

Fig. 1.

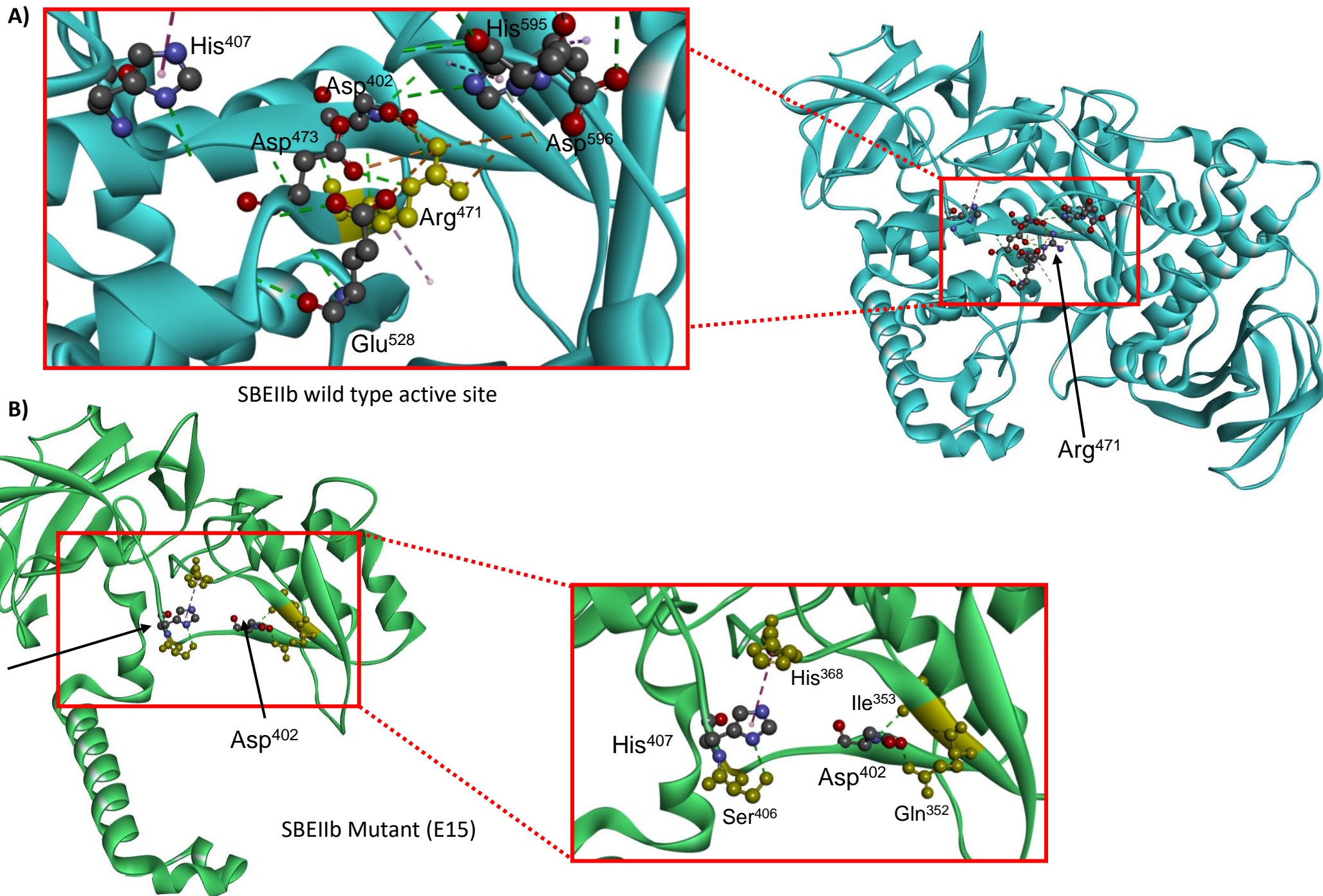


Fig. 2.

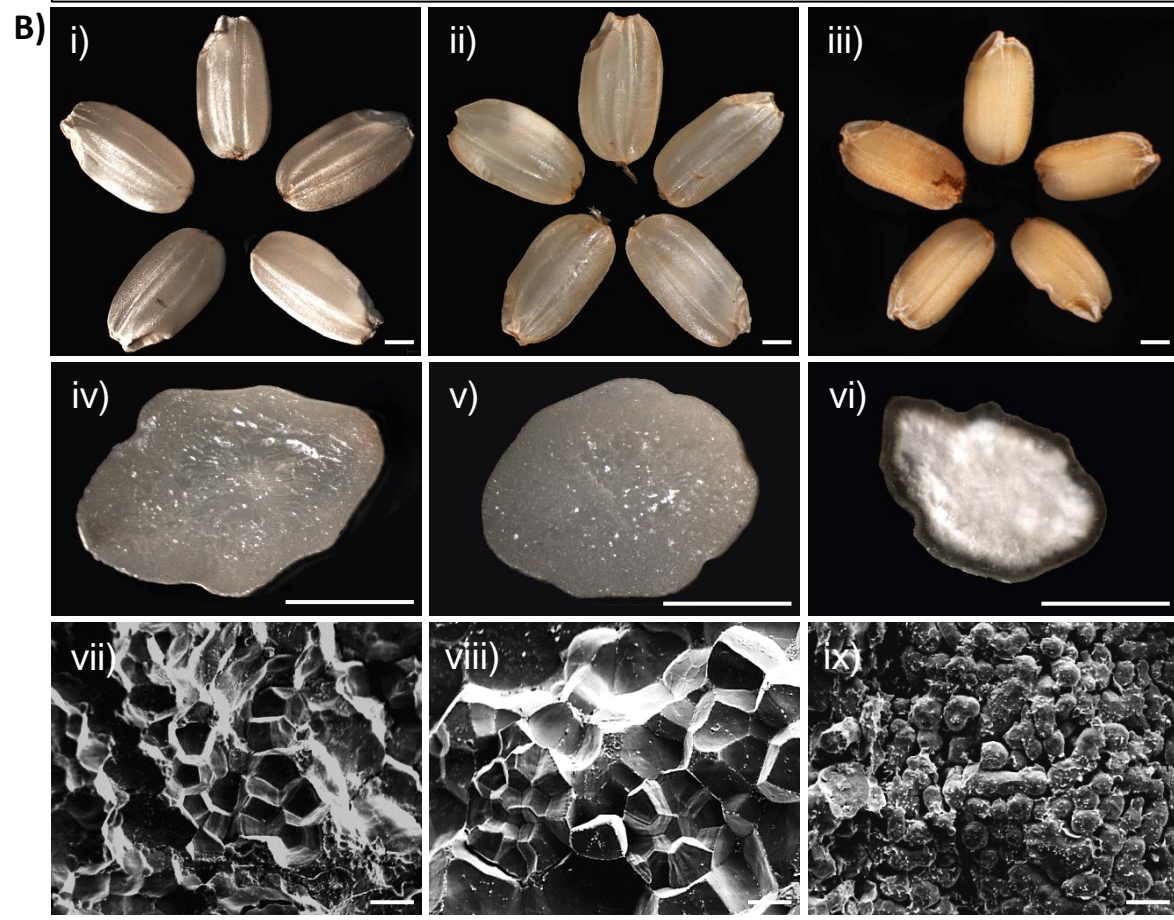
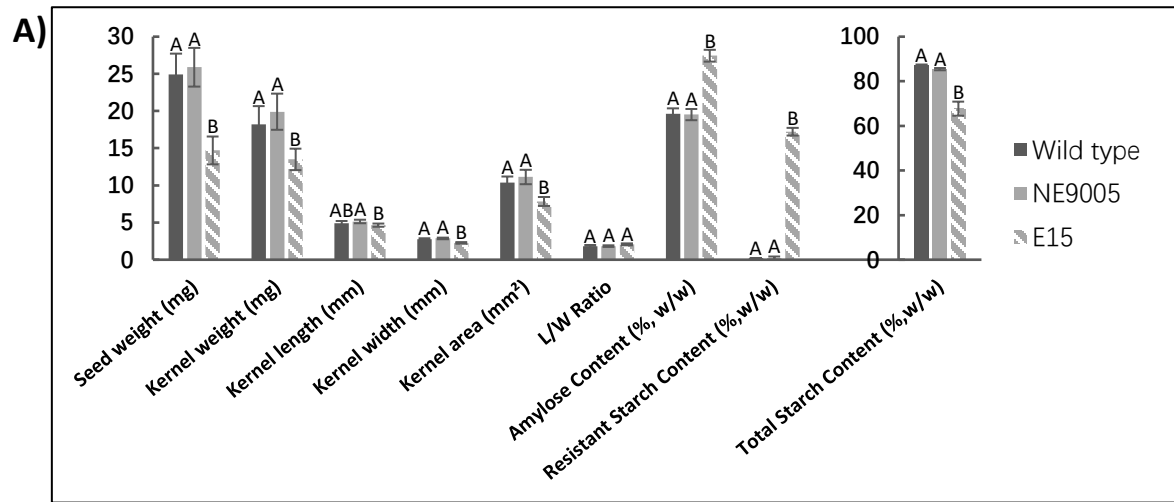


Fig. 3.

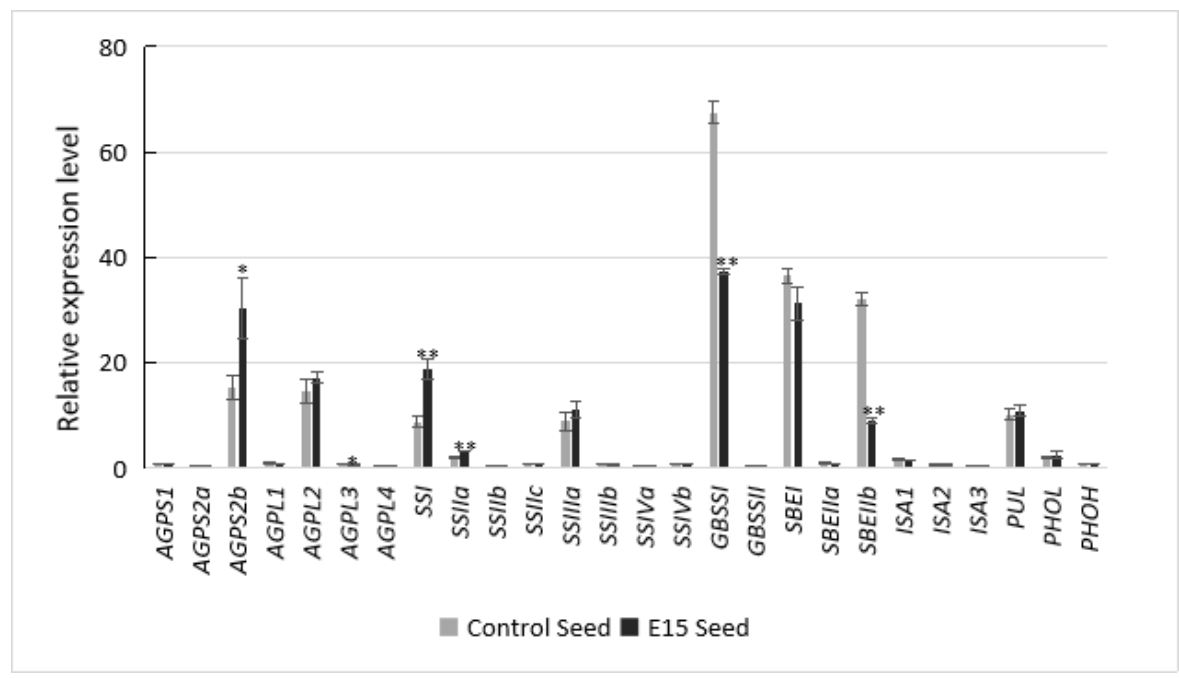
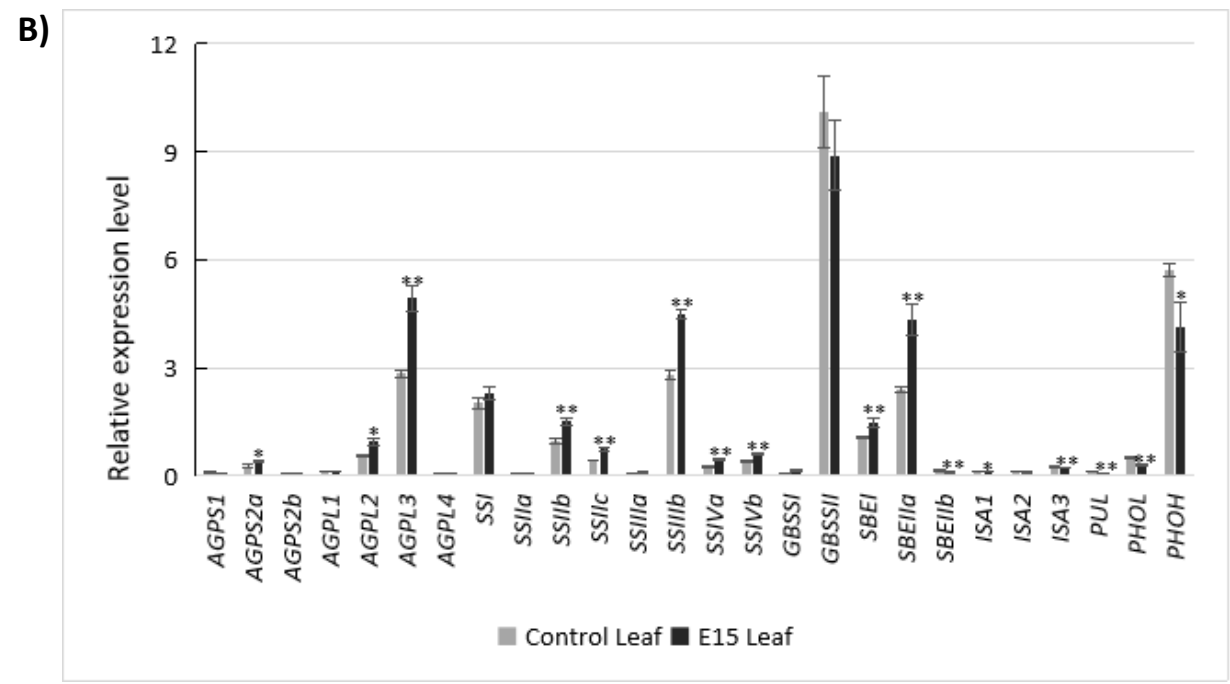
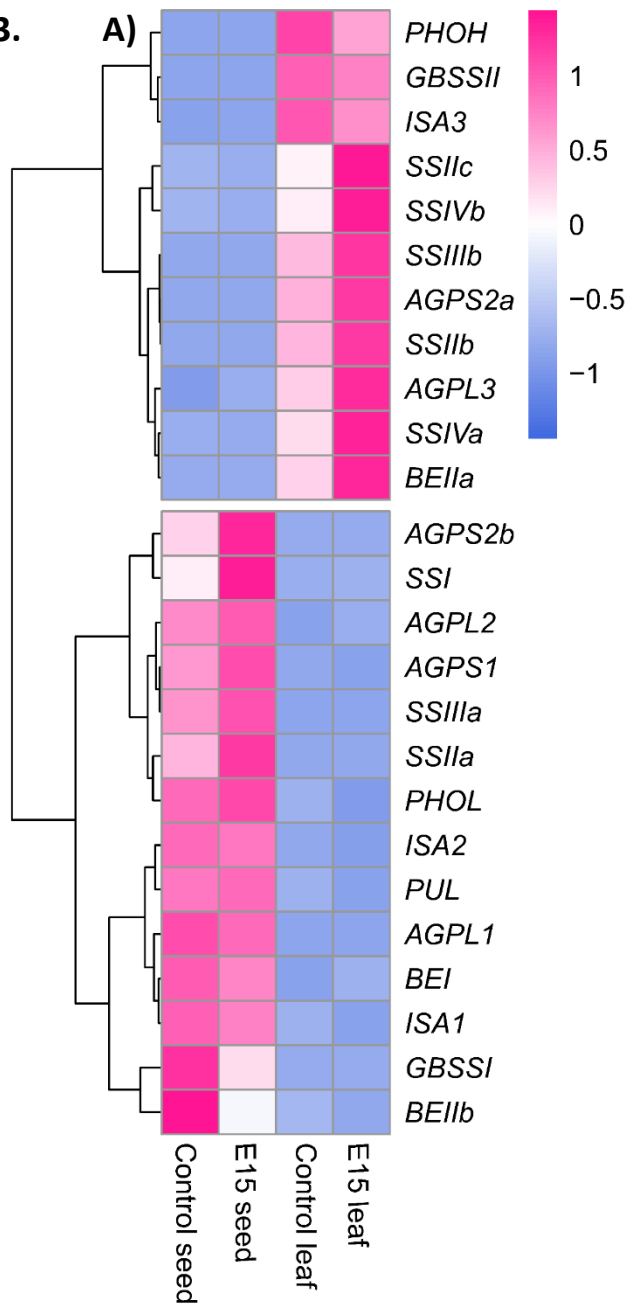


Fig. 4.

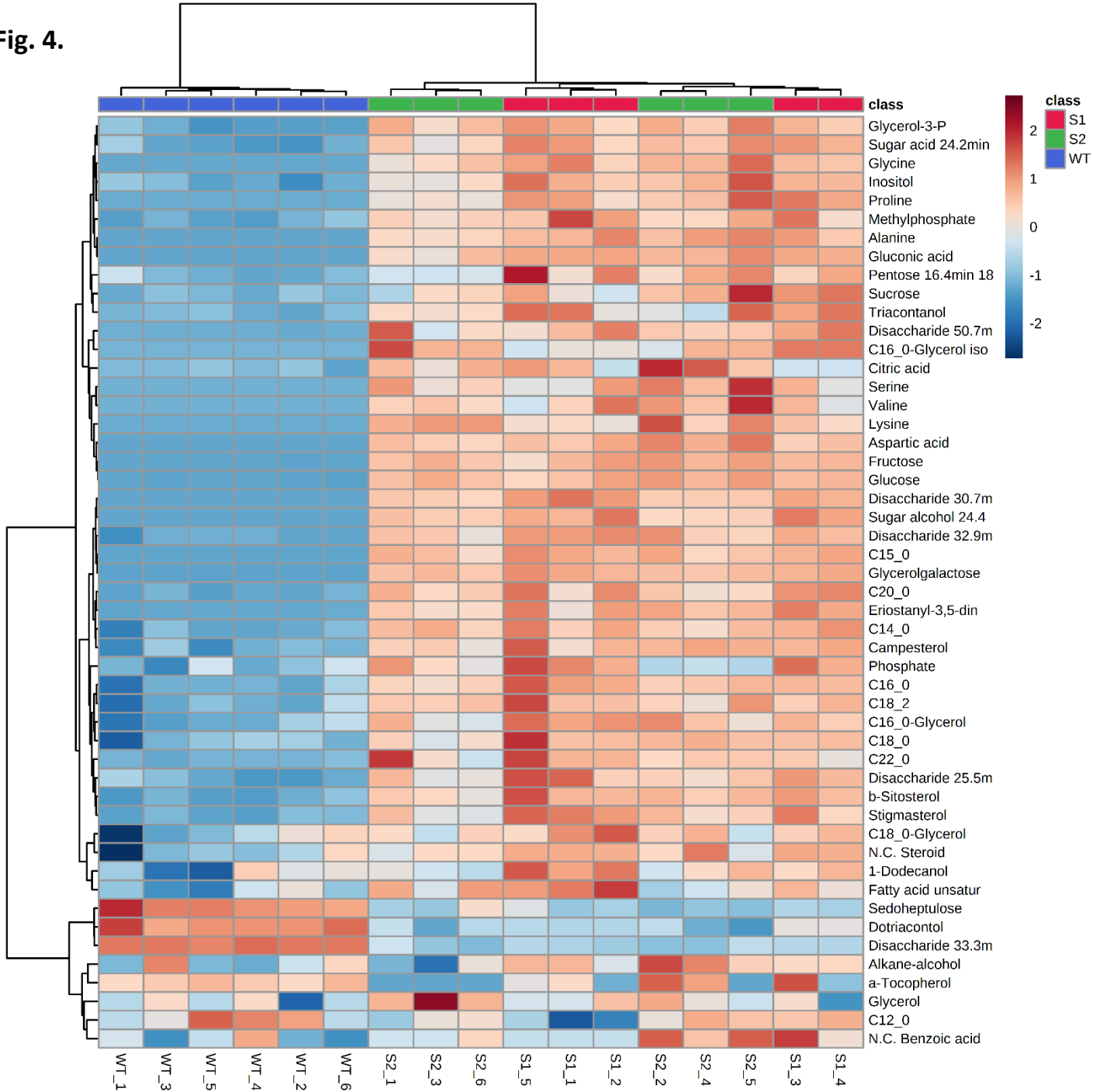


Fig. 5.

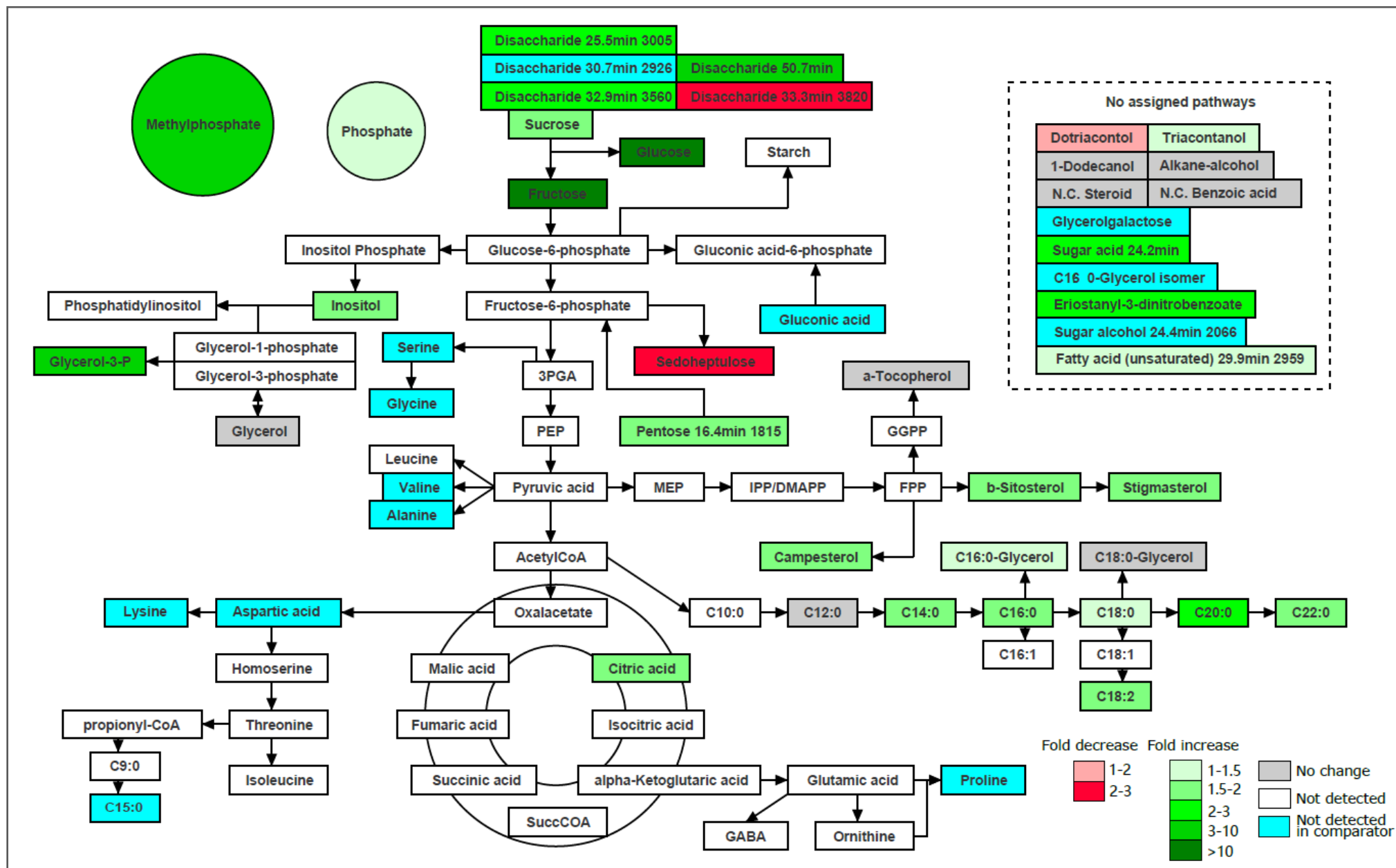


Fig. S1.

A) Amino acid alignment and comparison of amino acid sequences of wild type SBEIIb protein versus mutant SBEIIb protein.

>Rice SBEIIb Protein

MAAPASAVPGSAAGLRAGAVRFPVPAGARSWRAAAELPTSRSLLSGRRFPGAVRVGGSGGRVAVRAAGASGEVM IPEGESDGMPVSAGSDDLQLPALDDELSTEVGAEVEIESSGASDVEGVKRVVEELAAEQKPRVVPPTGDGQKIFQMDSMLNGYKYHLEYRYSLYRRLRSDIDQYEGGLETF SRGYEKFGFNHSAEGVTYREWAPGAHSAALVGD FNNWNP NADRMSKNEFGVWEIFLPNNADGSSPIPHGSRVKVRMETPSGIKDSIPAWIKYSVQAAGEIPYNGIYYDPPEEEKYIFKHPQPKRPKSLRIYETHVGMSSSTEPKINTYANFRDEVLPRIKKLGYN AVQIMAIQEHAYYGSFGYHVTNFFAPSSRFGT PEDLKSLIDKAHELGLVVLMDVVHSHASNNTLDGLNGFDGTDTHYFHSGRGHHWMWDSRLFN YGNWEVLRFLSNARWWLEEYKFDGFRFDGVTSM MYTHHGLQVAFTGN YSEYFGFATDADAVVYLMLVNDLIHGLYPEAITIGEDVSGMPTFALPVQDGGVGF DYRLHMAVPDKWIELLKQSDSWKMGDIVHTLTNRRWSEKCVTYAESHDQALVGDKTIAFWLMDKDMYDFMALDRPATPSIDRGIALHKMIRLITMGLGGEGYLNFMGNEFGHPEWIDFPRAPQVLPNGKFIPGNNNSYDKCRRRFDLGDADYLRYRGMLEFDRAMQSLEEKYGFMTSDHQYISRKHEEDKMIIFEKGLVVFVFNHWSNSYFDYRVGCLKPGKYKVVLDSDAGLFGGFGRHHHTAEHFTADCSDHNRPYFSVYSPSRTC VVYAPAEStop

>Rice SBEIIb Mutant (E15) Protein

MAAPASAVPGSAAGLRAGAVRFPVPAGARSWRAAAELPTSRSLLSGRRFPGAVRVGGSGGRVAVRAAGASGEVM IPEGESDGMPVSAGSDDLQLPALDDELSTEVGAEVEIESSGASDVEGVKRVVEELAAEQKPRVVPPTGDGQKIFQMDSMLNGYKYHLEYRYSLYRRLRSDIDQYEGGLETF SRGYEKFGFNHSAEGVTYREWAPGAHSAALVGD FNNWNP NADRMSKNEFGVWEIFLPNNADGSSPIPHGSRVKVRMETPSGIKDSIPAWIKYSVQAAGEIPYNGIYYDPPEEEKYIFKHPQPKRPKSLRIYETHVGMSSSTEPKINTYANFRDEVLPRIKKLGYN AVQIMAIQEHAYYGSFGYHVTNFFAPSSRFGT PEDLKSLIDKAHELGLVVLMDVVHSHASNNTLDGLNGLVQIRITFIVVHAAIIGCGILAFSTMIGIGKStop

B) Amino acid residues shown as different colors represent different domains of rice SBEIIb protein. Sequence alignment and homology modelling was performed and modified from the data of (4).

OsSBEIIb **178 Y E 206 W 208 P 233 E 234 F 423 D T 448 W E 452 R** **222 W 258 K 269 D 288 N** **160 H 163 Y 481 T 498 G F 501 T 503 A**
Maltopentaose Binding Sites Glucose Binding Sites I Glucose Binding Sites II

OsSBEIIb **367 Y 402 D 407 H 471 R 473 D 528 E 595 H** **368 H 428 H 596 D 598 A** **324 S T - 663 W I D F P 680 P**
Catalytic residues Active Sites I *CD Binding Sites I

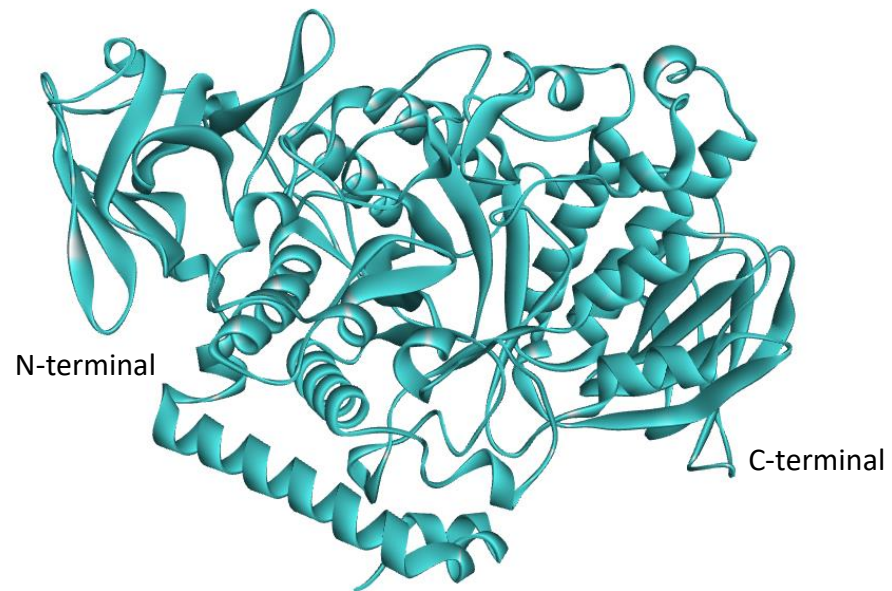
OsSBEIIb **621 D 636 K 685 S Y** **538 L P 545 V G F D 587 K** **- 259 V 282 A 286 P** **632 I 634 L H 755 W 758 S 786 F**
CD Binding Sites II CD Binding Sites III CD Binding Sites IV CD Binding Sites V

OsSBEIIb **574 D 577 H T 580 T N 729 Y** **225 P 329 I N - -**
CD Binding Sites VI CD Binding Sites VII

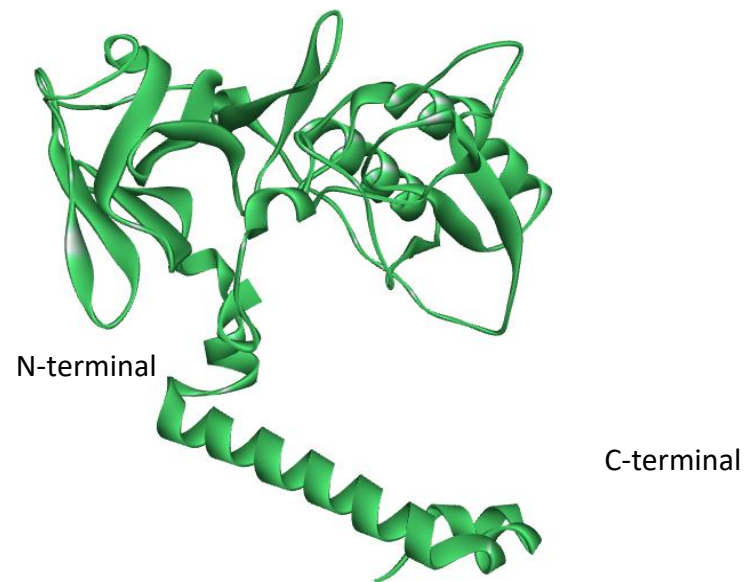
*cyclodextrin (CD)-binding sites

Fig. S2.

A)



B)



C)

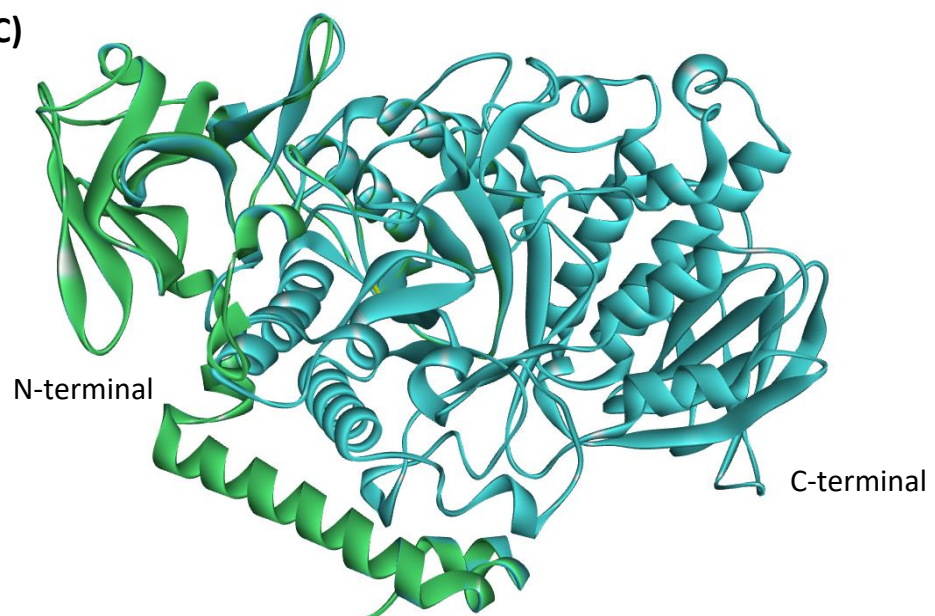


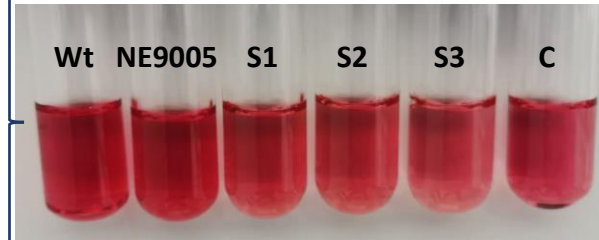
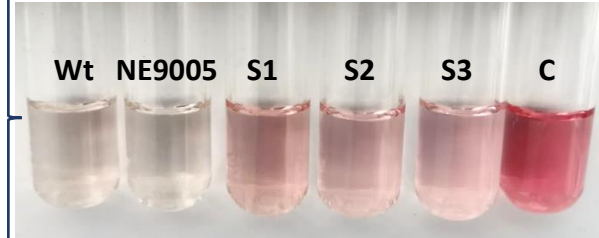
Fig. S3.

Absorbance values for 100 micrograms of D-glucose standard

Rep. 1	Rep. 2	Rep. 3	Rep. 4	Average Abs
1,1060	1,1200	1,1430	1,1240	1,1233

89,0274 Factor [=100 (micrograms of D-glucose)/Absorbance for 100 micrograms of D-glucose]

Sample identifier	Absorbance values (510 nm)			Sample weight (mg)	Extract volume (mL)	Resistant Starch (g/100 g) "as is"	Non Resistant Starch (g/100 g) "as is"	Moisture Content %	Resistant Starch (g/100 g) "dwb"	Non Resistant Starch (g/100 g) "dwb"	Total Starch (g/100 g) "dwb"
	R1	R2	Δ Abs								
Wild type	0.025	0.0230	0.024	100	10.3*	0.1981	-	10.4	0.2211	-	87.3656
NE9005	0.0240	0.0230	0.0235	100	10.3*	0.1939	-	10	0.2155	-	85.2366
E15 (S1)	0.2090	0.1920	0.2005	100	100	16.0650	-	9.7	17.7907	-	70.4529
E15 (S2)	0.2070	0.1820	0.1945	100	100	15.5842	-	8.9	17.1067	-	68.383
E15 (S3)	0.1970	0.1830	0.1900	100	100	15.2237	-	9.2	16.7662	-	64.2409
Control 39%	0.4320	0.4110	0.4215	100	100	33.7725	-	12	38.3779	-	89.1387
Wild type	0.9740	0.9750	0.9745	100	100	-	78.0815	10.4	-	87.1445	-
NE9005	0.9630	0.9470	0.9550	100	100	-	76.5190	10	-	85.0211	-
E15 (S1)	0.5750	0.6120	0.5935	100	100	-	47.5540	9.7	-	52.6622	-
E15 (S2)	0.6080	0.5580	0.5830	100	100	-	46.7127	8.9	-	51.2763	-
E15 (S3)	0.5560	0.5200	0.5380	100	100	-	43.1071	9.2	-	47.4747	-
Control 39%	0.5400	0.5750	0.5575	100	100	-	44.6695	12	-	50.7608	-



R1 and R2 are technical replicates

S1, S2, S3 are 3 biological replicates (T3 seeds from 3 independent siblings) of *BE11b* mutant line E15

*Extract volume for samples containing < 10% RS (See the protocol)

Rep. 1,2,3,4 are the absorbance values for 100 ug of D-glucose standard

Fig. S4.

Scores Plot

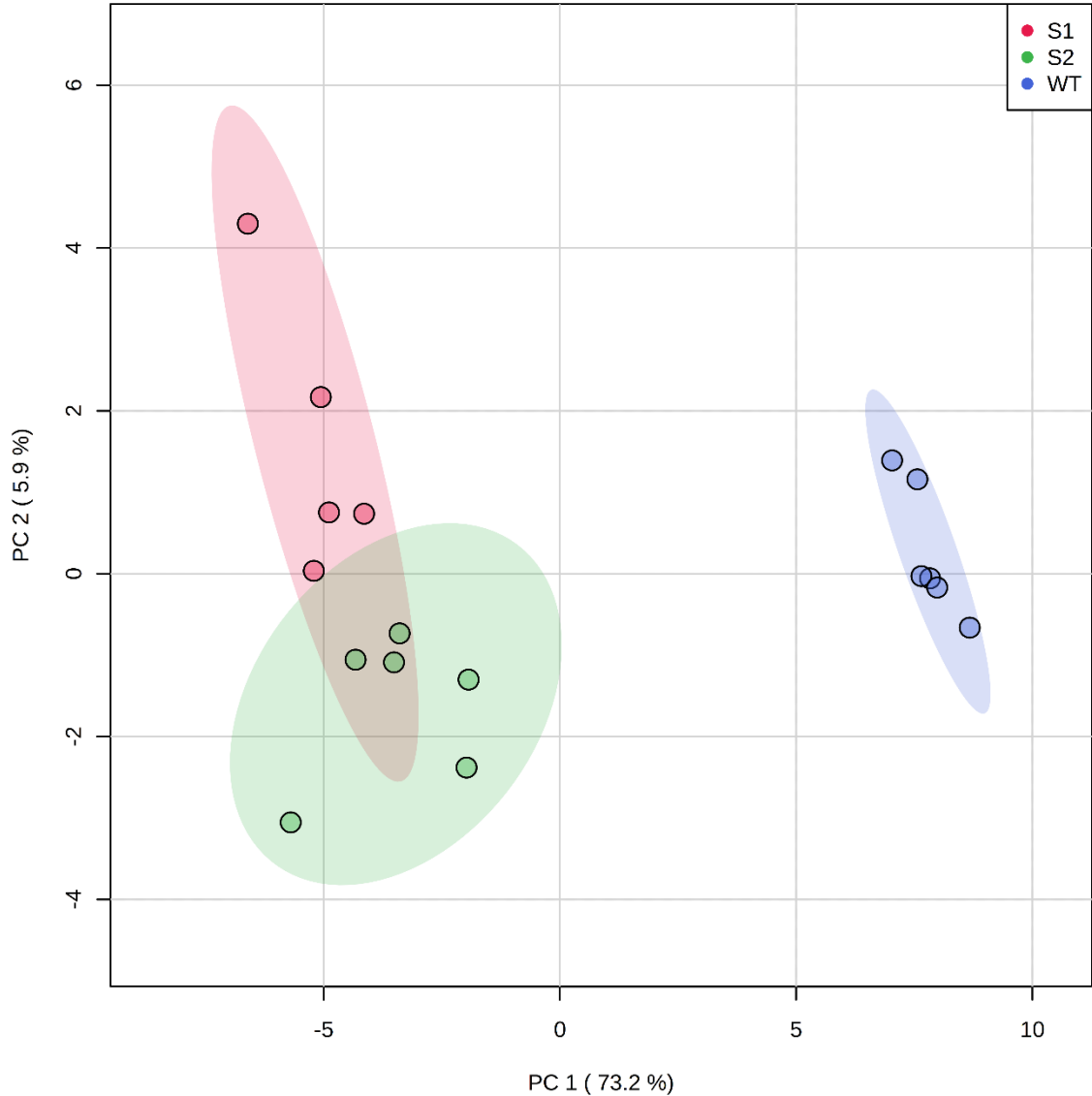


Table S1.

Sample	Seed weight (mg)	Kernel weight (mg)	Kernel length (mm)	Kernel width (mm)	Kernel area (mm ²)	L/W Ratio	Amylose Content (% w/w)	Resistant Starch Content (% w/w)	Total Starch Content (% w/w)
Wild type	24.9±2.8	18.2±2.4	4.9±0.3	2.8±0.1	10.4±0.8	1.8±0.1	19.6±0.7	0.2±0	87±0.5
NE9005	25.9±2.6	19.9±2.4	5.1±0.2	2.9±0.1	11.1±1	1.8±0.1	19.5±0.7	0.2±0.2	85.4±0.5
E15	14.7±1.9	13.5±1.4	4.7±0.2	2.3±0.1	7.8±0.6	2.1±0.1	27.4±0.8	17.2±0.5	67,7±3,2

Table S2.

	<i>AGPS1</i>	<i>AGPS2a</i>	<i>AGPS2b</i>	<i>AGPL1</i>	<i>AGPL2</i>	<i>AGPL3</i>	<i>AGPL4</i>	<i>SSI</i>	<i>SSIIa</i>	<i>SSIIb</i>	<i>SSIIc</i>	<i>SSIIIa</i>	<i>SSIIIb</i>
Control Leaf	0.02	0.21	0.00	0.05	0.55	2.86	0.01	1.86	0.00	0.90	0.40	0.02	2.68
	0.02	0.27	0.00	0.05	0.54	2.94	0.01	2.13	0.00	0.94	0.40	0.02	2.82
	0.04	0.29	0.00	0.05	0.53	2.74	0.01	2.06	0.00	1.04	0.41	0.02	2.92
E15 Leaf	0.02	0.42	0.00	0.06	0.97	5.00	0.01	2.46	0.00	1.62	0.80	0.02	4.48
	0.02	0.36	0.00	0.04	0.84	4.54	0.01	2.08	0.00	1.40	0.69	0.01	4.36
	0.02	0.38	0.00	0.04	1.00	5.22	0.01	2.33	0.00	1.50	0.74	0.02	4.63

	<i>SSIVa</i>	<i>SSIVb</i>	<i>GBSSI</i>	<i>GBSSII</i>	<i>SBEI</i>	<i>SBEIIa</i>	<i>SBEIIb</i>	<i>ISA1</i>	<i>ISA2</i>	<i>ISA3</i>	<i>PUL</i>	<i>PHOL</i>	<i>PHOH</i>
Control Leaf	0.23	0.40	0.07	8.99	1.05	2.33	0.14	0.06	0.09	0.24	0.13	0.48	5.50
	0.25	0.35	0.07	10.36	1.10	2.33	0.14	0.06	0.11	0.24	0.13	0.51	5.79
	0.27	0.40	0.07	10.92	1.04	2.49	0.15	0.06	0.12	0.25	0.14	0.49	5.87
E15 Leaf	0.47	0.59	0.07	7.92	1.62	4.40	0.10	0.05	0.09	0.22	0.08	0.29	4.01
	0.44	0.61	0.05	8.95	1.38	3.86	0.09	0.05	0.08	0.20	0.08	0.24	3.53
	0.48	0.58	0.07	9.84	1.43	4.75	0.09	0.05	0.08	0.20	0.08	0.28	4.89

	<i>AGPS1</i>	<i>AGPS2a</i>	<i>AGPS2b</i>	<i>AGPL1</i>	<i>AGPL2</i>	<i>AGPL3</i>	<i>AGPL4</i>	<i>SSI</i>	<i>SSIIa</i>	<i>SSIIb</i>	<i>SSIIc</i>	<i>SSIIIa</i>	<i>SSIIIb</i>
Control Seed	0.21	0.02	14.24	0.42	12.58	0.33	0.01	7.74	1.97	0.01	0.20	8.75	0.13
	0.28	0.02	13.75	0.38	13.85	0.30	0.01	8.73	1.94	0.01	0.21	7.19	0.12
	0.33	0.02	17.83	0.50	17.08	0.41	0.01	9.67	2.17	0.01	0.21	10.50	0.16
E15 Seed	0.37	0.02	36.05	0.40	18.22	0.61	0.01	18.67	3.33	0.01	0.23	12.82	0.13
	0.33	0.02	24.21	0.31	16.72	0.51	0.01	16.94	3.15	0.01	0.16	9.67	0.11
	0.35	0.02	30.68	0.33	16.28	0.50	0.01	20.67	3.07	0.01	0.19	11.13	0.12

	<i>SSIVa</i>	<i>SSIVb</i>	<i>GBSSI</i>	<i>GBSSII</i>	<i>SBEI</i>	<i>SBEIIa</i>	<i>SBEIIb</i>	<i>ISA1</i>	<i>ISA2</i>	<i>ISA3</i>	<i>PUL</i>	<i>PHOL</i>	<i>PHOH</i>
Control Seed	0.06	0.26	65.49	0.08	35.59	0.40	30.55	1.43	0.61	0.04	10.63	1.64	0.28
	0.06	0.25	67.36	0.08	35.84	0.37	32.95	1.62	0.59	0.04	8.82	1.89	0.25
	0.08	0.32	69.66	0.11	38.10	0.50	32.40	1.75	0.54	0.04	11.08	2.15	0.35
E15 Seed	0.07	0.22	37.59	0.09	27.65	0.40	9.61	1.54	0.67	0.05	12.00	1.81	0.35
	0.05	0.22	37.43	0.08	33.00	0.40	8.56	1.35	0.55	0.04	9.83	2.51	0.29
	0.06	0.22	36.66	0.08	33.25	0.40	8.91	1.44	0.45	0.04	10.69	3.15	0.31

Table S3a.

Genotype	Sample	Dodecanol	Alanine	Alkane-alcohol	Aspartic acid	a-Tocopherol	b-Sitosterol	C12_0	C14_0	C15_0	C16_0	C16_0-Glycerol	C18_0	C18_0-Glycerol	C18_2	C20_0	C22_0	Campesterol
WT	WT_1			26.48		23.69	397.88	9.87	43.3		2669.72	62.53	1389.14	41.1	1864.56	4.12		135.05
	WT_2	14.24				19.06	446.93	13.46	54.52		3414.23	78.89	1767.61	52.4	2324.18	4.24		172.53
	WT_3	12.61		34.93			462.49	12.53	59.96		3570.62	70.3	1669.88	46.65	2347.86	4.93	1.85	185.97
	WT_4	14.77		31.56			404.12	13.71	53.24		3604	72.22	1773.9	49.98	2411.19	4.36	2	164.98
	WT_5	12.37		37.08		19.14	412.52	14	52.84		3575.01	72.18	1723.31	47.81	2543.85	3.98		137.2
	WT_6	14.37		33.75		24.59	492.53	412.53	14.33	58.59		4128.9	82.4		53.7	2862.9	4.8	2.15
S1	S1_1	15.19	178.35	29.44	230.21	21.35	803.36	10.42	87.68		5908.2	101.51	2110.71		3547.04	9.7		245.96
	S1_2		221.11	33	276.97	19.63	799.53	10.9	97.83	2.19	5766.57	103.3	2118.32	58.61	3574.11	13.36		279.41
	S1_3	14.62	203.39	33.66	219.32	23.01	854.31	13.09	94.57	2.23	5619.54	98.94	2109.66	53.79	3458.38	13.06	3.74	277.41
	S1_4	16.56	160.47	33.72		19.91	785.68	13.33	100.98	2.33	5592.87	94.83	2122.88	54.95	3656.33	13.44	3.23	287.3
	S1_5	15.78	172	39.09			980.06		104.94	2.49	6606.35	108.29	2451.02	59.2	4295.19	14.07	5.1	328.84
S2	S2_1	14.35	140.01	31.7	245.51	17.89	762.86	11.78	92.78	2.27	5279.86	99.74	2063.35	47.35	3492.79	11.99	5.21	259.58
	S2_2		166.84	35.66	316.37	22.83	805.01	12.62	88.62	2.35	5312.93	104.7	2138.37	60.65	3421.7	11.1	3.56	278.41
	S2_3		134.06	30.49	222.07	17.51	730.05	12.64	96.06	2.16	5063.92	87.77	1906.09	50.33	3450.36	10.18	3.45	264.02
	S2_4	14.61	201.59	34.94		22.17	750.9	13.36	83.48	1.96	5445.54	96.57	2156.33	55.21	3226.66	9.6		288.51
	S2_5	13.46	221.36	33.84	330.99	25.52	798.67	13.11	92.64	2.1	5663.21	90.24	2108.64	50.46	3844.52	10.14		281.87
	S2_6	13.89	146.25		209.99	17.06	667.73	667.73	12.73	86.73	1.89	5331.94	86.17	2008.11	47.05	3553.12	10.85	2.83

Table S3b.

Genotype	Sample	Citric acid	Disaccharide 50.7min	Dotriacontol	Eriostanyl- 3,5-dinitro- benzoate	Fructose	Gluconic acid	Glucose	Glycerol	Glycerol-3-P	Glycerol- galactose	Glycine	Inositol	Lysine	Methyl- phosphate	N.C. Benzoic acid	N.C. Steroid	Phosphate
WT	WT_1		11.68	10.45	6.46	71.17		339.21		129.21			128.81		3.2		22.47	182.75
	WT_2	99.9	10.85	9.61	6.74	50.77		290.08	946.38	83.28			91.37		4.76	1.72	27.67	
	WT_3			9.37		66.52		300.75	859.84	102.73			121.89		4.78		26.56	153.25
	WT_4			9.6		62.73		324.56	1740.75	82.44			109.61		2.94	1.81		175.55
	WT_5	98.98	11.26	9.61		57.47		311.51	1182.65	72.2			104.34		3.41	1.75	27.05	224
	WT_6	81.36		10	7.03	57.67		262.06		87.24			112.29		6.14		29.98	222.09
S1	S1_1	168.02	33.45	6.31	15.68	1370.65	72.36	2982.62		294.7		35.5	211.94		23.03	1.75		
	S1_2	119.67	40.62	9.08	21.8	1583.6	73.21	3504.65	1348.19	243.7	1038.02	23.63	195.27	4.12			33.95	344.17
	S1_3	124.56			23.76				1293.7	283.52	1051.23	27.52	209.1	5.6	20.59	1.86	31.29	310.45
	S1_4	123.5	41.31	8.33	21.02	1399.56	69.56	3188.25	1039.3	257.51		25.97	206.54		13.28	1.78	28.22	216.8
	S1_5	180.19	27.65	9.81	23.81	1069.29		2653.71		314.46	1228.9	31.42	241.14	4.55	15.4			327.03
S2	S2_1	165.98	44.51	7.91	18.69	1311.56	51.88	2998.2		291.89		19.11	173.93	6.13		1.84	23.08	292.35
	S2_2	222.44		7.86	21.27	1614.81	66.92	3593.79	1387.71	292.86	980.2	28.78	198.47	8.37	13.99	1.76		207.22
	S2_3	141.01	22.22	6.91	16.71	1456.42	45.18	3335.11	1619.31	232.97	1023.35	22.37	171.6		13.02	1.67		254.68
	S2_4	203.95	30.61	7.03	19	1393.69	67.83	3170.45	1269.17	257.77	943.33	28.27	209.65	5.1	14.14		32.25	217.84
	S2_5	160.94		6.71	19.91	1565.39	81.87	3545.32	1208.79	332.16	1002.98	38.3	253.54	7.17	17.36	1.93	34.36	208.71
	S2_6	171.44	29.25	5.71	17.08	1271.77	65.85	2967.77		274.21	926.77	26.61	186.31		14.64	1.79		

Table S3c.

Genotype	Sample	Proline	Pentose 16.4min 1815	Disaccharide 30.7min 2926	Disaccharide 25.5min 3005	Disaccharide 33.3min 3820	Sedoheptulose	Serine	Stigmasterol	Sucrose	Fatty acid (unsaturated) 29.9min 2959	Sugar acid 24.2min	Triaccontanol	C16_0- Glycerol isomer	Disaccharide 32.9min 3560	Sugar alcohol 24.4min 2066	Valine
WT	WT_1		18.87		38.78	1216.39	24.26		124.81	76774.52		55.1			12.61		
	WT_2		13.67		25.58		17.48		141.22	94254.37	261.87	37.22	3.47		15.62		
	WT_3		14.86		33.47				138.28	88665.39	221.29	42.61	3.6				
	WT_4		13.58		25.51	1257.08	18.15		123.59	76006.76	252.02	38.47	3.49				
	WT_5		14.15		28.81	1175.7	19.37		125.68		213.59	40.97	3.64				
	WT_6					29.39		16.77		139.72			45.65	3.61		14.87	
S1	S1_1	142.2	21.78	30.94	75.94	456.39	5.14	17.8	251.85	135046.5	293.54	96.21		2.94	31.98	43.07	
	S1_2	93.77	28.15		57.84	399.5	6.29	34.68	239.15	117710.85	307.13	80.77	4.17	2.94	33.34	55.9	6.21
	S1_3	165.42	23.12	26.01	68.25	485.06		30.92	253.36	178375.15	278.95	96.6		5.15	30.88	54.86	4.84
	S1_4	135.93	25.95	24.04	62.32	473.82	6.31	17.57	206.96	191392.78	262.55	90.36	4.92	5.15	29.47	47.04	3.06
	S1_5	148.41	33.36	26.81	79.31	480.99	10.15	17.69	261.94	173897.27	334.14	101.61	4.96	2.31	32.19	45.4	2.6
S2	S2_1	80.78	19.24	21.53	62.64	574.32		34.8	222.22	103389.38	282.68	85.7		5.92	29.15	41.03	4.18
	S2_2				57.8	332	3.67	38.55	225.78		241.59	88.01	4.12	2.49	32.89	34.47	5.5
	S2_3	91.09	19.04		48.74	359.78	5.2	20.07	185.6	145222.7		71.48	4.27		28.51	37.72	
	S2_4	119.59	25.68		53.59	334.52	4.84	28.8	200.23	167166.56	252.36	84.39	3.92		27.76	35.41	
	S2_5	181.54	27.75	21.36	59.87	530.23	4.47	49.17	210.71	221359.24	263.77	99.88	5	4.19	27.48	36.9	7.6
	S2_6	83.74	19.61	19.36	50.68	302.96	12.58	25.44	183.57	149067.11	237.16	80.94			24.7	37.48	3.9

Table S4.

Enzyme	Gene name	Accession number	Primer sequence	Amplicon size (bp)
1-ADP-glucose pyrophosphorylase small subunit 1	<i>OsAGPS1</i>	AK073146	[F] GTGCCACTTAAAGCACCATT [R] CCCACATTTTCAGACACGGTTT	97
2-ADP-glucose pyrophosphorylase small subunit 2a	<i>OsAGPS2a</i>	AK071826	[F] ACTCCAAGAGCTCGCAGACC [R] GCCTGTAGTTGGCACCCAGA	147
3-ADP-glucose pyrophosphorylase small subunit 2b*	<i>OsAGPS2b</i>	AK103906	[F] AACAAATCGAAGCGCGAGAAA [R] GCCTGTAGTTGGCACCCAGA	186
4-ADP-glucose pyrophosphorylase large subunit 1	<i>OsAGPL1</i>	D50317	[F] GGAAGACGGATGATCGAGAAAAG [R] CACATGAGATGCACCAACGA	140
5-ADP-glucose pyrophosphorylase large subunit 2*	<i>OsAGPL2</i>	U66041	[F] AGTTCGATTCAAGACGGATAGC [R] CGACTCCACAGGCAGCTTATT	96
6-ADP-glucose pyrophosphorylase large subunit 3	<i>OsAGPL3</i>	AK069296	[F] AAGCCAGCCATGACCATTG [R] CACACGGTAGATTCACGAGACAA	131
7-ADP-glucose pyrophosphorylase large subunit 4	<i>OsAGPL4</i>	AK121036	[F] TCAACGTCGATGCAGCAAAT [R] ATCCCTCAGTTCTAGCCTCATT	77
8-Starch synthase I	<i>OsSSI</i>	D16202	[F] GGGCCTTCATGGATCAACC [R] CCGCTTCAAGCATCCTCATC	279
9-Starch synthase IIa	<i>OsSSIa</i>	AF419099	[F] GCTTCCGGTTTGTGTGTTCA [R] CTTAATACTCCCTCAACTCCACCAT	54
10-Starch synthase IIb	<i>OsSSIb</i>	AF395537	[F] TAGGAGCAACGGTGAAGTGA [R] GTGAACGTGAGTACGTGACCAAT	89
11-Starch synthase IIc	<i>OsSSIc</i>	AF383878	[F] GACCGAAATGCCTTTTCTCG [R] GGGCTTGGAGCCTCCTTA	256
12-Starch synthase IIIa	<i>OsSSIa</i>	AY100469	[F] GCCTGCCCTGGACTACATTG [R] GCAAACATATGTACACGGTTCTGG	334
13-Starch synthase IIIb	<i>OsSSIb</i>	AF432915	[F] ATTCGCTCGAAGAAGTGA [R] CAACCGCAGGATAACGGAAA	224
14-Starch synthase IVa	<i>OsSSIVa</i>	AY100470	[F] GGGAGCGGCTCAAACATAAA [R] CCGTGCACTGACTGAAAAT	237
15-Starch synthase IVb	<i>OsSSIVb</i>	AY373258	[F] ATGCAGGAAGCCGAGATGTT [R] ACGACAATGGGTGCCAAGAT	75
16-Granule-bound starch synthase I	<i>OsGBSSI</i>	X62134	[F] AACGTGGCTGCTCCTTGAA [R] TTGGCAATAAGCCACACACA	218
17-Granule-bound starch synthase II	<i>OsGBSSII</i>	AY069940	[F] AGGCATCGAGGGTGAGGAG [R] CCATCTGGCCACATCTCTA	246
18-Starch branching enzyme I	<i>OsBEI</i>	D11082	[F] TGGCCATGGAAGAGTTGGC [R] CAGAAGCAACTGCTCCACC	191
19-Starch branching enzyme IIa	<i>OsBEIIa</i>	AB023498	[F] GCCAATGCCAGGAAGATGA [R] GCGCAACATAGGATGGGTTT	128
20-Starch branching enzyme IIb	<i>OsBEIIb</i>	D16201	[F] ATGCTAGAGTTTGACCGC [R] AGTGTGATGGATCCTGCGC	261
21-Starch debranching enzyme: Isoamylase I	<i>OsISA1</i>	AB093426	[F] TGCTCAGCTACTCCTCCATCATC [R] AGGACCGCACAACTCAACATA	132
22-Starch debranching enzyme: Isoamylase II	<i>OsISA2</i>	AC132483	[F] TAGAGGTCTCTTGAGG [R] AATCAGCTTCTGAGTCACCG	170
23-Starch debranching enzyme: Isoamylase III	<i>OsISA3</i>	AP005574	[F] ACAGCTTGAGACTGGGTTGAG [R] GCATCAAGAGGACAACCATCTG	100
24-Starch debranching enzyme: Pullulanase	<i>OsPUL</i>	AB012915	[F] ACCTTTCTCCATGCTGG [R] CAAAGGTCTGAAAGATGGG	202
25-Starch phosphorylase L	<i>OsPHOL</i>	AK063766	[F] TTGGCAGGAAGGTTTCGCT [R] CGAAGCCTGAAGTGAACCTTGCT	66
26-Starch phosphorylase H*	<i>OsPHOH</i>	AK103367	[F] CACCAAGACGAAGCTCATCAAG [R] TTCACTCGTTGCTGGTTCTC	126

* Cytosolic type