

Supplemental Materials

Table S1. Gene Ontology (GO) terms enriched within the sets of significantly ($FDR < 0.05$) differentially expressed genes (DEGs) between reciprocal hybrid pairs with significant reciprocal effects (ST8-2/GY14-15 and ST8-4x/9930-3) and no reciprocal effects (controls; ST8-4/TMG1-5 and GY14-15/ST8-4) compared to number of genes represented in reference set (Ref) of all detected genes across samples in the experiment. Significance was tested based on Fisher's exact test with the false discovery rate (FDR) correction.

<i>Significant reciprocal effects: ST8-2xGY14-15 vs GY14-15xST8-2</i>					
Domain*	GO Term	Ref (#/20429)	DEGs (#/33)	Raw p- value	Adjusted p-value (FDR)
BP	negative regulation of endopeptidase activity (GO:0010951)	35	4	4.43E-07	2.05E-03
BP	negative regulation of peptidase activity (GO:0010466)	35	4	4.43E-07	1.03E-03
BP	negative regulation of proteolysis (GO:0045861)	35	4	4.43E-07	6.84E-04
BP	regulation of endopeptidase activity (GO:0052548)	36	4	4.92E-07	5.69E-04
BP	regulation of peptidase activity (GO:0052547)	37	4	5.44E-07	5.04E-04
BP	regulation of proteolysis (GO:0030162)	64	4	4.24E-06	3.28E-03
BP	negative regulation of hydrolase activity (GO:0051346)	65	4	4.50E-06	2.98E-03
BP	negative regulation of cellular protein metabolic process (GO:0032269)	105	4	2.77E-05	1.60E-02
BP	negative regulation of protein metabolic process (GO:0051248)	105	4	2.77E-05	1.42E-02

BP	negative regulation of catalytic activity (GO:0043086)	146	4	9.62E-05	4.46E-02
BP	negative regulation of molecular function (GO:0044092)	148	4	1.01E-04	4.27E-02
BP	regulation of hydrolase activity (GO:0051336)	156	4	1.23E-04	4.77E-02
MF	cysteine-type endopeptidase inhibitor activity (GO:0004869)	17	3	4.28E-06	2.09E-03
MF	endopeptidase inhibitor activity (GO:0004866)	35	4	4.43E-07	1.08E-03
MF	peptidase inhibitor activity (GO:0030414)	35	4	4.43E-07	5.40E-04
MF	endopeptidase regulator activity (GO:0061135)	36	4	4.92E-07	4.00E-04
MF	peptidase regulator activity (GO:0061134)	37	4	5.44E-07	3.32E-04
MF	enzyme inhibitor activity (GO:0004857)	139	4	7.99E-05	3.25E-02
CC	No significant results				
<i>Significant reciprocal effects: ST8-4x9930-3 vs 9930-3xST8-4</i>					
Domain	GO Term	Ref (#/20429)	DEGs (#/153)	Raw p-value	FDR
BP	photorespiration (GO:0009853)	12	3	1.72E-04	4.68E-02
BP	regulation of transcription by RNA polymerase II (GO:0006357)	379	12	3.72E-05	1.43E-02
BP	regulation of transcription, DNA-templated (GO:0006355)	1308	27	1.79E-06	8.31E-03

BP	regulation of RNA biosynthetic process (GO:2001141)	1318	27	2.07E-06	4.79E-03
BP	regulation of nucleic acid-templated transcription (GO:1903506)	1318	27	2.07E-06	3.19E-03
BP	regulation of RNA metabolic process (GO:0051252)	1372	27	4.31E-06	5.00E-03
BP	regulation of nucleobase-containing compound metabolic process (GO:0019219)	1409	27	6.98E-06	6.46E-03
BP	regulation of cellular macromolecule biosynthetic process (GO:2000112)	1437	27	9.91E-06	7.65E-03
BP	regulation of macromolecule biosynthetic process (GO:0010556)	1449	27	1.15E-05	7.60E-03
BP	regulation of cellular biosynthetic process (GO:0031326)	1463	27	1.36E-05	7.88E-03
BP	regulation of biosynthetic process (GO:0009889)	1467	27	2.37E-05	1.22E-02
BP	regulation of gene expression (GO:0010468)	1596	28	2.61E-05	1.10E-02
BP	regulation of nitrogen compound metabolic process (GO:0051171)	1690	29	2.53E-05	1.17E-02
BP	regulation of primary metabolic process (GO:0080090)	1710	29	4.92E-05	1.75E-02
BP	regulation of cellular metabolic process (GO:0031323)	1760	29	6.29E-05	2.08E-02
BP	regulation of macromolecule metabolic process (GO:0060255)	1873	30	6.55E-05	2.02E-02

BP	regulation of metabolic process (GO:0019222)	1928	30	1.32E-04	3.83E-02
MF	RNA polymerase II cis-regulatory region sequence-specific DNA binding (GO:0000978)	157	11	5.29E-08	3.23E-05
MF	cis-regulatory region sequence- specific DNA binding (GO:0000987)	158	11	5.63E-08	2.29E-05
MF	RNA polymerase II transcription regulatory region sequence-specific DNA binding (GO:0000977)	174	11	1.42E-07	3.46E-05
MF	DNA-binding transcription factor activity, RNA polymerase II- specific (GO:0000981)	192	12	4.23E-08	3.44E-05
MF	regulatory region nucleic acid binding (GO:0001067)	301	14	1.03E-07	3.58E-05
MF	transcription regulatory region sequence-specific DNA binding (GO:0000976)	301	14	1.03E-07	3.14E-05
MF	sequence-specific double-stranded DNA binding (GO:1990837)	321	14	2.18E-07	4.84E-05
MF	double-stranded DNA binding (GO:0003690)	385	14	1.76E-06	3.30E-04
MF	sequence-specific DNA binding (GO:0043565)	554	19	5.41E-08	2.64E-05
MF	protein dimerization activity (GO:0046983)	265	9	2.16E-04	3.52E-02
MF	DNA-binding transcription factor activity (GO:0003700)	682	22	1.27E-08	1.55E-05

MF	transcription regulator activity (GO:0140110)	782	22	1.31E-07	3.56E-05
MF	DNA binding (GO:0003677)	1405	33	4.75E-09	1.16E-05
MF	molecular function regulator (GO:0098772)	1139	25	1.58E-06	3.21E-04
MF	nucleic acid binding (GO:0003676)	2477	36	9.23E-05	1.61E-02
CC	nuclear chromatin (GO:0000790)	155	10	4.47E-07	2.07E-04
CC	chromatin (GO:0000785)	204	12	7.92E-08	7.33E-05
CC	host cellular component (GO:0018995)	122	6	3.94E-04	7.28E-02
CC	host cell (GO:0043657)	122	6	3.94E-04	6.07E-02
CC	host intracellular region (GO:0043656)	122	6	3.94E-04	5.20E-02
CC	host cell nucleus (GO:0042025)	122	6	3.94E-04	4.55E-02
CC	host intracellular membrane-bounded organelle (GO:0033648)	122	6	3.94E-04	4.05E-02
CC	host intracellular organelle (GO:0033647)	122	6	3.94E-04	3.64E-02
CC	host intracellular part (GO:0033646)	122	6	3.94E-04	3.31E-02
CC	host cell part (GO:0033643)	122	6	3.94E-04	3.03E-02
CC	nuclear chromosome (GO:0000228)	226	10	1.11E-05	2.57E-03
CC	chromosome (GO:0005694)	355	13	3.88E-06	1.20E-03
<i>Control: ST8-4xTMG1-5 vs TMG1-5xST8-4</i>					

Domain	GO Term	Ref (#/20429)	DEG (#/216)	Raw p- value	FDR
BP	protein folding (GO:0006457)	163	11	5.59E-07	2.59E-03
MF	protein folding chaperone (GO:0044183)	14	4	1.79E-05	2.18E-02
MF	unfolded protein binding (GO:0051082)	98	9	5.62E-07	1.37E-03
CC	No significant results				
<i>Control: GY14-15xST8-4 vs ST8-4xGY14-15</i>					
Domain	GO Term	Ref (#/23710)	DEGs (#/92)	Raw p- value	FDR
BP	No significant results				
MF	No significant results				
CC	No significant results				

*BP, MF, and CC represent biological process, molecular function, and cellular component domains, respectively.

Table S2. Gene Ontology (GO) terms overrepresented within sets of significantly ($FDR < 0.05$) differentially expressed genes (DEGs) that are exclusive to each reciprocal hybrid pair with significant reciprocal effects compared to number of genes represented in reference set (Ref) of all detected genes across all samples in the experiment. Significance was tested based on Fisher's exact test with the false discovery rate (FDR) correction.

<i>Significant reciprocal effects: Exclusive to ST8-2xGY14-15 vs GY14-15xST8-2</i>					
Domain*	GO Term	Ref (#/20429)	DEG (#/25)	Raw p-value	Adjusted p-value (FDR)
BP	No significant results				
MF	No significant results				
CC	No significant results				
<i>Significant reciprocal effects: Exclusive to ST8-4x9930-3 vs 9930-3xST8-4</i>					
Domain	GO Term	Ref (#/20429)	DEG (#/126)	Raw p-value	FDR
BP	No significant results				
MF	RNA polymerase II cis-regulatory region sequence-specific DNA binding (GO:0000978)	157	10	8.19E-08	1.00E-04
MF	cis-regulatory region sequence-specific DNA binding (GO:0000987)	158	10	8.67E-08	7.05E-05
MF	RNA polymerase II transcription regulatory region sequence-specific DNA binding (GO:0000977)	174	10	2.03E-07	9.91E-05
MF	DNA-binding transcription factor activity, RNA polymerase II-specific (GO:0000981)	192	11	5.02E-08	1.22E-04

MF	regulatory region nucleic acid binding (GO:0001067)	301	12	5.21E-07	1.82E-04
MF	transcription regulatory region sequence-specific DNA binding (GO:0000976)	301	12	5.21E-07	1.59E-04
MF	sequence-specific double-stranded DNA binding (GO:1990837)	321	12	1.00E-06	2.72E-04
MF	double-stranded DNA binding (GO:0003690)	385	12	6.13E-06	1.25E-03
MF	sequence-specific DNA binding (GO:0043565)	554	15	2.17E-06	4.82E-04
MF	DNA-binding transcription factor activity (GO:0003700)	682	18	2.75E-07	1.12E-04
MF	transcription regulator activity (GO:0140110)	782	18	1.87E-06	4.57E-04
MF	DNA binding (GO:0003677)	1405	27	1.27E-07	7.74E-05
MF	molecular function regulator (GO:0098772)	1139	20	2.52E-05	4.73E-03
CC	nuclear chromatin (GO:0000790)	155	9	7.80E-07	3.61E-04
CC	chromatin (GO:0000785)	204	11	9.01E-08	8.33E-05
CC	nuclear chromosome (GO:0000228)	226	9	1.48E-05	3.42E-03
CC	chromosome (GO:0005694)	355	12	2.75E-06	8.48E-04

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