SUPPLEMENTAL MATERIAL

Supplemental Tables:

Table S1. Trait summary for Northern Leaf Blight resistance in the maize nested association mapping (NAM) population and individual NAM families

Family	# of lines	Rating 1		Rating 2		Rating 3	
Founders	**27**	**7.8**	**(1.3; 27.6)**	**11.8**	**(1.7; 43)**	**20.1**	**(4.1; 59.4)**
B97 x B73	**189**	**14.9**	**(4.1; 41.8)**	**22.5**	**(7.1; 58)**	**35.3**	**(13; 79.6)**
CML103 x B73	**177**	**9.3**	**(1.8; 23.4)**	**14.3**	**(2.5; 35.9)**	**23.5**	**(8.6; 45.9)**
CML228 x B73	**161**	**7.5**	**(2; 20.1)**	**11.7**	**(2.9; 24.9)**	**22.6**	**(8.9; 46.4)**
CML247 x B73	**182**	**7.6**	**(1.5; 20)**	**11.8**	**(1.6; 33.8)**	**23.0**	**(5.7; 53.3)**
CML277 x B73	**151**	**5.6**	**(0.6; 13.9)**	**8.1**	**(1; 20.9)**	**15.7**	**(2.7; 36.5)**
CML322 x B73	**175**	**11.8**	**(2.4; 30.9)**	**17.7**	**(3; 43.7)**	**30.0**	**(9.4; 62.6)**
CML333 x B73	**183**	**14.5**	**(1.5; 34.6)**	**21.6**	**(2.9; 50.7)**	**32.4**	**(9.5; 63.1)**
CML52 x B73	**163**	**7.6**	**(0.7; 21.1)**	**11.1**	**(1.5; 33.3)**	**19.5**	**(4.4; 51.4)**
CML69 x B73	**186**	**6.7**	**(0.7; 26.9)**	**10.3**	**(1.2; 43.7)**	**18.3**	**(3.6; 59.8)**
Hp301 x B73	**182**	**20.1**	**(8.2; 46)**	**30.4**	**(13; 63.4)**	**45.3**	**(27.7; 76)**
Il14H x B73	**187**	**14.1**	**(4.1; 31.6)**	**21.5**	**(5; 49.3)**	**36.1**	**(10.3; 75.4)**
Ki11 x B73	**168**	**9.0**	**(0.3; 27.2)**	**13.5**	**(0.3; 39.9)**	**23.4**	**(2.6; 52.5)**
Ki3 x B73	**191**	**6.0**	**(0.8; 15.5)**	**8.8**	**(1.2; 21.7)**	**16.4**	**(4.2; 34.7)**
Ky21 x B73	**191**	**16.5**	**(5.2; 31.5)**	**24.4**	**(10.5; 40.5)**	**37.8**	**(17.2; 60.6)**
M162W x B73	**187**	**6.5**	**(1; 17.4)**	**9.6**	**(0.8; 28.9)**	**17.5**	**(2.5; 43.8)**
M37W x B73	**187**	**7.0**	**(1.6; 22.1)**	**10.5**	**(1.9; 36.3)**	**19.1**	**(6.1; 53.2)**
Mo17 x B73	**179**	**11.8**	**(1.5; 32.1)**	**17.8**	**(3.5; 43.3)**	**29.8**	**(10.2; 60)**
Mo18W x B73	**173**	**9.5**	**(0.6; 31.5)**	**14.8**	**(1.1; 45.7)**	**26.1**	**(6.3; 60.8)**
MS71 x B73	**191**	**15.7**	**(2.2; 50.2)**	**23.4**	**(5.1; 62.1)**	**35.0**	**(11.1; 79.2)**
NC350 x B73	**182**	**12.3**	**(1.5; 28.2)**	**18.6**	**(2.3; 40.6)**	**29.4**	**(5.6; 57.4)**
NC358 x B73	**182**	**7.8**	**(2.2; 21.6)**	**12.2**	**(2.8; 36)**	**22.8**	**(7.5; 54.7)**
Oh43 x B73	**180**	**13.6**	**(6.3; 26.6)**	**20.7**	**(9.5; 40.1)**	**32.4**	**(18.3; 57.6)**
Oh7B x B73	**176**	**22.5**	**(6.4; 53.4)**	**34.5**	**(8.4; 73.7)**	**48.9**	**(18.3; 79.3)**
P39 x B73	**174**	**16.1**	**(4.5; 37.4)**	**24.6**	**(8.9; 57.4)**	**39.0**	**(17.9; 73.4)**
Tx303 x B73	**188**	**12.6**	**(2.3; 24.5)**	**19.4**	**(4.1; 37.1)**	**32.4**	**(12.3; 52.8)**
Tzi8 x B73	**182**	**12.7**	**(1.4; 41.6)**	**18.9**	**(3; 52.1)**	**30.9**	**(7.1; 73.7)**
NAM	**4667**	**11.4**	**(0.3; 53.4)**	**17.2**	**(0.3; 73.7)**	**28.2**	**(2.5; 79.6)**

mean (min;max)

Table S2. Broad-sense heritability for resistance to Northern Leaf Blight in the maize nested association mapping (NAM) population and individual NAM families

Family	Rating 1	Rating 2	Rating 3	Index
NAM	0.75	0.82	0.81	0.87
B97	0.65	0.70	0.71	0.78
CML103	0.62	0.72	0.63	0.75
CML228	0.53	0.67	0.62	0.70
CML247	0.61	0.74	0.75	0.79
CML277	0.57	0.66	0.71	0.75
CML322	0.72	0.79	0.76	0.83
CML333	0.63	0.70	0.63	0.75
CML52	0.71	0.78	0.78	0.83
CML69	0.66	0.76	0.75	0.81
Hp301	0.63	0.70	0.55	0.74
Il14H	0.60	0.72	0.72	0.77
Ki11	0.74	0.81	0.78	0.85
Ki3	0.55	0.64	0.61	0.71
Ky21	0.46	0.41	0.48	0.58
M162W	0.54	0.71	0.72	0.76
M37W	0.54	0.68	0.66	0.74
Mo17	0.68	0.71	0.69	0.78
Mo18W	0.72	0.80	0.76	0.83
MS71	0.77	0.80	0.79	0.85
NC350	0.68	0.74	0.75	0.80
NC358	0.50	0.69	0.69	0.73
Oh43	0.46	0.56	0.55	0.65
Oh7B	0.69	0.78	0.65	0.79
P39	0.65	0.71	0.67	0.77
Tx303	0.64	0.71	0.64	0.76
Tzi8	0.74	0.75	0.76	0.83
Avg. within Family	0.63	0.71	0.68	0.77
Founders	0.80	0.87	0.88	0.90

Table S3. Joint Linkage Model for Northern Leaf Blight Resistance in the maize nested association mapping population

Model Effect	Df	Sum Sq	F value	Pr(>F)	Chr.	Marker Name	NAM Marker	Position (cM)	Lower CI	Upper CI	BAC		AGP Physical
factor(pop)	25	49.2	5.6463	< 2.2e-									
DaysToAnthesis	1	0.33	0.9567	3.28E-									
factor(pop):m25	26	27.91	3.0801	2.52E-	1	PZB00718.5	m25	33.9	20.1	37.8	AC211261.1	c0365I14	17595139
factor(pop):m69	26	25.41	2.8042	2.92E-	1	PZA00944.1/2	m69	84.9	77.9	87.9			
factor(pop):m87	26	38.06	4.2002	5.90E-	1	PZA03531.1	m87	99.3	97.7	100.3	AC183930.4	b0410I01	184088942
factor(pop):m107	26	24.46	2.6995	7.22E-	1	PZA02117.1	m107	131.6	127.8	133.9	AC210173.1	c0201I15	223466480
factor(pop):m118	26	28.56	3.152	1.32E-	1	PZA03301.2	m118	141.9	137.6	149.7	AC195814.2	c0245C01	240574247
factor(pop):m159	26	42.08	4.644	6.88E-	1	PZA00307.14	m159	191.5	190.5	191.7	AC185520.3	b0116L09	291983663
factor(pop):m178	26	30.34	3.3481	2.16E-	2	PZA00680.3	m178	212.4	0	1	AC190579.4	b0151L07	1081791
factor(pop):m189	26	22.54	2.487	4.31E-	2	PZA00172.12	m189	11.5	10.5	12.5	AC210003.1	c0468P22	4177515
factor(pop):m196	26	31.97	3.5275	4.02E-	2	PZB00901.3/4	m196	27.6	23.6	36.2			
factor(pop):m225	26	28.92	3.1915	9.17E-	2	PZA02450.1	m225	70.5	66.9	73.5	AC208083.1	b0498C16	47575949
factor(pop):m244	26	32.9	3.6302	1.52E-	2	PZA01537.2	m244	81.4	80.7	84	AC215308	c0276P12	150984061
factor(pop):m296	26	21.96	2.4232	7.26E-	2	PZA01352.5	m296	141.5	133.3	151.6	AC190841.2	b0457N09	226450170
factor(pop):m371	26	69.51	7.6703	< 2.2e-	3	PHM4621.57	m371	76.5	76	80.8			
factor(pop):m422	26	24.55	2.7091	6.65E-	3	PZA00219.7	m422	138.8	135.8	137.8			
factor(pop):m445	26	37.96	4.1889	6.60E-	4	PHM8527.2	m445	39.2	36.2	41.4	AC208695.1	b0318B02	17307041
factor(pop):m501	26	39.41	4.3493	1.34E-	4	PZA01976.9	m501	92.8	87.1	93.2	AC186143.3	c0337K02	179871677
factor(pop):m522	26	38.76	4.2768	2.76E-	4	PZA02479.1	m522	110.7	110.6	112.5	AC185302.4	c0422E05	218367682
factor(pop):m616	26	38.24	4.2194	4.88E-	5	PZA03049.24	m616	68.5	67.5	70	AC197061.1	b0395C18	88604977
factor(pop):m657	26	41.88	4.622	8.61E-	5	PHM532.23	m657	101.2	101.2	108	AC185506.4	c0190K23	193208321
factor(pop):m710	26	24.51	2.705	6.89E-	6	PZA02048.2	m710	41.6	41.5	41.5	AC208725.2	b0623J02	114891830
factor(pop):m728	26	26.25	2.8969	1.30E-	6	PZA02328.5	m728	52.5	48	57.5	AC204292.2	c0411A17	137254358
factor(pop):m740	26	45.39	5.0083	1.67E-	6	PZA02436.1	m740	61.4	59.5	62.8	AC213673.1	c0207M02	149251173
factor(pop):m791	26	25.07	2.7668	4.04E-	7	PZA01113.1	m791	50.2	49.5	63.2	AC186884.2	c0447O11	93101779
factor(pop):m812	26	66.92	7.3851	< 2.2e-	7	PZA02854.13	m812	76.3	74.3	78	AC204772.2	c0206P11	137834376
factor(pop):m909	26	46.26	5.1048	6.18E-	8	PZA00090.1	m909	69.8	69.8	72.6	AC191419.3	b0358B02	137480768
factor(pop):m914	26	81.95	9.0429	< 2.2e-	8	PHM4757.14	m914	76.1	78.2	82	AC199186.2	c0384O20	151452567
factor(pop):m951	26	22.45	2.4772	4.67E-	9	PZA00466.1	m951	18.7	13.6	24.8	AC207658.1	c0384C20	11972467
factor(pop):m1052	26	25.36	2.7987	3.07E-	10	PZA00409.17	m1052	36.3	27.5	41.1	AC199346.3	c0325G20	62062819
factor(pop):m1087	26	25.59	2.8235	2.47E-	10	PHM18513.156	m1087	61.3	52.2	64.8			
Residuals	3621	1270.77											

Supplemental Figures:

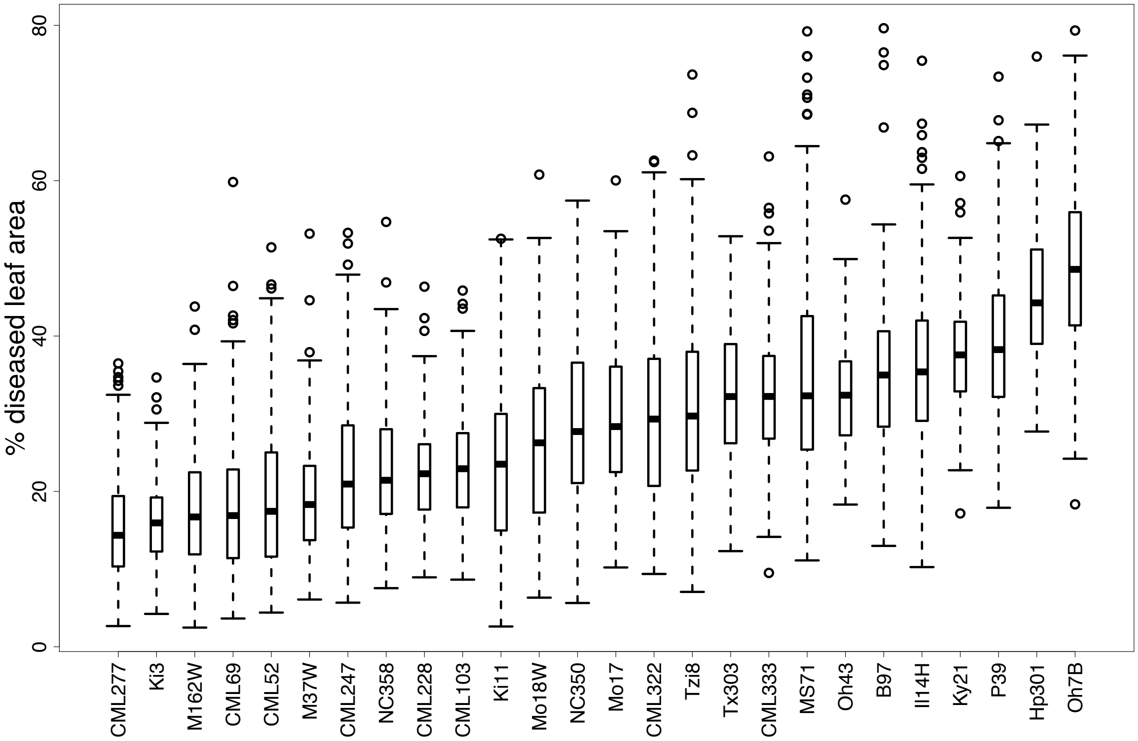

Fig. S1. Box-plot of trait variation of NLB resistance for individual families of NAM. The scale is percentage of total diseased leaf area at the third disease rating. For each family, the family median is shown as a bold line, the 25% and 75% percentiles with the box, and outliers with individual circles. Square-root transformation of the phenotype produced normal distributions for the families and were used for analysis (see text).

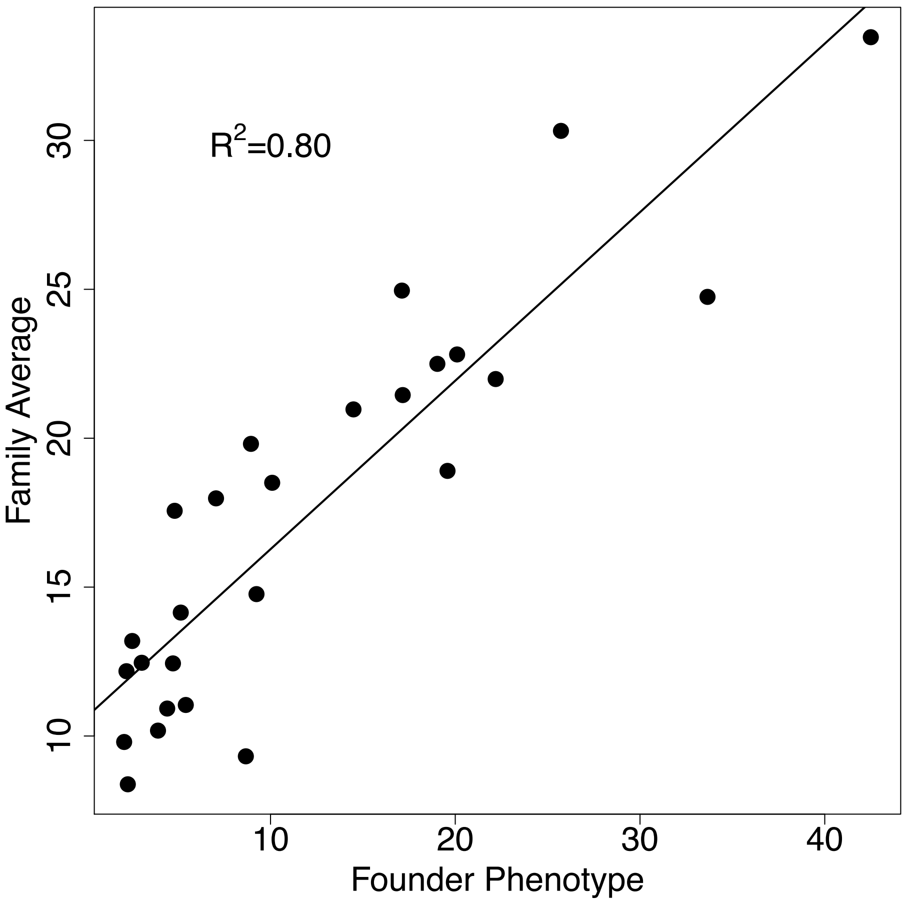

Fig. S2. Comparison of NAM founder phenotypes and mean phenotype of progeny. For each NAM founder the observed phenotype was compared to the average observed phenotype for its respective family. Regression of the family means on the founder phenotype explained 80% of the variance.

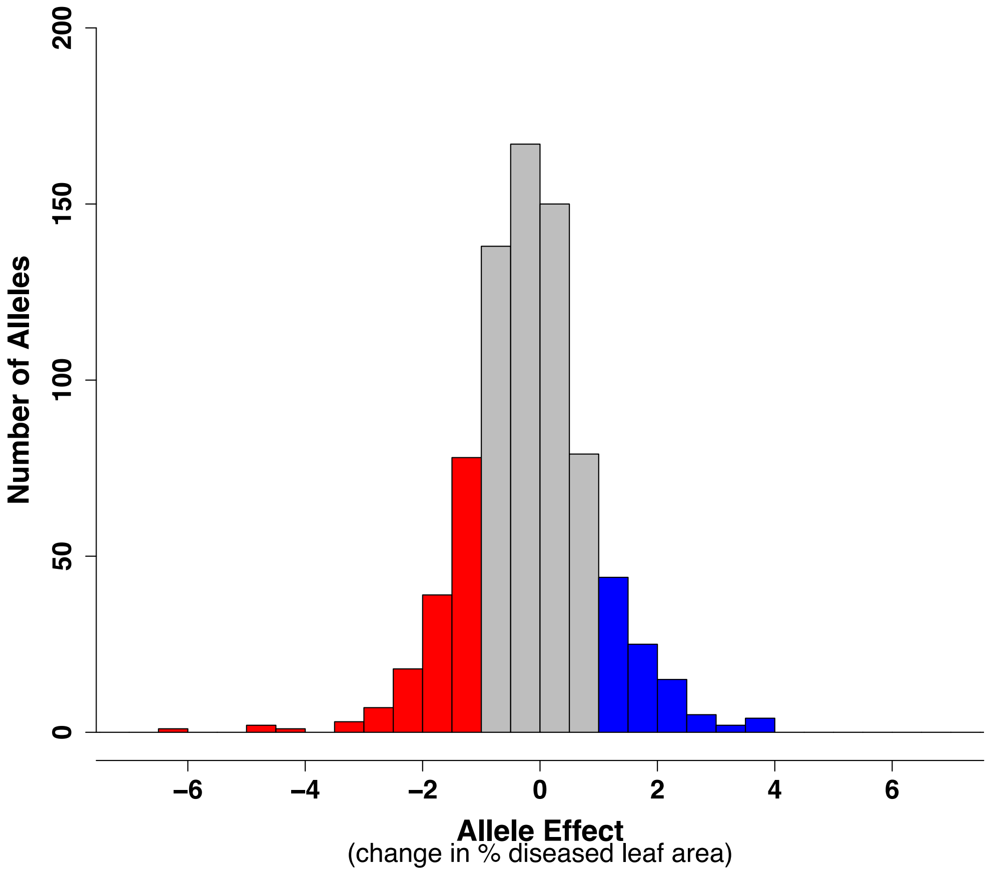

Fig. S3. Histogram of allele effects for all modeled alleles at QTL. The nested model give an estimated allele effect for each founder line at each QTL resulting in #QTL x #Founder estimates. The nesting of marker effects allows for pooling data among families to increase power in testing for QTL effects and estimating the total percentage of explained genetic variation accounted by the multiple SNP model of the NAM pop as a whole. Most of these allele effects are estimated to be close to zero and non-significant (grey). The significant positive and negative allele effects are shown in blue and red. Most observed effects were less than a 5% difference in diseased leaf area.

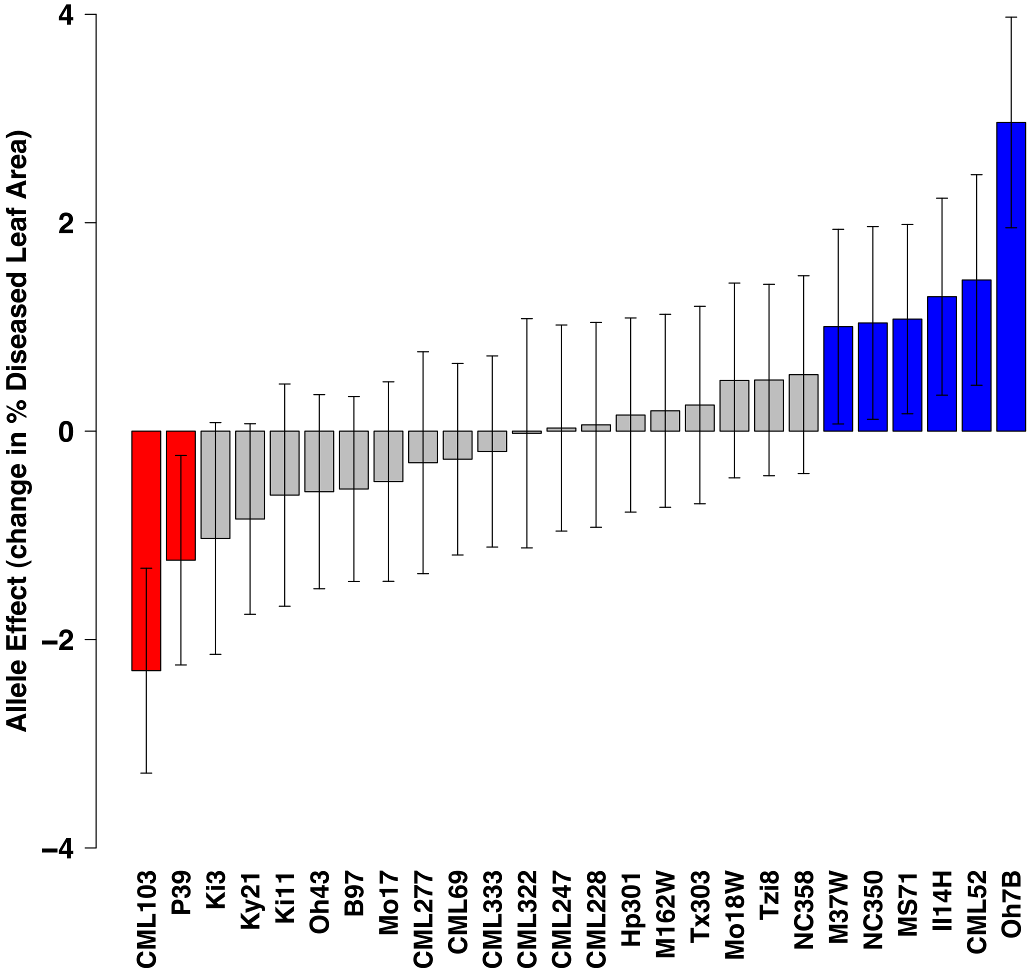

Fig. S4. It was observed that many of the QTL (21 of 29) had allele effects that were estimated both above and below the B73 allele (the zero reference point). Shown here are the estimated allele effects for a single QTL (m616, Chr.5 at 69.5 cM, 88.6 Mb) showing both positive and negative alleles relative to B73. Confidence intervals (95%) are shown in brackets. We can conclude that there are at least three alleles at this locus by comparing to B73, and possibly more considering differences within both the positive and the negative allele groups.

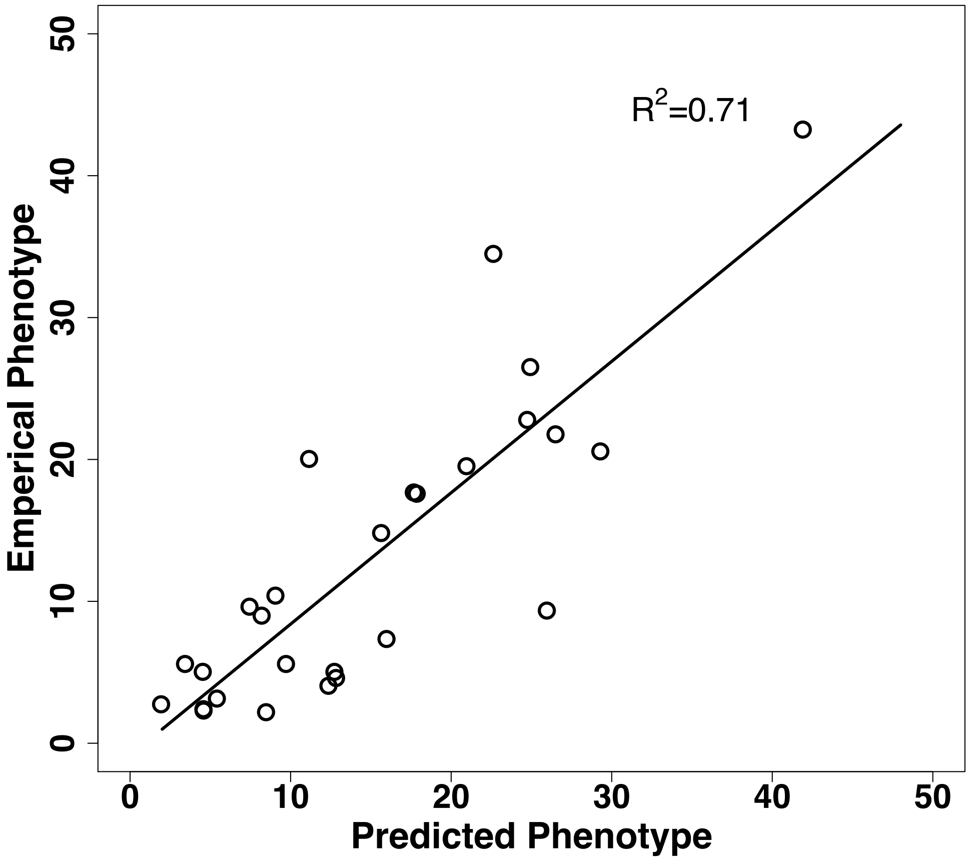

Fig. S5. Additive genetic model for NLB resistance gives accurate prediction of the observed phenotypes for the nested association mapping (NAM) population founders. Linear fit of predicted phenotypic values for each of the diverse founder inbred lines of NAM against the empirical phenotypic observations. Predicted phenotypes were determined by summing the allele effect for each respective founder line at all of the QTL identified while the empirical phenotypes are best linear unbiased predictions from three years of replicated field trials. Units are shown in percentage diseased leaf area.

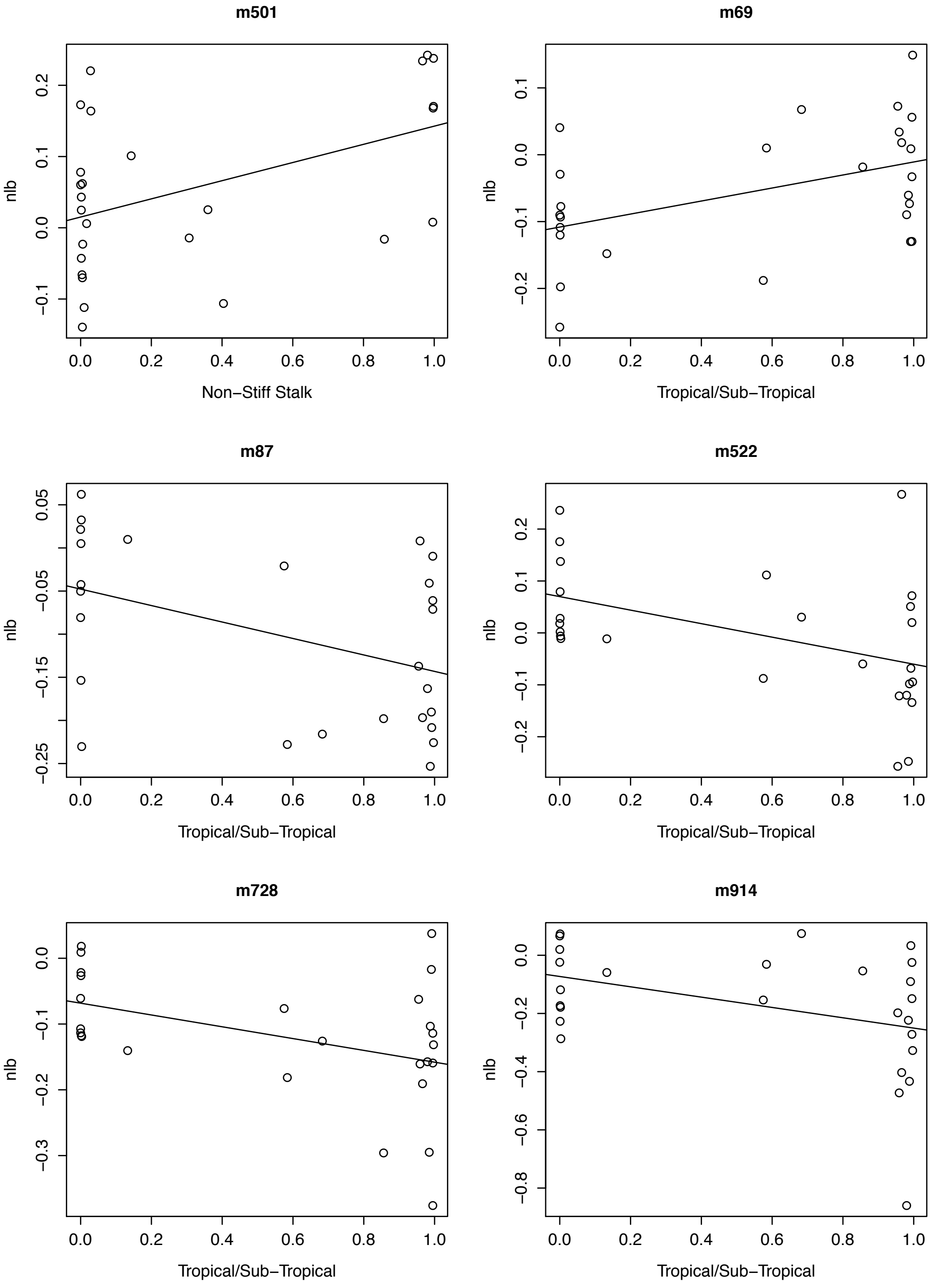

Fig. S6. Test for allele origins showing QTL markers that had significant association with quantitative estimates of allele origins. The horizontal axis in each graph shows the origin of a given founder for either non-stiff stalk (first graph) or Tropical/Sub-tropical (remaining five graphs). The estimated allele effect is plotted on the vertical axis. The linear regression line is also shown.