

**Supplemental Table S19. Summary of *cis*- and *trans*-regulatory differences in their reciprocal cross hybrids**

		BT						TB				
		Expression in parents <sup>a</sup>	Expression in progeny	F <sub>1</sub> (%) <sup>b</sup>	F <sub>2</sub> (%) <sup>b</sup>	F <sub>3</sub> (%) <sup>b</sup>	Shared among BT	F <sub>1</sub> (%) <sup>b</sup>	F <sub>2</sub> (%) <sup>b</sup>	F <sub>3</sub> (%) <sup>b</sup>	Shared among TB	Shared among BT and TB
Conserved		B=T	B=T	1055 (10.82%)	912 (9.35%)	966 (9.90%)	359 (3.68%)	1194 (12.24%)	1045 (10.71%)	803 (8.23%)	378 (3.88%)	205 (2.10%)
		B>T <sup>c</sup>	B>T <sup>c</sup>	1373 (14.08%)	803 (8.23%)	396 (4.06%)	209 (2.14%)	1119 (11.47%)	718 (7.36%)	480 (4.92%)	257 (2.64%)	108 (1.11%)
		B<T <sup>c</sup>	B<T <sup>c</sup>	131 (1.34%)	199 (2.04%)	247 (2.53%)	56 (0.57%)	149 (1.53%)	174 (1.78%)	198 (2.03%)	61 (0.63%)	35 (0.36%)
<i>Cis</i> + <i>trans</i>	Parental condition	B>T <sup>c</sup>	B>T <sup>c</sup>	450 (4.61%)	182 (1.87%)	108 (1.11%)	16 (0.16%)	344 (3.53%)	171 (1.75%)	112 (1.15%)	20 (0.21%)	2 (0.02%)
		B<T <sup>d</sup>	B<T <sup>d</sup>	59 (0.60%)	60 (0.62%)	75 (0.77%)	4 (0.04%)	58 (0.59%)	72 (0.74%)	69 (0.71%)	7 (0.07%)	2 (0.02%)
Total in parental condition				3068 (31.46%)	2156 (22.11%)	1792 (18.37%)	644 (6.60%)	2864 (29.37%)	2180 (22.35%)	1662 (17.04%)	723 (7.41%)	352 (3.61%)
<i>Trans</i> only	No bias in progeny	B>T	B=T	1005 (10.30%)	1789 (18.34%)	2333 (23.92%)	767 (7.86%)	1209 (12.40%)	1924 (19.73%)	2343 (24.02%)	904 (9.27%)	508 (5.21%)
		B<T	B=T	1643 (16.85%)	2285 (23.43%)	2341 (24.00%)	1176 (12.06%)	1815 (18.61%)	2230 (22.86%)	2484 (25.47%)	1340 (13.74%)	845 (8.66%)
Compensatory	Novel bias in progeny	B=T	B>T	273 (2.80%)	131 (1.34%)	69 (0.71%)	29 (0.30%)	247 (2.53%)	115 (1.18%)	67 (0.69%)	22 (0.23%)	13 (0.13%)
		B=T	B<T	50 (0.51%)	89 (0.91%)	61 (0.63%)	16 (0.16%)	49 (0.50%)	52 (0.53%)	54 (0.55%)	13 (0.13%)	9 (0.09%)
<i>Cis</i> x <i>trans</i>	Novel bias in progeny	B>T	B<T	130 (1.33%)	256 (2.62%)	293 (3.00%)	43 (0.44%)	171 (1.75%)	231 (2.37%)	247 (2.53%)	57 (0.58%)	32 (0.33%)
		B<T	B>T	1358 (13.92%)	594 (6.09%)	297 (3.05%)	151 (1.55%)	1069 (10.96%)	488 (5.00%)	318 (3.26%)	147 (1.51%)	68 (0.70%)
Total in novel in progeny				1811 (18.57%)	1070 (10.97%)	720 (7.38%)	2046 (20.98%)	1536 (15.75%)	886 (9.08%)	686 (7.03%)	2159 (22.14%)	1840 (18.87%)
Ambiguous				2226 (22.82%)	2453 (25.15%)	2567 (26.32%)	2285 (23.43%)	2329 (23.88%)	2533 (25.97%)	2,578 (26.43%)	2398 (24.59%)	1962 (20.12%)

Abbreviation: SNP, single nucleotide polymorphism. B = T denotes equal expression; B > T and B < T denote B-biased and T-biased expression, respectively.

<sup>a</sup> Based on comparison of parental B and parental T.

<sup>b</sup> Based on comparison of gene expression values of B and T which were divided by genome-diagnostic SNPs.

<sup>c</sup> The significant differential expression between the  $\log_2$  (B/T) in parents and hybrids.

<sup>d</sup> The no significant differential expression between the  $\log_2$  (B/T) in parents and hybrids.