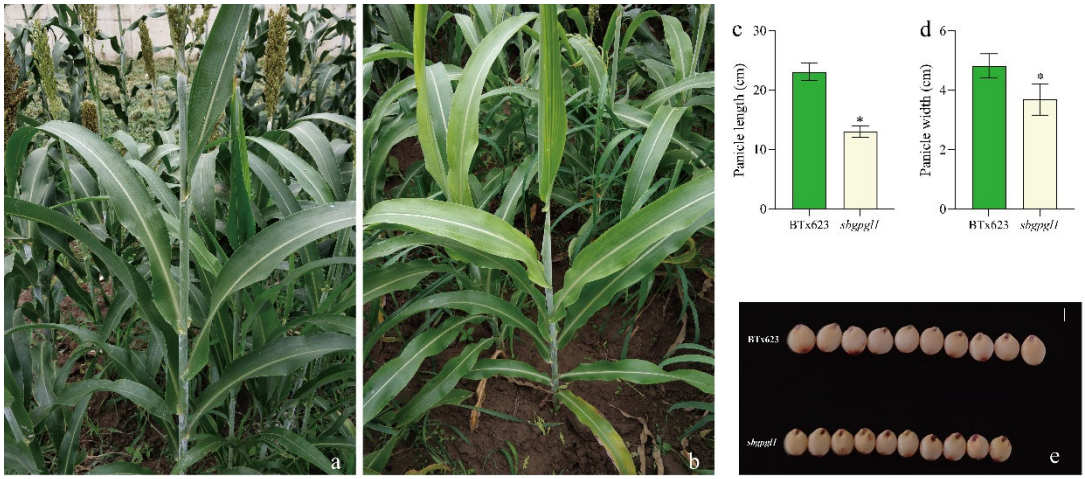


Figure S1. Phenotype in field and panicle traits of BTx623 and *sbgpgl1*. (a) Phenotype of BTx623 in the field. (b) Phenotype of *sbgpgl1* in the field. (c) Panicle lengths of BTx623 and *sbgpgl1*. (d) Panicle widths of BTx623 and *sbgpgl1*. (e) Seed phenotypes of BTx623 and *sbgpgl1*. The data are presented as the average and SD ($n \geq 3$), and are analyzed using t-test, * $p < 0.05$.

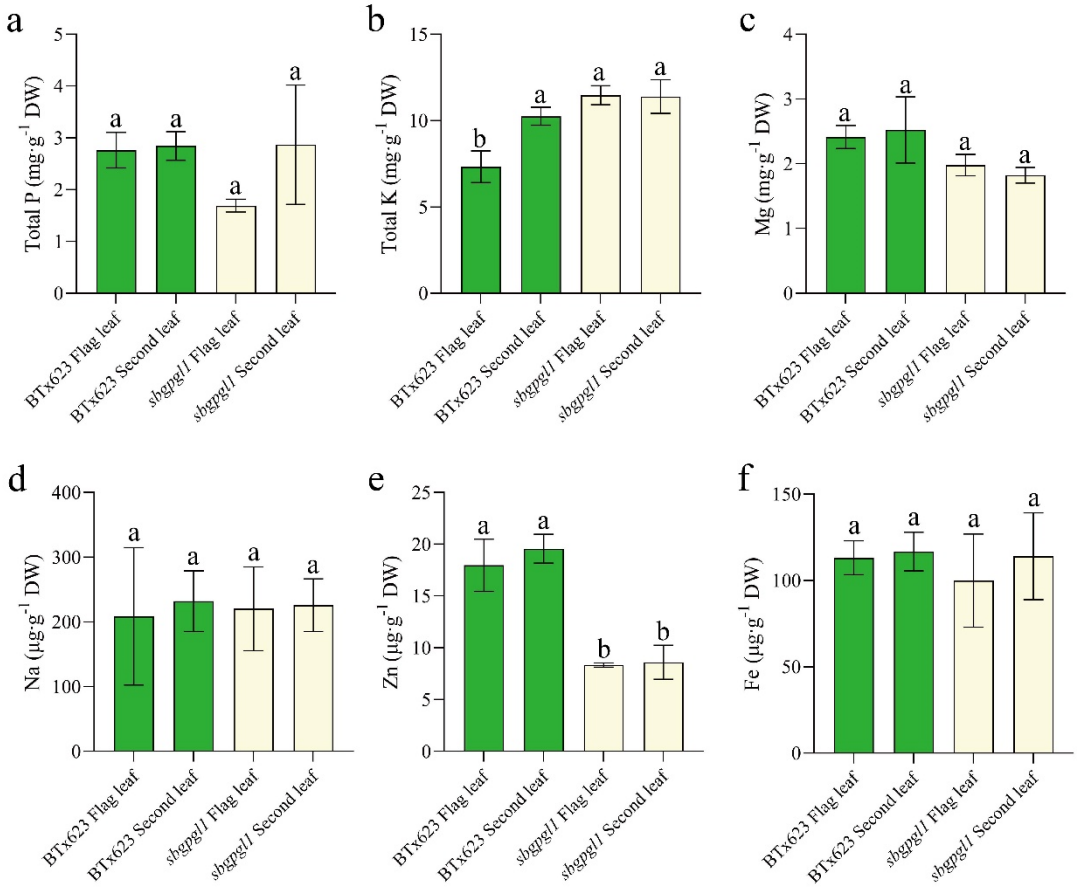


Figure S2. Total P, K and other mineral element contents of BTx623 and *sbgpgl1*. (a) Total P of BTx623 and *sbgpgl1*. (b) Total K of BTx623 and *sbgpgl1*. (c) Mg contents of BTx623 and *sbgpgl1*. (d) Na contents of BTx623 and *sbgpgl1*. (e) Zn contents of BTx623 and *sbgpgl1*. (f) Fe contents of BTx623 and *sbgpgl1*. The data are presented as the average and SD ($n \geq 3$), and are analyzed using Tukey-HSD test. Different letters indicate significant differences ($p < 0.05$).

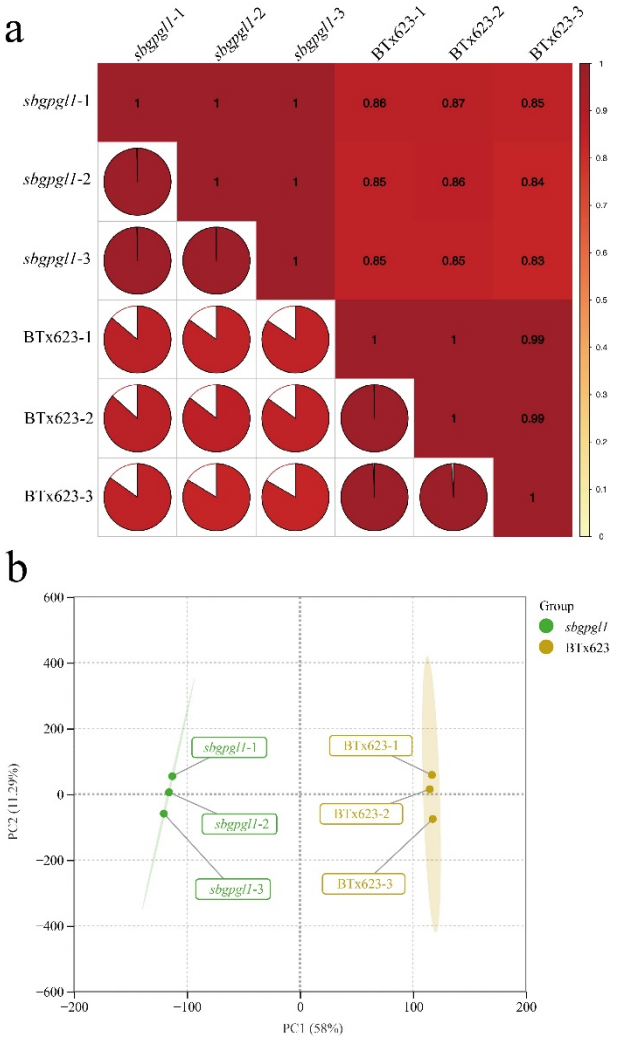


Figure S3. Transcriptomic correlation analysis of *sbgpgl1* and BTx623. (a) Correlation matrix of BTx623 and *sbgpgl1*. The horizontal and vertical axes represent different samples, and the color difference in the pie chart represents the Pearson correlation coefficient of gene expression levels between two samples; (b) PCA diagram of BTx623 and *sbgpgl1*.

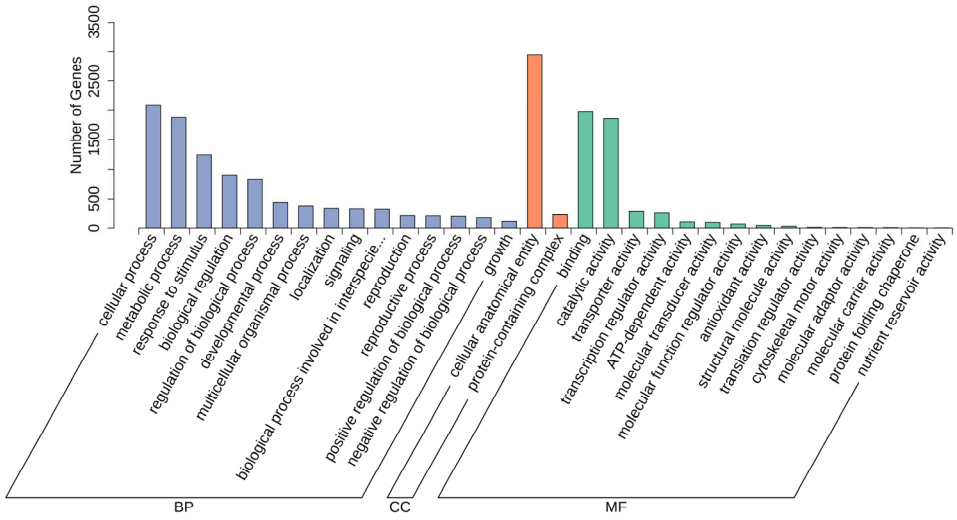


Figure S4. Up- and down-regulated number of genes of *sbgpgl1* and BTx623 by GO classification. The horizontal axis represents the secondary GO entries, and the vertical axis represents the number of DEGs in the GO entries.

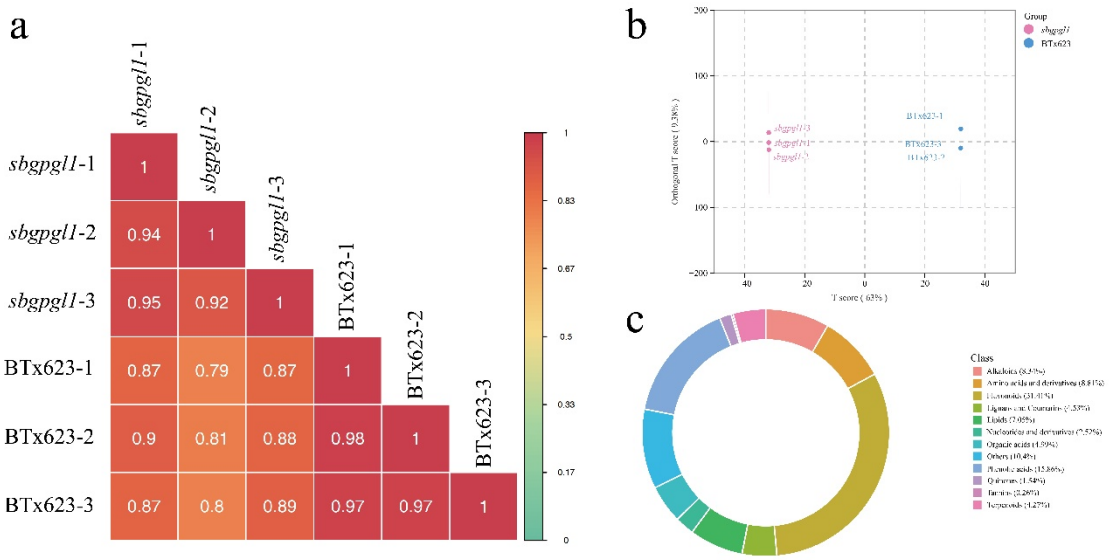


Figure S5. Metabolic correlation analysis of *sbgpgl1* and BTx623. (a) Correlation matrix of BTx623 and *sbgpgl1*; Different colors represent different sizes of Pearson correlation coefficients, and the size of the correlation coefficient between two samples is marked in the grid. (b) OPLS-DA diagram of BTx623 and *sbgpgl1*. PC1 represents the first principal component, and PC2 represents the second principal component. (c) Ring diagram of metabolites class. Each color represents a metabolite category, and the area of the color block indicates the proportion of that category.

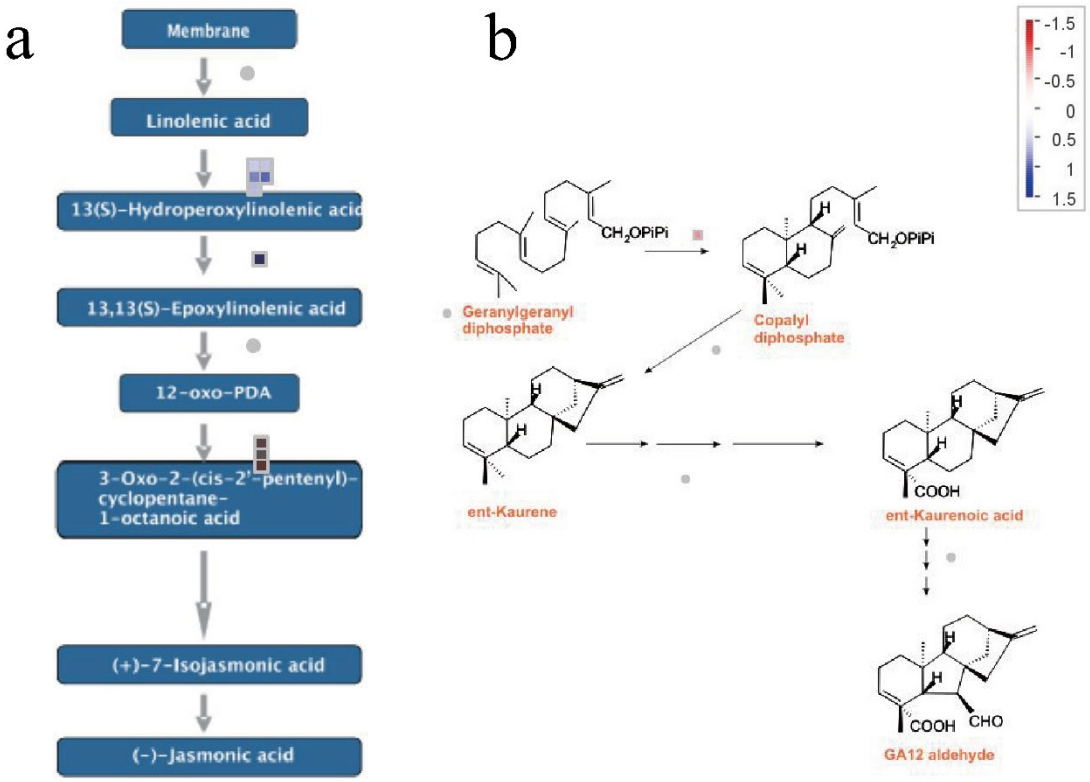


Figure S6. DEGs analysis of *sbgpgl1* and BTx623 in hormone synthesis. (a) JA synthesis. (b) GA synthesis.