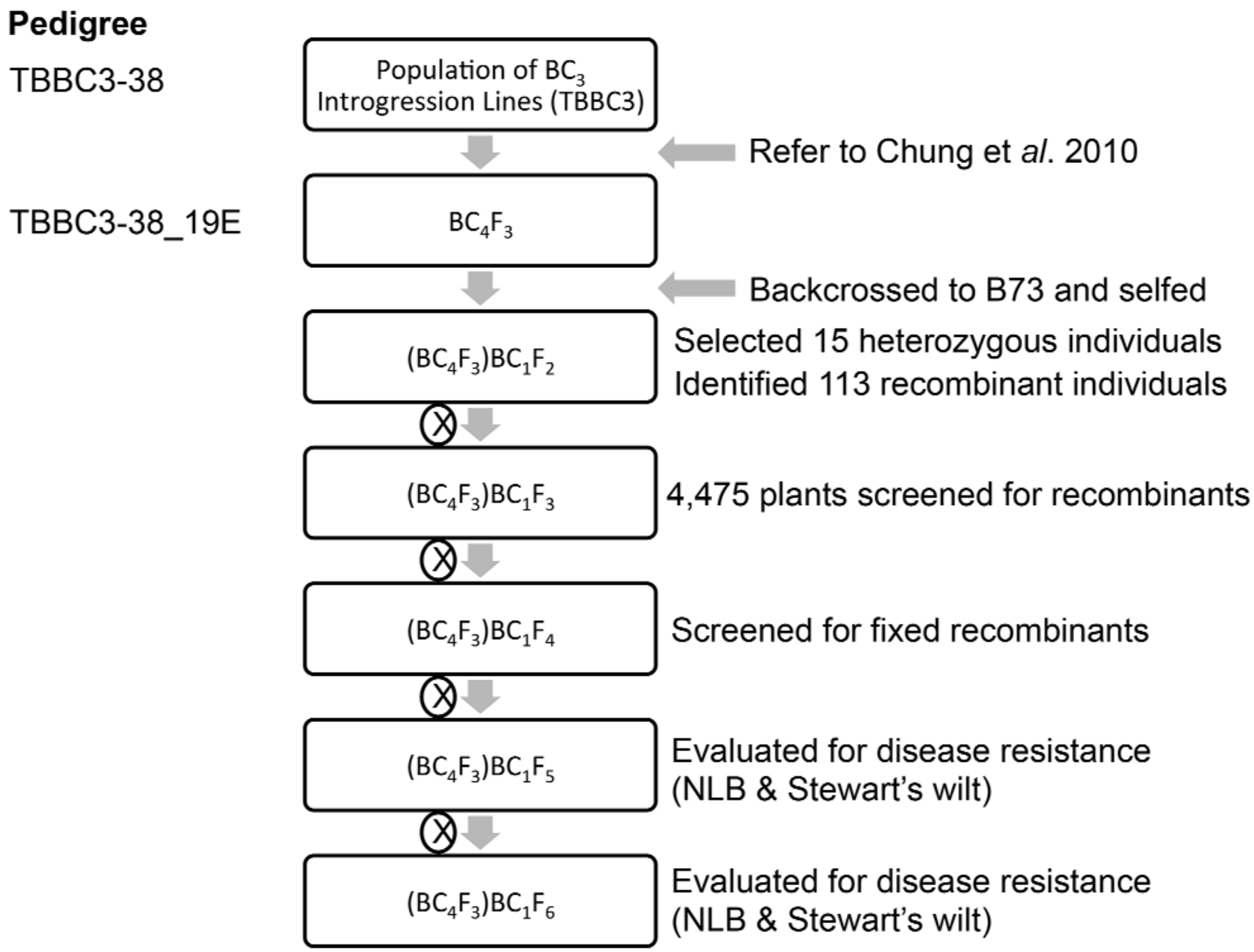

Figure S1 Near-isogenic line development. Near-isogenic line development is shown beginning with population development by Szalma et *al*. (2007) and Chung et *al*. (2010), through homozygous recombinant screening.

File S1

Genotypic and phenotypic data for fine-mapping study

Available for download as an Excel file at http://www.genetics.org/lookup/suppl/doi:10.1534/genetics.114.167486/-/DC1

Table S1 Markers

Marker ID	Locus name	Physical position*	Forward primer 1	Forward primer 2	Common reverse primer
snp_01_0042	ch1_AC202158_78820	180,394,890	GAAGGTGACCAAGTTCATGCTGCCGATACCAATCACTGACA	GAAGGTCGGAGTCAACGGATTCTGCCGATACCAATCACTGACG	GCCCCGGTCGGTACACAGTTA
snp_01_0057	chr1|183107525|C/T	184,016,638	GAAGGTGACCAAGTTCATGCTCCCTCACCAGCGACCACC	GAAGGTCGGAGTCAACGGATTCTTCCCTCACCAGCGACCACT	GGCAGGCAAGGTCACAGAGGAA
snp_01_0015	PZA00068.1	183,986,082	GAAGGTGACCAAGTTCATGCTGACAGGGAACCGGATTCTATAG	GAAGGTCGGAGTCAACGGATTGTGACAGGGAACCGGATTCTATAA	GTTAATCTTCACCTGGTGCATCGTGTA
snp_01_0059	chr1|184516928|G/A	184,633,349	GAAGGTGACCAAGTTCATGCTCCAGGGCCTGCTAACGCTGTT	GAAGGTCGGAGTCAACGGATTCAGGGCCTGCTAACGCTGTC	CGTACATGTGCCGCGCGTTTATATA
snp_01_0047	chr1|185582569|A/C	185,737,089	GAAGGTGACCAAGTTCATGCTGAATTGCTATTATTATATAACTCAACCCGT	GAAGGTCGGAGTCAACGGATTAATTGCTATTATTATATAACTCAACCCGG	TCGGCCATCTCGGCAACCTCAA
snp_01_0136	ss229502009	187,090,230	GAAGGTGACCAAGTTCATGCTGCAATAACCATTGAACCAACGAC	GAAGGTCGGAGTCAACGGATTCTGCAATAACCATTGAACCAACGAG	GTCCAGCTATAGGATAGGAAGAGCAT
snp_01_0137	ss229502244	187,245,104	GAAGGTGACCAAGTTCATGCTGCGTCATTTTCTCGTCAGGGC	GAAGGTCGGAGTCAACGGATTCTGCGTCATTTTCTCGTCAGGGA	ACTCCATTATTCATGCTTGATGGACCTA
snp_01_0138	ss229502327	187,272,680	GAAGGTGACCAAGTTCATGCTACTGCTAGCAGCTACTGCAGG	GAAGGTCGGAGTCAACGGATTCTACTGCTAGCAGCTACTGCAGA	CCAACCTTTACCTAAACATGTTTGCTGTT
snp_01_0139	ss229502401	187,341,010	GAAGGTGACCAAGTTCATGCTGCGCCTCTCCTCCACGGC	GAAGGTCGGAGTCAACGGATTGCGCCTCTCCTCCACGGT	ACGGTGCCCGGCGCGTGAA
snp_01_0115	ss229502466	187,399,046	GAAGGTGACCAAGTTCATGCTCGTAACGGCAAGCTTCTCTGTGT	GAAGGTCGGAGTCAACGGATTGTAACGGCAAGCTTCTCTGTGC	TCTCTGGCGTAGGGTCCTCTCT

snp_01_0116	ss229502486	187,400,044	GAAGGTGACCAAGTTCATGCTTCCGCTGCCGCTGCGGA	GAAGGTCGGAGTCAACGGATTCCGCTGCCGCTGCGGG	GCAGTCGTGGCGGTCCGAGTA
snp_01_0117	ss229502506	187,401,161	GAAGGTGACCAAGTTCATGCTGGACAGCGAACCCGGGGA	GAAGGTCGGAGTCAACGGATTGGACAGCGAACCCGGGGG	CCTTGGTCGCGTCTGGCTGCT
snp_01_0118	ss229502527	187,436,581	GAAGGTGACCAAGTTCATGCTTTGTTAAGCAAGCACACAGAAGCG	GAAGGTCGGAGTCAACGGATTTGTTAAGCAAGCACACAGAAGCA	CAGCTGCTCGTCGTCTGTTGTTAAT
snp_01_0079	ss196501884	187,588,467	GAAGGTGACCAAGTTCATGCTACCGGAACATCGTCAAGATGGAA	GAAGGTCGGAGTCAACGGATTCCGGAACATCGTCAAGATGGAG	CGGAGAGGATCACGCCGAAGTT
snp_01_0082	ss229504554	189,336,643	GAAGGTGACCAAGTTCATGCTCCTTGCGCTCTCAGGTTTTTGCA	GAAGGTCGGAGTCAACGGATTCTTGCGCTCTCAGGTTTTTGCG	TCATTCAGGTGGGCCCAGGCT
snp_01_0083	ss196429231	189,352,206	GAAGGTGACCAAGTTCATGCTCAGCCCCCTCTGTCCGTT	GAAGGTCGGAGTCAACGGATTCAGCCCCCTCTGTCCGTC	CCTTCAAGCTCGAGCTGGGACT
snp_01_0085	ss196516288	190,594,339	GAAGGTGACCAAGTTCATGCTGTTTAAGAATTGGATATCATTGATCGAC	GAAGGTCGGAGTCAACGGATTCTGTTTAAGAATTGGATATCATTGATCGAT	GGCGTTGCTGATATCGCGTTCAATT
snp_01_0061	chr1|193313487|C/T	193,478,836	GAAGGTGACCAAGTTCATGCTGGTTCGTCCATTGCCGGAATC	GAAGGTCGGAGTCAACGGATTCGGTTCGTCCATTGCCGGAATT	CGAACTCAACAGAGGAATTCTTACCTT
snp_01_0005	PZA00619.3	195,557,990	GAAGGTGACCAAGTTCATGCTGAAGCACTCAACGCCGCCAGA	GAAGGTCGGAGTCAACGGATTAGCACTCAACGCCGCCAGG	GMCATGCATATATATATGGCTGCCTCAT
snp_01_0088	ss229511302	196,306,976	GAAGGTGACCAAGTTCATGCTGATGTCCATGAATTTTCCAGTTCCAA	GAAGGTCGGAGTCAACGGATTGATGTCCATGAATTTTCCAGTTCCAT	AGCTCAGTACACTAGTAAAAATTAGGGTAA

*Physical positions are AGP_V2.

Table S2 NLB QTL mapping studies.

Reference	Parents	Resistance source	Population	QTL mapping	Trait	Flanking markers		Lower CI*	Upper CI*
Balint-Kurti *et al.* 2010	B73 x Mo17	B73	RIL	Composite interval mapping	AUDPC (AU06WMD)	bnlg1598	umc1396	187.8	191.1
Freymark *et al.* 1993	B52 x Mo17	B52	$F_{2:3}$	Interval mapping	Average Number of lesions/leaf	umc157	umc67	12.2	175.6
					Average percentage leaf tissue diseased	umc157	umc67	12.2	175.6
Welz *et al.* 1999	D32 x D145	D32	F_3	Composite interval mapping	% diseased leaf area	csu61b	dup12 (dupssr12)	181.0	239.6
Wisser *et al.* 2008	-	-	Recurrent selection	Selection mapping	-	bnlg615		201.0	
Chung *et al.* 2010	B73 x Tx303	Tx303	NILs	-	IP, AUDPC	umc1754	umc2234	180.0	187.4
Chung *et al*. 2011	B73 x CML52	CML52	HIFs	-	IP, lesion number, diseased leaf area, AUDPC			182.6	189.8
	B73 x CML52	CML52	RIL	ICIM	3 diseased leaf area ratings			200.4	205.8
Zwonitzer *et al.* 2010	Ki14 × B73	Ki14	RIL	Multiple interval mapping	sAUDPC	PZA01041.2	bnlg1057	157.1	190.0
Poland *et al.* 2011	NAM	B97 CML103 CML247 CML52 CML69	NAM	Joint linkage mapping	AUDPC	PZA02191.1	PZA00619.3	182.5	195.6

Ki11
Ki3
M37W
Mo17
Mo18W
NC358
Tzi8

Previous QTL studies that identified QTL for NLB resistance at maize bin 1.06 are listed. Confidence interval (CI) locations are based on AGP_V2.

Table S3 Candidate genes

Gene ID	Start (AGP_V2)	Stop (AGP_V2)	Interpro Description
GRMZM2G119511	185735951	185738575	Pyridoxal phosphate-dependent transferase
GRMZM2G419430	185737836	185738414	Calcium-binding EF-hand
GRMZM2G419431	185739064	185740761	
GRMZM2G419436	185739619	185740699	Serine/threonine-protein kinase, active site
GRMZM2G119547	185741603	185742128	Actin cross-linking
GRMZM2G124428	185777384	185779013	Wall-associated receptor kinase galacturonan-binding domain
AC190935.2_FG001	186007538	186008047	
GRMZM2G116254	186214773	186215342	Calcium-binding EF-hand
GRMZM2G552586	186230672	186232165	Aldehyde/histidinol dehydrogenase
GRMZM2G116236	186236715	186237201	
GRMZM2G417360	186237596	186238072	HAT dimerisation
AC186416.3_FG001	186340690	186342603	
GRMZM2G037493	186468876	186472999	SANT/Myb domain
GRMZM2G037581	186533673	186537407	WD40 repeat
GRMZM2G502940	186538248	186538450	
AC215187.3_FG003	186593280	186593915	
AC205695.3_FG008	186615110	186616941	
GRMZM2G362303	186633675	186639255	Protein kinase, catalytic domain
GRMZM2G308597	186640159	186640742	Calcium-binding EF-hand
GRMZM2G449226	186652945	186655618	
GRMZM2G391281	186674312	186675233	
GRMZM2G391288	186675613	186678029	S-receptor-like serine/threonine-protein kinase
GRMZM5G811972	186678239	186678787	
AC208564.3_FG004	186736360	186737646	Transcription factor, K-box
GRMZM2G061739	186964841	186965674	
AC211887.3_FG001	186964865	186965437	
GRMZM5G832154	186972934	186973635	
GRMZM5G800323	186973040	186973858	
GRMZM2G061791	186995763	186999056	
GRMZM2G359559	187002125	187004115	Aminotransferase, class V/Cysteine desulfurase
AC211887.3_FG004	187003702	187004115	Calcium-binding EF-hand
GRMZM2G059012	187055101	187062082	Wall-associated receptor kinase galacturonan-binding domain
AC211887.3_FG006	187063931	187064597	

GRMZM2G359434	187065602	187069942	Pentatricopeptide repeat
AC211887.3_FG007	187065698	187066120	Calcium-binding EF-hand
GRMZM2G059129	187091607	187095345	Glycerophosphoryl diester phosphodiesterase
GRMZM2G085210	187118709	187121135	Proton-dependent oligopeptide transporter family
GRMZM2G119381	187179081	187180794	
GRMZM2G419267	187190806	187194254	Glycosyltransferase AER61, uncharacterised
GRMZM2G445684	187269130	187271929	Zinc finger, C2H2
GRMZM2G445676	187271948	187272122	
AC213857.4_FG001	187338417	187341110	
GRMZM2G083755	187341766	187344871	Frataxin/CyaY
GRMZM2G083803	187344872	187345544	
AC213857.4_FG003	187344907	187345239	EF-Hand 1, calcium-binding site
GRMZM2G552850	187353437	187354156	
AC212463.3_FG001	187368059	187379099	
GRMZM5G834455	187379121	187379438	
GRMZM2G142507	187380518	187384704	
GRMZM2G441888	187383447	187384622	Photosystem II PsbP, oxygen evolving complex
GRMZM2G142597	187387273	187397432	RNA recognition motif domain
GRMZM2G441903	187398921	187400738	Zinc finger, AN1-type
GRMZM2G142638	187403377	187407974	Poly(A) polymerase, central domain
AC212463.3_FG009	187435427	187436221	
GRMZM2G020478	187441277	187443050	Serine/threonine- / dual specificity protein kinase, catalytic domain
GRMZM2G132763	187587612	187591058	Leucine-rich repeat
GRMZM2G132748	187626539	187627195	NADH:ubiquinone oxidoreductase, ESSS subunit
GRMZM2G132704	187635249	187640520	Dilute
GRMZM2G132623	187641040	187642585	Ribosomal protein L31e
GRMZM2G435224	187641060	187642612	
GRMZM2G132607	187643004	187646940	Carbohydrate kinase PfkB
GRMZM2G563405	187649672	187650116	
GRMZM2G141320	187667515	187670309	Diacylglycerol glucosyltransferase, N-terminal
GRMZM2G040129	187753619	187755711	DNA-directed DNA polymerase, family B, mitochondria/virus
GRMZM2G580853	187842642	187843102	
GRMZM2G163771	187843888	187844570	
GRMZM2G163783	187845063	187845576	
GRMZM2G121302	187877315	187877869	Cyclophilin-like peptidyl-prolyl cis-trans isomerase domain
GRMZM5G873791	187877340	187877853	

GRMZM2G121312	187883668	187885516	Leucine-rich repeat-containing N-terminal, type 2
GRMZM2G121398	187889142	187892150	
GRMZM5G839014	187975033	187977356	Ovarian tumour, otubain
GRMZM5G836190 (*pan1*)	187978007	187980515	Leucine-rich repeat-containing N-terminal, type 2
GRMZM5G854901	188014689	188017810	tRNA/rRNA methyltransferase, SpoU
GRMZM5G879527	188031610	188034600	Myc-type, basic helix-loop-helix (bHLH) domain
GRMZM2G703846	188036995	188037538	
GRMZM5G861100	188059257	188062957	
AC234203.1_FG009	188060402	188062129	rRNA-processing protein EFG1
AC234203.1_FG010	188063594	188066385	
AC234203.1_FG011	188071750	188073648	Ethylene insensitive 3-like protein, DNA-binding domain
AC234203.1_FG004	188083185	188089513	ABC transporter, transmembrane domain
AC234203.1_FG005	188092362	188092850	
GRMZM5G822593	188114875	188119970	Lipoxygenase, LH2
GRMZM2G161004	188169374	188172490	G-patch domain
GRMZM2G160917	188181863	188185970	Transcription factor, SBP-box
GRMZM2G159263	188256572	188256759	
GRMZM2G413230	188333139	188333371	
GRMZM2G115436	188342737	188344114	
GRMZM2G115442	188344346	188355656	Short-chain dehydrogenase/reductase SDR
GRMZM2G115462	188386434	188386882	Ribonuclease T2-like
GRMZM2G022499	188457694	188461344	SANT/Myb domain
GRMZM2G403669	188600179	188600736	
GRMZM2G403667	188601086	188602301	
GRMZM2G403664	188601935	188602807	
GRMZM2G007681	188719663	188811722	RNA polymerase, N-terminal
GRMZM2G325543	188733228	188736419	Zinc finger, BED-type predicted
GRMZM2G430455	188855847	188859402	KOW
GRMZM2G130659	188880026	188886014	Nonaspanin (TM9SF)
GRMZM2G430522	188906106	188908967	No apical meristem (NAM) protein
GRMZM2G467263	188927396	188928192	
GRMZM2G168669	188928450	188929193	
GRMZM2G342437	188983389	188985663	
GRMZM2G042622	188986180	188988366	Serine-threonine/tyrosine-protein kinase catalytic domain
GRMZM5G847243	189045340	189045985	
GRMZM2G357919	189077793	189078897	Protein kinase, catalytic domain
GRMZM2G055992	189081768	189085843	Leucine-rich repeat

GRMZM2G056056	189088108	189090646	
GRMZM2G056122	189091152	189093163	Pentatricopeptide repeat
GRMZM2G088627	189145769	189150346	Peptidase M20
GRMZM2G009009	189188469	189190473	
GRMZM2G009117	189191520	189193031	Heavy metal-associated domain, HMA
AC186691.4_FG009	189196177	189197677	
GRMZM2G009154	189200093	189201905	Glycosyl-phosphatidyl inositol-anchored, plant
GRMZM2G308873	189200780	189201223	
GRMZM2G158182	189276877	189277368	
GRMZM2G458441	189278497	189283529	Peptidase C54
AC186691.4_FG003	189334539	189334808	