

**Supplemental Table 1. Excel sheet summarizes SCA at 15,658 SNPs.**

**Supplemental Table 2. The set of  $\tau$  estimates for wet and dry tissue as a function of read depth at a**

**SNP.**

read depth	tau-wet	tau-dry
1	0.0000	0.000
2	0.0426	0.028
3	0.1837	0.141
4	0.2043	0.149
5	0.3384	0.246
6	0.3498	0.251
7	0.4632	0.326
8	0.4728	0.336
9	0.5691	0.405
10	0.5748	0.405
11	0.6415	0.466
12	0.6524	0.463
13	0.6969	0.520
14	0.6807	0.492
15	0.6993	0.516
16	0.7157	0.536
17	0.7581	0.560
18	0.7607	0.572
19	0.7852	0.597
20	0.7126	0.543
21	0.7653	0.589
22	0.7653	0.589
23	0.7653	0.589
24	0.7653	0.589
25	0.8179	0.634
26	0.8179	0.634
27	0.8179	0.634
28	0.8179	0.634
29	0.8399	0.687
30	0.8399	0.687
31	0.8399	0.687
32	0.8399	0.687
33	0.8399	0.687
34	0.8864	0.710

35	0.8864	0.710
36	0.8864	0.710
37	0.8864	0.710
38	0.8887	0.737
39	0.8887	0.737
40	0.8887	0.737
41	0.8887	0.737
42	0.8952	0.724
43	0.8952	0.724
44	0.8952	0.724
45	0.8952	0.724
46	0.9083	0.766
47	0.9083	0.766
48	0.9083	0.766
49	0.9083	0.766
50	0.9380	0.815
51	0.9380	0.815
52	0.9380	0.815
53	0.9380	0.815
54	0.9380	0.815
55	0.9396	0.833
56	0.9396	0.833
57	0.9396	0.833
58	0.9396	0.833
59	0.9503	0.852
60	0.9503	0.852
61	0.9503	0.852
62	0.9503	0.852
63	0.9525	0.875
64	0.9525	0.875
65	0.9525	0.875
66	0.9525	0.875
67	0.9696	0.887
68	0.9696	0.887
69	0.9696	0.887
70	0.9696	0.887
71	0.9806	0.887
72	0.9806	0.887
73	0.9806	0.887
74	0.9806	0.887
75	0.9806	0.887
76	0.9975	0.906
77	0.9975	0.906

78	0.9975	0.906
79	0.9975	0.906
80	0.9973	0.900
81	0.9973	0.900
82	0.9973	0.900
83	0.9973	0.900
84	1.0000	0.914
85	1.0000	0.914
86	1.0000	0.914
87	1.0000	0.914
88	1.0000	0.937
89	1.0000	0.937
90	1.0000	0.937
91	1.0000	0.937
92	1.0000	0.937
93	1.0000	0.937
94	1.0000	0.937
95	1.0000	0.937
96	1.0000	0.937
97	1.0000	0.937
98	1.0000	0.937
99	1.0000	0.937
100+	1.0000	1.0000

**Supplemental Table 3. Replicate STRUCTURE runs for K ranging from 1-4 with 10 replicates per K.**

K	rep	LN prob of data
1	0	-314443
1	1	-314458
1	2	-314463
1	3	-314459
1	4	-314446
1	5	-314446
1	6	-314458
1	7	-314435
1	8	-314449
1	9	-314469
2	0	-294549
2	1	-294706
2	2	-294601
2	3	-294615

2	4	-294673
2	5	-294583
2	6	-294848
2	7	-294621
2	8	-294693
2	9	-294672
3	0	-295226
3	1	-294864
3	2	-296034
3	3	-294695
3	4	-295223
3	5	-294754
3	6	-342774
3	7	-294937
3	8	-294898
3	9	-294823

4	0	-294929
4	1	-368494
4	2	-295312
4	3	-423949
4	4	-296421
4	5	-297542
4	6	-294892
4	7	-355275
4	8	-319750
4	9	-343484

**Supplemental Table 4. Mean Fst values for SNPs categorized by significance for viability selection (top) and qM/qS.**

		Mean Fst	n	SE
Significance based on delta32				
fst(BR vs Quarry)	ns	0.123	13911	0.001
	sig	0.156	343	0.009
fst(IM vs Quarry)	ns	0.131	13978	0.001
	sig	0.170	344	0.010
fst(BR v IM)	ns	0.065	10508	0.001
	sig	0.062	261	0.007
Significance based on delta31				
fst(BR vs Quarry)	ns	0.120	12622	0.001
	sig	0.152	1632	0.004
fst(IM vs Quarry)	ns	0.127	12688	0.001
	sig	0.169	1634	0.005
fst(BR v IM)	ns	0.065	9527	0.001
	sig	0.061	1242	0.003

**Supplemental Table 5.** We considered genotypes in isolation from any information about parents or progeny and calculated a confidence score (CS) as the difference between the likelihood of the most likely genotype (RR, RA, and AA) and the second most likely. GATK standardizes the likelihoods such that the highest has value 1. As a consequence, the maximum CS is 1 (which happens when we are certain of the genotype; likelihood of other two genotypes is zero). Across SNPs, the mean CS is very similar for S (0.731) parents and D parents (0.723).

**If we parse all SNPs according significance for the viability selection test:**

Offspring genotypes	ns	N = 15291	Mean CS score = 0.70
	sig	367	0.74
Parent genotypes	ns	15291	0.73
	sig	367	0.74

**If we parse all SNPs according significance for the fecundity selection test:**

Offspring genotypes	ns	N = 13925	Mean CS score = 0.69
	sig	1733	0.74
Parent genotypes	ns	13925	0.72
	sig	1733	0.74

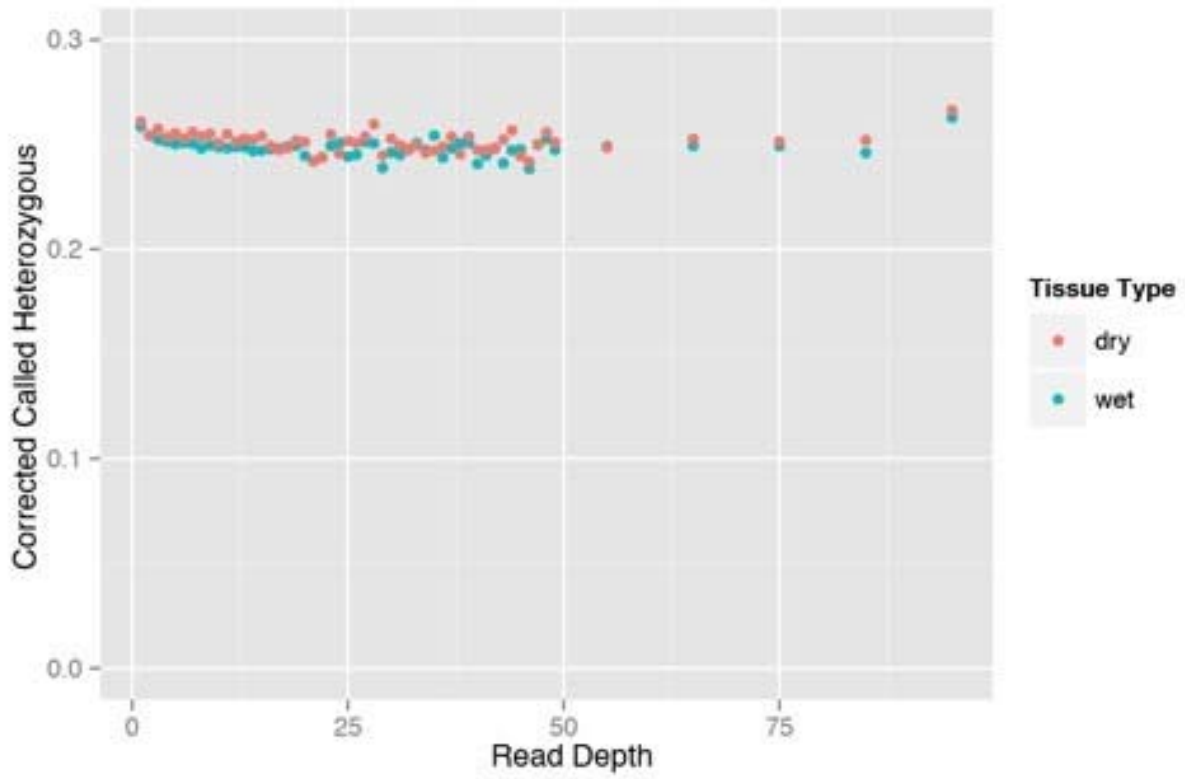
**Supplemental Table 6.** Excel sheet summarizes SCA at 15,658 SNPs when analysis was redone assuming external survey had 600 of 1000 plants survive.

**Supplemental Table 7.** Excel sheet summarizes SCA at 15,658 SNPs when analysis was redone assuming external survey had 800 of 1000 plants survive.

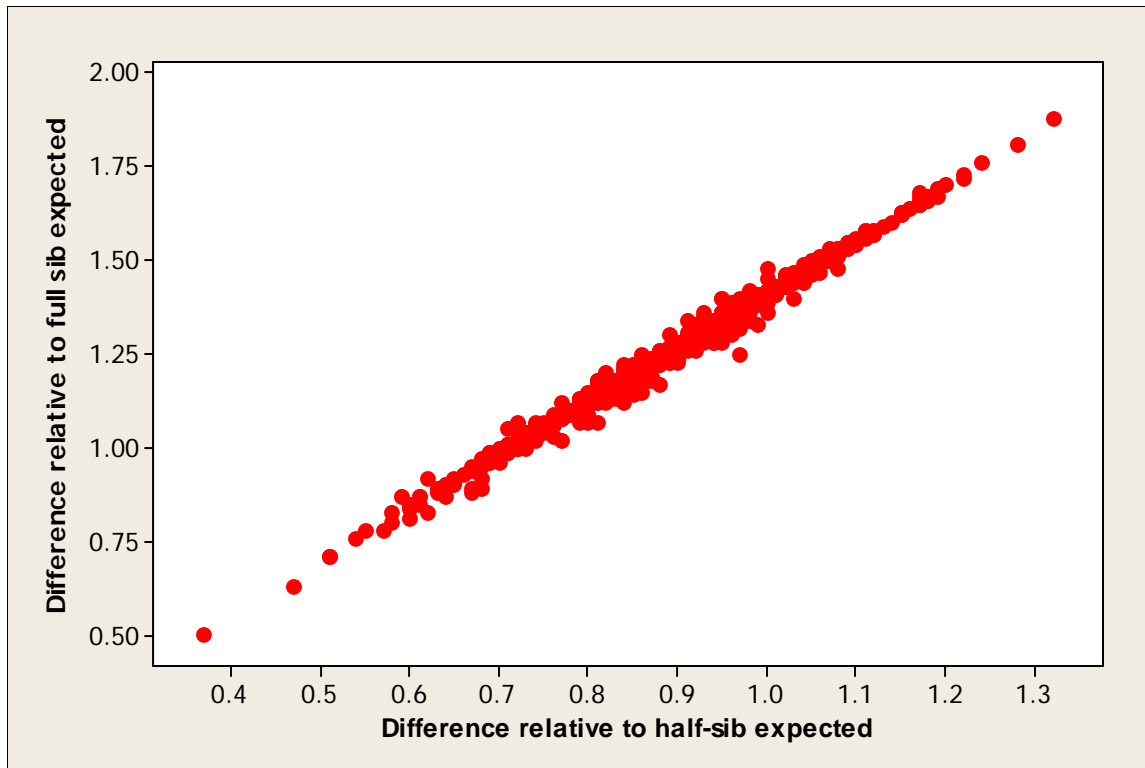


Supplemental Figures:

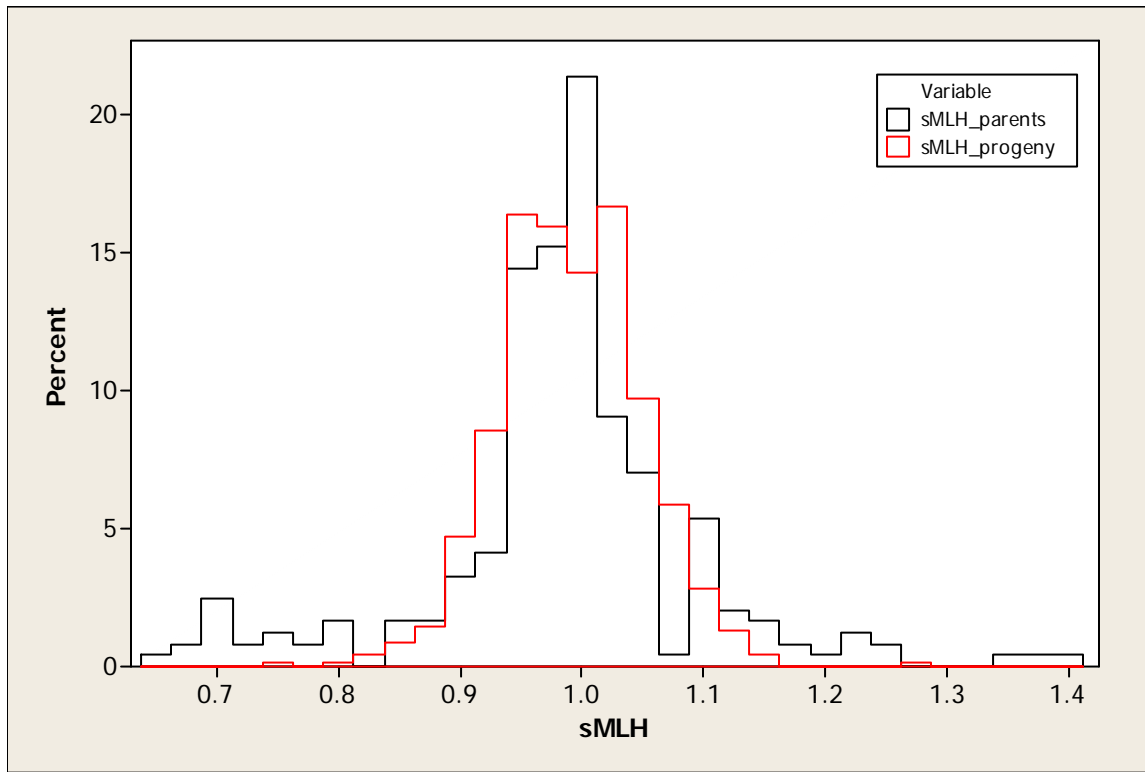
**Supplemental Figure 1.** The y-axis is the sum of posterior probabilities of heterozygotes (across individual and SNPs) divided by the number of calls (across individual and SNPs) at a given read depth.



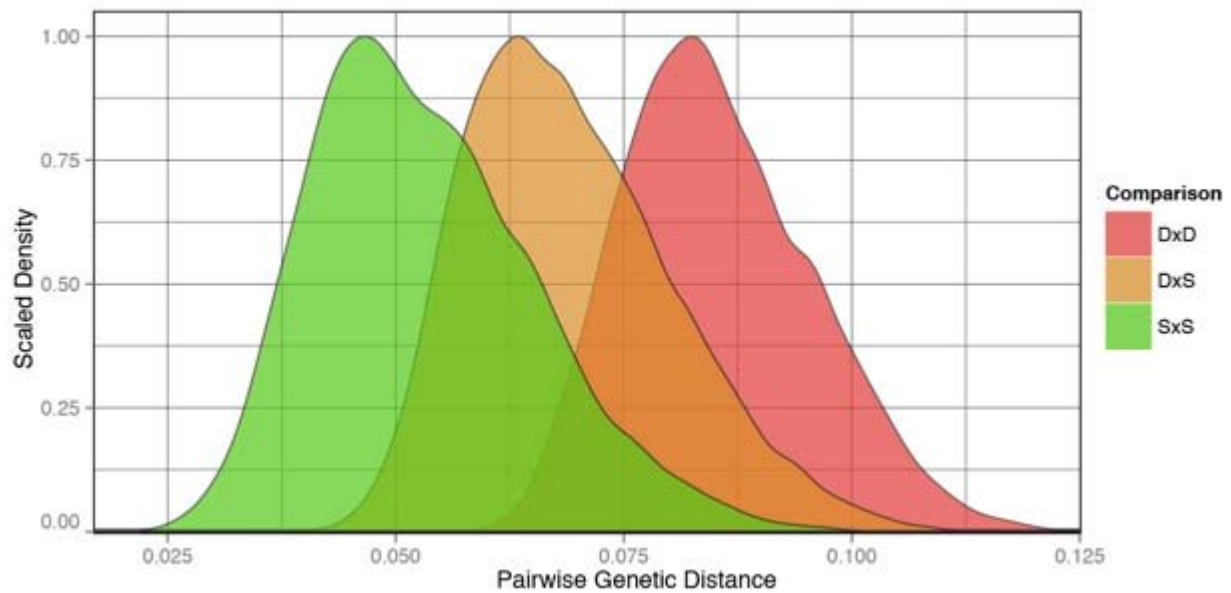
**Supplemental Figure 2. The relationship between two measures of inter-sibling distance**



**Supplemental Figure 3. The distributions of sMLH in parents and offspring (all plants with at least 1000 genotype calls).**



**Supplemental Figure 4. Density plots for three contrasts of pairwise genetic distance between parental plants: D versus D (red), D versus S (orange), and S versus S (green). Contrasts were limited to plant pairs with at least 500 common SNPs.**



Supplemental Figure 5. The predicted difference in allele frequency between successful male gametes and all surviving adults ( $\Delta q_{MS} = q_M - q_S$ ) as a function of initial frequency for significant (red) and non-significant (black) SNPs. Here, significance is according to the  $q_M / q_S$  test.

