



Supplementary Material: *De novo* Assembly and Analysis of *Polygonatum sibiricum* Transcriptome and Identification of Genes Involved in Polysaccharide Biosynthesis

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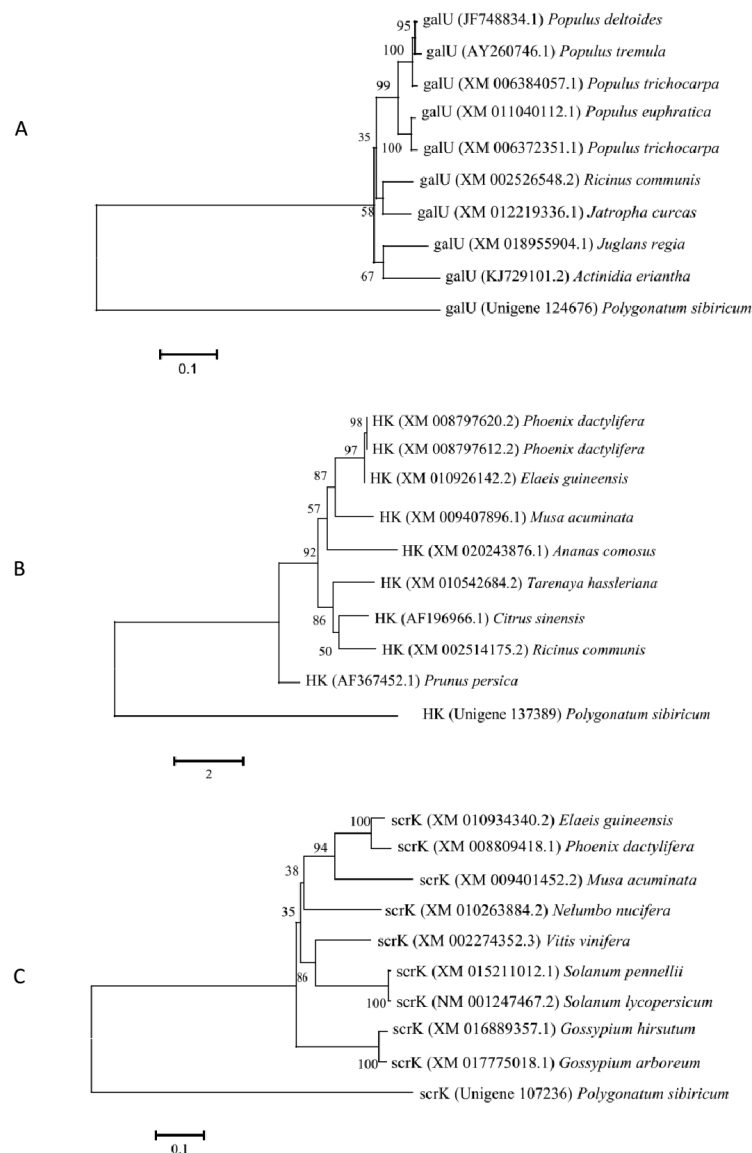


Figure S1. Trees produced from Neighbor-joining phylogenetic analysis of homologs for *galU* (A), *HK* (B), and *scrK* (C) in various plant species, as performed with MEGA 6 software.

PREDICTED: Ricinus communis UTP--glucose-1-phosphate uridylyltransferase (LOC8266519), transcript variant X2, mRNA
Sequence ID: [XM 002526548.2](#) Length: 1889 Number of Matches: 1

Range 1: 777 to 1870				GenBank	Graphics	Next Match	Previous Match
Score	Expect	Identities	Gaps	Strand			
1151 bits(623)	0.0	953/1111(86%)	28/1111(2%)	Plus/Minus			
Query	54	TGCCAGAGATTGGGGCTCAAGTTTCCAAATT-TA-TAAGTCTGTAGGAGCTATC---ACA					108
Sbjct	1870	TGCCAGAGATCGAGGCACAAGTTTGCACATTATACTAA-TCTGTAGAAGTTATCCGAACA					1812
Query	109	CTCCAACCTAGTTTACACCTTATATTATAAAGTTTGTATG-A-ACaaaaaaCAGGTTTC					166
Sbjct	1811	C-CC-ATGTAGTTTACATCCTCT-TTAT-CAGATTGTATGTATACACAAAAATAATATC					1756
Query	167	A-CCGTATCTAG-GCAGACATTCCAAATTCA-GACTCAGCAAACAAATGCAACTCTCTTA					223
Sbjct	1755	ATAAGTA-GAAGAGC-GGCATTCCGAATTCAAGACACAGGAAAGGGAA-CCACTCTCTTA					1699
Query	224	TTCTCCCAT-AAAAATGTAAGGGCATTCCGAGATGCAGAAAGGACTCCTCAAAGAGCCAC					282
Sbjct	1698	TTCTGCTATCAAAAATACATGAGCATTGTAAGATGGAGAAATGACTCCTCAAAGAG----					1643
Query	283	CACGTCTCCCCACACTTTTAGCAACCGCTACTTTCTTAGAGGTCTTCAGGACCATTAAAT					342
Sbjct	1642	----TCTCCAACACAATGTGAGCCAA-GCAACTCTTTTACAGGTCTCAGGGCCATTAAAT					1588
Query	343	ATCCTTGTTCACAATTATGGCTCCATCAGGTATTTCCAATTTTACACCAGGTTTTCAGC					402
Sbjct	1587	ATCCTTGTTCACAATTATGGCTCCATCAGGTATTTCCAATTTTACACCAGGTTTTCAGC					1528
Query	403	AATGTTGACTTTCCCTTGGAGTAATACCAGCACCACCAACACATCACCAGTCACCTT					462
Sbjct	1527	AATAGTCACTTTCCCTTGGAGTATAACACCAGCACCACCAACATACATCACCAGCCACTT					1468
Query	463	AAGGCTATCAAGCTCAATGATACTAGGGATCGACTTAAATCGACTCAAGAAGTTTGAAC					522
Sbjct	1467	AAGGCTATCAAGCTCAATGATGCTTGGGATTGACTTAAATCGACTCAAGAAGTTTGAAC					1408
Query	523	CTTCTTAAATTCTGGGCCCAATTCAATAGAAGGATTTCAGGATTTTGCCTGGCTTTATT					582
Sbjct	1407	CTTCTTAAATTCTGGGCCCAATTCAATAGAAGGATTTCAGGATTTTGCCTGGCTTTATT					1348
Query	583	TCGGATAACATAGCCATCCTCCAAGATGTAAGATCAGACTGGACAAGAAGCAAATCTGA					642
Sbjct	1347	TCTGATAACAAAGCCACCGTCTAAGGTGTAAGATCAGACTGGACAAGAAGCAAATCTGA					1288
Query	643	AGTTGCCTTCACTGGAAGGAATCGGGATCGAGGAACATTTATGCCAATTGCATGGTCAAA					702
Sbjct	1287	GGTTGCCTTCACTGGAAGGAATCGAGATCGAGGAACATTTATACCAATTGCATGATCAAA					1228
Query	703	GAACCTAATAGCGGCACAGCTGCAGTTTCTAGTTGAAGAACTTTGACTCCATCTACTTC					762
Sbjct	1227	AAACCTAATAGCTGCACAGCGCAGTTTCAAGCTGAAGAACTTTGACGCCATCCACTTC					1168
Query	763	CTTTGGGTTAGGAATTATCTCCATCTTTAGAGCATCAGCTTCCACCAGCCTTTTAATTGC					822
Sbjct	1167	CTTTGGGTTAGGAATTATCTCCATCTTTAATGCATCAGCTTCCACAAGCCTTTTAATTGC					1108
Query	823	TGACAAGCTCACCCACAAGTTGTTGTATTGAAAATTTGAACTTCTCTATTGATTGAA					882
Sbjct	1107	TGACAAGCTCACCCACAATTTGTTGTATTGAAAATTTGAACTTCTCTATTGACTTGAA					1048
Query	883	TTCATGACATGCTCATCAGGGACTTGCGCAATCTCCAACAGCTGAACCTTCCCTTCATA					942
Sbjct	1047	TTCATTGACATGCTCATCAGGGACTTGTGCAATTTCCAATAACTGAACCTTCCCTTCGTA					988
Query	943	GGAGATGAGAGTACCGCCCTTTACATCAGCCAGGGTTTTGGGTGTCACCTCCATGCAGTA					1002
Sbjct	987	AGAGATGAGAGTGCACCCCTTCACATCAGCCAGGGTTTTGGGTGTCACCTCCATGCAGTA					928
Query	1003	TTCATTCTTGTCTGATTAGATGACTTAAGATTTTCAAATCAACTATAGCACCAGGTT					1062
Sbjct	927	TTCATTCTTGTCTGATCAGATGATTTAAATTTTCAAATCAACAATAGCACCAGGTT					868
Query	1063	ATCTGAGTTGGCAATAAATACGTACTCCTTGCCCTGTAATAACAAGAATCAAGCTTGCC					1122
Sbjct	867	ATCTGAGTTGGCAGCAACACATACTCCTTGCCCTGAGATAACAGAGCATCAAGCTTGCC					808
Query	1123	ACTGTTCTTCAAGGATGGGAACACATCACCA	1153				
Sbjct	807	ACTGTTCTTCAAGGATGGGAACACATCACCA	777				

Figure S2. Alignment of *galU* between *Polygonatum sibiricum* and *Ricinus communis*.

PREDICTED: *Elaeis guineensis* hexokinase-2 (LOC105047281), transcript variant X2, mRNA
Sequence ID: [XM_010926142.2](#) Length: 2414 Number of Matches: 1

Range 1: 570 to 1983		GenBank	Graphics			Next Match	Previous Match
Score	Expect	Identities		Gaps	Strand		Plus/Minus
881 bits(477)	0.0	1111/1421(78%)		27/1421(1%)			
Query	354	ACAC-TTGGGACTCCTCGAGTTCAACGTACTGAGAGTGAGTGGCAGCAACGAGAGCTGCT				412	
Sbjct	1983	ACACTTTAGGATTCTTCAAGCTCAAGATACTGAGAGTGAGATGCAGCAAGGAGAGCTGCT				1924	
Query	413	CCGATGCCGTGAGCCATCATTGGCATGCTTGACATA-AACAGAATCTGAGGCCCTCTTCTCC				471	
Sbjct	1923	CCAATGCCGTGATCCGTCACCTGGCAAGCTTGA-TGACAATAGAAGCTGTGGCTTCTTCTCC				1865	
Query	472	AAGAAGTTCITTGAGGGTGCTCTGCAAGCATTTGCTGAATATGGCGTAGTGCTCAAAAAG				531	
Sbjct	1864	GAGCATCTCTCTAAGTGTGGTTTCCAACAATTTGCTAAATATAGTGTAAATGTTTATAAAG				1805	
Query	532	GGCTCCATCAATAGCAATCACCGTTCTCTGC-T-T--GTCGA-CACT---TGCCACATC				582	
Sbjct	1804	CCCACCATCCATAGCAATACTGCTCTGCTGCTCACTTCCATCCCTCAATGCAGTATC				1745	
Query	583	-CTTCCCTAACTTCTTCAATATGCCTACTATGCCTGCAGCAGCTAGGCGTGACCCACGCT				641	
Sbjct	1744	ACGGCCCT-GCTTCTTCAAGACGCCAGTATTCAGCAGCAGCCAGACGAGCCCCACGCT				1686	
Query	642	TTGCGATGACATCAGACCTCAACAATCAGTTTCTTGT-ACCGA-GA-GAAGTGGTGA				698	
Sbjct	1685	TGGCTATGATATCAGACCTTGACAACCAAGCTTCTTGTTTTCAAGGAGGTATTAGAGA				1626	
Query	699	TCCTTAAATTTTCCCTCCAGCTTCTTTCCAAAGACATTAAGATCAGATGATGATCATGAT				758	
Sbjct	1625	TCCTTAAATGTCTTTAGTTTAGTCCCAACAACCTCTGAGATCGGATGATGTGTCATGAT				1566	
Query	759	GCATGGAAGACACGACAGGTGCTCCTTAATACAAAAGGAACCTTGAAGTTAAGAGGGACAG				818	
Sbjct	1565	GCATGGCTGACATGTCTGGAGTCCGTAGTATAAATTGAACCTCAAGTTT-TGGCGGAATG				1507	
Query	819	-TATCCCCAAA-AAGGTGAGCCCTTTTCAGCCATTTTCAATAGGGCTCTGCGTACAAATTC				876	
Sbjct	1506	CTGTCTCCAAACAAGG-CAGCTTCTCTGAGCCATTTTCAACAGGACTCTTCTGACAAATTC				1448	
Query	877	ACCCAAATACATTCCTGAAAATAACTTCTCAAAGATCTGCTCACCAGGATTCAGGCTTTC				936	
Sbjct	1447	TCCCAAGTACATTCAGAAATTAACCTTCTCAAAGATCTGCTCACCAGGATTCAGAACTTTC				1388	
Query	937	AGCATCCAAGGCATGATCATGTTCCATCAAAGGAAGATGAGGTGAGAGGAAGTTTCCCCA				996	
Sbjct	1387	AGCATCTAATGCTTGATCATATTCGTATAGSAAAGATGAGATGACCTGAAATTTCCCCA				1328	
Query	997	TTCCATGTTAATAACCATCTGTCCAGATTTAGGCAAAAGGCCTTGCCACTTAGGAATTGC				1056	
Sbjct	1327	TTCCATGTTGATAACCATCTTTCCTGATTTTGGTAAAAGGCCATGCCATTAGGAATTGC				1268	
Query	1057	TTGTGCATGCTCTACATATGCTGCATTACTTCCAGTTCCCAATATCACTGCAGCAATGAC				1116	
Sbjct	1267	TTGTGCATGCTCTACATATGCTGCATTCTGTTCCAGTACCCAGTATGACAGCAGCAACCAC				1208	
Query	1117	ATCATCATCATAATATCTGCCACCAGCCAAAGTTCCAACTGTATCATTTGACTAATGCTGC				1176	
Sbjct	1207	GTGATTATCATAATATCTTCCCGCAGCAATGTCCCAATTGTGTCATTTACCAATGCTGT				1148	
Query	1177	CACTCGCATATCAAGACCCCTTTCTTTCCATTGCTTTAGTCAATTCAGCCACCACATCTTG				1236	
Sbjct	1147	AACTCGCATATCAAGACCTTGCTTTCAATGGCTTGGTCAACTCAGCCACCACATCTTC				1088	
Query	1237	GCCAAGCGTTCTGTCAATGTTGAAGCCCTTTGTCCATTAAATTAAGTTCTGTATGCAAT				1296	
Sbjct	1087	CCCAACCGTGCCATTATAGCGAAACCCCTTTGTCCACTTAATAAGAGTGCTGTATGAGAT				1028	
Query	1297	GGAAGTTTGTGCGCACGGGAAAAGAGAATGTAACCCCAAGCTCTCTCTGCTGCCCTCAGC				1356	
Sbjct	1027	TGAGGTTTGTCTCACTGGGAAAGAGAAAGTAAACCAAGTTCTCTCTGCTGCCACAGG				968	
Query	1357	AAGGCGAAATCTTCACTTCCGTAGCAACAAATTTAGCTAATTCTGCTGCAATGAATC				1416	
Sbjct	967	AAGGTGAATTTCTTCACTTCTGAAGCAACAACTTTGCCAATGCTGCAGCAATGAATC				908	
Query	1417	GAATAGTTTCATCAGAACCTCCGATCATCAAATGTGGTGAATAGAGACCTCTACCGCTTC				1476	
Sbjct	907	AAATAGTTCACTGGAGCTTCCAACCATCAAATTTGGTGAATGGAACTTCTTCAAATTC				848	
Query	1477	TCGTTTAAACAACACGCTCTTCTTCCACCCAGTTGTACACGTAA-ACAACGGAAGTTTG				1535	
Sbjct	847	TTGCTTGACAACACGCCCTCCCTTTCTTCCCAATTGTACACGTAGTAC-ACGGAAGTTGG				789	
Query	1536	TTCTTCAAGATCCAATGCATAAAACAATCCT-TCTTCGTTCCCAAGTGGGAGATTGTCA				1594	
Sbjct	788	TTCCACCAAGGTCCAACGCATAAAACAATCCTGTC-TCATCCCGTTTAGGGAGGTTATCA				730	
Query	1595	ACATAGCTGATGAGCATCTTGAGCTTGCTCCCGCCGTCCCGCTGCAGCCCCGCGTGCATC				1654	
Sbjct	729	ACGTAGCTAATGAGCATCTTGAGCTTGCTCCCGCCCTCCGAAGCGAGCCCGCGAGCATC				670	
Query	1655	TCCTCCACCATCGCCTCTGCCCACC-GCCGCCAGCCTCCCGCCGCGCTGCGCACCAGGctc				1713	
Sbjct	669	TCCACCGCTCATCGCATCGCCACCTGCCTC-AGCTTCCGATCGGCGTGCGCAATTTCTC				611	
Query	1714	ctccagctccctcaccatccctctcgcccgggcccaactcc 1754					
Sbjct	610	CTCCAGCTCCTTTAGTATCTCCATCGCCCGGCCACCAGCC 570					

Figure S3. Alignment of HK between *Polygonatum sibiricum* and *Phoenix dactylifera*.

PREDICTED: *Elaeis guineensis* probable fructokinase-6, chloroplastic (LOC105053244), mRNA
Sequence ID: [XM_010934340.2](#) Length: 1496 Number of Matches: 1

Range 1: 223 to 1179 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand	
992 bits(537)	0.0	817/957(85%)	0/957(0%)	Plus/Minus	
Query 384	AGCAACTACATTAACCAGAGCATCGAGCACAGCTTGTGCGGTTGGAAGAGCTGGTATGGC	443			
Sbjct 1179	AGCAACTATATTAACCAAGGCATTTCATCACCGCATCTCGAGTTGGTAAAGCAGGGATTGC	1120			
Query 444	TCCTCTCTCCATCACTGTCAATGCTCCGCATGCATTGCAAACCTTGAGAGCATCTGAAAG	503			
Sbjct 1119	TCCTCTCTCCATCACGGTCAGTGCACCACATGCATTGCAAACCTAAGGGCTTCTACTAG	1060			
Query 504	TCGACCTTCATCCTGAAGCAAAGAAATATCACCAGCTAATTGAGATAATATCCAGCAAC	563			
Sbjct 1059	TCGACCTTCATCCTGGAGCAAGGAAATATCAGTGGCTAATTGCGATAAAATCCAGCAAC	1000			
Query 564	AAAAGCATCCCCAGCGCCAGTCGTGTCTACTTGATTACCTTTAAACCACTAACCCCTCCC	623			
Sbjct 999	AAAAGCATCCCCAGCACCAGTAGTGCCACCGCATTCACTTTTAGTCCACTTACCCTCCC	940			
Query 624	ATGGAATTCCTTAGTATAATATCTGCAGCCATCTGGGCCCTCAGTGACGAGAAGCAACTT	683			
Sbjct 939	ACTGAATTCCTTGGTATAATATCTGCAGCCCTGTGGGCCCTCAGTGACAAGAAGCAACTT	880			
Query 684	CAGATTTGGATGGAAGGCTTACGGACAACATTATCATCATAAGGATCTTCACCTTTAGT	743			
Sbjct 879	AAGATTTGGGTGGAAGAGCTTGCCTACAACATGCATCATATGGATCTTCTCCTTTAGT	820			
Query 744	TAAAAAGGAGATTTCTTCTTCACTTATCTTGATTATATCAGCAAAGTCCCATATGCTTAA	803			
Sbjct 819	CAAAAGGAAATTTCTTCTTCACTTATCTTGATAATATCAGCAGCATCCCATATGCTCAA	760			
Query 804	GATTCCATCTCTAGCACTCTCAGCAGAAGGCCATAGCGGAAGTCGTAGATTGGATCATA	863			
Sbjct 759	GATTCCATCTCTAGCACTCTCTGCAGATGGCCATAGTGAAGCCTCAGATTGGATCATA	700			
Query 864	TGACAGAAGAACTCCAGCATCCTTAGCAGCTTTAGCTGCTGCAATATGTGCTGACTTGCA	923			
Sbjct 699	AGAAAGAAGCACTCCAGCATCCTTAGCAACCATAGCTGCTGCAATATGTGCTGATTTACA	640			
Query 924	TGGTTCTGTGATCAGACTTATAGATCCATAGTGAAATATTTTGCCTTCTTTATGATATC	983			
Sbjct 639	TGGTTCCGGTGATAAGACTTATAGATCCATAGTGGAAGATCTTTGCCTTCCTAATGATGTC	580			
Query 984	CAGTTCAAGTTCTTCTTCTTGAAGAAGCATATCGGCAGCTGGGATTACGATAAAACATGAA	1043			
Sbjct 579	AAGGTCAAGTTCTTCTTCTCGAGCAGCATATCAGCACTGGGATTACGATAAAACATGAA	520			
Query 1044	TTACAGTTCACCATCACTTCTCAACGTGACAAAAGCCAAAGCTGTTCTCGCACCAGGATC	1103			
Sbjct 519	CTCAGTTCACCATCATTTCTCAATGTAACAAAAGCCAAAGCTGTTTCGAGCACCAGGATC	460			
Query 1104	AAAACGCATTTCCTTCGTTGTTTACATTATTTTCTTTAAATGTCAGCCAGCATATAGCC	1163			
Sbjct 459	GAACCGCATTCCTTGATTGTTTACATTATTTTCTTTAAATATCAGCTAGCATATACCC	400			
Query 1164	AAACTCATCTTCACCAACCTTCCCAATGAAGGCAGCTGAACCACCGAGCCGAGCAATTCC	1223			
Sbjct 399	AAACTCATCTTCACCAACCTTCCCAATAAAGGCTGATGAACCACCAAGACGAGCTATGCC	340			
Query 1224	AACGGCAACATTGGCCGGTGCTCCCCAGGAGCCTTCTTGAACGCAGGGGCTCAGCCAA	1283			
Sbjct 339	AACAGCAACATTAGCCGGTGCTCCTCCAGGAGCCTTCTTGAAGCTGGAGATTACCTAA	280			
Query 1284	CGACAGCCCACTAATCGTCGGAACAAAGTCGATCAGCATCTCCCAAGCACACGAC	1340			
Sbjct 279	TGATAAGCCCACTAATCGTGGGGACAAAATCAATTAGCATTTCCCAAAACACACGAC	223			

Figure S4. Alignment of scrK between *Polygonatum sibiricum* and *Elaeis guineensis*.

Table S1. Number of unigenes from *Polygonatum sibiricum* assigned to KEGG reference pathways.

Pathway	Pathway_ID	Number of unigenes
Ribosome	KO03010	891
Carbon metabolism	KO01200	657
Biosynthesis of amino acids	KO01230	578
Protein processing in endoplasmic reticulum	KO04141	473
Spliceosome	KO03040	402
Oxidative phosphorylation	KO00190	397
RNA transport	KO03013	365
Glycolysis/Gluconeogenesis	KO00010	304
Plant hormone signal transduction	KO04075	295
Starch and sucrose metabolism	KO00500	284
Plant-pathogen interaction	KO04626	282
RNA degradation	KO03018	245
Purine metabolism	KO00230	243
Carbon fixation in photosynthetic organisms	KO00710	236
Phagosome	KO04145	233
Ubiquitin-mediated proteolysis	KO04120	232
Endocytosis	KO04144	229
Pyruvate metabolism	KO00620	227
mRNA surveillance pathway	KO03015	224
Cysteine and methionine metabolism	KO00270	215
Amino sugar and nucleotide sugar metabolism	KO00520	215
Phenylpropanoid biosynthesis	KO00940	206
Ribosome biogenesis in eukaryotes	KO03008	199
Glyoxylate and dicarboxylate metabolism	KO00630	176
Citrate cycle (TCA cycle)	KO00020	170
Pyrimidine metabolism	KO00240	170
Glutathione metabolism	KO00480	169
Peroxisome	KO04146	165
Fatty acid metabolism	KO01212	160
Arginine and proline metabolism	KO00330	152
Glycine, serine and threonine metabolism	KO00260	149
Phenylalanine metabolism	KO00360	149
2-Oxocarboxylic acid metabolism	KO01210	136
Photosynthesis	KO00195	135
Proteasome	KO03050	133
Pentose phosphate pathway	KO00030	128
Galactose metabolism	KO00052	128
Glycerophospholipid metabolism	KO00564	119
Fructose and mannose metabolism	KO00051	113
Alanine, aspartate and glutamate metabolism	KO00250	111
Aminoacyl-tRNA biosynthesis	KO00970	110
Fatty acid degradation	KO00071	107
Inositol phosphate metabolism	KO00562	103
alpha-Linolenic acid metabolism	KO00592	100
Pentose and glucuronate interconversions	KO00040	98
Glycerolipid metabolism	KO00561	98
Terpenoid backbone biosynthesis	KO00900	98

Valine, leucine and isoleucine degradation	KO00280	97
Phosphatidylinositol signaling system	KO04070	96
Phenylalanine, tyrosine and tryptophan biosynthesis	KO00400	91
Ascorbate and aldarate metabolism	KO00053	88
Nucleotide excision repair	KO03420	85
Protein export	KO03060	81
Cyanoamino acid metabolism	KO00460	80
beta-Alanine metabolism	KO00410	78
Biosynthesis of unsaturated fatty acids	KO01040	77
Fatty acid biosynthesis	KO00061	76
Circadian rhythm – plant	KO04712	76
Porphyrin and chlorophyll metabolism	KO00860	75
N-Glycan biosynthesis	KO00510	74
Tyrosine metabolism	KO00350	71
Regulation of autophagy	KO04140	70
Sulfur metabolism	KO00920	69
Lysine degradation	KO00310	68
Propanoate metabolism	KO00640	67
DNA replication	KO03030	66
Ubiquinone and other terpenoid-quinone biosynthesis	KO00130	65
Other glycan degradation	KO00511	65
Flavonoid biosynthesis	KO00941	64
Homologous recombination	KO03440	63
Sphingolipid metabolism	KO00600	61
Basal transcription factors	KO03022	61
Photosynthesis - antenna proteins	KO00196	60
Nitrogen metabolism	KO00910	59
ABC transporters	KO02010	59
Steroid biosynthesis	KO00100	56
Base excision repair	KO03410	56
SNARE interactions in vesicular transport	KO04130	56
RNA polymerase	KO03020	55
Tryptophan metabolism	KO00380	54
Mismatch repair	KO03430	53
One carbon pool by folate	KO00670	49
Pantothenate and CoA biosynthesis	KO00770	49
Selenocompound metabolism	KO00450	47
Valine, leucine and isoleucine biosynthesis	KO00290	46
Carotenoid biosynthesis	KO00906	44
Fatty acid elongation	KO00062	41
Tropane, piperidine and pyridine alkaloid biosynthesis	KO00960	39
Ether lipid metabolism	KO00565	38
Histidine metabolism	KO00340	37
Butanoate metabolism	KO00650	37
Biotin metabolism	KO00780	32
Glycosylphosphatidylinositol(GPI)-anchor biosynthesis	KO00563	31
Degradation of aromatic compounds	KO01220	31
Cutin, suberine and wax biosynthesis	KO00073	30

Linoleic acid metabolism	KO00591	30
Thiamine metabolism	KO00730	29
Folate biosynthesis	KO00790	29
Stilbenoid, diarylheptanoid and gingerol biosynthesis	KO00945	29
Arachidonic acid metabolism	KO00590	28
Lysine biosynthesis	KO00300	27
Diterpenoid biosynthesis	KO00904	25
Isoquinoline alkaloid biosynthesis	KO00950	24
Glycosaminoglycan degradation	KO00531	23
Vitamin B6 metabolism	KO00750	23
Zeatin biosynthesis	KO00908	23
Nicotinate and nicotinamide metabolism	KO00760	22
Brassinosteroid biosynthesis	KO00905	21
C5-Branched dibasic acid metabolism	KO00660	18
Taurine and hypotaurine metabolism	KO00430	17
Glycosphingolipid biosynthesis - globo series	KO00603	17
Sulfur relay system	KO04122	17
Riboflavin metabolism	KO00740	16
Non-homologous end-joining	KO03450	15
Other types of O-glycan biosynthesis	KO00514	13
Monoterpenoid biosynthesis	KO00902	12
Sesquiterpenoid and triterpenoid biosynthesis	KO00909	12
Glycosphingolipid biosynthesis - ganglio series	KO00604	11
Limonene and pinene degradation	KO00903	11
Caffeine metabolism	KO00232	9
Flavone and flavonol biosynthesis	KO00944	8
Synthesis and degradation of ketone bodies	KO00072	7
Lipoic acid metabolism	KO00785	7
Vancomycin resistance	KO01502	6
Betalain biosynthesis	KO00965	2
Glucosinolate biosynthesis	KO00966	2
Polyketide sugar unit biosynthesis	KO00523	1
Anthocyanin biosynthesis	KO00942	1

Table S2. Monosaccharide composition of PSP.

Monosaccharide species	RT (min)	Start time	End time	Area	Area %	Height	Height %	A/H	Mole ratio
Ara	18.342	18.167	18.517	3507611	6.36	601690	11.62	5.83	0.064
Man	28.077	27.942	28.175	26357768	47.81	5142115	19.81	5.13	0.478
Gal	28.266	28.167	28.492	15724869	28.52	3293556	17.41	4.77	0.285
Glc	28.884	28.775	29.042	7688552	13.95	1413024	31.27	5.44	0.139
Rha	17.656	17.542	17.792	1076870	1.95	185790	13.34	5.80	0.020
Fuc	18.319	18.008	18.217	772584	1.40	130211	6.55	5.93	0.014

Table S3. Functional annotations of unigenes identified as NDP-sugar interconversion enzymes (NSEs) in *Polygonatum sibiricum*.

Enzyme abbreviation	Gene_ID	KO e_value Database_Genes Anno
GALE	c51042.graph_c0	K01784 0 pda:103714167 bifunctional UDP-glucose 4-epimerase and UDP-xylose 4-epimerase 1; K01784 UDP-glucose 4-epimerase [EC:5.1.3.2] (A)
	c71739.graph_c0	K01784 3.23118e-42 sly:101248179 UDP-glucose 4-epimerase GEPI48-like; K01784 UDP-glucose 4-epimerase [EC:5.1.3.2] (A)
	c103420.graph_c0	K01784 1.4068e-167 cmo:103482842 UDP-glucose 4-epimerase GEPI48; K01784 UDP-glucose 4-epimerase [EC:5.1.3.2] (A)
	c161496.graph_c0	K01784 4.81375e-171 tcc:TCM_016202 UDP-D-glucose/UDP-D-galactose 4-epimerase 1 isoform 1; K01784 UDP-glucose 4-epimerase [EC:5.1.3.2] (A)
UGD	c143337.graph_c0	K12451 1.23939e-36 pmum:103337384 probable rhamnose biosynthetic enzyme 1; K12451 3,5-epimerase/4-reductase [EC:5.1.3.- 1.1.1.-] (A)
	c143337.graph_c1	K12451 1.38416e-160 fve:101295808 probable rhamnose biosynthetic enzyme 1-like; K12451 3,5-epimerase/4-reductase [EC:5.1.3.- 1.1.1.-] (A)
	c144506.graph_c0	K18121 1.04555e-167 mus:103995976 glyoxylate/succinic semialdehyde reductase 1; K18121 glyoxylate/succinic semialdehyde reductase [EC:1.1.1.79 1.1.1.-] (A)
	c151030.graph_c0	K18121 5.3521e-95 mus:103992702 glyoxylate/succinic semialdehyde reductase 2, chloroplastic isoform X1; K18121 glyoxylate/succinic semialdehyde reductase [EC:1.1.1.79 1.1.1.-] (A)
UGE	c170719.graph_c0	K08679 1.34076e-09 pda:103701187 UDP-glucuronate 4-epimerase 1-like; K08679 UDP-glucuronate 4-epimerase [EC:5.1.3.6] (A)
	c94561.graph_c0	K08679 1.49726e-12 vvi:100241904 UDP-glucuronate 4-epimerase 6; K08679 UDP-glucuronate 4-epimerase [EC:5.1.3.6] (A)
	c132132.graph_c0	K08679 0 vvi:100241904 UDP-glucuronate 4-epimerase 6; K08679 UDP-glucuronate 4-epimerase [EC:5.1.3.6] (A)
	c153724.graph_c0	K08679 0 pvu:PHAVU_003G152300g hypothetical protein; K08679 UDP-glucuronate 4-epimerase [EC:5.1.3.6] (A)
	c154937.graph_c0	K08679 0 pda:103701187 UDP-glucuronate 4-epimerase 1-like; K08679 UDP-glucuronate 4-epimerase [EC:5.1.3.6] (A)
	c161016.graph_c1	K08679 0 pda:103710561 UDP-glucuronate 4-epimerase 3-like; K08679 UDP-glucuronate 4-epimerase [EC:5.1.3.6] (A)
	c161619.graph_c0	K08679 0 vvi:100241904 UDP-glucuronate 4-epimerase 6; K08679 UDP-glucuronate 4-epimerase [EC:5.1.3.6] (A)
	c110330.graph_c0	K08679 0 rcu:RCOM_0782170 UDP-glucuronate 5-epimerase, putative (EC:5.1.3.12); K08679 UDP-glucuronate 4-epimerase [EC:5.1.3.6] (A)
UGDH	c168782.graph_c0	K00012 2.98471e-61 mtr:MTR_7g012950 UDP-glucose 6-dehydrogenase; K00012 UDP-glucose 6-dehydrogenase [EC:1.1.1.22] (A)
	c169751.graph_c0	K00012 1.16617e-110 pmum:103330088 UDP-glucose 6-dehydrogenase 1-like; K00012 UDP-glucose 6-dehydrogenase [EC:1.1.1.22] (A)
	c171350.graph_c0	K00012 7.26368e-97 cmo:103492904 UDP-glucose 6-dehydrogenase 1; K00012 UDP-glucose 6-dehydrogenase [EC:1.1.1.22] (A)
	c85329.graph_c0	K00012 3.2189e-12 cme:CYME_CMB031C UDP-glucose 6-dehydrogenase; K00012 UDP-glucose 6-dehydrogenase [EC:1.1.1.22] (A)
	c137637.graph_c0	K00012 7.88132e-130 ccp:CHC_T00008869001 UDP-glucose dehydrogenase; K00012 UDP-glucose 6-dehydrogenase [EC:1.1.1.22] (A)
	c104353.graph_c0	K00012 4.36344e-73 pda:103695952 UDP-glucose 6-dehydrogenase 5; K00012 UDP-glucose 6-dehydrogenase [EC:1.1.1.22] (A)
	c153987.graph_c0	K00012 0 mus:103981423 UDP-glucose 6-dehydrogenase 4; K00012 UDP-glucose 6-dehydrogenase [EC:1.1.1.22] (A)
	c156202.graph_c0	K00012 0 mus:103980185 UDP-glucose 6-dehydrogenase 4; K00012 UDP-glucose 6-dehydrogenase [EC:1.1.1.22] (A)
	c109773.graph_c0	K00012 7.5067e-31 pda:103718180 UDP-glucose 6-dehydrogenase 5-like; K00012 UDP-glucose 6-dehydrogenase [EC:1.1.1.22] (A)

UXE	c70998.graph_c0	K12448 1.97108e-171 rcu:RCOM_0771330 UDP-glucose 4-epimerase, putative (EC:5.1.3.5); K12448 UDP-arabinose 4-epimerase [EC:5.1.3.5] (A)
	c90008.graph_c0	K12448 1.09507e-36 mus:103979020 probable UDP-arabinose 4-epimerase 2 isoform X1; K12448 UDP-arabinose 4-epimerase [EC:5.1.3.5] (A)
	c126582.graph_c0	K12448 0 pxb:103952320 UDP-arabinose 4-epimerase 1-like; K12448 UDP-arabinose 4-epimerase [EC:5.1.3.5] (A)
	c152282.graph_c0	K12448 0 vvi:100259390 UDP-arabinose 4-epimerase 1; K12448 UDP-arabinose 4-epimerase [EC:5.1.3.5] (A)
	c153844.graph_c0	K12448 0 pda:103720550 probable UDP-arabinose 4-epimerase 3; K12448 UDP-arabinose 4-epimerase [EC:5.1.3.5] (A)
RHM	c169139.graph_c0	K12450 5.78399e-13 cit:102619504 probable rhamnose biosynthetic enzyme 1-like; K12450 UDP-glucose 4,6-dehydratase [EC:4.2.1.76] (A)
	c180306.graph_c0	K12450 4.12276e-13 gsl:Gasu_48500 dTDP-glucose 4,6-dehydratase (EC:4.2.1.46); K12450 UDP-glucose 4,6-dehydratase [EC:4.2.1.76] (A)
	c90376.graph_c0	K12450 4.4872e-59 bdi:100829812 probable rhamnose biosynthetic enzyme 1; K12450 UDP-glucose 4,6-dehydratase [EC:4.2.1.76] (A)
	c132526.graph_c0	K12450 1.49864e-72 csv:101223284 probable rhamnose biosynthetic enzyme 2-like; K12450 UDP-glucose 4,6-dehydratase [EC:4.2.1.76] (A)
	c134353.graph_c0	K12450 0 pda:103708634 probable rhamnose biosynthetic enzyme 1; K12450 UDP-glucose 4,6-dehydratase [EC:4.2.1.76] (A)
	c139404.graph_c0	K12450 0 gmx:100785885 probable rhamnose biosynthetic enzyme 1-like; K12450 UDP-glucose 4,6-dehydratase [EC:4.2.1.76] (A)
	c142186.graph_c0	K12450 0 pop:POPTR_0001s39210g hypothetical protein; K12450 UDP-glucose 4,6-dehydratase [EC:4.2.1.76] (A)
	c147565.graph_c0	K12450 3.9146e-90 aly:ARALYDRAFT_478892 hypothetical protein; K12450 UDP-glucose 4,6-dehydratase [EC:4.2.1.76] (A)
	c109180.graph_c0	K12450 1.82623e-153 mus:103980241 probable rhamnose biosynthetic enzyme 1; K12450 UDP-glucose 4,6-dehydratase [EC:4.2.1.76] (A)
	c166824.graph_c0	K12450 0 vvi:100260586 trifunctional UDP-glucose 4,6-dehydratase/UDP-4-keto-6-deoxy-D-glucose 3,5-epimerase/UDP-4-keto-L-rhamnose-reductase RHM1; K12450 UDP-glucose 4,6-dehydratase [EC:4.2.1.76] (A)
UER1	c174959.graph_c0	K12451 4.18211e-43 tcc:TCM_016154 Nucleotide-rhamnose synthase/epimerase-reductase; K12451 3,5-epimerase/4-reductase [EC:5.1.3.- 1.1.1.-] (A)
	c120308.graph_c0	K12451 0 rcu:RCOM_1683000 NAD dependent epimerase/dehydratase, putative; K12451 3,5-epimerase/4-reductase [EC:5.1.3.- 1.1.1.-] (A)
	c143337.graph_c0	K12451 1.23939e-36 pnum:103337384 probable rhamnose biosynthetic enzyme 1; K12451 3,5-epimerase/4-reductase [EC:5.1.3.- 1.1.1.-] (A)
	c143337.graph_c1	K12451 1.38416e-160 fve:101295808 probable rhamnose biosynthetic enzyme 1-like; K12451 3,5-epimerase/4-reductase [EC:5.1.3.- 1.1.1.-] (A)
GMDS	c69282.graph_c0	K01711 7.57744e-65 csv:101208005 GDP-mannose 4,6 dehydratase 2-like; K01711 GDP-mannose 4,6-dehydratase [EC:4.2.1.47] (A)
	c86965.graph_c0	K01711 4.79449e-24 mus:103970338 GDP-mannose 4,6 dehydratase 1-like; K01711 GDP-mannose 4,6-dehydratase [EC:4.2.1.47] (A)
	c128821.graph_c0	K01711 1.22005e-141 cit:102613014 GDP-mannose 4,6 dehydratase 2-like; K01711 GDP-mannose 4,6-dehydratase [EC:4.2.1.47] (A)

Table S4. Identities of candidate unigenes related to PSP biosynthesis, analyzed at nucleotide level. Sequence similarities with each specified gene from *Polygonatum sibiricum* (% Identity in last column) were calculated by the Basic Local Alignment Search Tool (BLAST) (<http://blast.ncbi.nlm.nih.gov/>).

A) *sacA*

Gene	Species	Accession number	Max score	Total score	Query cover	E-value	Identity
<i>AtsacA1</i>	<i>Agave tequilana</i>	JN790054.1	883	883	77%	0.0	77%
<i>AtsacA2</i>	<i>A. tequilana</i>	DQ535031.1	880	880	77%	0.0	77%
<i>AtsacA3</i>	<i>A. tequilana</i>	JN790053.1	869	869	77%	0.0	77%
<i>AtsacA4</i>	<i>A. tequilana</i>	EU026119.2	399	399	45%	1e-106	75%
<i>AtsacA5</i>	<i>A. tequilana</i>	JN790060.1	239	443	37%	2e-58	76%

B) *GALE*

Gene	Species	Accession number	Max score	Total score	Query cover	E-value	Identity
PdGALE	<i>Phoenix dactylifera</i>	XM_008801334.2	815	815	77%	0.0	81%
MaGALE	<i>Musa acuminata</i>	XM_009414368.2	749	749	78%	0.0	80%
OIGALED	<i>Ornithogalum longebracteatum</i>	KU664038.1	652	652	78%	0.0	78%
PbGALE	<i>Pyrus x bretschneideri</i>	XM_009347175.2	545	545	76%	8e-151	77%
FvGALE	<i>Fragaria vesca</i>	XM_004298698.2	540	540	76%	4e-149	77%
AiGALE	<i>Arachis ipaensis</i>	XR_001618403.1	538	538	76%	1e-148	76%

C) UGDH

Gene	Species	Accession number	Max score	Total score	Query cover	E-value	Identity
EgUGDH	<i>Elaeis guineensis</i>	XM_010938031.2	998	998	64%	0.0	83%
BdUGDH	<i>Brachypodium distachyon</i>	XM_003577751.3	998	998	64%	0.0	83%
BoUGDH	<i>Bambusa oldhamii</i>	AY773130.1	985	985	64%	0.0	83%
SiUGDH	<i>Setaria italica</i>	XM_004981649.3	953	953	64%	0.0	82%
PdUGDH	<i>Phoenix dactylifera</i>	XM_008787743.2	944	944	65%	0.0	82%
OsUGDH	<i>Oryza sativa</i>	XM_015764669.1	937	937	64%	0.0	82%
AtUGDH	<i>Aegilops tauschii</i>	XM_020331265.1	926	926	64%	0.0	82%
CeUGDH	<i>Colocasia esculenta</i>	AY222335.1	920	920	64%	0.0	82%

D) UXE

Gene	Species	Accession number	Max score	Total score	Query cover	E-value	Identity
PdUXE	<i>Phoenix dactylifera</i>	XM_008810308.2	896	896	82%	0.0	82%
EgUXE	<i>Elaeis guineensis</i>	XM_019851960.1	867	867	80%	0.0	82%
MaUXE	<i>Musa acuminata</i>	XM_009395015.2	800	800	81%	0.0	81%
AcUXE	<i>Ananas comosus</i>	XM_020240417.1	732	732	84%	0.0	80%
ObUXE	<i>Oryza brachyantha</i>	XM_006657370.2	649	649	69%	0.0	80%

E) RHM

Gene	Species	Accession number	Max score	Total score	Query cover	E-value	Identity
JcRHM	<i>Jatropha curcas</i>	XM_012225546.1	2451	2451	99%	0.0	90%
PeRHM	<i>Populus euphratica</i>	XM_011008510.1	2109	2109	99%	0.0	87%
JrRHM	<i>Juglans regia</i>	XM_018993306.1	1881	1881	99%	0.0	85%
TcRHM	<i>Theobroma cacao</i>	XM_007021946.2	1836	1836	99%	0.0	84%
VvRHM	<i>Vitis vinifera</i>	XM_002285598.3	1810	1810	99%	0.0	84%
CsRHM	<i>Citrus sinensis</i>	XM_006477756.2	1790	1790	100%	0.0	84%
PmRHM	<i>Prunus mume</i>	XM_016793132.1	1760	1760	99%	0.0	84%
PbRHM	<i>Pyrus x bretschneideri</i>	XM_009378452.2	1688	1688	99%	0.0	83%

F) scrK

Gene	Species	Accession number	Max score	Total score	Query cover	E-value	Identity
EgscrK	<i>Elaeis guineensis</i>	XM_010934340.2	992	992	53%	0.0	85%
PdscrK	<i>Phoenix dactylifera</i>	XM_008809418.1	937	937	53%	0.0	84%
NnscrK	<i>Nelumbo nucifera</i>	XM_010263884.2	817	817	53%	0.0	82%
MasscrK	<i>Musa acuminata</i>	XM_009401452.2	815	815	52%	0.0	82%
VvscrK	<i>Vitis vinifera</i>	XM_002274352.3	749	749	50%	0.0	82%
PtscrK	<i>Populus trichocarpa</i>	XM_002305164.2	754	754	51%	0.0	81%

G) GMPP

Gene	Species	Accession number	Max score	Total score	Query cover	E-value	Identity
PdGMPP	<i>Phoenix dactylifera</i>	XM_008804913.2	1070	1070	72%	0.0	84%
EgGMPP	<i>Elaeis guineensis</i>	XM_010939248.2	1059	1059	72%	0.0	84%
AcGMPP	<i>Ananas comosus</i>	XM_020252994.1	870	870	72%	0.0	81%
ObGMPP	<i>Oryza brachyantha</i>	XM_015835653.1	806	806	72%	0.0	80%
MnGMPP	<i>Morus notabilis</i>	XM_010096733.1	798	798	72%	0.0	80%
VvGMPP	<i>Vitis vinifera</i>	XM_002282386.3	793	793	72%	0.0	80%

H) HK

Gene	Species	Accession number	Max score	Total score	Query cover	E-value	Identity
EgHK	<i>Elaeis guineensis</i>	XM_010926142.2	881	881	69%	0.0	88%
PdHK	<i>Phoenix dactylifera</i>	XM_008797620.2	845	845	72%	0.0	77%
MaHK	<i>Musa acuminata</i>	XM_009407896.1	732	732	66%	0.0	77%
CsHK	<i>Citrus sinensis</i>	NM_001288857.1	612	612	61%	1e-170	76%
AcHK	<i>Ananas comosus</i>	XM_020243876.1	597	597	72%	4e-166	74%
RcHK	<i>Ricinus communis</i>	XM_002514175.2	436	436	54%	8e-118	74%
ThHK	<i>Tarenaya hassleriana</i>	XM_010542684.2	398	398	71%	4e-106	72%

Table S5. UDP-glycosyltransferases found in *Polygonatum sibiricum*.

Gene_ID	KO e_value Database_Genes Anno
c169792.graph_c0	K13496 0 sly:101257246 UDP-glycosyltransferase 73C1-like; K13496 UDP-glucosyltransferase 73C [EC:2.4.1.-] (A)
c170030.graph_c0	K13679 0 tcc:TCM_015612 UDP-glycosyltransferase superfamily protein isoform 1; K13679 granule-bound starch synthase [EC:2.4.1.242] (A)
c172989.graph_c0	K13679 9.18547e-141 tcc:TCM_015612 UDP-glycosyltransferase superfamily protein isoform 1; K13679 granule-bound starch synthase [EC:2.4.1.242] (A)
c1875.graph_c0	K13691 6.33653e-84 cit:102619890 UDP-glycosyltransferase 74F2-like; K13691 pathogen-inducible salicylic acid glucosyltransferase [EC:2.4.1.-] (A)
c56959.graph_c0	K13496 1.10568e-100 pda:103708808 UDP-glycosyltransferase 73C6-like; K13496 UDP-glucosyltransferase 73C [EC:2.4.1.-] (A)
c6752.graph_c0	K13496 5.76012e-38 gmx:100790358 UDP-glycosyltransferase 73C3-like; K13496 UDP-glucosyltransferase 73C [EC:2.4.1.-] (A)
c70862.graph_c0	K08237 1.3681e-56 sita:101764556 UDP-glycosyltransferase 72B3-like; K08237 hydroquinone glucosyltransferase [EC:2.4.1.218] (A)
c78024.graph_c0	K13496 0 pda:103708833 UDP-glycosyltransferase 73C6-like; K13496 UDP-glucosyltransferase 73C [EC:2.4.1.-] (A)
c85443.graph_c0	K08237 5.1431e-25 tcc:TCM_005182 UDP-glycosyltransferase superfamily protein; K08237 hydroquinone glucosyltransferase [EC:2.4.1.218] (A)
c90528.graph_c0	K13496 3.17133e-144 pda:103708808 UDP-glycosyltransferase 73C6-like; K13496 UDP-glucosyltransferase 73C [EC:2.4.1.-] (A)
c96476.graph_c0	K13679 0 tcc:TCM_015612 UDP-glycosyltransferase superfamily protein isoform 1; K13679 granule-bound starch synthase [EC:2.4.1.242] (A)
c118861.graph_c0	K13496 1.49414e-20 pda:103708833 UDP-glycosyltransferase 73C6-like; K13496 UDP-glucosyltransferase 73C [EC:2.4.1.-] (A)
c130195.graph_c0	K13496 0 pda:103708834 UDP-glycosyltransferase 73C6-like; K13496 UDP-glucosyl transferase 73C [EC:2.4.1.-] (A)
c132414.graph_c0	K13496 4.15324e-43 pda:103708808 UDP-glycosyltransferase 73C6-like; K13496 UDP-glucosyl transferase 73C [EC:2.4.1.-] (A)
c139423.graph_c0	K13496 0 pda:103717036 UDP-glycosyltransferase 73C6-like; K13496 UDP-glucosyl transferase 73C [EC:2.4.1.-] (A)
c146981.graph_c0	K13496 9.06307e-44 mus:103969971 UDP-glycosyltransferase 73C6-like; K13496 UDP-glucosyl transferase 73C [EC:2.4.1.-] (A)
c161382.graph_c1	K13496 0 pda:103708808 UDP-glycosyltransferase 73C6-like; K13496 UDP-glucosyl transferase 73C [EC:2.4.1.-] (A)
c167564.graph_c0	K09480 1.05443e-39 tcc:TCM_022931 UDP-Glycosyltransferase superfamily protein isoform 1; K09480 digalactosyldiacylglycerol synthase [EC:2.4.1.241] (A)

Table S6. Primary selection of reliable internal control for analyzing gene expression in different tissues from *Polygonatum sibiricum*.

Gene symbol	Gene name	Primer sequence (5'-3')	Product size (bp)	PCR efficiency (%)	Mean expression stability (Rank by geNorm)	Stability (Rank by NormFinder software)	CV±SD (Rank by BestKeeper software)
18S	18S rRNA	F:TCAAGCTTCTCTCCCACCAG R:TGGTCTCCTCGGTTCTATGC	227	98.5	0.49	0.19	3.12±0.66
ACT	actin, other eukaryote	F:AGTACTGTTCCAACCGTCGT R:GCGCAGTAATCTCCTTGCTC	182	99.2	0.96	1.04	5.50±1.21
CYP	peptidyl-	F:TCGCTGATGACCACCTTCTT	221	98.8	0.69	0.29	4.59±1.05

GAPDH	prolyl						
	cis-trans	R:TTCAAGTTGGTGCATGTGGG					
	isomerase B						
	glyceraldehyd	F:CCATGGTCAACGTCGGAATC					
	e 3-phosphate						
	dehydrogenas	R:GCGAAGATGTGGATGGCTTT	229	96.7	0.56	0.21	2.50±0.65
	e						
		F:TGAGGAGGTTGGTGTGAAT					
TUA2	tubulin alpha	R:AGAGAGAGAATCAGGCAGC	219	97.7	1.61	1.20	8.29±2.55
	C						
		F:ATCTGGCCAAAAGGACCTGA					
TUB1	tubulin beta	R:GGTGCTAAGTTCTGGGAGGT	203	99.4	0.41	0.09	1.38±0.36
	small subunit	F:AGCTCTGACACCATCGACAA					
UBQ10	ribosomal	R:AATGGTGTCACTGCTCTCCA	243	97.6	1.25	0.37	5.13±1.35
	protein S27Ae						
		F:CAAGAAGGTCAAGCTCGCTG					
UBQ5	ubiquitin C	R:ACCGCTACAACAGATCAAGC	204	96.3	0.52	0.12	2.06±0.76

Table S7. Origins of rhizome samples collected from different germplasms of *Polygonatum sibiricum*.

Origin	Abbreviation	Longitude	Latitude	Elevation (m)
Xiakou Yi, ShaanXi, China	SXXKY	33°12'31"	106°25'32"	909
Shangluo, ShaanXi	SXSL	34°02'18"	109°81'18"	1044
ZhenAn, ShaanXi	SXZA	33°48'84"	109°02'02"	1086
Danfeng, ShaanXi	SXDF	33°68'24"	110°29'66"	953
Liuba, ShaanXi	SXLB	33°37'27"	106°54'55"	1288
Lueyang, ShaanXi	SXLY	33°17'56"	105°51'12"	1192
Foping, ShaanXi	SXFP	33°52'86"	108°01'71"	1494
Luoyang, HeNan, China	HNLY	34°39'41"	112°24'7"	1193
Anyang, HeNan	HNAY	33°30'00"	112°43'50"	820
Yingshan, HuBei, China	HBYS	30°73'79"	115°69'55"	291
Shiyan, HuBei	HBSY	32°45'46"	111°11'54"	705
Tiantai, ZheJiang, China	ZJTT	29°12'83"	120°98'97"	426
Jiangxian, ShanXi, China	SXJX	111°40'38"	35° 27'1"	1085

Table S8. *Polygonatum sibiricum* genes and primers used in real-time PCR.

Gene ID	Candidate gene*	Forward (5' -3')	Tm (°C)	Reverse (5' -3')
c143943.graph_c0	scrA	CTTACATGGCCACGAATGTG	59.90	CACACCCGCCAGTTTATGAT
c157362.graph_c0	sacA	GGCCGATGTCACCTACAAC	60.00	CTATTTCTCCGGCCTTGGAT
c152224.graph_c0	Pgm	CCCAGATTCCATCCTTCTCA	60.00	TTCTGGACTAAAGGGCGTTG
c124676.graph_c0	galU	CAGCTTCCACCAGCCTTTTA	60.38	ATGGAGGTGACACCCAAAAC
c51042.graph_c0	GALE	TTGCAAGGCTGCTATGTGAC	60.02	TGTGGGAGCTCATGAAAGTG
c143337.graph_c1	UGD	ACTATCACCTTCGCCTGCTC	59.46	GACATCCCCAACTCCATGAC
c110330.graph_c0	UGE	AAGGCTGTGTCGGTTCTTTG	60.29	AATGGTACGTACCGTTTCC
c153987.graph_c0	UGDH	GCACAAACATAGCCCAAACA	59.59	CTTCAAACCTGCATCCTGCAA
c140053.graph_c0	AXS	CCTTCCGGAGAGGACTGTCT	60.78	ATCAATCTGGCGGCTATCTG
c153844.graph_c0	UXE	AGCAATCTCCTGTTTTGGA	59.67	AAAAAGCTCTTGACGCTTCG

c142186.graph_c0	<i>RHM</i>	TAAACATGGCCAACCTCTCC	59.93	ATAACGACCCGTGGAAACAA
c120308.graph_c0	<i>UER1</i>	GGTTCCTCTTTGCCATCTCA	60.20	CAAAGCCATGGTGGGAAGAGT
c149264.graph_c0	<i>GPI</i>	GGCCATTTTTTGGTGATGAAT	59.63	ATGGGATGGACAAGCACTTC
c137389.graph_c0	<i>HK</i>	TCCTCATCCTCCACCTAACG	60.07	CAAGAAAACGACGAACACCA
c107236.graph_c0	<i>scrK</i>	AACGCTGCACTTTCCAGTTT	59.92	TCCTCCTCTCGTCAGTGGAT
c157674.graph_c0	<i>MPI</i>	GGCTTATGGTTTGGGTCCTT	60.19	ACGCTGAAGTCGTGGGTTAG
c134455.graph_c0	<i>PMM</i>	CCAGAGGACACTGCAGAACA	60.02	AAGGATCGCCGGTCTTTTAT
c151473.graph_c0	<i>GMPP</i>	TGGTTCTACCTGGGTTCTGG	59.96	CTGGTCCAATCGCAACATC
c128821.graph_c0	<i>GMD5</i>	GTGGGTTTGAAGTGAAGGA	59.94	TAACCAGCATCAACGAGCAC
c149334.graph_c0	<i>TSTA3</i>	GGTGGAGGAGGAAGAAGGAC	60.05	TCTCTCCAATGGCAGACTCC

**scrA*, Phosphotransferase System; *sacA*, beta-fructofuranosidase; *pgm*, phosphoglucomutase; *galU*, uridine-diphosphate glucose pyrophosphorylase; *GALE*, UDP-glucose 4-epimerase; *UGD*, UDP-D-galactose dehydrogenase; *UGE*, UDP-glucuronate 4-epimerase; *UGDH*, UDP-glucose 6-dehydrogenase; *AXS*, UDP-apiose/xylose synthase; *UXE*, UDP-arabinose 4-epimerase; *RHM*, UDP-glucose 4,6-dehydratase; *UER1*, 3,5-epimerase/4-reductase; *GPI*, glucose-6-phosphate isomerase; *HK*, hexokinase; *scrK*, fructokinase; *MPI*, mannose-6-phosphate isomerase; *PMM*, phosphomannomutase; *GMPP*, mannose-1-phosphate guanylyltransferase; *GMD5*, GDP-mannose 4,6-dehydratase; *TSTA3*, GDP-L-fucose synthase