Supplemental Data

Deep Sequencing of Voodoo Lily (*Amorphophallus konjac*): An approach to identify relevant genes involved in the synthesis of the hemicellulose glucomannan

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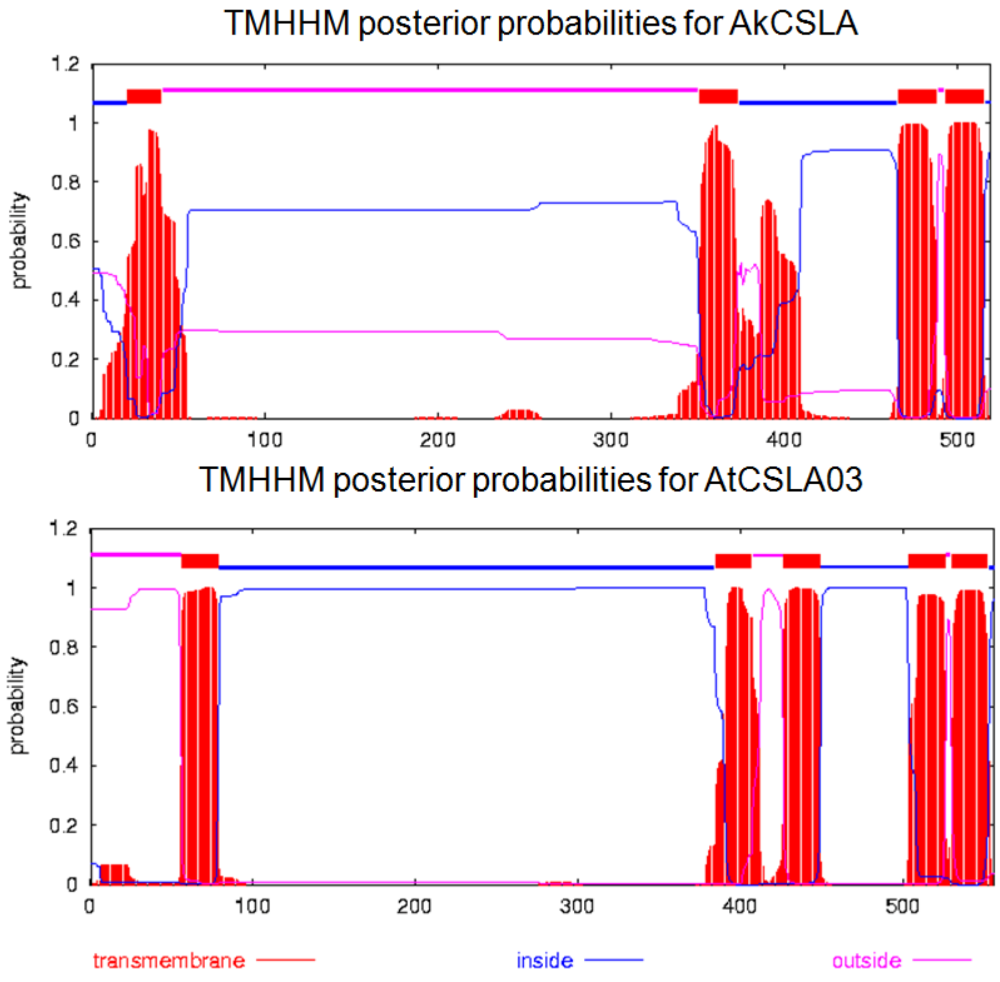

Supplemental Fig.1 Predicted topology of the identified putative *A.konjac* glucomannan synthase AKCSLA03 and the *A.thaliana* mannan synthase ATCSLA03. The proteins were analyzed using TMHHM server v2.0 (http://www.cbs.dtu.dk/services/TMHMM-2.0/). The red colored areas represent predicted transmembrane domains

Description	***A.thaliana* genetic locus**	**454 contig length**	**EST reads**	**E value**
hydrogen ion transmembrane transporter	At2g07707	1132	34041	0.0
26S rRNA	At2g01015	2352	27449	2e -146
metallothionein 3,MT3, copper ion binding	At3g15353	767	21098	7e -19
rRNA repeat unit	X52323	2209	11931	3e -157
rRNA	At3g41979	1759	11220	2e -58
18S rRNA	At3g41768	1243	8152	0.0
late embryogenesis abundant (LEA) family protein	At2g44060	2539	8101	3e -163
mitochondrial	mit. genome	692	7956	1e -124
rRNA repeat unit	X52322	1328	7461	0.0
unknown protein	At1g01430	2301	7310	9e -37
cytosolic O-acetylserine(thiol)lyase	At4g14880	1431	5609	6e -90
PDF2.5 (plant defensin)	At5g63660	651	4920	3e -04
ATP:ADP antiporter (ATNTT2)	At1g15500	3551	4661	0.0
EF-1 alpha (enlongation factor)	At1g07920	2090	4531	0.0
ACT7 (actin 7) cytoskeleton	At5g09810	1646	4283	0.0
rRNA repeat unit	X52322	1418	4023	8e -139
EF-1 alpha (enlongation factor)	At1g07940	1967	3810	0.0
rRNA repeat unit	X52321	1250	3671	4e -09
PP2A-3 protein serine/threonine phosphatase	At3g58500	2129	3407	0.0
GR-RBP8 RNA binding / nucleic acid binding	At4g39260	678	3361	2e -14
basic chitinase (ATHCHIB)	At3g12500	1182	3083	7e -57
ATPase subunit 6	At2g07741	1375	2985	0.0
PP2A-2 protein serine/threonine phopshatase	At1g10430	1557	2979	9e -176
rRNA repeat unit	X52320	562	2642	1e -54
ATJ3 chaperonin, protein binding, HeatShock protein	At3g44110	2173	2283	9e -132
mitochondrial	mit. genome	4530	2254	0.0
MTA2A (Metallothionein 2A) copper ion binding	At3g09390	786	2166	4e -28
ECT2, protein binding, interacts w CIPK1	At3g13460	3221	2109	2e -114
ribosomal protein	mit. genome	2131	2094	0.0
LOS2 phosphopyruvate hydratase	At2g36530	1804	2044	0.0
chloroplast	chl. genome	2792	1937	0.0
mitochondrial transcription termination factor related	At1g62010	1796	1883	0.60
maturase K (plastid gene product)	plastid	2441	1841	0.0
rRNA repeat unit	X52322	1825	1791	6e -147
chloroplast	chl. genome	1705	1791	0.0
40S ribosomal protein S7	At5g16130	1554	1761	1e -66
prxp5 peroxidase	plastid	1470	1756	7e -89
ribulose-1,5-bisphopshate carboxylase/oxygenase	chl. genome	3451	1749	0.0
ATCSLA03	**At1g23480**	**2014**	**1706**	**2e -140**

Description	*A.thaliana* genetic locus	454 contig length	EST reads	E value
putative starch synthase, glycosyltransferase	**At1g32900**	**2186**	**1649**	**7e -171**
HSP60 heat-shock protein 60, ATP binding	At3g23990	590	1603	1e -66
chloroplast	chl. genome	2636	1578	0.0
rRNA repeat unit	X52320	659	1578	0.0
unknown mRNA	AF083679	1452	1515	1e -67
translation initiation factor SUI1	At4g27130	993	1512	1e -86
ACT3 (actin 3) cytosceleton	At3g53750	808	1498	1e -123
Histone H3.2	At4g40040	1216	1495	5e -110
60S ribosomal protein L39	At4g31985	889	1443	6e -39
chloroplast	chl. genome	2401	1413	0.0
ribulose-1,5-bisphopshate carboxylase/oxygenase	chl. genome	4129	1381	0.0
ARFA1D GTP binding, phospholipase activator	At1g70490	1206	1356	4e -169
chloroplast	chl. genome	1893	1351	2e -103
ubiquitin-protein ligase, ribosome constituent	At2g28830	5838	1347	2e -70
60S acidic ribosomal protein P0	At3g09200	1455	1305	0.0
UBC10 ubiquitin-protein ligase	At5g53300	920	1291	6e -115
S-adenosyl-L-homocystein hydrolase	AY256916	1836	1278	0.0
unknown protein	At1g15270	587	1256	5e -15
other RNA, unknown	At4g36648	2019	1255	1e -04
30S ribosomal protein	AB022325	1483	1201	4e -136
ribosomal protein S27	mit. genome	1425	1193	6e -58
ARFA1D GTP binding, phospholipase activator	At1g70490	1910	1191	1e -161
ATGPX6 glutathione peroxidase 6	At4g11600	879	1171	2e -109
chloroplast	chl. genome	1526	1139	6e -83
senescense accosiated protein	At3g48140	1283	1133	5e -27
60S ribosomal protein L28	At2g19730	1476	1129	7e -57
ribosomal protein S12	mit. genome	1163	1120	0.0
UTP-glucose-1-phosphate uridylyltransferase	**At5g17310**	**2602**	**1101**	**0.0**

Supplemental table 1. Contigs with ≥ 1100 EST reads (top 67). The 454 sequencing data were assembled into contigs and aligned to the *A.thaliana* nucleotide sequence collection using BLASTN (Altschul *et al.* 1997). Contigs in bold type are part of Table 2 and Fig.4

Supplemental table 2. Assembled contig sequences and Genbank accession numbers of identified *A. konjac* (Ak) glucomannan and starch biosynthetic genes. N.A. – not assigned as the coding sequence is not complete.

AkCSLA3	**GenBank accession: HQ833588**
assembled contig sequence	AACGTACCAGGGGAGCCAAGAAATGGAGGGCCTAATGAAGGTCGCCTACCTGCCTCGCTCCCTCATGTACTCGATCATGGGGGCCGGGAATTGTCGTTTTGGCCGGAGATGGCCATCGACTGGGCGAGAATCCTCTACATTTGGGGTCAGGTGAGAACCATGGTGCTTATTCCGGCAATGAGGATCGCCGTGTTGCTGTGCCTCATCATGTCGGTGATGCTGCTAATGGAGAAGCTCCTCATGGGTGGTGTGAGCCTGTACGTGAAGGTCTTCCGCCGGCGGCCCAAGAAGGTCTACAGGTGGGAGCCCGTGGGAGGGGACGAGGAGTTGGGCACTGCAGCCTACCCAATGGTCCTCGTCCAAATACCCATGTACAATGAGAGAGAGGTTTACCACCTGTCGATCAAAGCTGCATGCTGCCTCCAATGGCCGTCGGATCGGCTGATCGTCCAAGTTCTTGATGATTCCACAGACCCAATGATTAAGGATCTCGTGTACAAGGAATGCCAGAAATGGGCTTTGGATGGGGTGAACATAAAATATGAGACCAGGGCCAACAGAAATGGGTACAAGGCGGGTGCCCTCAAGGAAGGAATGAAGTACAGTTACGTGGAGGAGTGCGACTACGTCGCCATCTTTGATGCCGACTTCCAAGCAGACCCCGACTACCTTGTGCAGATGGTACCTTTTCTCATCCACAACCCGGAGATCGGTCTCGCTCAGGCTCGCTGGAACTTTGTAAATGCTGAGGAGTGCTTGATGACAAGACTACAAGAGATGTCAATGGACTACCACTTCAAGGTGGAGCAGGAGTCAGGCTCATCCATTCATGCATTCTTCGGCTTCAATGGAACTGCTGGGGTTTGGAGAATCCGGGCCCTTAATGAAGCCGGAGGTTGGAAGGACCGCACCACTGTGGAGGACATGGACTTGGCCATTAGGGCGACTCTTGAAGGTTGGAAGTTTGTCTACGTGGGAGACGTCAAGGTTAAAAGTGAATTACCAAGCACTTTCAAGGCTTTTCGCTACCAACAGCATCGATGGTCATGCGGGCCCGCAAATCTGGTGAGGAAGATGGCAATAGAAATCCTGATGACTAAGAAAGTGCCACTGTGGAAGAAATTCTACTTACTCTACAATTTCTTCCTCACTCGAAAGATCGTAGCTCATTTCGTCACCTTCTTCTTCTATTGTGTCGTGTTTCCAACAGCCGTGTTCTTTCCTGAAATCAGTATTCCATTATGGGCAGTAGTGCATCTCCCGACAACCATCACGATCCTTAATGCTTGTGGAACGCCAAGGTCTATTCATCTGATAGTGTTCTGGACCCTATTTGAGAATGTCATGGCACTCCACCGTTGCAAAGGTGTAATCATCGGTTTGTTGGAGATCGGGAGGGTCAACGAGTGGGTCGTCACAGAGAAGTTGGGTGATGCACTCAAACTCAAACCGAATGGTAATCAAAACTTTGCAAGGAAAGCTCGTACCAAGTACTTCCAGAGATTCCACTTCTTGGAGATTGGGCTTGCACTATACCTCATCATCTGTGCATCCTATAATTACATGCATGCAAACAACTATTGCTACATTTACATCTATCTACAATCTCTCGCATTTTTGGTGATGGGACTTGGTTATGTTGGCACCTTTGTTCCTAGTGAAAAGTAGAGGATGAAAGGAGATGAAGCCACCATTGTTCCAATGTTTCCTTGTGGTGGATGCCATTGATGGCGGAGAAAATCTACCTTTGGTGCTTTTGTTTGTAATGGTTGACCAAATATGGCCACCAATATTTTATTCCTATATATGTGAAGTGGATGTATTCTATTGAAAGAGCTTGTAAGGTCATCTTACAATTTTGAAAAAAAAAAGAAAAAAAAACAAAACATGTCGGCCGCCTCGGCCTCTATGGCCACTCTGCGTTGATACCACTGCTTCCCGGCAGTAATGGCCACTCTGCGTTGATACCACTGCTTCCCGGCCGTAATGGCCACTCTGCGTTGATACCACTGCTT

Ak starch synthase	**GenBank accession: JF727262**
assembled contig sequence	TATTTTTTTTTTTTTTTTTTTTTTTTTTTTGTTTTTTTTTTTTTTTTTTTCGGCAATCGTAGGTAATACCTTCCCCTTCTGGGTCAAAACATCCTAAGATTATTACAAGGTCCAAGATAGGAGGCTTTATCAAGAAGAACAAGCCTCGAAGGCGTGTCTCAGCCTTTTATCTTCATCTAAAGGCTTAGGCATATATAGAACGGGAACAACAGGAAACTACAAAACAAGGGAGCAGGCAACGCCTATTAACTTGCTGATGATCCCCTTCAGGCGGCAGTCACTTTGTCAGCAACGACGAACTCTTCCTCTTCTACCTCGATCTCAGCTCCACTTGGGGCACGTAGAAGGCCTCGTAGCTCCTCCTCCCACTTCTTGGAAGGCCCCTTCCAGGAAAGATCTTTAGCCATGCAGTTTCGGATCATCTGAGAGAATTGGTCTGTCCCATACACCCGAATAGCCCTCCTCACAGTCGTCGCAACTGCTTCAACATCCTTTGGGTCCACGGCATCACAATCAACATGGAAGGCTCCCATATGAAAACCAGTGACACCATCAACAATGGTGTTCACTAGCCCACCCGTGCTGGCACACATAGATGGCGTCCCATACTGCATTGCCTGCAACTGAATAAGACCACATGGCTCAAATCTGCTGGTAATTATCATAAGATCAGCTCCAGCAAAAAGCTTGTGAGCCAAGACAGCATCAAATTTTGCTATTCCTCTTGCTTTGTCTGGATAATCTTCCTCGAGCTTCATAATTTGCTTCTCCATGACTTTCTTTCCAGTACCAAGGACCACTATCTGAACATTTTCACGAATGAACTTGGGAATGGCAGCAACTAAGATGTCTGAACCTTTCTGTTCCTCTAGTCTACCAATAAAAGCTATGAGAGGGATGTCAGGATCCACTGGCAACCCAACTGTTGCTTGGACATCCTCCTTGTTAAGACGTTTTGCATCAAGGACCGTTGTAGAATCATAATTTGCACAGATATATTTGTCAGTAACTGGATTCCACACATCAACATCCATTCCGTTCACAATCCCAGTAATGCCAGTCTTGCGGATGATGTTATCCAGTTCAACACCTCTAGCGACACCAGAGACAACCTCTTCAGCGTAATATGGGCTCACAGTGAAGACTTTGTCTGCTTCTAGAATTCCAGCTTTCATCCAGTTAATTTTCCTCCCTTTCACAGGCTTGTTATATCCATCAATAAAATCAAACGAGCTCTTAAATGTTTCTGGGAGATTAAGAAATGAAAAGTCAGAGAAGGCAAATCTGCCCTGGTATGCCATATTGTGAATGCAAAAGGCCACCTTCGCGTTCTTGTAGAGCCCATGCAGTTTGTACATGCTCTTCAGGTAGCATGGGAGAACTCCAGTGTGCCAATCATTACAGACAAATACAACATCCTCTCCATAAGGCCCAGAAAATGATTTGTTGTTATTCAGATTTAGAATGCGAGGAGCTTCCAAAGCAGCAAGACATAGCAAAGTGAACCTTATCTGGTTGTCTTTGTAATCTTCCCCAGCGACGGGACCATACAATTTTCCTCCAGTTTTCCCCCATACCTTTTCCAGAAATAAAGGATGGTCAATGAACACACGATCAACACCTCTTTTATAGCAGTGGAAGAAACGTACAGTGTACACAGTGTCCCGGACTTTGATCTCAAGCAGAACACTGGTATCCCATGCATCCTTGTATTGATCATAGCGTGGTGATACGGTCATGACACGGTGCCCAAGTTTCGCAAGAGCAGGAGGCAAGCCCCCAGCAACGTCACCTAAACCGCCAGTTTTGCTCCATGGGGCCACCTCTGTTGATACAAAGACTATGTTCATGCTGTCTTCACAAGTGATAGCTTCAGAAGGGTTTGCACTTTTTACACAAACAACAACCCCAGAACGTCTAGCTTGCTCATCCCGGATGCCCCTCCTTACGGCTTGTGTGGAGCTCACTTTCCCGACCGCCCTCAGCCCATGAAAAGTGGTGGCTTGGTTTCTCAAGCAAGCAGCCTTCCTGCTTCCTGATGCTCTTGGTTCCACGTCAGCTACTCCCCCATGAGCACTCCTCGAGATGATCGTTGAAGCAGTCACAGTTGCCATTTGCACGATTTTAACTCTGATCTCTCACCGCAGGTTTGGGGGGTGATCGCGAGACTTCCCCCGGCCGTAATG

Ak UDP-D-glucose pyrophosphorylase (UGP2)	**Genbank accession: JF727263**
assembled contig sequence	ATCTCTTTCCAGGCCGCTCGAGTCCCTTTCTCTACTTGCGCTCCGCTTCCGTCCCGGGAAGCTAGGTCGGCTCC CGATCTCCAATGGCTGCCGTCGCCGAGGCTCCCCTCGTCAACGAGGCCGAGAAGCTCGCGAAGCTTCAGGCCG CAGTCGCAGGCCTCGACCAGATCAGTGAGAACGAGAAATCTGGTTTCATCAGCCTCGTTTCGCGGTATCTGAGT GGAGAAGCACAGGAAATCGAATGGAGTAAGATCCAGAGTCCTACTGAGGAAGTGGTCGTGCCTTATGATAGCTT GGCGCCTGCCCCAGAAGATTTTCCGTCAACGAAGAAACTCTTGGACAAGCTTGTTGTGCTAAAGCTCAATGGAGG TCTGGGAACAACGATGGGTTGCACTGGTCCAAAGTCTGTTATTGAAGTTCGAAATGGCTTGACATTTCTTGACCTG ATTGTCATCCAAATTGAGTCTCTGAACATCAAGTATGGATGCAATGTTCCCCTCCTTTTAATGAACTCATTTAACAC ACATGAAGATACACAGAAGATTGTAGAGAAATATTCCAACTCAAAAATTGAGATACATACCTTTAATCAGAGTCAAT ACCCTCGTTTGGTTGTTGAAGATTTTCTGCCACTACCAAGCAAGGGAAAGACTGAGAAAGATGGCTGGTATCCTC CGGGGCATGGTGATGTGTTCCCTTCTTTGATGAACAGTGGTAAACTAGAGGCCATGTTATCACAGGGTAAAGAGT ATGTCTTCATCGCTAACTCTGATAACCTGGGTGCTGTTGTTGATTTGAAAATAATTAATCACTTAATCCACAATCAG AATGAATACTGCATGGAGGTGACGCCAAAACCTTGGCAGATGTTAAGGGTGGTACCTTAATTTCATATGAAGGAA GGGTTCAGCTCCTTGAAATAGCACAGGTTCCCAGTGAACATGTCAATGAATTCAAGTCAATCGAAAAATTCAAGAT ATTCAACACCAACAACTTGTGGGTGAACCTGAAGGCCATTAAGCGCCTTGTTGAGGCTGACGCACTTAAAATGGA GATCATTCCCAACCCTAAGGAAGTCGATGGTGTGAAAGTTCTTCAGCTAGAAACTGCAGCTGGTGCAGCCATTCG TTTCTTTGATAATGCTATTGGAGTCAATGTTCCTCGATCTCGGTTTCTCCCTGTGAAAACGACTTCAGACTTGCTG CTTGTTCAGTCAGATTTGTATACATTAGTTGACGGCTTTGTTATACGGAATGAAGCCAGAAATAATCCGGCAAATC CTTCTATTGACCTGGGGCCTGAATTTAAGAAGGTTGGGGACTTCCTCAAACGCTTCAAGTCCATCCCGAGCATCA TTGAGCTTGATAGTTTAAAGGTTTCTGGTGACGTGTGGTTTGGTGCTGGCATAGTCGTCAAGGGCAAGGTGGTCG TCAGTGCAAATCCTGGGGTGAAATTGGAAATTCCAGACGGGGTTGTCATCGAGAACAAGGTGATCAACAGTCCTG ATGACATTTGAACGCGCACACGATTCCTTTTCGACGATGTTTTCTTCTCGCTGGGGCGTAGCTTTGCCATGTTGC GGCCAAAGCATGACGTGTTTTGTTCAGTTTGAATGTCAACTCGTACCTTGTTAAATAAAAACCTTGAGCTTTTGAG AATGCCCTCTGAGAATGTTCTTCTCGTTACAAAAAAAAAGAAAAAAACAAAACATGTCGGCCGCCTCGGCCTCTAA AGCAGTGGTATCAACGCAGAGTGGCCATTACGGCCGGGGCTCCCCTGCCGGCCACCGCTTCGCCAGCCCCTTG GCTCTCCTCTGCGATCTCCTGCGGCTTCTTCACTCCCAGGAGAGCGAAGATGTTGGTTTATCAGGATCTGCTCAC AGGTGACGAGCTTCTCTCTGACTCATTCCCATACAAAGAGATTGAGAATGGAATGCTGTGGGAAGTTAACGGGAA GTGGGTGGTTAAAGGAGCCGTTGACGTAGATATTGGAGCAAACCCATCTGCTGAAGGTGGAGGGGAAGATGAAG GTGTTGACGATCAAGCTGTGAAAGTTGTTGATATTGTGGACACATTCCGCCTTCAGGAGCAACCTCCTTTCGACA AAAAGCAATTTGTCACCTTCATGAAGCGGTACATCAAGAACTTGACACCTAAGTTGGATGCCGAAAAGCAGGAGA CATTTAAAAAGCACATTGAGGCTGCTACAAAATTTCTGCTTTCAAAACTGAATGACTTGCAATATTTCGTTGGTGAG AGCATGCATGACGATGGTAGCTTGGTGTTTGCTTACTACAAGGACGGTGCCACCGACCCCACATTTTTGTACTTC GCTTATGGTCTAAAGGAGGTGAAGTGCTAAGCAGGAGAGAGGAGATTACCACCAGGGGCCTGGACGTGTTGTAC TCTAAGCTTTTCTTAAAGTTTCAACTTTACTTCTATCTTAAACTTCTTATTATGTTTGGAGAGACTCAAAACTGTGGT GGCTTTCTTTTTATTGTTTTTTTTGTTTATCCTGGCCCTTCAAGTAAGTAACTCTCGGTGCTTCGATTTTGCCAAACT GACTTCATATTTATCTATTTGAATTTAGAAGAAAAAAAAAA

Ak Phosphoglucomutase	**Genbank accession: JF727264**
assembled contig sequence	AAGCAGTGGTATCAACGCAGAGTGGCCATTACGGCCGGGAAGCAGTGGTATCAACGCAGAGTGGCCACGGCCG GAAAGCAGTGGTATCAACGCAGAGTGGCCATTACGGCCGGGAAGCAGTGGTATCAACGCAGAGTGGCCATTACG GCCGGGAAGCAAGTGGTATCAACGCAGAGTGGCCATCAACGCAGAGTGGCCATTACGCCGGGAAGCAGTGGTA TCAACGCAGAGTGGCCATTACGCCGGGAAGCAGTGGTATCAACGCAGAGTGGCATTACGGCCGGGAAGCAGTG GTATCAACGCAGAGTGGCCATTACGGCCGGGGAAGCAGTGGTATCAACGCAGAGTGGCCATTACGGCCGGGGA CTGTGAGCACCGAGCACCCTCCTCCTCCCTTCTCTGTACTCTCAGGATAGAGAGAGCGATGGTGCTGTTCACGG TCGCCAAGAAAGAGACCGCTCCAATCGATGGCCAGAAGCCCGGCACCTCCGGCCTCAGGAAGAAGGTAACAGT GTTCCAGCAACCTAATTATCTCCACAACTTTGTTCAAGCTACATTCAATGCGCTTTCACCCAGCAATGTCAGAGGT GCAACCATTGTTGTTTCTGGGGATGGTCGCTATTTCTCTGAGGAAGCAATCCAGATTATCGCTAAAATGGCTGCT GCAAATGGAGTAAGACGTGTTTGGGTTGGACAAAATGGACTGCTCTCAACACCTGCTGTATCTTGTGTCATACGT GAAAGAGTTGGTGCAGATGGATCTAAGGCATCTGGAGGCTTTATCTTGACAGCAAGTCACAATCCTGGTGGTCCA CATGAGGACTTTGGAATCAAGTACAACATGGAAAATGGTGGACCTGCTCCTGAGGGCATTACTGACAAGATCTAT GCCAACACGACGACAATTAAAGAATATTTTATAGCAGAAGATCTTCCAGATGTAGACATTTCTACTGTTGGGGTAA CAAGCTTTGAGGGACCTGATGGACCATTCGATGTGGATATTTTTGATTCAACAGATGATTACGTCAAGTTGATGAA GACAATTTTTGACTTTGAGTCCATCCAGAAACTTCTGGCATCTCCAAAATTCACATTTTGTTATGATGCACTTCATG GTGTTGCTGGAATTTATGCCAAGCGTATTTTTGTGGAAGAGCTCGGGGCAAATGAGAGTTCATTGCTGAACTGTA CACCTAAGGAGGACTTTGGTGGTGGGCATCCAGATCCCAACCTCACCTATGCAAAAGAATTGGTGGCACGCATG GGACTAGGCAAGACAGCCCTGGAGGGTGAACCACCAGAGTTTGGTGCTGCTGCTGATGGCGATGCTGATCGTAA TATGATCCTTGGTAAAAGATTTTTTGTGACTCCTTCGGATTCTGTTGCCATCATTGCTGCAAATGCAGTTCAATCCA TTCCTTATTTCAGCTCCGGCTTGAAGGGTGTTGCCAGGAGCATGCCCACATCAGCTGCACTTGATGTTGTAGCAA AAAATTTAAATCTGAAATTCTTTGAGGTGCCCACTGGCTGGAAATTTTTCGGGAATCTGATGGATGCTGGAGTTTG TTCAATATGTGGTGAAGAAAGCTTTGGGACTGGTTCTGACCATATAAGGGAGAAGGATGGAATCTGGGCAGTCTT AGCTTGGCTCTCTATCCTTGCCTTCAGAAACAGGGACAACCTTAATGGAGGCAAACTTGTGACTGTGGAAGACAT AGTTAAGGAGCACTGGGCTACTTATGGTCGCCACTATTATACTCGTTATGACTATGAAAATGTTGATGCAGGTGCA GCAAAAGAGCTCATGGCATATTTGGTTAAACTGCAGTCATCGCTTCCTGATGTGAACAAGATTATAAAGGAGATCA GATCAGATGTTTCAGATGTTGTAGAAGCAGATGAGTTCGAATACAAAGATCCTGTTGACGGTTCTATATCAAAGCA CCAGGGAATCCGTTATCTGTTTGGGGATGGATCAAGATTGGTTTTCCGCCTCTCTGGAACCGGTTCTGTGGGTGC AACTATTCGTCTCTACATCGAGCAATATGAGAAGGATTCGTCAAAGACTGGAAGGGATTCTCAAGAGGCACTTGC TCCTCTCGTGGATGCTGCGTTAAAGCTTTCAAAGATGCAGGAATTCACTGGGCGCTCGGCTCCCACTGTCATCAC ATAGATCGAACAACCGAGGCTAAAGGCAGACGCTGATCAACTGTTATCCTATAGTATTTCAATTTTGTCCAACCTT AAATGTTTGGCTGTGACATTGAGATATAATGCCTCAGTTTCCCGTTTTCACCCCGTGCATAAAAGAAACTCTACAG ATCAACATGTGATGTCTGTTTTCACATAATATGAATACTGCATGCCCGCAGGGTGTTCGGGACCAATAAGAAGCTA CAGGATGATGCCATGTTGGTAATTAATCCTGGCGTTCTTTTTAGTCTTTTTGGCGAGGGTTTGAAAGGCTACCCTG AAATTTGCTTTGTTCTTGAGCCACCCATATTCCGGTGCTTCTGATGTATTTCTATGTGAATGTGAGGGCCGAAGTT GGCAGGCGTTGATCCTAGTAACCTCCAATGTATGGATTCTGCTTTATGTTAGGCTGATGTTCGCAGACATACTAGA AGGTACTTCAAACAGTCAAGAGATCTGAGTTTGTTTATATATCATAATTCGGAAAGATTGTGGTTGGCGTTTTA

Ak sucrose synthase	**Genbank accession: JF727265**
assembled contig sequence	AGACCACTGTATATGCGTGTGGGTGGGCGGTTGCTCCCAAAGCGATGGTGGTAGCATCAACCACTCCGACGACTGGTCCCTTGTTACGCTCGCCGACGAACTAGAAACTCCGTAGGGAAAACCAGCCCCGCAGGGAGCAACCACGAGCCCAACGCGCGCTCACCCTCGTTCTGTTCCTTCTTTTTCCTCCTCGGAGGACAGAGAGACAAAGAAGCGGTCGCCGTCGGGAAACCATGCCTCCCAAGCTAGGCCGGGTTCCGAGCATCCGGGATAGGGTGGAGGACACCCTTTCCGAGCACCGCAATGAGCTCGTCGCCCTCCTCTCCAGGTACATGGGGCAGGGAAAGGGCATCCTGCAGCCCCACCACCTGCTCGACGAGTTCTCCAGCGTCATCGCAGAGGACCGCGGGCGCAAGCTCGAGGATGGACCCTTCTTCGAGGTCCTCAAGACTGCCCAGGAAGCCATAGTTCTGCCTCCATTCGTGGCCATCGCAGTCCGCCCCCGGCCCGGAGTCTGGGAGTATGTCAGGGTTAACGTGTACGAGCTCAGCGTCGAGCAGCTGAGCGTGTCCGAGTACCTCGGCTTCAAAGAGGAGCTCGTCGATGGACACTTCAACGATCGTTACGTGCTGGAGCTGGATTTCGAGCCCTTCAACGTGTCCTTCCCCAGACCGAGCCTGTCGTCGTCCATCGGCAACGGGGTGCAGTTCCTCAATCGCCACCTCTCCTCCATCATGTTCCGCAACAAGGATTGCTTGGAGCCGCTGCTCGACTTCCTTCGAGCCCATAAGTACAAGGGCCATGTCTTGATGGTAAACGATAGAATACAAAGTTTATACAGACTCCAGTCCTGTTTGGCAAAGGCAGAGGAGCTCTTGTCCAAGCTATCTCCAGAAGCACCTTTCTTTGAATTTGCATACAAATTCCAAGAACTGGGATTGGAGAAAGGGTGGGGAGATACAGCTAAACGTGCATTGGAGATGATACATCTCCTTCTGGACATTCTTCAAGCCCCTGATCCTTCCACTTTGGAGACATTTCTGGGGAGGATTCCTATGGTGTTCAATGTAGTCATTGTTTCTCCTCATGGATACTTTGGCCAAGCAAATGTCCTAGGCTTGCCTGACACAGGTGGACAGATTGTATACATATTGGACCAAGTTCGTGCATTGGAGAATGAAATGCTTTTAAGAATTGAACATCAGGGGCTGAGTGTGGAACCTAGAATTCTTGTGGTAACGAGATTGATACCCGATGCAAAAGGAACAACATGCAACCAGCGGCTTGAAAGGATCAGTGGAACGCAGCACTGTCATATCCTAAGGGTTCCTTTCAGGACTGAAAAAGGAATTCTTCGCAAATGGATATCAAGGTTTGATGTATGGCCCTACCTAGAGACATTTGCAGAGGATGCATCAAGTGAGATTGCTGCAGAGTTGCAGGGCATTCCAGATTTAATCATTGGCAACTATAGTGATGGAAATCTTGTTGCATCTTTGCTAGCGTATAAGCTAGGAATCACGCAGTGCAACATTGCGCACGCGTTGGAGAAAACCAAGTATCCTGACTCCGACATTTATTGGAAAAATTATGAGGACAAGTATCATTTTTCATGTCAATTCACGGCTGATTTAATTGCAATGAACAATGCAGATTTTATCATAACCAGTACCTACCAAGAGATTGCAGGAAGCAAAAATACTGTTGGGCAATATGAGAGCCATACTGCTTTTACTCTTCCTGGACTTTACCGTACTGTCCATGGCATTGATGTTTTTGATCCCAAATTTAACATTGTTTCTCCGGGAGCAGACATGGCTATTTATTTTCCATACTCTGAACATGAAAAACGACTGACTTCTCTTCATGGTTCAATTGAAAAGCTATTATTTGATCCAGAGCAAAATGAGGAGCACATTGGTCGATTGGATGACCGGTCAAAGCCCATTATATTCTCCATGGCAAGGCTTGATAAAGTGAAAATATCAGTGGCCTGGTTGAGTGGTTTGGTCAAAGCCCTCGACTAAGGGAATTAGCTAACCTTGCTGTGGTTGCTGGTCACAACGATGCAAAGAAATCAAATGACAGGGAAGAAGTTAAAGAGATTGAAAAGATGCATGAACTTATGAAGAAATATAACATGGATGGTCAGTTCCGATGGATATCTGCCCAAACGAACAGGGCCCGTAATGGTGAGCTCTACCGTTATATAGCAGACACAGGAGGTATCTTTGTGCAGCCTGCTTTTTATGAAGCATTTGGGCTGACAGTCATTGAGGCTATGACTTGTGGTCTTCCAACATTTGCTACTTGCCACGGAGGCCCTGCGGAGATCATTGAGCATGGTGTATCAGGGTTTCATATAGACCCATATCATCCAAACCAGGCAACCAATCTCATGATAGACTTCTTTGAAAAGTGTAAGGAAGACCCAGGATATTGGACTAACATATCTGAGGCAGGACTAAAACGAATCCATGAAAGGTACACATGGAAGATTTACTCTGAAAGGCTGATGACATTGGCTGGGGTTTATGGTTTCTGGAAGTACGTTTCGAAGCTTGAAAGGCGCGAGACCCGGCGATATATTGAGATGTTCTACATTCTAAAATTCCGTGATCTGGTGAAATCTGTGCCACTTGTAACTGATGATTAAAAGCAATGTGCCTTAAAGGCAGGCAGATGAATCCGGTGGCAGCAGCTGTAAAATTTCCATGGGCAGTATAGGGTGTTGAAGGGGTGTCGGTGTCACCTGAGGGCAGCAGTTTATCGTCTGCCTGCTTCCTGTTGATAAATAATCAGGTGATTAAGGTTTCCTCGAATAAAAGGAAATCCCGAATACATGTGTTTTTCTTAACCAGTTGAGAACAAATATGCCCTGCATTTATGTTGTGTGGATATTTCATATGAATATTGAGGGCTACATGCCATGTTTGACTTTAA

Ak ADP-glucose pyrophosphorylase	**Genbank accession: JF727266**
assembled contig sequence	CTTCCTCCTCCTCCTCCTCCTCCTCTGCCCCTGTTTCTTCTCACTGCTGGAGAAACCTGCGGCAGAGACCTTTCTGGCTCTCAAGGGTCTGGACATCGGGTCCTCCTCGGCTTAGAGGTGGTCTCTCTCTCTCTGTATGTGTGTGTGGATCAGCACCAGAGAGCTGACTCTTCAGTAGGTTCTGGTGACTGGGCACTTATAACGCCTCTTCCGGACCTTAACAACAGAGGAAGCAAAAAGAAAGGGAGAAAAAGAAAGGAGACAGAGAGGGAGAGAGAGATTCTGATTCTGCAAACATGGATGCCAGCAGTATGATGGTCACAAGCTTCGGTGCCAACGCCCCGTTTGTGAACCGGTCACACCGCCAAGGGGGTGGCGGTGGCATCATGGGAGGGAGACCAATCTGGGGAGATGAAGTGCGTGGTGGCAGTTCAGAGAGCAGAGGAATATGGGGCACCACCAAGTTGCCAATGAGCTCTCTGGGCAACAGGGCTCCGGCTGCCAGAAGGCACACAGGTCCCGCGGGCGCGACTGTCTCTGCCATCCTTACTCCAGAAATCAGCAAGGATACCTTGACCTTCCAGTCGCCATTCTTTGAGAAGGAGTGGGCAAACCCGAAGAACGTGGCTGCGATCATCCTCGGTGGAGGTGCCGGGACTAAATTGTTCCCTCTGACTGGCAGAAGAGCTGAGCCTGCTGTCCCCATTGGAGGTTCCTATCGGCTTATTGACATTCCAATGAGCAACTGCATCAACAGTGGGATAAACAAGATTTATGTGATGACCCAGTTCAATTCTTGGTCTCTTAACCGCCATCTCGCTCGCACGTACAACTTTGGGAATGGTGTTAATTTTGGGGATGGATTTGTTGAGGTACTGGCAGCCACCCAAACTTCTGGTGAAGCTGGAATGAACTGGTTTCAGGGAACGGCAGATGCTGTGAGACAATTCATCTGGGTCTTTGAGGATCCAAGGAACAAGAACATAGAGCACGTACTGATCTTGTCTGGTGATCAGCTTTACAGAATGGATTATATGGACTTGGTGCAGAGGCACATGGACACTCGGGCAGATATTACGGTTTCATGTGTACCCGTGGACGACAGCCGTGCATCTGACTTCGGATTGATGAAGATCGATAAGGTTGGCCGGATTGTCCATTTCTCTGAGAAACCTAAGGGTTCTGTTCTGGATGCCATGAAGGTTGACACCACAATTCCTGGGTTATCTCCTTATGAAGCCAAAAATTTTCCCTACATTGCATCGATGGGAGTATATGCCTTCAGAACAGAAATCCTTCTAAACCTCTTGAGGTGGAGGTACCCAACATCCAATGATTTTGGATCTGAAATCATTCCTTCTGCTGTGAATGAGTACAATGTACAGGCTTATCTCTTCAAGGACTACTGGGAGGACATTGGAACAATTAAGACATTCTTTGAGGCAAATTTGGCTCTCACAGATCAGTCCCCAAAATTTCAATTTTATGATCCTCAGACACCATTCTACACATCACCTCGTTATTTGCCGCCTACCAAAGTGGATAAATGCAGGATTGTGGACTCCATCATATCCCATGGGTGTTTCCTAGATCAATGCAGTATTGAACATTCAATTGTAGGTGATCGGTCACGCTTGGAGTACAACGTCGAACTGAAGGACACCATGATGATGGGTGCCGACTACTATCAAACTGAAGTAGAGAGAGCTGCCCTCCTAGCAGAAGGAAAGGTTCCTATTGGTGTGGGGCAACAGACTAAAATGAGGAATTGCATCATTGACAAGAATGCTAAGATCGGGAAAAATGTTATCATTACAAACAAAGATGGTGTGCAGGAAGCTGATCGGCCAAGTGAAGGGTTCTATATCAGGTCTGGGCACACTATAATACTGAAGAACACAACAATCAAGGATGGGACAGTCATATGAAAATGCTTGGGGACAATAAAGAAACCGTTTTCTGTGGTTATCCGGACTAAGGAGAATAGTCCTGGACCTCCTGGTGTTGATCAAATCATGTACAGATGAAACGTAGAAATTGACACCTCTACTTTAGTTCTCTCTGTCCGCAACCCAGCAGCATATTGGTACCGGAGGAAGGTCTATGATGACAGTCTGCTAGGATTAATACGTAGTGAATAAAAGGATTGTAGCAGCTACAATGTTGTATACATTAGAATTTCGTATCCATGCTTAGAGCTTAATAATTGTATACGATGTTCCTGAAACGCGCCGATGGCAGTGTCCATCTCTGTTTTTGTGAATGTTTTCTTCTTTATCTGTTGTTGGGAGACAATAAATTTTACTTGTTGGTCCTTGTGCCAGCAACTTGTATACATGTTTATGAGTTTGTAGCTGCCA

Ak ADP-glucose pyrophosphorylase	**Genbank accession: JF727266**
assembled contig sequence	CTTCCTCCTCCTCCTCCTCCTCCTCTGCCCCTGTTTCTTCTCACTGCTGGAGAAACCTGCGGCAGAGACCTTT CTGGCTCTCAAGGGTCTGGACATCGGGTCCTCCTCGGCTTAGAGGTGGTCTCTCTCTCTCTGTATGTGTGTGT GGATCAGCACCAGAGAGCTGACTCTTCAGTAGGTTCTGGTGACTGGGCACTTATAACGCCTCTTCCGGACCTT AACAACAGAGGAAGCAAAAAGAAAGGGAGAAAAAGAAAGGAGACAGAGAGGGAGAGAGAGATTCTGATTCTG CAAACATGGATGCCAGCAGTATGATGGTCACAAGCTTCGGTGCCAACGCCCCGTTTGTGAACCGGTCACACC GCCAAGGGGGTGGCGGTGGCATCATGGGAGGGAGACCAATCTGGGGAGATGAAGTGCGTGGTGGCAGTTC AGAGAGCAGAGGAATATGGGGCACCACCAAGTTGCCAATGAGCTCTCTGGGCAACAGGGCTCCGGCTGCCA GAAGGCACACAGGTCCCGCGGGCGCGACTGTCTCTGCCATCCTTACTCCAGAAATCAGCAAGGATACCTTGA CCTTCCAGTCGCCATTCTTTGAGAAGGAGTGGGCAAACCCGAAGAACGTGGCTGCGATCATCCTCGGTGGAG GTGCCGGGACTAAATTGTTCCCTCTGACTGGCAGAAGAGCTGAGCCTGCTGTCCCCATTGGAGGTTCCTATC GGCTTATTGACATTCCAATGAGCAACTGCATCAACAGTGGGATAAACAAGATTTATGTGATGACCCAGTTCAAT TCTTGGTCTCTTAACCGCCATCTCGCTCGCACGTACAACTTTGGGAATGGTGTTAATTTTGGGGATGGATTTGT TGAGGTACTGGCAGCCACCCAAACTTCTGGTGAAGCTGGAATGAACTGGTTTCAGGGAACGGCAGATGCTGT GAGACAATTCATCTGGGTCTTTGAGGATCCAAGGAACAAGAACATAGAGCACGTACTGATCTTGTCTGGTGAT CAGCTTTACAGAATGGATTATATGGACTTGGTGCAGAGGCACATGGACACTCGGGCAGATATTACGGTTTCAT GTGTACCCGTGGACGACAGCCGTGCATCTGACTTCGGATTGATGAAGATCGATAAGGTTGGCCGGATTGTCC ATTTCTCTGAGAAACCTAAGGGTTCTGTTCTGGATGCCATGAAGGTTGACACCACAATTCCTGGGTTATCTCCT TATGAAGCCAAAAATTTTCCCTACATTGCATCGATGGGAGTATATGCCTTCAGAACAGAAATCCTTCTAAACCT CTTGAGGTGGAGGTACCCAACATCCAATGATTTTGGATCTGAAATCATTCCTTCTGCTGTGAATGAGTACAATG TACAGGCTTATCTCTTCAAGGACTACTGGGAGGACATTGGAACAATTAAGACATTCTTTGAGGCAAATTTGGCT CTCACAGATCAGTCCCCAAAATTTCAATTTTATGATCCTCAGACACCATTCTACACATCACCTCGTTATTTGCCG CCTACCAAAGTGGATAAATGCAGGATTGTGGACTCCATCATATCCCATGGGTGTTTCCTAGATCAATGCAGTAT TGAACATTCAATTGTAGGTGATCGGTCACGCTTGGAGTACAACGTCGAACTGAAGGACACCATGATGATGGGT GCCGACTACTATCAAACTGAAGTAGAGAGAGCTGCCCTCCTAGCAGAAGGAAAGGTTCCTATTGGTGTGGGG CAACAGACTAAAATGAGGAATTGCATCATTGACAAGAATGCTAAGATCGGGAAAAATGTTATCATTACAAACAA AGATGGTGTGCAGGAAGCTGATCGGCCAAGTGAAGGGTTCTATATCAGGTCTGGGCACACTATAATACTGAA GAACACAACAATCAAGGATGGGACAGTCATATGAAAATGCTTGGGGACAATAAAGAAACCGTTTTCTGTGGTT ATCCGGACTAAGGAGAATAGTCCTGGACCTCCTGGTGTTGATCAAATCATGTACAGATGAAACGTAGAAATTG ACACCTCTACTTTAGTTCTCTCTGTCCGCAACCCAGCAGCATATTGGTACCGGAGGAAGGTCTATGATGACAG TCTGCTAGGATTAATACGTAGTGAATAAAAGGATTGTAGCAGCTACAATGTTGTATACATTAGAATTTCGTATCC ATGCTTAGAGCTTAATAATTGTATACGATGTTCCTGAAACGCGCCGATGGCAGTGTCCATCTCTGTTTTTGTGA ATGTTTTCTTCTTTATCTGTTGTTGGGAGACAATAAATTTTACTTGTTGGTCCTTGTGCCAGCAACTTGTATACA TGTTTATGAGTTTGTAGCTGCCA

Ak Glucose-6-phosphate isomerase	**Genbank accession: JF727267**
assembled contig sequence	CCAGAGGCCGCAGAATGTGCAAAAGGCAGGCAGTTGAGATTCCTTGCAAATGTTGATCCAATCGATGTTGC TCGAAGCATTGCTGGCCTTGATCCTGAAACTACATTAGTTGTGGTGGTTTCAAAAACTTTTACAACAGCTGAA ACTATGCTGAATGCTCGAACACTGAGAGAATGGATTTCTTCTGCACTAGGGCCTGAGGCAGTTGCAAAGCAT ATGGTAGCTGTCAGTACAAACCTTGAGCTTGTACAGAAGTTTGGCATTGACCCTAATAATGCTTTCGCATTTT GGGACTGGGTTGGTGGTCGTTATAGTGTCTGCAGTGCTGTTGGTGTCCTTCCTTTGTCCCTACAATATGGTT TTTCAGTAGTTGAAAAGTTTCTGAATGGTGCGGCGAGCATTGACAACCATTTTCGTTCCACTCCATTTGAGAA AACGTGCCTGTTCTTCTGGGTTTATTAAGCGTGTGGAATGTATCTTTTCTTGGATATCCTGCCAGAGCTATAC TACCATATTCTCAGGCCTTGGAAAAATTTGCACCACATATTCAACAGGTAAGCATGGAGAGTAATGGGAAGG GTGTATCAATTGATGGAATCCCTCTTCCCTTTGAGACAGGGGAGATTGATTTTGGAGAGCCTGGAACAAATG GTCAGCATAGCTTTTATCAGCTGATCCATCAGGGCCGGGTTATCCCATGCGATTTTATTGGTGTCGTGAAGA GTCAGCAGCCAGTTTACTTGAAAGGTGAACCAGTGAGTAATCATGATGAGCTTATGTCCAACTTTTTTGCACA ACCAGATGCCCTTGCTTATGGGAAGACACCTGAACAGCTGTTGAGTGAGAAAGTCTCTGATCATCTTATTCC TCACAAGACCTTCTCTGGAAATCGGCCATCATTGAGTATTTTGCTGCCTGCCTTAAGTGCTTATAACATTGGA GAGTTGTTGGCGATGTATGAGCACAGGATTGCTGTTGAAGGTTTCATCTGGGGTATCAATTCTTTTGATCAG TGGGGAGTGGAGCTAGGCAAGTCTCTGGCTTCTCAAGTGAGGAAGCAACTTCACTTATCTCGCACAGCAGG GGAGCCTGTTAAGGGATTTAACTACAGTACTACAGCACTGCTAACAAGATATCTCGAGGCTGAAACCGGTCT CCCATCTGGTTCTTCCACTGTGCTACCGAAGGTTTAATTTTCACATCCTCGGTGAATGTTTTTCGCGGCTTTT TCCACAAACTGCAGCTGAGATATCTGAGTTATGTGAACCCTTGGTTGAAATTCCTGAGCTGGGACTGTAGTG GCTTCCACTTGTCGTAATCGATGTGTAATAACCCAAAACTGTCTTATTACAATAAATTCCCCCCCCCGTTTTA CGTGTACTATTTATTTCAACCTTTTGTGAATGTTCATATCCTGTTGGAAAATGGTGTAAATGGTGCATCCAAGT ATGAGATAAGTTGCAATCTCAGCTTTTTT

Ak Phosphomannomutase	**Genbank accession: JF727268**
assembled contig sequence	CGGCCGGGGAGATCTGGGGCGGCTTTGTTTCTTTTTGGGTTTATACTCAAGAGGAATCTGGGAAGAGAAG GGAGCAGAATCTGATCGGAGCTCTGATCTGTAACATAGCGTAAAAATATGGCTGGAAGGAAGCCGGGTGT GATTGCTCTGTTCGATGTGGATGGGACACTAACAGCTCCAAGAAAGGTGGTGACCCCTGAGATGCTCGAG TTCTTGCATAAGCTACAAGAGGTTGTTACCGTCGGTGTTGTTGGAGGATCTGATCTTGTAAAGATATCTGAA CAACTTGGGAAAACAGTTATCACTGACTATGATTATGTCTTTTCTGAAAATGGCCTCGTTGCCCACAAAAAT GGGGAATTAATTGGAAGTCAGAGCTTGAAACAGTTTCTTGGGGAGGATAAGCTCAAGGAGTTCATTAATTT TACCCTTCATTACATTGCAGACTTGGATATTCCAATAAAAAGGGGAACATTCATTGAGTTCCGAAGCGGGAT GCTTAATGTTTCACCAATTGGGCGAAACTGTAGCCAAGAGGAGCGTGATGAGTTTGAAAAGTATGATAAGG TTCATAATATAAGGCCAAAAATGGTGTCTGTGCTTCGGGAAAAATTTGCACACTTGAGCTTGGCATTTTCTA TTGGAGGGCAAATAAGTTTTGATGTGTTTCCTCAAGGTTGGGATAAGACCTACTGTTTGAGATACCTGGAG GGCTTTGAAGAAATACACTTCTTTGGGGACAAAACATACAAGGGAGGAAATGATCATGAGATTTATGAATCT GAAAGAACTGTGGGTCACACAGTCAAAAGCCCTGAGGATACGGCAGCACAGTGCACTGCTCTCTTTCTGA CCAAGCAGGCTGGAGTGGAATGAGCTTGTGGTGTCACGCTAGATTATTTTTTCGCGATTACATGTCAACCG ACGATTCAGGAGCTAAGCCATTTCTGTTGATTATTTGATTATAGTAGTTTTACGATGAATGTCAAATTGCATA TGTAATCCCACATACTACCCAGCCCCATATTTCACTTGAATGAACAAGCCGAAATAAAAGTCTTT

Ak GDP-D-mannose pyrophosphorylase	**Genbank accession: JF727269**
assembled contig sequence	CGTACGCTTGTTCAAATCAAATGTTTAAATTAAAGAAAGAAATGGCATATCCTCTGTGCAAGGGTGAGGAAACAAACACCAATTACGGTGTGTTCGGAAATGGCTGCAATAATCTTCCGAAGATGTCCCAGGAAATCTCTGTGAGGGAGACACAAAGAAAGGCTAAACAGAGCAGCTGGAGGGATGGTGATCGGTTATCGATGCGAAACCATGGTCTCGAAGCAGTTGATCCCGTCGAACTCCGGAGCCAACCGCGGCCCCCGGTGCGGCCTCTTCCCCAGTTCTTGCGGCATGTCCTGCTGCTGTGGCTTCCCTTCCGCCGCCGCCGCCGCCGCCCCCTTATGGTTGCTCCTAGGGACTTCCCAAGCCCAGATCCACTCCCGGGCCTTCCCTTTCTCGCGGGACAAGTCCGGGGTGGAGCTGAAAATAGACATGGCCAAGAAGAAGTCCATCGTCGAATACCCACCAAGACAACTGGTGAGAGAGAGAGAGAGAGAGGACGCAGCTTGGAACAGTGACATGGACAACATGGACTTGGGCCACTCACATCACATGACGATCTCAGGCTTCAATATGCTGGACTTGATCTCCTTGTGGGGGAGCACCACCCCGCCATTGCTGTAAATCTCATCGCCCACATGCACGTCCTCCCCGAGGATGGTCATGTTCTCCACCCGCGCCCACTGCCCAACAGTGGAGTGCCACCCGATGATACTGCTGGAGACGCAGGCGTGCTTCTTGATGCGGGCCCCGCGCATCACCGTGCACCTCGACAGCCGGACGCCGGGCTCGACGACGCAG

Ak Cytosolic invertase	**Genbank accession: N.A.**
assembled contig sequence	AAAGGATTATGACATGACTCCGCTTAAAATCCAATATTTACACACATTTTCCACGGGGAACAAAGTCATACAGGATCTAACCATTATAACAAAATATCCAACAACAGAAACGACGCTCGAGTGACCAACCCAGAGTGGCGATTGACATGGCCGCCCAGTTTAGCAGCGATCACCTTCAAGAGGGCCTGTGGCGGCTCCAGAACTGTGAATTGCACGGCGAAGCTCAGCCAGAAAGTCCATCTGATGAGGTAGTTTCAAGTGTCCCCACGACGATCCACTAGCTCCAGAATACATAATTGGTCTCTCAGATAAATCTACCGATGGGTCATTGTAGGAATGCATGGCAGCCGCCCAACGTTCACTCAGAAGTTGTGCAGCCTCACCACTACAGCACCCATTTATTGGAATCATCCCAAAATAAGGATTTTCATTTTGATTCGTGCTGTTTCCAACTTCCCCATTATCCATAGCCGAAAAAGTTCTTGCATGAGCCTGGTTCTTCTCTCCATCATTTCCATACGCATAGTTTACTTTTTCAAATCGTTCTCCAGACTTCCGCCGGTTGAGCACACGGTTCCTCTGAGGCGGCGGAGCATATCGCTTAACATTCTCTGCGGCGTCCTCGAGCATCTCCGCTGCCGCACGCAGAAGCAGAGCGAGACCCCGAGGAAGACGAAGAAGGCGGGTCTTCCCACCTCTTCCGAGCGCGGTTTCTCCTCCTCCGACTCCGGCTCTGCGCGGCCGCCCCTTCTCCCCGCCTCTTTCGACGGTGCAGAAGGCAA

Ak Starch branching enzyme	**Genbank accession: N.A.**
assembled contig sequence	ACCTTAAAACATATATTTTCTGGTAGGTCTGCAAGTTAATTAACATATAGATAAATAAATGCTTGTCACGCTACATGCTCGTGCGCAGCTACCTGGCAAGGATGCCAATTCCAACTCACTTGACAAAAATTACGGCCAGCGAAAAAGAAAGACTACAATCTGGAGGCAACAAAAGCTGAAGAGGCTGACGGAAGAACCTGCCGGACGGATTGTAAGCAGCTGTTTCCAGTTGGGGGATGATAAAGAAATGGTGCTCGTGAGGTGCGTGCTTCCGTTCTATGCACGTCCTGAATGCCCTGTGCCCCATGAGGTCGACTTTCTCTGAAATGCCAAGAAGATATAAGTCCAACGTAGGAGTTGCACGTTCTCCGGCGGAGCGCTGGCTACTAGAACCTATGATATTCTTGGACTCAAAAAACTCTTCAGCCCCGGTCAGTCCTCGCACAGGGCATAAACAACACAAGTTCTACTTGGGGAATACACACAGAAAGATCGAGGCCTCTTGTCAAACCATCCTTCAGCAGTGAAGTACTCTGCGGTTGGATCTACTCGGCCGAACCCACCAAATAGTTTATCATCGGAATCTAAGACCACCTTGTATTTTCCAGGCTTTGCACAGCCAACTCTGTAGTCGAAGTAGCT

Ak Mannose-6-phosphate isomerase	**Genbank accession: N.A.**
assembled contig sequence	AAACAACAACATACTATATATATATCAAAAGGCAATCATAGGTTAGGACAATTCTTCAGAATAATATTTTAATTTTCTAAGATAAATTTTCACATCTCCAGCGCGCACAAGAACAAGATTAATCTACAACACTACCGTAGTCATCTAACAAGTCTAGTGCGGTATTCCTCACTACACTCCACCATCTTCACACCTCATGGGCCGCAGCCACAAGCTAGCTAGCTAGTCGAGGCGGATGCGACCGATGTGGTGCGCAACCACCGAGCCGTAGTAGAGATGCCTCCCTATCTTGAGGCCGCCGGTGACCACCGCCATGTCTGGGTCCGTGTACAGAGCGAGCGCCTCCCCTTCCAAGCTCGCGCGCAGCACGCCGCCTCCCTTCAGGAAACGGG

Ak Phosphofructokinase	**Genbank accession: N.A.**
assembled contig sequence	TAATGGCAACAGAATAAGATGGGACAAATCCGCAAAGGATCAAACAACCGGCTGACCTCATAACTTTTGACCTTTTCAACGTAACAATGCAATGATGGGGCATCTCGTAGCCTCAGACATGAACTTCTTCCCTCTCATTCAACATACATCCGAGGTGAATGACTACAGGTTAGGGGAGAGAAAAGATAGAAGCAATAGTGTAAAGAGATCAGTAACAACATAAGAGCATACAGATTCACTAATCAACTGCAGTACTTTGGCATTCTCCAGATAATGAGGAAGAAAGTAGACACTACACACACACTTGAGTTTGTCAGACTAGAACCTTTCTCATGAACAATGACATGCATTCCTGGACATTCCCATGTGGGTCTCTTTCTAAAAGCAGCTGCTCCTGAATTGCTTGTGGCAGAAGTTCAAAAAGCAACTGAGATTGATTCCGGAGTTTCTTTTTCCACAACCCACCTTCATCAACAACATCATGAGCTAGAATTTCATTAAGTTCTGCAATGAGTTGTTGCACCTCGGGAATAAAATCAATTAAGCCTTCTGGTATGAGAATGACACCATAGTTGTAGCCAAGCTCTCCACGCTTGCAGATTATATCTGTTATGTAGTCAGTGACATTTTTCAACGTTTGCTTTTTGGCAGCAACCTCTTCTCCAATTAAGGTAATGTTGGGATGAGTTTGCAAAGCACATTCCAAGGTAATGTGAGAAGCAGCACGGCCCATAAGCCTGACAAA

Ak Hexokinase	**Genbank accession: N.A.**
assembled contig sequence	CCGGCTACCATCCCTTGGGGCAGTATCTCTGCCCAACTTCTTCAGAATGCCGACAACCCCAGCGGCGGCCAGCTGAGCTCCTCGCTTGGCCACAGCATCACATACCTCAATGACTAACTTCCTCTTCTCGAGGGAAGTATTAGTAATCTCTAGAATATCCTTTAACGTGGTCCCAACAGCTTTGAGATCAAGGGATGTATCATGATGCATGGCTGACATATGAGGAGTCCGTAATATGAAAGGAATTGCTAGT