

**Table S3.** KEGG pathways enrichment results of diterpene treatments.

	KEGG pathways	Sg3a-5h			Sg6-5h			Sg3a-1h			Sg6-1h		
		UP/DOWN	UP	DOWN	UP/DOWN	UP	DOWN	UP/DOWN	UP	DOWN	UP/DOWN	UP	DOWN
bst02010	ABC transporters	35 <sup>a</sup>	36										12
bst02030	Bacterial chemotaxis			20	2	21	21			9			5
bst02040	Flagellar assembly	2	28		1	37	37			12			
bst00552	Teichoic acid biosynthesis		13										
bst00300	Lysine biosynthesis		9										
bst00230	Purine metabolism				10	34	34						
bst00240	Pyrimidine metabolism				3	23	23						
bst00640	Propanoate metabolism				9	15							
bst01120	Microbial metabolism in diverse environments				72	45	72						
bst01110	Biosynthesis of secondary metabolites				83	112		48			65	13	65
bst00650	Butanoate metabolism				13	6	13						
bst00190	Oxidative phosphorylation				3	25	25						
bst03010	Ribosome						34						
bst01232	Nucleotide metabolism						29						
bst00670	One carbon pool by folate						9						
bst00500	Starch and sucrose metabolism					23							
bst00920	Sulfur metabolism					11							
bst00562	Inositol phosphate metabolism					9							
bst02060	Phosphotransferase system (PTS)					15							
bst00520	Amino sugar and nucleotide sugar metabolism					16							
bst00071	Fatty acid degradation					8			8				
bst04122	Sulfur relay system								7				
bst00740	Riboflavin metabolism								6				
bst01240	Biosynthesis of cofactors								29				
bst00130	Ubiquinone and other terpenoid-quinone biosynthesis								6		7	1	7
bst01230	Biosynthesis of amino acids										32	5	32
bst00220	Arginine biosynthesis					10							8
bst00340	Histidine metabolism										6	1	6
bst00380	Tryptophan metabolism												6
bst00290	Valine, leucine and isoleucine biosynthesis												9
bst00280	Valine, leucine and isoleucine degradation										7	1	7
bst00561	Glycerolipid metabolism										4	4	4
bst00630	Glyoxylate and dicarboxylate metabolism										10	1	10
bst01210	2-Oxocarboxylic acid metabolism					14							15
bst00010	Glycolysis / Gluconeogenesis											10	
bst00400	Phenylalanine, tyrosine and tryptophan biosynthesis												5

<sup>a</sup>The number of the genes up- or down-regulated in the significantly enriched pathways is marked in red and green, respectively.