Figure 1: Representation of the upstream regulatory region of *tb1*, showing the *tb1* coding region (green) and the *Hopscotch* insertion (red). Arrows show the location of primer sets; in black, primers used for amplification and sequencing (Sequenced region 1; within the 5' UTR, and sequenced region 2; 66,169 bp upstream from the tb1 ORF); in blue, primers used to genotype the *Hopscotch* insertion.

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Table 2: Accessions of *Zea mays* ssp. *mexicana* (RIMME) and *Zea mays* ssp. *parviglumis* (RIMPA) sampled. RIHY is a *Z. mays* ssp. *parviglumis* and *Zea mays* ssp. *mays* hybrid.

Accession	USDA ID	Locality	Alleles Sampled	*Hopscotch* Frequency	No *Hopscotc*
RIHY0009	N/A	N/A	2	0.5	0.5
RIMME0006	566673	Durango	2	0	1
RIMME0007	566680	Guanajuato	2	0	1
RIMME0008	566681	Michoacan	2	0	1
RIMME0009	566682	Distrito Federal	2	0	1

Table 2: Accessions of *Zea mays* ssp. *mexicana* (RIMME) and *Zea mays* ssp. *parviglumis* (RIMPA) sampled. RIHY is a *Z. mays* ssp. *parviglumis* and *Zea mays* ssp. *mays* hybrid.

Accession	USDA ID	Locality	Alleles Sampled	*Hopscotch* Frequency	No *Hopscotc*
RIMME0011	566685	Mexico	2	0	1
RIMME0014	714151	Breeders line; Puga: 11066	6	0	1
RIMME0017	699874	Ayotlan	8	0	1
RIMME0021	N/A	El Porvenir	69	0.17	0.83
RIMME0026	N/A	Opopeo	42	0.07	0.93
RIMME0028	N/A	Puruandiro	28	0.04	0.96
RIMME0029	N/A	Ixtlan	35	0	1
RIMME0030	N/A	San Pedro	27	0	1
RIMME0031	N/A	Tenango del Aire	25	0.08	0.92
RIMME0032	N/A	Nabogame	24	0	1
RIMME0033	N/A	Puerta Encantada	25	0	1
RIMME0034	N/A	Santa Clara	23	0	1
RIMME0035	N/A	Xochimilco	25	0	1
RIMPA0001	87168	El Salado	4	0	1
RIMPA0003	87171	Mazatlan	8	0.13	0.87
RIMPA0017	87200	N/A	4	0	1
RIMPA0019	87213	El Salado	2	0.50	0.50
RIMPA0029	87244	N/A	2	0.50	0.50
RIMPA0031	87249	N/A	2	0.5	0.5
RIMPA0035	87288	Jalisco	4	0	1
RIMPA0040	288185	Mexico	4	0	1
RIMPA0042	288187	Guerrero	4	0.25	0.75
RIMPA0043	288188	Guerrero	4	0	1
RIMPA0045	288193	Guerrero	4	0	1
RIMPA0055	714152	Breeders line	2	0	1
RIMPA0056	714153	Breeders line	2	0.50	0.50
RIMPA0057	714154	Breeders line	2	0.50	0.50
RIMPA0058	N/A	N/A	4	0.50	0.50
RIMPA0059	N/A	N/A	4	1	0
RIMPA0060	714157	Breeders line: CIMMYT 11355	2	0	1
RIMPA0061	714158	Breeders line: USDA PI566686	4	0.5	0.5
RIMPA0062	714159	Breeders line	4	0.5	0.5
RIMPA0063	714160	Breeders line	4	0	1
RIMPA0064	714161	Breeders line	3	0	1
RIMPA0065	714162	Breeders line	4	0.25	0.75
RIMPA0068	699861	Jalisco, Mexico	16	0	1
RIMPA0069	699862	Ixtlan	14	0.14	0.86
RIMPA0070	699863	Benito Jaurez	16	0	1
RIMPA0071	699864	Tuzantla	28	0	1
RIMPA0072	699865	Tiquicheo	16	0	1
RIMPA0073	699866	Tiquicheo	16	0.12	0.88
RIMPA0074	699867	Huetamo	12	0	1
RIMPA0075	699868	Huetamo	2	0	1
RIMPA0076	699869	Huetamo	4	0	1
RIMPA0077	699870	Caracuaro	2	0	1
RIMPA0078	699871	Caracuaro	2	0.5	0.5

Table 2: Accessions of *Zea mays* ssp. *mexicana* (RIMME) and *Zea mays* ssp. *parviglumis* (RIMPA) sampled. RIHY is a *Z. mays* ssp. *parviglumis* and *Zea mays* ssp. *mays* hybrid.

Accession	USDA ID	Locality	Alleles Sampled	*Hopscotch* Frequency	No *Hopscotc*
RIMPA0079	699872	Villa Madero	14	0	1
RIMPA0080	699873	Guachinango	12	0	1
RIMPA0081	699875	Ameca	16	0	1
RIMPA0083	699877	Tepoztlan	14	0	1
RIMPA0084	699878	Tepoztlan	16	0	1
RIMPA0085	699879	Miahuatlan	16	0	1
RIMPA0086	699880	Miahuatlan	16	0.06	0.94
RIMPA0087	699881	Tecoanapa	24	0	1
RIMPA0089	699883	Guerrero	12	0	1
RIMPA0090	699884	Guerrero	10	0	1
RIMPA0091	699885	Guerrero	16	0	1
RIMPA0092	699886	Guerrero	10	0	1
RIMPA0093	699887	Guerrero	26	0.08	0.92
RIMPA0094	699888	Guerrero	2	0	1
RIMPA0095	699889	Guerrero	4	0	1
RIMPA0096	699890	Guerrero	26	0.04	0.96
RIMPA0097	699891	Guerrero	6	0	1
RIMPA0098	699892	Guerrero	4	0	1
RIMPA0099	699893	Guerrero	4	0	1
RIMPA0100	699894	Guerrero	6	0	1
RIMPA0101	699895	Guerrero	2	0	1
RIMPA0103	699897	Guerrero	2	0	1
RIMPA0104	699898	Guerrero	22	0.09	0.91
RIMPA0105	699899	Guerrero	6	0	1
RIMPA0106	699900	Guerrero	6	0.33	0.67
RIMPA0107	699901	Guerrero	4	0	1
RIMPA0108	699902	Guerrero	6	0	1
RIMPA0109	699903	Michoacan	4	0.25	0.75
RIMPA0110	699904	Michoacan	2	0	1
RIMPA0111	699905	Michoacan	4	0	1
RIMPA0112	699906	Michoacan	4	0.25	0.75
RIMPA0114	699908	Michoacan	6	0.17	0.83
RIMPA0116	699910	Mexico	2	0	1
RIMPA0117	699911	Mexico	4	0	1
RIMPA0118	699912	Mexico	6	0.17	0.83
RIMPA0119	699913	Mexico	2	0	1
RIMPA0120	699914	Mexico	1	1	0
RIMPA0121	699915	Mexico	2	0	1
RIMPA0128	699922	Mexico	2	0.5	0.5
RIMPA0129	699923	Michoacan	2	0.5	0.5
RIMPA0135	699929	Nayarit	24	0	1
RIMPA0138	699932	Jalisco	2	0.5	0.5
RIMPA0139	699933	Jalisco	1	1	0
RIMPA0142	699936	Colima	18	0.44	0.56
RIMPA0144	699938	Jalisco	2	1	0
RIMPA0145	699939	Michoacan	1	1	0

Table 2: Accessions of *Zea mays* ssp. *mexicana* (RIMME) and *Zea mays* ssp. *parviglumis* (RIMPA) sampled. RIHY is a *Z. mays* ssp. *parviglumis* and *Zea mays* ssp. *mays* hybrid.

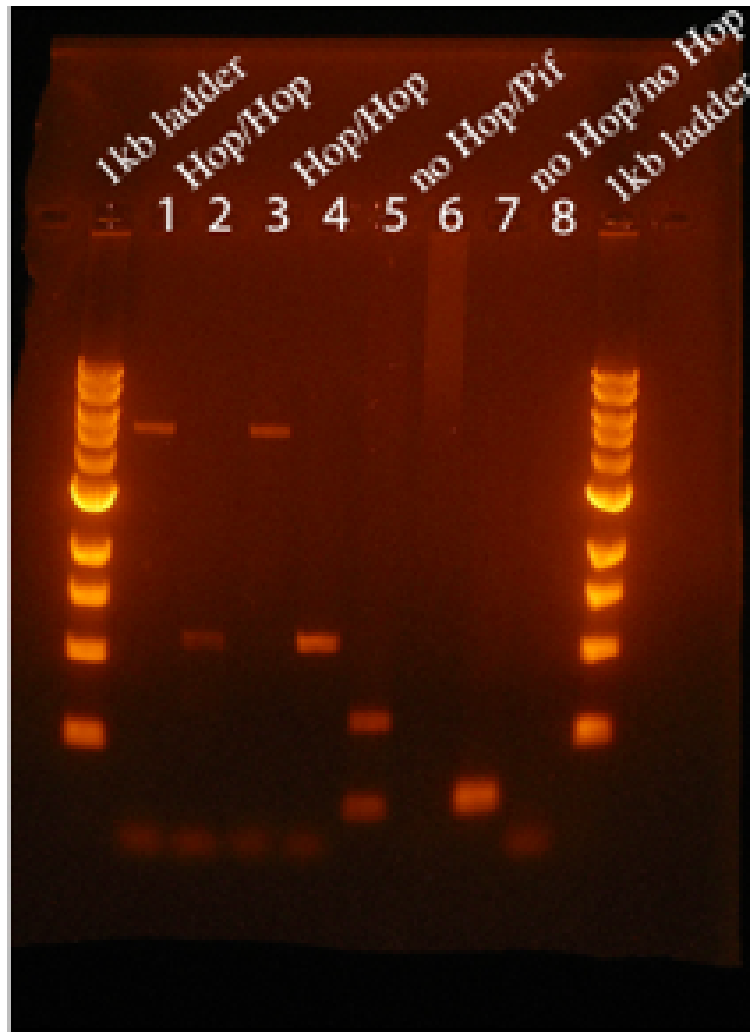| Accession	USDA ID	Locality	Alleles Sampled	*Hopscotch* Frequency	No *Hopscotc*
RIMPA0147	699941	Jalisco	1	1	0
RIMPA0155	N/A	Jalisco	73	0.01	0.99
RIMPA0156	N/A	Jalisco	20	0	1
RIMPA0157	N/A	Jalisco	58	0.34	0.66
RIMPA0158	N/A	Jalisco	64	0.53	0.47
RIMPA0159	N/A	Jalisco	26	0	1
RIMPA0162	21785	N/A	4	0	1

Figure 2: Agarose gel image of amplification products using our primer sets. Genotypes are indicated at the top of the gel.

Figure 3: Neighbor-Joining tree of the sequenced region in the 5? UTR (right; sequenced region 1) and the 66,169 bp upstream region (left; sequenced region 2) of *tb1*. Individuals with genotype data are colored: Homozygous for the teosinte (no *Hopscotch*) allele (red), homozygous for the maize (*Hopscotch*) allele (blue), heterozygotes (purple). TILs (teosinte inbred lines) are colored in green, with stars indicating the 3 TILs known to have the *Hopscotch* insertion. Black indicates individuals not genotyped for the *Hopscotch* insertion.

Table 1: Pairwise F_{ST} values from sequence and *Hopscotch* genotyping data

Comparison	Region 1	Region 2	*Hopscotch*
EjuA & EjuB	0	0	0
EjuA & MSA	0.326	0.328	0.186
EjuA & SLO	0.416	0.258	0.280
EjuB & MSA	0.397	0.365	0.188
EjuB & SLO	0.512	0.290	0.280
MSA & SLO	0.007	0	0.016

Table 3: *Zea mays* ssp. *mays* (RIMMA) sampled for genotyping

Accession	Number of alleles sampled	*Hopscotch* Frequency
RIMMA0066	2	1
RIMMA0075	2	1
RIMMA0077	2	1
RIMMA0079	2	1
RIMMA0081	2	1
RIMMA0084	2	1
RIMMA0086	2	1
RIMMA0088	2	1
RIMMA0089	2	1
RIMMA0090	2	1
RIMMA0092	4	1
RIMMA0094	4	1
RIMMA0097	2	1
RIMMA0099	2	1
RIMMA0100	2	1
RIMMA0101	2	1
RIMMA0104	2	1
RIMMA0108	2	1
RIMMA0111	6	1
RIMMA0115	2	1
RIMMA0117	2	1
RIMMA0130	2	1
RIMMA0133	2	1
RIMMA0134	2	1
RIMMA0135	2	1
RIMMA0142	2	0.5
RIMMA0143	4	1
RIMMA0146	4	1
RIMMA0149	2	1
RIMMA0152	2	1
RIMMA0153	2	1
RIMMA0154	2	1
RIMMA0155	2	1
RIMMA0156	2	1
RIMMA0157	2	1
RIMMA0158	2	1
RIMMA0159	2	1
RIMMA0160	2	1
RIMMA0162	2	1
RIMMA0166	2	1
RIMMA0167	2	1
RIMMA0168	2	1
RIMMA0169	2	1
RIMMA0172	2	1
RIMMA0174	4	1
RIMMA0177	2	1
RIMMA0178	2	1
RIMMA0179	2	1
RIMMA0181	2	1

Table 4: Variables and rotations used for the 6 principal components used for BayEnv calculations and their corresponding Bayes Factors. Modified from **?**.

PC1		PC2		PC3		PC4		PC5		PC
Var	**Rot**	**Var**	**Rot**	**Var**	**Rot**	**Var**	**Rot**	**Var**	**Rot**	**Va**
bio1	0.146	bio4	0.244	prec7	0.287	ts_clay	0.41	bio2	0.38	bio
tmean11	0.146	bio3	0.241	prec8	0.276	v_mod	0.359	sq4	0.328	x_mo
tmean12	0.145	bio7	0.241	prec11	0.262	ts_sand	0.329	ts_loam	0.289	sc
bio11	0.145	prec6	0.237	bio13	0.247	bio15	0.272	ts_sand	0.266	bio
tmax12	0.145	sq7	0.218	prec1	0.246	prec4	0.259	sq7	0.231	v_mo
tmin5	0.145	prec9	0.217	bio16	0.242	x_mod	0.244	bio18	0.213	prec1
tmean1	0.145	sq3	0.207	prec12	0.24	prec3	0.226	bio13	0.207	bio1
tmean2	0.145	prec12	0.207	bio19	0.238	sq3	0.21	prec11	0.183	sc
tmin4	0.145	bio12	0.204	bio12	0.231	prec5	0.21	bio7	0.17	sc
tmax1	0.145	bio19	0.196	prec2	0.222	prec7	0.19	bio16	0.163	ts_san
tmean4	0.145	prec2	0.188	bio18	0.221	sq4	0.186	bio4	0.157	bio
tmin11	0.144	prec1	0.185	sq4	0.2	bio3	0.185	bio12	0.156	prec
tmax11	0.144	prec10	0.184	prec9	0.18	bio18	0.178	bio3	0.155	tmax
tmin12	0.144	bio16	0.183	prec10	0.171	sq7	0.132	prec6	0.154	tmax
tmin2	0.144	prec8	0.17	prec5	0.161	bio14	0.116	x_mod	0.152	bio
tmean5	0.144	prec5	0.165	prec4	0.154	bio13	0.099	prec9	0.144	tmax
tmean10	0.144	bio14	0.158	sq3	0.147	bio16	0.095	prec8	0.143	bio
bio6	0.144	bio13	0.151	bio2	0.143	prec8	0.09	v_mod	0.142	ts_loa
tmax2	0.144	bio17	0.149	bio17	0.129	bio7	0.077	bio15	0.136	ts_cla
tmean3	0.144	prec3	0.144	ts_loam	0.127	bio4	0.075	prec7	0.112	tmin
tmin1	0.143	ts_clay	0.141	v_mod	0.123	bio2	0.074	prec4	0.108	tmin
tmin10	0.143	bio2	0.129	prec3	0.113	prec2	0.074	bio14	0.096	prec
Altitude	0.143	prec7	0.108	x_mod	0.111	bio19	0.068	tmax7	0.093	tmin1
bio9	0.143	tmax6	0.107	bio14	0.099	prec12	0.056	tmax8	0.092	tmin1
tmin3	0.143	x_mod	0.106	bio4	0.07	ts_loam	0.053	prec1	0.091	tmin
bio10	0.142	bio15	0.098	tmax3	0.067	tmax12	0.047	prec2	0.086	tmean
tmax10	0.142	ts_loam	0.088	ts_clay	0.065	bio17	0.047	tmin11	0.086	tmax
tmax3	0.142	tmean6	0.085	bio15	0.056	bio9	0.043	prec5	0.082	tmax
tmax4	0.142	tmin7	0.082	tmax2	0.055	tmax8	0.042	bio17	0.082	tmean
tmin6	0.142	bio5	0.082	tmean3	0.052	tmax1	0.041	tmin12	0.08	bio
tmean9	0.141	tmean7	0.081	ts_sand	0.05	tmax5	0.039	prec3	0.078	tmin1
tmin9	0.141	prec4	0.08	prec6	0.048	tmax7	0.039	tmax9	0.078	prec
tmean8	0.141	tmax7	0.079	sq7	0.048	prec10	0.038	tmin1	0.077	tmean
bio8	0.14	bio8	0.079	tmin7	0.046	Altitude	0.037	tmin10	0.074	bio1
tmean6	0.14	tmax9	0.077	bio3	0.044	tmax10	0.035	bio6	0.071	bio1
tmean7	0.14	tmean8	0.076	tmax4	0.043	tmax2	0.033	prec12	0.067	tmin
tmin8	0.14	tmin8	0.076	bio7	0.042	tmax9	0.03	tmin2	0.061	prec1
tmax5	0.14	tmax5	0.074 9	tmax1	0.036	tmean12	0.029	tmin6	0.061	bio
tmax9	0.139	tmax8	0.074	tmin3	0.035	tmax11	0.027	tmax6	0.059	tmean1
tmax8	0.139	tmean9	0.072	bio9	0.035	tmean1	0.027	tmin3	0.052	prec
bio5	0.139	bio18	0.07	tmin8	0.034	bio5	0.026	bio8	0.046	Altitud
tmax7	0.139	v_mod	0.066	tmean4	0.031	tmean5	0.026	tmean11	0.041	bio
tmin7	0.138	tmin9	0.066	tmean2	0.031	bio11	0.025	tmean1	0.04	tmin
tmax6	0.135	bio10	0.065	tmax12	0.03	tmean2	0.022	tmin9	0.04	tmean1
bio17	0.107	tmax10	0.063	tmean7	0.028	tmin6	0.022	tmean12	0.04	tmean
bio14	0.095	tmin6	0.061	tmin9	0.023	prec1	0.022	tmax10	0.038	prec

Table 5: Diversity in the *tb1* region based on the maize SNP50 genotyping data

Population	# Seg Sites	$\hat{\theta}_\pi$) / bp	$\hat{\theta}_W$ / bp	Tajima's D
Ejutla A	4	0.15217	0.11902	0.76191
Ejutla B	5	0.15258	0.14877	0.07412
La Mesa	3	0.12802	0.08926	1.09209
San Lorenzo	3	0.09098	0.08926	0.04845