

Supplemental Figure S5; Alignment of maize sucrose synthase isoforms and location of recovered peptides
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SUS-SH1      ----MAAKLTRLHSLRER GAITSSHPNELIALES YVHQGKGLQRHQLLAEFD-ALF
SUS1         MGEAGADRVL SRLH SVRERIGDSL SAHPNELVAVFTRLKNLGKGLQPHQIIAEYNNAI P
SUS2         ----MSAPKLD RNP SIRDVVEDTLHAHRNELVALLSKYV NKGKGI LQPHHILDALD- EVQ
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SUS-SH1      DSDKE--KYAPETTLAAQEAIVLPPVVALAIRPRPGVWDYIRVNVSELAVEELSVSEY
SUS1         EAEREKLDGAFEDVLRAAQEAIVPPWVALAIRPRPGVWEYVRVNVSELAVEELRVPEY
SUS2         GSGGRALAE GPF LDVLRSAQEAIVLPPVVAIAVRPRPGVWEYVRVNVHEL SVEQLTVSEY
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SUS-SH1      LAFKEQLVDGQSNFVLELDFEFPNASFPRPSMSKSI GNGVQFLNRHLSSKLFDKRS
SUS1         LQFKEQLVEEGPNNNFVLELDFEFPNASFPRPSLSKSI GNGVQFLNRHLSSKLFHDKESM
SUS2         LRFKEELVDGQHNDPYVLELDFEFPNVSVPRPNRSSI GNGVQFLNRHLSSIMFRNRDCL
              * * * * * : * . : * * * * * * * * * * * * * * * * * * * * * * * * * * * *

SUS-SH1      YPLLNFLRAHNYKGTMMMLNDRIQSLRGLQSSLRKAERYLSVPOQTPYSENEFQELG
SUS1         YPLLNF LRAHNYKGMTMMLNDRIRLSALQCALRKA EHLSTLQADTPYSEFHHRFQELG
SUS2         EPLLDFLRGRHRKHGVMMLNDRIQSLRGLQSVLTKA EHL SKLPADTPYSQFAYKFQEWG
              * * * * * : . . : * * * * * * * * * * * * * * * * * * * * * * * * * *

SUS-SH1      LEKGWGDTAKRVLDTLHLLLDLLEAPDPANLEKFLGTIPMMFNVVILSPHGYFAQSNVLG
SUS1         LEKGWGDCAKRAQETIHL LLDLLEAPDPSTLEKFLGTIPMVFNVVILSPHGYFAQANVLG
SUS2         LEKGWGDTAGHVLEMIHLLLDIIQAPDPSTLEKFLGRIPMIFNVVVVSPHGYFQANVLG
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SUS-SH1      YPDTGGQVVYILDQVRLENEMLEIKQGLDITPILIVTRLLPDAAGTTCGQRLEKIT
SUS1         YPDTGGQVVYILDQVRAMENEMLLRIKQCGLDITPKILIVTRLLPDAAGTTCGQRLEKVL
SUS2         LPDTGGQIVYILDQVRALENEMVLRLLKQGLDVSPKILIVTRLIPDAGTSCNQRLEKIT
              * * * * * : * * * * * * * * * * * * * * * * * * * * * * * * * * * *

SUS-SH1      GTEHTDILHVPFRNENGLRKKWISRFDVWPYLETYTEDVSSEIMKEMQAKPDLIIGNYSD
SUS1         GTEHCHILRVPPFRTENGIVRKKWISRFEVWPYLETYTDDVAHEIAGELQANPDLIIGNYSD
SUS2         GTQHTYILRVPPFRNENGLKKKWISRFDVWPYLETFAEDAAGEIAAELQGTDPDFIIGNYSD
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SUS-SH1      GNLVATLLAHKLGVTQCTIAHALEKTKYPNSDIYLDKFD SQYHFSCQFTADLIAMNHDF
SUS1         GNLVACLLAHKMGVTHCTIAHALEKTKYPNSDLYWKKFEDHYHFSCQFTD L IAMNHADF
SUS2         GNLVASLLSYKMGITQCNIAHALEKTKYPNSDIYLDKFDSEKQYHFSCQFTADLIAMNADF
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SUS-SH1      IITSTFQEIAGSKDVTGQYESHIAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSIYFPYT
SUS1         IITSTFQEIAGNKDVTGQYESHMAFTMPGLYRVVHGIDVFDPKFNIVSPGADLSIYFPYT
SUS2         IITSTYQEIAGSKNTVGQYESHIAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSIYFPH
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SUS-SH1      STDRLTAFHPEIEELIYSDVENSEHKFVLKDKKKPIIFSMARLDRVKMTGLVEMYGRN
SUS1         ESKRLTSLHPEIEELIYSDVENSEHKFVLNDRNKPIIFSMARLDRVKNLTGLVEMYGRN
SUS2         EKAKRLTSLHGSIENTIYDPEQND EHTGHLDDR SKPIIFSMARLDRVKNITGLVEAFAC
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SUS-SH1      ARLRELANLVTVAG-DHGNESKDREEQAEFKKYSLTDEYLKGHIRWISAQMNRVRNGE
SUS1         KRLQELVNLVVVCG-DHGNPSKDEEQAEFKKMFDLIEQYNLNGHIRWISAQMNRVRNGE
SUS2         AKLRELVNLVVVAGYNDVNKSKDREEIAEIEKMH ELIKTHNLFQGRWISAQTNRRANGE
              : * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

SUS-SH1      LYRYICDTKGAFVQPAFYEAFLTVIESMTCGLPTIATCHGGPAEIIVDGVSGLHIDPYH
SUS1         LYRYICDTKGAFVQPAFYEAFLTVVEAMTCGLPTFATAYGGPAEIIVHGVSGLHIDPYQ
SUS2         LYRYIADTHGAFVQPAFYEAFLTVVEAMTCGLPTFATLHGGPAEIEHGVSGFHIDPYH
              * * * * * : * * * * * * * * * * * * * * * * * * * * * * * * * * * *

SUS-SH1      SDKADLLVNFFKCKADPSYWDEISQGLQRIYEKYTWKLYSERLMTLTGVYGFWKYVS
SUS1         GDKASALLVDFDKCQAEPSHWSKISQGLQRIYEKYTWKLYSERLMTLTGVYGFWKYVS
SUS2         PEQAANLMADFFDRCKQDPDHWVNISGAGLQRIYEKYTWKLYSERLMTLAGVYGFWKYVS
              : : * * * * : * * * * * * * * * * * * * * * * * * * * * * * * * * * *

SUS-SH1      NLERRETRRYTEMYALYRSASQVPLSF-----
SUS1         NLERRETRRYLEMALYALKYRTMASTVPLAVEGEPSSK
SUS2         KLERLETRRYLEMFYILKFRELAKTVPLAIDQPQ---
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Supplemental Figure S5. Alignment of maize sucrose synthase isoforms and location of recovered peptides. Sequences were aligned using the program CLUSTALW. Genbank

accession numbers providing each sequence are as follows: SUS-SH1, P04712; SUS1, L22296; SUS2, NP001105194. Highlighted residues indicate peptide sequences from proteins that associate with starch biosynthetic enzymes (see Supplemental Table S1 for details). Grey highlighted residues indicate peptide sequences that are identical in all three sucrose synthase isoforms. Green highlighted residues indicate peptide sequences that are identical only to SUS-SH1. Yellow highlighted residues indicate peptide sequences that are identical in both SUS-SH1 and SUS1. The data indicate that the starch biosynthetic enzymes associate specifically with SUS-SH1.