Table S1   Trait-specific means and two standard errors for control genotypes from each of the two populations (Klamath and Marie) for each of the three phenotypic assays.

Klamath						
SM	Mean 1	2SE1	Mean 2	2SE2	Mean 3	2SE3
G	2.23	0.06	2.42	0.06	2.25	0.05
I	2.05	0.08	2.36	0.04	2.15	0.06
K	1.83	0.06	2.32	0.06	1.95	0.06
CL1	Mean 1	2SE1	Mean 2	2SE2	Mean 3	2SE3
G	3.79	1.58	6.53	1.16	4.16	0.88
I	2.92	1.42	3.47	1.06	1.73	0.8
K	3.5	1.26	6.61	1.52	0.73	0.54
CL2	Mean 1	2SE1	Mean 2	2SE2	Mean 3	2SE3
G	7.46	3.42	19	2.44	10.23	1.72
I	6.83	1.76	8.87	2.46	4.79	1.52
K	8.76	1.88	13.67	2.12	1.33	0.98
CL3	Mean 1	2SE1	Mean 2	2SE2	Mean 3	2SE3
G	13.27	4.84	20.3	2.74	10.43	1.86
I	8.33	2.68	8.07	2.54	5.51	1.98
K	10.61	3.24	18.11	2.78	2.79	1.22
CL4	Mean 1	2SE1	Mean 2	2SE2	Mean 3	2SE3
G	15.9	4.38	24	4.48	11.17	2.72
I	8.92	3.72	11.63	3.76	7.51	2.12
K	13.46	2.5	21.72	3.58	2.48	1.58
AM	Mean 1	2SE1	Mean 2	2SE2	Mean 3	2SE3
G	6.07	0.66	6.17	0.42	6.91	0.4
I	6.76	0.6	6.06	0.3	6.65	0.46
K	6.02	0.5	6.34	0.5	6.6	0.26

Marie						
SM	Mean 1	2SE1	Mean 2	2SE2	Mean 3	2SE3
B	1.71	0.104	1.8	0.056	1.83	0.084
K	1.89	0.076	1.93	0.056	1.9	0.108
CL1	Mean 1	2SE1	Mean 2	2SE2	Mean 3	2SE3
B	3.54	1.476	0.87	0.92	1.1	1.26

K	4.93	1.48	4.7	2.12	1.39	0.96

CL2	Mean 1	2SE1	Mean 2	2SE2	Mean 3	2SE3
B	4.46	2.424	1.95	1.8	3.5	3
K	11.71	4.76	11.23	4.24	4.96	3.2

CL3	Mean 1	2SE1	Mean 2	2SE2	Mean 3	2SE3
B	6.92	3.152	1.86	1.92	4.13	2.96
K	16.93	5.24	12.7	5.36	6.46	3.8

CL4	Mean 1	2SE1	Mean 2	2SE2	Mean 3	2SE3
B	7.15	3.84	1.84	1.48	7.33	4.48
K	16.21	6.8	11.31	5.6	6.53	3.88

AM	Mean 1	2SE1	Mean 2	2SE2	Mean 3	2SE3
B	6.66	1.572	6.35	0.56	6.91	0.576
K	6.13	0.96	6.46	0.76	6.92	1.16