SUPPLEMENTARY MATERIALS

Table S1. DON levels for lines with resistance alleles present and absent with respect to four QTL, probability of Type I and Type II errors and the power of a test contrasting two sample means.

	1A_N		4A_N		1B_J		*Fhb1*	
	Present	**Absent**	**Present**	**Absent**	**Present**	**Absent**	**Present**	**Absent**
DON (ppm)	6.1	5.3	5.5	6.2	6.7	5.5	5.4	6.0
Alpha %	5		5		5		5	
Beta %	8.5		13		32.7		7.3	
Power %	91.5		87		67.3		92.7	

Table S2: Least Square (LS) means for sedimentation volume (cm^3) in order of highest to lowest by combination code, where combinations that had less than 5 lines were removed from analysis. QTL refers to the QTL that comprise each combination code. QTL followed by "(h)" means that this QTL is present in the heterozygous form. Count signifies the number of observations for each combination code.

LS Mean Sedimentation Volume (cm^3)	**Combination Code**	**QTL**	**Count**	**T- Test Grouping (0.05)**
7.7	21	4A_N (h), *Fhb1*	7	a
7.5	20	1A_N (h), *Fhb1*	8	b
7.1	28	*Fhb1*	5	c
6.9	9	1A_N (h), 4A_N (h), *Fhb1*	11	d
6.8	16	4A_N (h), 1B_J (h)	9	e
6.8	19	4A_N (h)	21	f
6.6	15	1A_N (h)	27	g
6.5	4	1A_N (h), 4A_N (h), 1B_J ((h)	6	h
6.4	7	1A_N (h), 3B_M (h), *Fhb1* (h)	9	i
6.3	8	1A_N (h), 4A_N (h)	26	j
6.3	5	1A_N (h), 4A_N (h), 1B_J (h), *Fhb1*	9	j
6.1	1	None	55	k
6.1	25	1B_J (h)	10	k
5.9	11	1A_N (h), 1B_J (h)	5	l

Note: 1A_N = 1A Neuse; 4A_N = 4A Neuse, 1B_J = 1B_Jamestown, 3B_M = 3B Massey.

Table S3: Least Square (LS) means and Standard Error (SE) for heritable flavor traits by combination of resistance genes.

	Nutty		Earthy		Intensity	
Combination	**LS Mean**	**SE**	**LS Mean**	**SE**	**LS Mean**	**SE**
1	1.8	0.1	1.3	0.1	2.4	0.1
2	1.7	0.2	0.3	0.2	2.5	0.2
3	2.2	0.2	2	0.2	2.9	0.2
5	1.8	0.2	1.2	0.2	2.2	0.2
7	2.2	0.1	1.6	0.1	2.6	0.1
8	1.9	0.1	1.2	0.1	2.2	0.1
9	2	0.1	1.5	0.1	2.4	0.1
11	1.7	0.2	1.4	0.2	2.4	0.2
12	2.3	0.1	1.6	0.1	2.6	0.1
15	2.2	0.1	1.4	0.1	2.5	0.1
16	2	0.2	1.2	0.2	2.4	0.2
18	2.2	0.2	1.3	0.2	2.8	0.2
19	2.1	0.1	1.4	0.1	2.5	0.1
20	2	0.1	1.6	0.1	2.8	0.1
21	2.1	0.2	1.5	0.1	2.7	0.2
25	1.8	0.3	1.2	0.2	2.4	0.3
29	2	0.1	1.5	0.1	2.3	0.1

Table S4: Least Square (LS) means and Standard Error (SE) for agronomic and quality traits by combination of resistance genes.

	Yield		Test Weight		DON		Protein		Sedimentation	
Combination	**LS Mean**	**SE**	**LS Mean**	**SE**	**LS Mean**	**SE**	**LS Mean**	**SE**	**LS Mean**	**SE**
1	3231.0	1.0	71.0	0.2	6.0	0.3	10.5	0.0	6.1	0.0
2	4080.6	4.9	68.0	1.1	5.6	1.5	10.5	0.1	7.3	0.0
3	3896.1	6.9	69.3	1.6	7.5	2.1	12.1	0.1	7.3	0.0
4	3312.7	2.8	72.4	0.7	9.6	0.9	10.8	0.0	6.5	0.0
5	3514.8	2.3	68.4	0.5	4.3	0.7	9.9	0.0	6.3	0.0
6	3550.0	4.0	67.8	0.9	4.5	1.2	9.2	0.0	6.0	0.0
7	3649.9	2.3	67.9	0.5	5.4	0.7	9.7	0.0	6.4	0.0
8	3407.4	1.3	71.9	0.3	5.7	0.4	10.5	0.0	6.3	0.0
9	3735.7	2.1	69.8	0.5	5.4	0.6	10.2	0.0	6.9	0.0
10	3403.3	6.9	71.8	1.6	2.0	2.1	11.2	0.1	6.8	0.0
11	3463.4	3.1	72.4	0.7	8.9	0.9	10.1	0.0	5.9	0.0
12	3594.2	3.4	67.3	0.8	6.7	1.1	9.1	0.0	6.4	0.0
13	3576.1	6.9	63.3	1.6	9.6	2.1	9.1	0.1	4.7	0.0
14	3368.2	4.9	70.5	1.1	5.6	1.5	10.5	0.1	6.4	0.0
15	3480.0	1.3	71.3	0.3	6.5	0.4	10.7	0.0	6.6	0.0
16	3243.0	0.3	72.2	0.5	6.3	0.7	10.9	0.0	6.8	0.0
17	4455.0	4.6	68.2	1.1	5.6	1.5	10.2	0.1	5.9	0.0
18	3376.3	4.9	68.6	1.1	5.0	1.5	9.7	0.1	6.8	0.0
19	3439.9	1.5	73.1	0.4	4.6	0.5	11.0	0.0	6.8	0.0
20	3597.7	2.4	67.9	0.6	5.6	0.7	10.6	0.0	7.5	0.0
21	3538.8	2.6	70.0	0.6	4.8	0.8	11.1	0.0	7.7	0.0
22	2963.3	6.9	73.1	1.6	7.4	2.1	11.2	0.1	6.7	0.0
23	3149.0	6.9	72.1	1.6	10.6	2.1	9.6	0.1	4.8	0.0
24	4195.7	6.9	76.6	1.6	4.6	2.1	10.8	0.1	6.3	0.0
25	3498.9	2.2	73.6	0.5	5.2	0.7	10.5	0.0	6.1	0.0
26	3856.9	6.9	67.4	1.6	4.8	2.1	9.0	0.1	4.7	0.0
27	3453.6	3.4	71.6	0.8	4.9	1.1	10.5	0.0	7.1	0.0
28	3423.0	3.1	68.2	0.7	6.2	0.9	10.3	0.0	7.1	0.0

Table S5: Gene state impacts on flavor traits by significant QTL (P<0.05).

	1A Neuse	1B Jamestown	*Fhb1*	
	Sweet	Sweet	Earthy	Flavor Intensity
Homozygous Positive	NA	NA	1.49a	2.65a
Heterozygous	1.83a	1.66b	1.62a	2.74a
Homozygous Negative	1.67b	1.84a	1.33b	2.38b

Table S6: LS Means for agronomic and quality traits by QTL combination code for yield, test weight, DON, sedimentation volume, and protein content. QTL followed by "(h)" means that this QTL is present in the heterozygous form.

Combination	**QTL**	**Yield (kg/ha)**	**Test Weight (kg/hl)**	**DON (ppm)**	**Sedimentation Volume (cm^3)**	**Protein Content (%)**
1	None	3201.1	71.1	6.0	6.1	10.5
2	1A_N (h), 4A_N (h), 1B_J (h), 3B_M (h), *Fhb1* (h)	4055.2	68.0	5.6	7.3	10.5
3	1A_N (h), 4A_N (h), 1B_J (h), *Fhb1* (h)	3873.6	69.4	7.5	7.3	12.1
4	1A_N (h), 4A_N (h), 1B_J (h)	3288.5	72.5	9.6	6.5	10.8
5	1A_N (h), 4A_N (h), 1B_J (h), *Fhb1*	3490.3	68.4	4.2	6.2	9.9
6	1A_N (h), 4A_N (h), 3B_M (h)	3523.9	67.9	4.5	6	9.2
7	1A_N (h), 3B_M (h), *Fhb1* (h)	3624.8	68.0	5.4	6.4	9.7
8	1A_N (h), 4A_N (h)	3376.0	72.0	5.7	6.3	10.5
9	1A_N (h), 4A_N (h), *Fhb1*	3692.0	69.8	5.4	6.9	10.2
10	1A_N (h), 1B_J (h), *Fhb1* (h)	3376.0	71.8	2.0	6.8	11.2
11	1A_N (h), 1B_J (h)	3436.5	72.4	8.9	5.9	10.1
12	1A_N (h), 3B_M (h)	3571.0	67.4	6.7	6.4	9.1
13	1A_N (h), 3B_M (h), *Fhb1*	3550.8	63.3	9.6	4.7	9.1
14	1A_N (h), *Fhb1* (h)	3342.3	70.5	5.6	6.4	10.5
15	1A_N (h)	3456.7	71.4	6.5	6.6	10.7
16	4A_N (h), 1B_J (h)	3221.3	72.3	6.3	6.8	10.9
17	4A_N (h), 3B_M (h)	4438.5	68.3	5.6	5.9	10.2
18	4A_N (h), *Fhb1* (h)	3349.1	68.6	5.0	6.8	9.7
19	4A_N (h)	3416.3	73.0	4.6	6.8	11.0
20	1A_N (h), *Fhb1*	3571.0	67.9	5.6	7.5	10.6
21	4A_N (h), *Fhb1*	3517.2	70.0	4.8	7.7	11.1
22	4A_N (h), 1B_J (h), *Fhb1* (h)	2938.8	73.1	7.4	6.7	11.2
23	4A_N (h), 1B_J (h), *Fhb1*	3127.1	72.1	10.6	4.8	9.6
24	1B_J (h), *Fhb1* (h)	4169.5	76.6	4.6	6.3	10.8
25	1B_J (h)	3476.8	73.6	5.2	6.1	10.5
26	1B_J (h), *Fhb1*	3833.3	67.5	4.8	4.7	9.0
27	*Fhb1* (h)	3430.1	71.6	4.9	7.0	10.5
28	*Fhb1*	3557.5	68.8	6.2	7.0	10.3

Table S7: KASP primers used to identify presence or absence of FHB resistance QTL.

QTL	Primer Name	Primer Sequence
1A Neuse	IWA1587_AL1	**GAAGGTGACCAAGTTCATGCT**CTATCTATATTCTTTGTTCTTCAAGTCCA
	IWA1587_AL2	**GAAGGTCGGAGTCAACGGATT**CTATCTATATTCTTTGTTCTTCAAGTCCG
	IWA1587_C1	GATTGTTGCAACTAGCAACAGCTGTTTAT
	IWA886_AL1	**GAAGGTGACCAAGTTCATGCT**GTAAGCTGCTAGGTCTTGTAGCC
	IWA886_AL2	**GAAGGTCGGAGTCAACGGATT**AAGTAAGCTGCTAGGTCTTGTAGCA
	IWA886_C1	TACGTGCACGGTCGATCAGTTTCTA
	IWA3805_AL1	**GAAGGTGACCAAGTTCATGCT**AACTTTGCTGTCAACTTTGAGGA
	IWA3805_AL2	**GAAGGTCGGAGTCAACGGATT**CTAACTTTGCTGTCAACTTTGAGGG
	IWA3805_C1	TTACTGCAACTGATGGGTGCACTTTATAT
4A Neuse	IWA2793_AL1	**GAAGGTGACCAAGTTCATGCT**CACAATTTCCCGCTCAGCG
	IWA2793_AL2	**GAAGGTCGGAGTCAACGGATT**CCTCACAATTTCCCGCTCAGCA
	IWA2793_C1	GATCTCACCGATCACCTCATGAAGAT
	IWA2900_AL1	**GAAGGTGACCAAGTTCATGCT**AGGAGGCCTGCATGCACGC
	IWA2900_AL2	**GAAGGTCGGAGTCAACGGATT**CAGGAGGCCTGCATGCACGT
	IWA2900_C1	CTTGCACAACCACACGCAGAGGAA
	IWA402_AL1	**GAAGGTGACCAAGTTCATGCT**ATATCAATTAAATGCTACATCATGAACATAGT
	IWA402_AL2	**GAAGGTCGGAGTCAACGGATT**ATCAATTAAATGCTACATCATGAACATAGC
	IWA402_C1	TTTAGGAATGGAAGGAGTATCATTCACCA
	IWA482_AL1	**GAAGGTGACCAAGTTCATGCT**GATCAATTGGTTCCTGTGATATCATTC
	IWA482_AL2	**GAAGGTCGGAGTCAACGGATT**ATGATCAATTGGTTCCTGTGATATCATTT
	IWA482_C1	TGGGACAACACATTCTTGGGCCATT
1B Jamestown	IWB43992_AL1	**GAAGGTGACCAAGTTCATGCT**CATTACTGTCGATATGGATCTTGTGC
	IWB43992_AL2	**GAAGGTCGGAGTCAACGGATT**ACATTACTGTCGATATGGATCTTGTGT
	IWB43992_C1	TGCTGCTTGAAAAGAAATGCAGGATACTT
	IWA6259_AL1	**GAAGGTGACCAAGTTCATGCT**AACAATAACAGCGCACCAGCACT
	IWA6259_AL2	**GAAGGTCGGAGTCAACGGATT**ACAATAACAGCGCACCAGCACC
	IWA6259_C1	GGTGGCAATAAATCTGTGTCATTCAGTAT
	IWA7594_AL1	**GAAGGTGACCAAGTTCATGCT**ACGGTGTTAGATATGTCACATACTCA
	IWA7594_AL2	**GAAGGTCGGAGTCAACGGATT**CGGTGTTAGATATGTCACATACTCC
	IWA7594_C1	GGCACTCTTGAAAGGAAGGGTGCA
3B Massey	Fhb3Bc_6105_AL1	**GAAGGTGACCAAGTTCATGCT**CGAGTTCTGACTTCTGGCTACC
	Fhb3Bc_6105_AL2	**GAAGGTCGGAGTCAACGGATT**ACGAGTTCTGACTTCTGGCTACT
	Fhb3Bc_6105_C1	GCACCTGTAGTAGCTTTTTAGAAGATGTA
	Fhb3Bc_8137_AL1	**GAAGGTGACCAAGTTCATGCT**CAGCACTTACCACAGCTTCTGGT
	Fhb3Bc_8137_AL2	**GAAGGTCGGAGTCAACGGATT**AGCACTTACCACAGCTTCTGGC
	Fhb3Bc_8137_C1	AGGACCAAGGAATCCTTGCAGGAAA
Fhb1	Snp3BS-8_AL1	**GAAGGTGACCAAGTTCATGCT**CACATGCATTTGCAAGGTTGTTATCC
	Snp3BS-8_AL2	**GAAGGTCGGAGTCAACGGATT**CACATGCATTTGCAAGGTTGTTATCG
	Snp3BS-8_C1	CAAAGCAGCCTTAGGTCAATAGTTTGAAA