Supplemental Table S1. Segregation of F_2 seeds derived from a cross between *ss3a* and *ss4b* mutants according to normal, white core, and opaque morphologies.

Supplemental Table S2. Log_2-fold changes in the lipid profiles of bran and polished rice grains from wild-type (Nipponbare) and *ss3a ss4b* (*#2012*).

Supplemental Table S3. Percentage of amyloplasts exposing inner starch granules when rice grains were cracked with a knife.

Supplemental Table S4. Composition of carbohydrate content (weight %) in endosperm starch fractions separated by gel filtration chromatography (Toyopearl HW55S/HW50S ×3).

Supplemental Table S5. Amino acid alignment used for phylogenetic analysis of starch synthases (SSs) and glycogen synthases (GSs).

Supplemental Tables

Supplemental Table S1. Segregation of F_2 seeds derived from a cross between *ss3a* and *ss4b* mutants according to normal, white core, and opaque morphologies.

Cross combination			F_1	Segregation in F_2				
(♀)	×	(♂)		Translucent	White core	Opaque	Total	$\chi^2_{(12:3:1)}$
e1 (*ss3a*)	×	*e8* (*ss4b*)	Translucent	140	29	10	179	0.99*
e1 (*ss3a*)	×	*e14* (*ss4b*)	Translucent	113	30	11	154	0.29*

*Significant at 0.1 % level.

Supplemental Table 2. Log2-fold changes in the lipid profiles of bran and polished rice grains from wild-type (Nipponbare) and *ss3a ss4b* (*#2012*).

				Bran		Polished rice grains	
Id	**Annotation level**	**Synonym**	**Line no**	**Log_2-fold change (*#2012* vs. Nip)**	**FDR (*#2012* vs. Nip)**	**Log_2-fold change (*#2012* vs. Nip)**	**FDR (*#2012* vs. Nip)**
100	A	lysoPC_16:0 ([M+H]+)	LIPID_88	-0.16	0.5286	1.59	**0.0000**
103	A	lysoPC_18:0 ([M+H]+)	LIPID_112	0.54	**0.0062**	2.60	**0.0000**
104	A	lysoPC_18:1 ([M+H]+)	LIPID_113	0.12	0.5261	1.68	**0.0000**
105	A	lysoPC_18:2 ([M+H]+)	LIPID_114	-0.09	0.7604	0.57	**0.0295**
109	A	DAG_34:1 ([M+NH4]+)	LIPID_169	ND	ND	ND	ND
110	A	DAG_34:2 ([M+NH4]+)	LIPID_170	ND	ND	ND	ND
111	A	DAG_34:3 ([M+NH4]+)	LIPID_171	ND	ND	ND	ND
113	A	DAG_36:2 ([M+NH4]+)	LIPID_182	ND	ND	ND	ND
114	A	DAG_36:3 ([M+NH4]+)	LIPID_184	-0.75	**0.0011**	2.39	**0.0000**
115	A	DAG_36:4 ([M+NH4]+)	LIPID_187	ND	ND	ND	ND
116	A	DAG_36:5 ([M+NH4]+)	LIPID_189	-0.61	**0.0422**	2.74	**0.0000**
117	A	DAG_36:6 ([M+NH4]+)	LIPID_190	-0.42	0.4153	2.63	**0.0037**
118	A	DAG_36:1 ([M+NH4]+)	LIPID_212	ND	ND	ND	ND
119	A	PE_34:2 ([M+H]+)	LIPID_214	-1.46	**0.0002**	1.97	**0.0000**
120	A	PE_34:3 ([M+H]+)	LIPID_215	-0.24	0.5843	-0.17	0.5879
122	A	PE_36:6 ([M+H]+)	LIPID_231	-0.50	0.8246	-2.91	0.1189
123	A	PE_34:1 ([M+H]+)	LIPID_243	-1.55	**0.0001**	2.11	**0.0000**
125	A	PC_34:6 ([M+H]+)	LIPID_246	ND	ND	ND	ND
126	A	PE_36:2 ([M+H]+)	LIPID_253	ND	ND	ND	ND
127	A	PE_36:3 ([M+H]+)	LIPID_257	ND	ND	ND	ND
128	A	PE_36:4 ([M+H]+)	LIPID_259	-1.20	**0.0002**	2.17	**0.0000**
129	A	PE_36:5 ([M+H]+)	LIPID_260	0.11	0.6969	0.27	0.2983
130	A	PG_34:1 ([M+NH4]+)	LIPID_262	-1.01	**0.0420**	2.02	**0.0020**
131	A	MGDG_34:5 ([M+NH4]+)	LIPID_263	ND	ND	ND	ND
132	A	PG_34:2 ([M+NH4]+)	LIPID_264	-1.28	**0.0247**	1.71	**0.0029**
133	A	MGDG_34:6 ([M+NH4]+)	LIPID_265	0.06	0.9535	-1.19	0.1072
134	A	PG_34:3 ([M+NH4]+)	LIPID_266	ND	ND	ND	ND
135	A	PC_34:1 ([M+H]+)	LIPID_268	-1.66	**0.0000**	1.78	**0.0000**
136	A	PG_34:4 ([M+NH4]+)	LIPID_269	1.05	0.1171	-0.94	0.0913
137	A	PC_34:2 ([M+H]+)	LIPID_270	-1.58	**0.0001**	1.81	**0.0000**
138	A	PC_34:3 ([M+H]+)	LIPID_273	-0.92	**0.0059**	1.14	**0.0010**
139	A	PC_34:4 ([M+H]+)	LIPID_274	ND	ND	ND	ND
140	A	PC_34:5 ([M+H]+)	LIPID_276	ND	ND	ND	ND
141	A	PC_36:6 ([M+H]+)	LIPID_279	-0.55	0.1382	-0.69	0.0504
142	A	MGDG_34:1 ([M+NH4]+)	LIPID_282	ND	ND	ND	ND
143	A	MGDG_34:2 ([M+NH4]+)	LIPID_284	ND	ND	ND	ND
144	A	MGDG_34:3 ([M+NH4]+)	LIPID_286	ND	ND	ND	ND
146	A	MGDG_34:4 ([M+NH4]+)	LIPID_290	ND	ND	ND	ND
148	A	MGDG_36:6 ([M+NH4]+)	LIPID_294	-1.71	**0.0015**	0.11	0.8132
149	A	PC_36:1 ([M+H]+)	LIPID_296	-1.48	**0.0001**	1.85	**0.0000**
150	A	PC_36:2 ([M+H]+)	LIPID_297	-1.69	**0.0000**	1.44	**0.0000**
151	A	PC_36:3 ([M+H]+)	LIPID_300	-1.60	**0.0000**	1.65	**0.0000**
152	A	PC_36:4 ([M+H]+)	LIPID_304	-1.51	**0.0000**	1.74	**0.0000**
153	A	PC_36:5 ([M+H]+)	LIPID_306	-1.52	0.1640	1.01	0.1940
154	A	MGDG_36:4 ([M+NH4]+)	LIPID_324	-2.21	**0.0031**	1.91	**0.0112**
155	A	MGDG_36:5 ([M+NH4]+)	LIPID_325	-1.92	**0.0247**	1.28	**0.0256**
156	A	TAG_48:0 ([M+NH4]+)	LIPID_327	-1.12	**0.0000**	2.51	**0.0000**

Supplemental Table 2. Log2-fold changes in the lipid profiles of bran and polished rice grains from wild-type (Nipponbare) and *ss3a ss4b* (*#2012*). Continued.

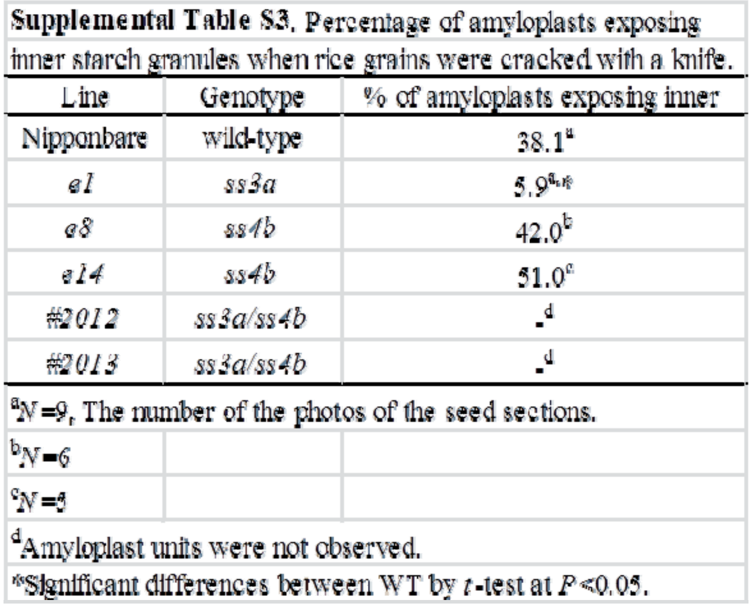
				Bran		Polished rice grains	
Id	**Annotation level**	**Synonym**	**Line no**	**Log$_2$-fold change (*#2012* vs. Nip)**	**FDR (*#2012* vs. Nip)**	**Log$_2$-fold change (*#2012* vs. Nip)**	**FDR (*#2012* vs. Nip)**
157	A	TAG_48:1 ([M+NH4]+)	LIPID_328	-1.60	**0.0000**	2.30	**0.0000**
158	A	TAG_48:2 ([M+NH4]+)	LIPID_329	-2.09	**0.0000**	1.71	**0.0000**
161	A	PC_38:3 ([M+H]+)	LIPID_337	-1.94	**0.0002**	1.03	**0.0092**
162	A	SQDG_34:2 ([M+NH4]+)	LIPID_345	ND	ND	ND	ND
163	A	SQDG_34:3 ([M+NH4]+)	LIPID_347	-0.52	0.7314	-1.12	0.2649
166	A	PI_34:2 ([M+NH4]+)	LIPID_362	-1.35	**0.0001**	1.54	**0.0000**
167	A	TAG_50:1 ([M+NH4]+)	LIPID_363	-1.27	**0.0000**	2.82	**0.0000**
168	A	PI_34:3 ([M+NH4]+)	LIPID_365	-0.28	0.5574	0.12	0.8488
169	A	TAG_50:2 ([M+NH4]+)	LIPID_367	-1.41	**0.0000**	2.49	**0.0000**
170	A	TAG_50:3 ([M+NH4]+)	LIPID_369	ND	ND	ND	ND
171	A	TAG_50:4 ([M+NH4]+)	LIPID_370	-2.12	**0.0000**	1.52	**0.0000**
172	A	SQDG_36:5 ([M+NH4]+)	LIPID_385	ND	ND	ND	ND
174	A	SQDG_36:6 ([M+NH4]+)	LIPID_388	-0.72	0.5933	0.29	0.7831
176	A	TAG_52:1 ([M+NH4]+)	LIPID_396	-1.14	**0.0000**	2.89	**0.0000**
177	A	TAG_52:2 ([M+NH4]+)	LIPID_398	-1.01	**0.0000**	2.37	**0.0000**
178	A	TAG_52:3 ([M+NH4]+)	LIPID_400	-0.90	**0.0000**	2.24	**0.0000**
179	A	TAG_52:4 ([M+NH4]+)	LIPID_401	-1.25	**0.0000**	2.36	**0.0000**
181	A	TAG_52:5 ([M+NH4]+)	LIPID_404	-1.13	**0.0000**	3.40	**0.0000**
182	A	TAG_54:8 ([M+NH4]+)	LIPID_406	-0.87	**0.0006**	3.87	**0.0000**
183	A	TAG_54:9 ([M+NH4]+)	LIPID_413	ND	ND	ND	ND
184	A	TAG_54:5 ([M+NH4]+)	LIPID_424	-0.90	**0.0000**	2.24	**0.0000**
185	A	TAG_54:6 ([M+NH4]+)	LIPID_426	-1.41	**0.0000**	2.55	**0.0000**
186	A	TAG_54:7 ([M+NH4]+)	LIPID_429	-1.17	**0.0001**	3.30	**0.0000**
189	A	TAG_54:1 ([M+NH4]+)	LIPID_445	-1.35	**0.0000**	2.46	**0.0000**
190	A	TAG_54:2 ([M+NH4]+)	LIPID_449	-1.14	**0.0000**	2.58	**0.0000**
191	A	TAG_54:3 ([M+NH4]+)	LIPID_451	-0.93	**0.0000**	2.23	**0.0000**
192	A	TAG_54:4 ([M+NH4]+)	LIPID_453	-0.77	**0.0000**	2.20	**0.0000**
193	A	DGDG_34:5 ([M+NH4]+)	LIPID_471	ND	ND	ND	ND
194	A	TAG_56:5 ([M+NH4]+)	LIPID_472	-1.73	**0.0000**	1.88	**0.0000**
195	A	DGDG_34:6 ([M+NH4]+)	LIPID_473	ND	ND	ND	ND
196	A	DGDG_34:1 ([M+NH4]+)	LIPID_488	-0.30	0.3849	5.68	**0.0000**
197	A	DGDG_34:2 ([M+NH4]+)	LIPID_492	0.06	0.8701	4.73	**0.0000**
198	A	DGDG_34:3 ([M+NH4]+)	LIPID_496	-0.68	**0.0247**	1.57	**0.0003**
199	A	DGDG_34:4 ([M+NH4]+)	LIPID_500	ND	ND	ND	ND
200	A	TAG_56:4 ([M+NH4]+)	LIPID_501	-1.37	**0.0001**	1.96	**0.0000**
201	A	DGDG_36:6 ([M+NH4]+)	LIPID_502	-0.90	**0.0018**	0.71	**0.0044**
202	A	TAG_58:1 ([M+NH4]+)	LIPID_520	-1.64	**0.0000**	2.36	**0.0000**
203	A	DGDG_36:2 ([M+NH4]+)	LIPID_522	ND	ND	ND	ND
204	A	TAG_58:2 ([M+NH4]+)	LIPID_524	ND	ND	ND	ND
205	A	DGDG_36:3 ([M+NH4]+)	LIPID_525	ND	ND	ND	ND
206	A	TAG_58:3 ([M+NH4]+)	LIPID_527	-1.50	**0.0000**	2.08	**0.0000**
207	A	DGDG_36:4 ([M+NH4]+)	LIPID_528	ND	ND	ND	ND
208	A	TAG_58:4 ([M+NH4]+)	LIPID_530	-1.65	**0.0000**	1.75	**0.0000**
209	A	DGDG_36:5 ([M+NH4]+)	LIPID_531	ND	ND	ND	ND
210	A	TAG_60:2 ([M+NH4]+)	LIPID_540	ND	ND	ND	ND
211	A	TAG_60:3 ([M+NH4]+)	LIPID_541	-1.59	**0.0000**	1.86	**0.0000**
212	A	TAG_60:4 ([M+NH4]+)	LIPID_542	-1.84	**0.0000**	1.45	**0.0000**

N=3 (analytical replications of polished seed powder and bran from 100 grains).

Identification/Annotation levels were determined according to Summuner et al. 2007. A, annotated (MSI-level 2).

ND, not detected; FDR, folse discovery rate; DAG, diacyl glycerol; DGDG, digalactosyldiacylglycerol;
MGDG, monogalactosyldiacylglycerol; PC, phosphatidylcholine; PE, phosphatidylethanolamine;
PG, phosphatidylglycerol; PI, phosphatidylinositol; SQDG, sulfoquinovosyl diacylglycerol; TAG, triacylglycerol.

Pink and Blue-shaded, |log2-fold change (*#2012* vs. Nip)| ≤ 1 and FDR < 0.05.



Supplemental Table S3. Percentage of amyloplasts exposing inner starch granules when rice grains were cracked with a knife.

Line	Genotype	% of amyloplasts exposing inner
Nipponbare	wild-type	38.1[a]
a1	*ss3a*	5.9[a,*]
a8	*ss4b*	42.0[b]
a14	*ss4b*	51.0[c]
#2012	*ss3a/ss4b*	-[d]
#2013	*ss3a/ss4b*	-[d]

[a] *N* =9, The number of the photos of the seed sections.

[b] *N* =6

[c] *N* =3

[d] Amyloplast units were not observed.

[*] Significant differences between WT by *t*-test at $P < 0.05$.

Supplemental Table S4. Composition of carbohydrate content (weight %) in endosperm starch fractions separated by gel filtration chromatography (Toyopearl HW55S/HW50S x 3).

Line		Frac. I[a] (%)	Frac. II (%)	Frac. III (%)	TAC[e] (%)	III/II
WT	starch[b]	$22.0 \pm 0.3^{d, **}$	$20.0 \pm 0.2^{**}$	$58.0 \pm 0.2^{**}$	$20.8 \pm 0.3^{**}$	$2.9 \pm 0.1^{**}$
(Nipponbare)	amylopectin[c]	$1.2 \pm 0.1^{c**}$	$21.2 \pm 0.5^{**}$	$57.6 \pm 0.4^{**}$		$2.6 \pm 0.1^{**}$
ss3a	starch	$30.8 \pm 0.0^{*}$	$12.7 \pm 0.1^{*}$	$56.5 \pm 0.1^{*}$	$27.9 \pm 0.2^{*}$	$4.4 \pm 0.0^{*}$
	amylopectin	$2.9 \pm 0.2^{*}$	$12.3 \pm 0.2^{*}$	$54.8 \pm 0.3^{*}$		$4.5 \pm 0.2^{*}$
ss4b	starch	$14.6 \pm 1.3^{*,**}$	$22.5 \pm 0.5^{*,**}$	$62.9 \pm 1.4^{*,**}$	$13.1 \pm 1.2^{**}$	$2.8 \pm 0.1^{**}$
(*e8*)	amylopectin	$1.5 \pm 0.0^{**}$	$19.2 \pm 0.6^{**}$	$59.4 \pm 0.6^{**}$		$3.1 \pm 0.2^{*,**}$
ss4b	starch	$11.9 \pm 2.0^{*,**}$	$23.4 \pm 0.1^{*,**}$	$64.7 \pm 1.9^{*,**}$	$10.5 \pm 1.9^{*,**}$	$2.7 \pm 0.1^{**}$
(*e14*)	amylopectin	$1.4 \pm 0.0^{**}$	$20.4 \pm 0.2^{**}$	$61.1 \pm 0.2^{*,**}$		$3.0 \pm 0.1^{*,**}$
ss3a/ss4b	starch	$33.3 \pm 0.3^{*,**}$	$11.4 \pm 0.1^{*,**}$	$55.4 \pm 0.3^{*,**}$	$30.3 \pm 0.3^{*,**}$	$4.9 \pm 0.1^{*,**}$
(*#2012*)	amylopectin	$2.9 \pm 0.1^{*}$	$11.1 \pm 0.1^{*,**}$	$56.0 \pm 0.1^{**}$		$5.0 \pm 0.1^{*}$
ss3a/ss4b	starch	$33.6 \pm 0.7^{*}$	$11.2 \pm 0.2^{*,**}$	$55.2 \pm 0.9^{*}$	$29.8 \pm 0.6^{*,**}$	$5.0 \pm 0.2^{*,**}$
(*#2013*)	amylopectin	$3.8 \pm 0.2^{*,**}$	$11.0 \pm 0.5^{*}$	$60.1 \pm 0.4^{*,**}$		$5.0 \pm 0.2^{*}$

[a] Three fractions (Fr. I, II and III) were divided at the valleys of the carbohydrate content curve equipped with refractive index detectors (Figure 2 and Supplemental Figure S3C).

[b] Total carbohydrate content was 100 %.

[c] The amylopectin area for Fr. II and Fr. III were superimposed on those of starch, and the amount of the amylopectin Fr. I (extra-long chain) was calculated.

[d] Mean±SE of at least three replications.

[e] True amylose content=apparent amylose content (Fr. I of starch) – extra-long chains (Fr. I of amylopectin).

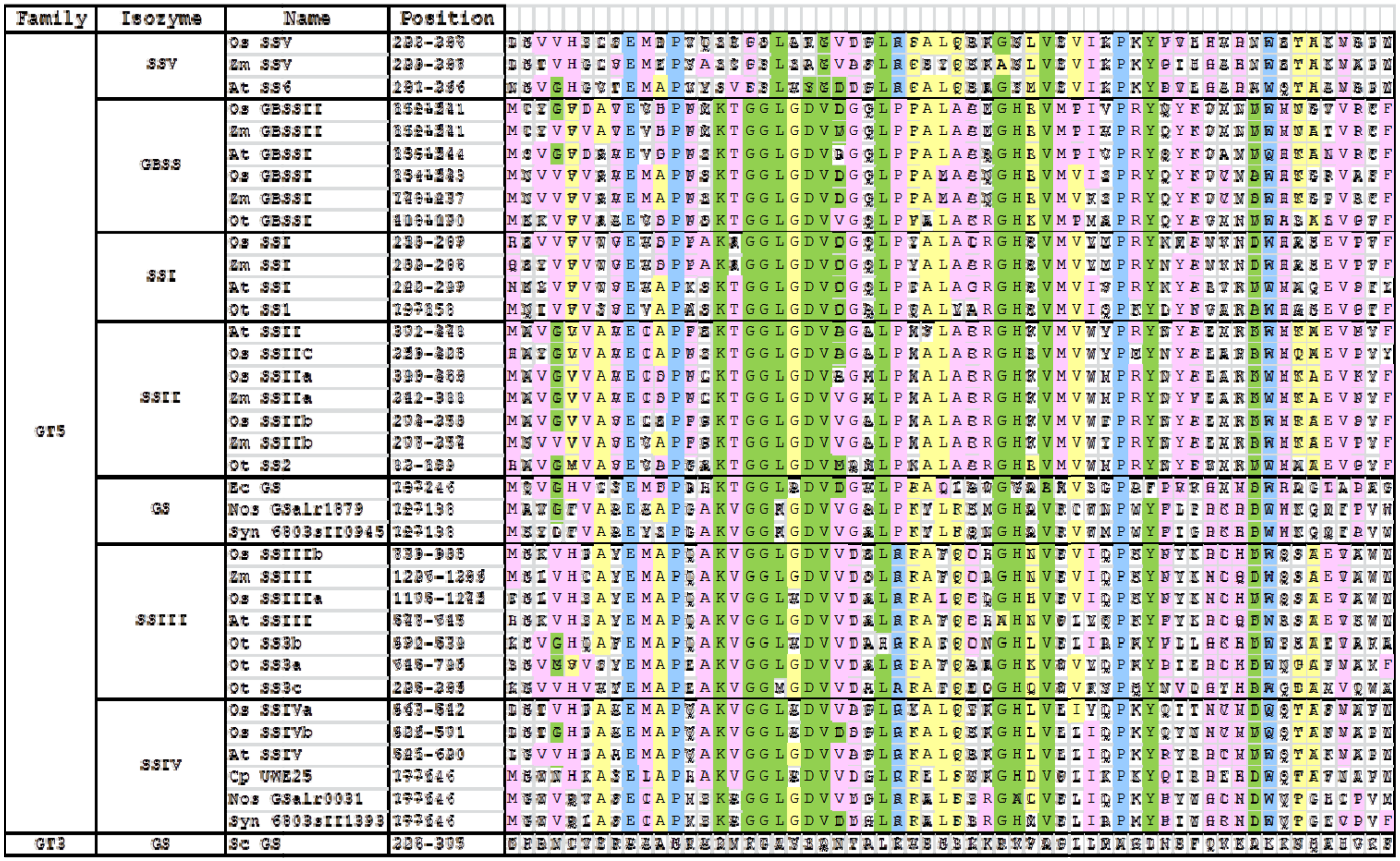
*Significant differences between WT and mutant lines by *t*-test at $P < 0.05$.

**Significant differences between *ss3a* and other lines by *t*-test at $P < 0.05$.

Supplemental Table S5. Amino acid alignment used for phylogenetic analysis of starch synthases (SSs) and glycogen synthases (GSs). Alignments were generated using ClustalW2 (Larkin *et al.*, 2007) and manually optimized. Gap regions were eliminated prior to phylogenetic analysis. Residues used for phylogenetic analysis are shown. Conserved residues among SSs and GSs , except for Sc GS , were indicated in colour as follows. Blue; 100% conservation, green; 80-99% conservation, yellow; 60-79% conservation, red; 40-59% conservation.

Family	Isozyme	Name	Position	
GT5	SSV	Os SSV	222-297	LHVVHICSEMDPITSRGSLATYVTGLSSALQRKGNLVEVILPKYVIHFADYESYHKNRIW
		Zm SSV	223-298	LHIVHICSEMYPVASCGPLSAYVASLSCEIQKKANLVEVILPKYGIHGAEYESYHKNKIW
		At SS6	191-266	LHVIHICTEMAPLVSVEPLASYITGLSCALQEEGYMVEVILPKYEIEGADAYSYHANRIW
	GBSS	Os GBSSII	81-151	MTIIFIATECHPWCKTGGLGDVLGGLPPALAAMGHRVMTIVPRYQYKDVLVEVNETVRFF
		Zm GBSSII	81-151	MTIVFVATEVHPWCKTGGLGDVVGGLPPALAAMGHRVMTIAPRYQYKDVLVEVNETVRFF
		At GBSSI	83-154	MSVIFIGAEVGPWSKTGGLGDVLGGLPPALAARGHRVMTICPRYQYKDAVVQIKENVRFF
		Os GBSSI	83-153	MNVVFVGAEMAPWSKTGGLGDVLGGLPPAMAANGHRVMVISPRYQYKDVVAEIKERVRFF
		Zm GBSSI	77-147	MNVVFVGAEMAPWSKTGGLGDVLGGLPPAMAANGHRVMVVSPRYQYKDVVSEIKETVRFF
		Ot GBSSI	41-107	MKIVFVSAECSPWSKTGGLGDVVGSLPVELAKRGHKVMTVSPRYQYAGVHVEALKSVGFF
	SSI	Os SSI	133-209	RSVVFVTGEASPYAKSGGLGDVCGSLPIALALRGHRVMVVMPRYNFANKHIKIPHEVTFF
		Zm SSI	132-208	QSIVFVTGEASPYAKSGGLGDVCGSLPVALAARGHRVMVVMPRYNYANKHIRIPHEVTFF
		At SSI	142-219	NNLVFVTSEAAPYSKTGGLGDVCGSLPIALAGRGHRVMVISPRYNYARIRVTVNQEVSFY
		Ot SS1	1-78	MNIVFVSSEVAPWSKTGGLGDVCGALPQALVARGHRVMVISPKYLYNGTRAKIGHEVGFF
	SSII	At SSII	301-371	MNVILVAAECAPFSKTGGLGDVAGALPKSLARRGHRVMVVVPRYEYAEVRKRYKMEVMYF
		Os SSIIC	258-328	INIILVAAECAPWSKTGGLGDVAGALPKALARRGHRVMVVVPMYNYAEEPRRYQMEVIYY
		Os SSIIa	319-389	MNVIVVAAECSPWCKTGGLGDVAGALPKALARRGHRVMVVVPRYDYAEIRKYYKLEVKYF
		Zm SSIIa	241-311	MNVIVVAAECSPWCKTGGLGDVVGALPKALARRGHRVMVVVPRYDYVEIRKYYKLEVNYF
		Os SSIIb	203-273	MNVIVVASECSPFCKTGGLGDVVGALPKALARRGHRVMVVIPRYEYAEVRKRYRSEVSYF
		Zm SSIIb	207-277	MNVVVVASECAPFCKTGGLGDVVGALPKALARRGHRVMVVIPRYEYAEVRRRYKSEVTYF
		Ot SS2	12-82	LNVIMVASECAPFSKTGGLGDVMQSLPKALAARGHRVMVVVPRYEYEEVRVTYNTEVGYF
	GS	Ec GS	1-72	MQVLHVCSEMFPLLKTGGLADVIGALPAAQIADGVDARVLLPAFIRRGVVSRRDITLLFG
		Nos GSalr1879	1-71	MRILFVAAEAAPIAKVGGMGDVVGALPKVLRKMGHDVRIFLPYYFLPDKDPIWKQDFTVH
		Syn 6803sII0945	1-71	MKILFVAAEVSPLAKVGGMGDVVGSLPKVLHQLGHDVRVFMPYYFIGDKEPVWKQQFAVY
	SSIII	Os SSIIIb	778-838	MHIVHIAVEMAPIAKVGGLGDVVTSLSRAVQDLGHNVEVILPKYNVKDLHYRQSTEIKVW
		Zm SSIII	1226-1296	MHIVHIAVEMAPIAKVGGLGDVVTSLSRAVQDLGHNVEVILPKYNVKNLQIHQSSEINVW
		Os SSIIIa	1105-1175	IHIVHIAVEMAPIAKVGGLADVVTSLSRAIQELGHHVEVILPKYNVKNLHVRQSTEIKVW
		At SSIII	577-647	LHIVHIAVEMAPIAKVGGLGDVVTSLSRAVQELNHNVDIVFPKYFVKDLQFNRSTEIKVW
		Ot SS3b	490-571	LHVCHIAVEMAPIAKVGGLADVVTAIGRAIQDNGHLVEIILPKYVLLGKEYETHTTIRVE
		Ot SS3a	645-715	LHVMSVSVEMAPIAKVGGLGDVVTSLGLAVQAEGHKVEVVLPKYLIEDLKEENGCYNKVF
		Ot SS3c	225-295	LKVVHVAVEMAPIAKVGGMGDVVTALARATQEDGHQVEVFVPHYNVDGYHRAGETVVQVY
	SSIV	Os SSIVa	467-542	LHIVHIAAEMAPVAKVGGLADVVAGLGKALQTKGHLVEIVLPKYQITNVVIQSYFSNNVW
		Os SSIVb	426-501	LHIIHIAAEMAPVAKVGGLADVISGLGKALQKKGHLVEIILPKYQVNNVVVQSYFNNKIW
		At SSIV	545-620	LYVVHIAAEMAPVAKVGGLGDVVAGLGKALQRKGHLVEIILPKYRVRDTVVESYYKNKIW
		Cp UWE25	1-76	MHIIHIASELAPLAKVGGLADVVLGLCRELSWKGHDVDIIIPKYQIRDFELPSFFFNTVW
		Nos GSalr0031	1-76	MYIVQIASECAPVIKAGGLGDVVYGLSRELEIRGNCVELILPKYHVWGLNLWVPIHCTVY
		Syn 6803sII1393	1-76	MYIVQIASECAPVIKAGGLGDVIYGLSRELELRGHCVELILPMYHIWGRNLEVPIFCDVF
GT3	GS	Sc GS	228-305	YHRYCIERAAAHTADVFTTVSQITALEAEHLLKRKPDGILPNGLHEFQKKDKINHFHGCF

Supplemental Table S5. Amino acid alignment used for phylogenetic analysis of starch synthases (SSs) and glycogen synthases (GSs). Continued.



Family	Isozyme	Name	Position	
GT5	SSV	Os SSV	238-296	DSVVHSCSEMDPTQSEGSLAKGVDGLRSALQEKGNLVEVIKPKYFVEHKHNWETAKNEFN
		Zm SSV	239-298	DSTVHGCVEMEPYASSGSLSRGVASLRCEYQEKANLVEVIKPKYGIHHARNWETAKNKEN
		At SS6	287-346	NSVGHGVTEMAPKYSVESLKSGDDGLRCALQEEGYMVEVIKPKYEVEHAHKWQTAENEEN
	GBSS	Os GBSSII	85-141	MCYGFDAVEVDPWMKTGGLGDVDGQLPFALAEMGHRVMPIVPRYQYKDKNDWHNETVREF
		Zm GBSSII	85-141	MCYVFVAVEVDPWMKTGGLGDVMGQLPFALAEMGHRVMPIMPRYQYKDKNDWHNATVREF
		At GBSSI	88-144	MSVGFDRAEVGPWSKTGGLGDVRGQLPFALAERGHRVMPIVPRYQYKDAMDQHKANVREF
		Os GBSSI	84-143	MNVVFVGAEMAPWSKTGGLGDVDGQLPFAMAENGHRVMVISPRYQYKDCMDWHKERVAFF
		Zm GBSSI	78-137	MNVVFVGAEMAPWSKTGGLGDVDGQLPFAMAENGHRVMVKSPRYQYKDCMDWHKEFVREF
		Ot GBSSI	41-100	MKKVFVAAEVDPWDKTGGLGDVVGQLPFALAERGHKVMPMAPRYQYEGKNDWHSAEVGFF
	SSI	Os SSI	230-289	REVVFVWGEWDPPAKAGGLGDVDGQLPYALACRGHRVMVYMPRYKNENKNDWHASEVPFF
		Zm SSI	228-286	QEYVFVWGEWDPPAKAGGLGDVDGQLPYALAERGHRVMVYMPRYNYENKNDWHASEVPFF
		At SSI	240-299	NKEVFVWSEWAPKSKTGGLGDVDGQLPFALAGRGHRVMVISPRYKYERTRDWHMQEVPFI
		Ot SS1	197-256	MNIVFVSSEVAPASKTGGLGDVDGALPQALYARGHRVMVIQPKYDYNGARDWHASEVGFF
	SSII	At SSII	302-378	MKVGVVAKECAPFEKTGGLGDVDGALPKSLAERGHKVMVWYPRYEYAENRDWHKMEVMVF
		Os SSIIC	229-288	HKYGVVAKECAPWSKTGGLGDVDGALPMALAERGHRVMVWYPMYNYAEARDWHQMEVPVY
		Os SSIIa	399-468	MKVGVVAKECDPWCKTGGLGDVEGMLPMALAERGHKVMVWHPRYDYAEARDWHKAEVRVF
		Zm SSIIa	242-308	MKVGVVAKECDPWCKTGGLGDVVGMLPMALAERGHKVMVWHPRYDYFEARDWHKAEVNVF
		Os SSIIb	198-258	MKVGVVASECSPFSKTGGLGDVVGALPMALAERGHKVMVWEPRYEYAENRDWHRAEVSVF
		Zm SSIIb	198-257	MSVVVVASECAPFSKTGGLGDVVGALPMALAERGHKVMVWTPRYEYAENRDWHKAEVPVF
		Ot SS2	82-139	HKVGMVASECDPEAKTGGLGDVMRNLPKALAERGHRVMVWHPRYEYEENRDWHMAEVGVF
	GS	Ec GS	187-246	MQVGHVCSEMDPRHKTGGLRDVDGMLPFAQIEDGVREKVSGPRFPVRHKHDWRRGIADEG
		Nos GSalr1879	127-186	MRTGFVARESAPGAKVGGMGDVVGALPKYLREMGHRVECWNPMYFLFHKHDWHKQNFPVH
		Syn 6803sll0945	127-186	MKYDFVAREYSPGAKVGGMGDVVGALPKYLFQNGHRVEVWMPMYFIGHKHDWHKQNFAVW
	SSIII	Os SSIIIb	839-898	MSKVHSAYEMAPQAKVGGLGDVVDELRRAFQDAGHNVEVIQPEYNYKHCHDWQSAEVAWN
		Zm SSIII	1226-1286	MSLVHCAYEMAPQAKVGGLGDVVDSLRRAFQDRGHNVEVIQPEYNYKNCQDWQSAEVAWN
		Os SSIIIa	1186-1245	FSLVHSAYEMAPQAKVGGLWDVVDALRRALQEDGHHVEVIQPEYNYKNCHDWQSAEVAWN
		At SSIII	688-745	HSKVHSAYEMAPQAKVGGLGDVVDALRRAYQEHAHNVDLYQPKYFYKHCQDWRSAEVSWN
		Ot SS3b	580-639	KSVGHQAYEMAPQAKVGGLWDVVDAHRRAFQDNGHLVELIRPKYFLLHKHDWESAEVRKA
		Ot SS3a	736-795	ESVNSVSYEMAPEAKVGGLGDVVDALREAYQERGHKVEVVQPKYEIEHCKDWNGAFNAKF
		Ot SS3c	226-285	KKVVHVHYEMAPEAKVGGMGDVVDALRRAFQEDGHQVEVKYPQYNVDHTHDWGEAKVQWA
	SSIV	Os SSIVa	553-612	DSTVHSAEEMAPWAKVGGLEDVVDGLRKALQFKGHLVEIVQPKYQITNCHDWQTASNMFN
		Os SSIVb	442-501	DSTGHSAEEMAPWAKVGGLEDVDDGLRKALQEKGHLVELIQPKYQYNNCHDWQTANNAFN
		At SSIV	621-680	LSVVHSAHEMAPWAKVGGLGDVVDGLRKALQEKGHLVELIQPKYRYEHCHDWQTAKNKFN
		Cp UWE25	187-246	MSNNHKASELAPHAKVGGLEDVVDGLRRELSWKGHDVELIKPKYQIRHEHDWQTAVNAFN
		Nos GSalr0031	187-246	MSNVRTASECAPHEKEGGLGDVVDGLRRALEERGALVELIQPKYHYNHCNDWVPGECPVM
		Syn 6803sll1393	187-246	MSNVRIASECAPKEKEGGLGDVDDGLRRALEERGHNVELIRPMYHINHRNDWVPGEVDVF
GT3	GS	Sc GS	246-305	CHENCTEREAAREMRMFGAYEQNTALKWEGEKKEKVAGILMAGDNEFQVEEKKNHEHVKE

Supplemental Table S5. Amino acid alignment used for phylogenetic analysis of starch synthases (SSs) and glycogen synthases (GSs). Continued.

Family	Isozyme	Name	Position	
GT5	SSV	Os SSV	380-476	R I L L T C Q D L T Q C V N V L K G G I V Y S N K V L L M S S T L P E T L T T E K L V A S H G L D
		Zm SSV	381-477	R I L L T C Q D L N E C V N I L K G G I V Y S N K V V L M S S T H S Q T L A A E K L V A S Y G L D
		At SS6	350-438	R I L L T C Q D F D K G V N I L K G G V V Y S N K V V I M S S S H S E T L A I D K F F A P F G M D
	GBSS	Os GBSSII	256-355	K V A F C I H N I A Q G I N W M K A G I T E C D L V M T V S P H Y V D I L R T P L T G I V N G M D
		Zm GBSSII	256-355	K V A F C I H N I A Q G L N W M K A G I I E S D L V L T V S P H Y V D V L R T P L I G I V N G M D
		At GBSSI	259-358	K V V F C I H N I A Q G R N W M K A A I L E A H R V L T V S P Y Y A K Y L R M K V S G I I N G M D
		Os GBSSI	258-356	K V A F C I H N I S Q G I N W M K A G I L E A D R V L T V S P Y Y A D N I M R L G I G I V N G M D
		Zm GBSSI	252-350	K T A F C I H N I S Q G I N W M K A G I L E A D R V L T V S P Y Y A D N I M R L G I G I V N G M D
		Ot GBSSI	205-320	K C A M T I H N I A Q G V N W L K A G F M N S D R N L T V S E N Y A D H V I R E G M G I V N G M D
	SSI	Os SSI	302-405	R S V L V I H N L A Q G V N F L K G A V V T A D R I V T V S Q G Y S N L L S S S V N G I V N G I D
		Zm SSI	304-404	R S I L V I H N L A Q G V N F L K G A V V T A D R I V T V S K G Y S N L L S S S V N G I V N G I D
		At SSI	312-415	R S I L I I H N L A Q G V N V L K G A I V T S D R I I T V S Q G Y A Q L L S S S V N G I T N G I N
		Ot SS1	173-276	R T I C A I H N I F Q G V N I L K G A I A T S D R V L T V S Q G Y A E L L L S N K D G I A N G I D
	SSII	At SSII	463-558	R S V L V I H N I A Q G F N I F A A G L K A A D R V L T V S H G Y S H I I N E W K R G I V N G I D
		Os SSIIC	420-505	R S V L V I H N I A Q G L N I F A A G I K A A D R L L T V S H G Y A H I I N E W K Q G I V N G I D
		Os SSIIa	481-576	R S V L V I H N I A Q G A N I F G A G L K M A D R V V T V S P G Y L H I I R E W K N G I V N G I D
		Zm SSIIa	403-498	R S V L V I H N I A Q G A N I F A A G L K M A D R V V T V S R G Y L H I I R S W K N G I V N G I D
		Os SSIIb	365-450	R S V L V I H N I A Q G S N V F A A G L K M A D R A V T V S H G Y L H I I N H W K Q G I V N G I D
		Zm SSIIb	369-464	R S V L V I H N I A Q G S N V F A A G L K T A D R V V T V S N G Y M H I I N Q W K Q G I V N G I D
		Ot SS2	174-270	R S C F V V H N M A Q G M N I M K A G L S L A T R V I A V S E G Y A A T I R D G K S G I V N G I D
	GS	Ec GS	155-249	K S V F T V H N L A Q G I S F L K A G L Y Y A D H I T A V S P T Y A E L L Q Q G R S G V P N G V D
		Nos GSalr1879	146-229	T T V F T I H N L A Q G H N T M A A A V Q F A D R V N T V S P T Y A E L L S F G K S G I V N G I D
		Syn 6803sII0945	146-230	A T V F T I H N L A Q G D N V M A A A I Q F A N R V T T V S P T Y A E L L S Y G N V G I L N G I D
	SSIII	Os SSIIIb	919-976	R V V F T I H N L E F G A H H I G K A M A R C D K A T T V S Y T Y S H A I A P S K H G I R N G I D
		Zm SSIII	1377-1434	R V V F T I H N L E F G A H H I G K A M R Y C D K A T T V S N T Y S H A I V P G K Y G I L N G I D
		Os SSIIIa	1256-1313	R I I F T I H N L E F G A H F I G K A M T Y C D K A T T V S H T Y S H A I A P G K Y G I L N G I D
		At SSIII	728-786	R I V F T I H N L E F G A N A I G K A M T F A D K A T T V S P T Y A N V I S A Y K H G I I N G I D
		Ot SS3b	653-710	K V A F T I H N M N Y G Q A K L G E A V H H S Q V A T T V S P S Y A S V I G N H K T G V R N G I D
		Ot SS3a	803-860	R I V F T I H N L D F G E G L V R E A M D Y T Q I G T T V S K T Y A H S I S H E K H G V V N G I D
		Ot SS3c	369-426	A T A L T V H N L Q F G V D R I R R G M E S C D I A T T V S P T Y A H A I A P D K I G I R N G I D
	SSIV	Os SSIVa	626-720	R I C F T C H N F E Q G I N V A K G G I V Y S N I V T T V S P T Y A Q T L K M R K V G I L N G I D
		Os SSIVb	584-679	R I C F T C H N F E Q G I N V V K G A I V Y S N I V T T V S P T Y A Q S L K L R K V G I L N G I D
		At SSIV	704-800	R I C F T C H N F E Q G V N P V K G A I I F S N I V T T V S P T Y A H T L N F K K I G I L N G I D
		Cp UWE25	160-256	K I L F T I H N M E Q G I N L L K G G I V Y S D F V T T V S P N Y A E T L V E H K K G I L N G I D
		Nos GSalr0031	160-257	R V C Y T I H N F K Q G L N Y M K G G I V Y S N A V T T V S P N H A G T L Y L E K S G V L N G I D
		Syn 6803sII1393	160-257	R V C Y T I H N F K Q G I N F M K G G I V Y S N Y V N T V S P H H A G T L E I Q K G G I L N G L D
GT3	GS	Sc GS	392-477	R I F E H T M R Y P N G K R V L A L R R P Y G E L P P V V T H N M C N I R H N D S D R V K V I F H