Table S2: Average phenotype ± standard deviation for given genotypic class. The marker closest to the QTL of interest, as indicated by the position (pos) and Chromosome (Chr), was used for the anlysis.

Trait	Chr	Pos (cM)	Marker	AA	A-	A?	DD	D-	D?	H
Melanin	A	15.6	CNA03050	38.21 ± 6.66^{ab}	35.83 ± 7.19^{ab}	36.70 ± 7.27^{ab}	39.08 ± 4.03^{ab}	33.73 ± 5.55^{ab}	31.18 ± 10.14^{b}	36.16 ± 8.89^{a}
	B	15.0	CNB03520	36.56 ± 10.35^{ab}	31.27 ± 9.19^{b}	39.20 ± 5.91^{a}	30.55 ± 11.96^{ab}	32.72 ± 7.07^{ab}	33.03 ± 7.91^{b}	38.40 ± 7.14^{a}
	G	3.6	CNG01240	43.51^{ab}	39.82 ± 4.28^{a}	39.40 ± 5.69^{a}	26.39 ± 8.91^{ab}	33.45 ± 2.80^{ab}	30.88 ± 8.61^{b}	38.03 ± 6.40^{a}
	L	0.0	CNL03990	38.32 ± 5.56^{a}	34.22 ± 7.71^{a}	38.05 ± 5.25^{a}	32.84 ± 7.14^{a}	27.43^{a}	33.23 ± 7.39^{a}	35.03 ± 9.69^{a}
	L	9.4	CNL06810	4.98^{a}	32.14^{ab}	38.05 ± 5.25^{b}	34.38 ± 5.80^{b}	34.87 ± 7.64^{b}	33.23 ± 7.39^{b}	35.29 ± 9.10^{b}
Cell Size	A	35.7	CNA06130	6.63 ± 0.78^{ac}	6.22 ± 0.86^{ab}	6.10 ± 0.54^{ab}	6.42 ± 0.88^{ab}	5.77 ± 0.67^{b}	5.87 ± 0.76^{bc}	6.44 ± 0.81^{a}
	A	54.2	CNA07310	6.39 ± 0.87^{ab}	5.85 ± 0.58^{b}	6.10 ± 0.54^{ab}	6.37 ± 0.83^{ab}	6.10 ± 0.94^{ab}	5.87 ± 0.76^{b}	6.48 ± 0.80^{a}
	A	64.0	CNA07990	6.59 ± 1.00^{ab}	5.91 ± 0.68^{b}	6.10 ± 0.54^{ab}	5.85 ± 0.77^{b}	5.99 ± 0.87^{b}	5.87 ± 0.76^{b}	6.60 ± 0.72^{a}
	D	41.6	RUM1	5.56 ± 0.68^{ab}	5.96 ± 0.75^{b}	5.94 ± 0.67^{b}	6.52 ± 0.82^{ab}	5.85 ± 0.70^{b}	5.99 ± 0.67^{b}	6.57 ± 0.88^{a}
	F	1.2	CNF00290	6.52 ± 0.33^{ab}	6.25 ± 0.77^{ab}	6.08 ± 0.59^{ab}	6.08 ± 0.76^{ab}	5.94 ± 0.69^{b}	5.83 ± 0.78^{b}	6.56 ± 0.81^{a}
	I	2.6	CNI01350	5.91 ± 0.62^{ab}	5.42 ± 0.55^{b}	6.15 ± 0.69^{ab}	5.79 ± 1.28^{ab}	6.03 ± 0.39^{ab}	5.72 ± 0.62^{b}	6.32 ± 0.82^{a}
Cell Wall Thickness	A	14.6	CNA02700	0.05 ± 0.00^{abc}	0.05 ± 0.01^{b}	0.05 ± 0.01^{abc}	0.04 ± 0.01^{ab}	0.05 ± 0.01^{ac}	0.06 ± 0.01^{c}	0.05 ± 0.01^{ac}
Capsule	A	0.0	CNA00050	0.27 ± 0.28^{ab}	0.19 ± 0.21^{ab}	0.22 ± 0.22^{ab}	0.12 ± 0.19^{ab}	0.07 ± 0.14^{b}	0.09 ± 0.16^{b}	0.22 ± 0.22^{a}
	B	0.6	CNB00360	0.07 ± 0.09^{ab}	0.19 ± 0.23^{ab}	0.21 ± 0.23^{ab}	0.07 ± 0.17^{b}	0.09 ± 0.12^{b}	0.10 ± 0.16^{b}	0.28 ± 0.22^{a}
	D	41.9	CND06160	0.16 ± 0.14^{ab}	0.05 ± 0.08^{b}	0.16 ± 0.19^{b}	0.14 ± 0.13^{ab}	0.12 ± 0.19^{b}	0.10 ± 0.16^{b}	0.29 ± 0.23^{a}
	H	0.0	CNH00030	0.24 ± 0.21^{a}	0.20 ± 0.24^{abc}	0.20 ± 0.22^{ab}	0.05 ± 0.12^{bc}	0.07 ± 0.12^{abc}	0.06 ± 0.12^{c}	0.23 ± 0.22^{a}
	L	2.2	CNL04620	0.00^{ab}	0.08 ± 0.14^{ab}	0.14 ± 0.18^{ab}	0.01 ± 0.02^{ab}	0.04 ± 0.04^{ab}	0.08 ± 0.13^{b}	0.23 ± 0.22^{a}
MIC on agar	A	4.2	CNA00290	6.33 ± 1.15^{abc}	6.74 ± 0.67^{a}	6.31 ± 1.20^{ac}	5.11 ± 1.17^{cd}	4.93 ± 1.21^{bd}	4.40 ± 1.76^{bd}	6.62 ± 0.95^{a}
	E	7.8	CNE01630	5.75 ± 1.50^{ab}	6.31 ± 1.14^{ab}	6.12 ± 1.32^{ab}	6.07 ± 1.77^{ab}	5.00 ± 1.15^{ab}	5.13 ± 1.77^{b}	6.15 ± 1.27^{a}
	N	15.0	CNN02060	5.67 ± 1.41^{ab}	5.46 ± 1.66^{ab}	6.43 ± 1.10^{b}	5.50 ± 2.12^{ab}	5.40 ± 1.78^{ab}	5.89 ± 1.36^{ab}	5.35 ± 1.81^{a}
MIC in Broth	A	4.2	CNA00290	6.67 ± 0.58^{a}	4.61 ± 1.24^{a}	5.69 ± 1.14^{a}	3.00 ± 2.55^{abc}	2.56 ± 3.00^{b}	1.00 ± 2.34^{c}	4.63 ± 2.17^{a}
	A	59.8	CNA07470	4.45 ± 1.97^{ab}	4.00 ± 2.65^{a}	5.69 ± 1.14^{a}	3.70 ± 2.54^{ab}	2.04 ± 2.42^{bc}	1.00 ± 2.34^{c}	4.79 ± 2.23^{a}
	C	9.4	CNC06110	1.60 ± 1.95^{a}	1.80 ± 1.92^{a}	4.08 ± 2.44^{a}	3.33 ± 2.66^{a}	4.00 ± 4.12^{a}	2.73 ± 2.88^{a}	4.10 ± 2.65^{a}

Superscript letters refer to significant differences between groups based on Tukey's HSD at $p<0.05$