

OAX68	111	ACAGGACACGAGT	GAAGGCTGTAAGGGTGAGGAGACTG	GACTGAGGCCTGGCCCGACGCCCGTCGGCGGCGAACGCCCTCCCTTGAGTGGCGCTAACAGGGCGC
URG_II	111	ACAGGACACGAGT	GAAGGCTGTAAGGGTGAGGAGACTG	GCGAACGCCCTCCCTTGAGTGGCGCTAACAGGGCGC
MEX48	111	ACAGGACACGAGT	GAAGGCTGTAAGGGTGAGGAGACTG	GACTGAGGCCTGGCCCGACGCCCGTCGGCGGCGAACGCCCTCCCTTGAGTGGCGCTAACAGGGCGC
SIN2	108	ACAGGACACGAGT	GAAGGCTGTAAGGGTGAGGAGACTG	GACTGAGGCCTGGCCCGACGCCCGTCGGCGGCGAACGCCCTCCCTTGAGTGGCGCTAACAGGGCGC
PUE32	111	ACAGGACACGAGT	GAAGGCTGTAAC-GAG-C	GACTGAGGCCTGGCCCGACGCCCGTCGGCGGCGAACGCCCTCCCTTGAGTGGCGCTAACAGGGCGC
VEN453	111	ACAGGACACGAGT	GAAGGCTGTAAGGGTGAGGAGACTG	GACTGAGGCCTGGCCCGACGCCCGTCGGCGGCGAACGCCCTCCCTTGAGTGGCGCTAACAGGGCGC
GUAI31	108	ACAGGACACGAGT	GAAGGCTGTAAGGGTGAGGAGACTG	GACTGAGGCCTGGCCCGACGCCCGTCGGCGGCGAACGCCCTCCCTTGAGTGGCGCTAACAGGGCGC
CHH160	108	ACAGGACACGAGT	GAAGGCTGTAAGGGTGAGGAGACTG	GACTGAGGCCTGGCCCGACGCCCGTCGGCGGCGAACGCCCTCCCTTGAGTGGCGCTAACAGGGCGC
MAG450	108	ACAGGACACGAGT	GAAGGCTGTAAGGGTGAGGAGACTG	GACTGAGGCCTGGCCCGACGCCCGTCGGCGGCGAACGCCCTCCCTTGAGTGGCGCTAACAGGGCGC
YUC7	108	ACAGGACACGAGT	GAAGGCTGTAAGGGTGAGGAGACTG	GACTGAGGCCTGGCCCGACGCCCGTCGGCGGCGAACGCCCTCCCTTGAGTGGCGCTAACAGGGCGC
APC13	111	ACAGGACACGAGT	GAAGGCTGTAAGGGTGAGGAGACTG	GACTGAGGCCTGGCCCGACGCCCGTCGGCGGCGAACGCCCTCCCTTGAGTGGCGCTAACAGGGCGC
SAN329	111	ACAGGACACGAGT	GAAGGCTGTAAGGGTGAGGAGACTG	GACTGAGGCCTGGCCCGACGCCCGTCGGCGGCGAACGCCCTCCCTTGAGTGGCGCTAACAGGGCGC
OAX70	111	ACAGGACACGAGT	GAAGGCTGTAAGGGTGAGGAGACTG	GACTGAGGCCTGGCCCGACGCCCGTCGGCGGCGAACGCCCTCCCTTGAGTGGCGCTAACAGGGCGC
GUAI4	108	ACAGGACACGAGT	GAAGGCTGTAAGGGTGAGGAGACTG	GACTGAGGCCTGGCCCGACGCCCGTCGGCGGCGAACGCCCTCCCTTGAGTGGCGCTAACAGGGCGC
JSGyMAS_401	108	ACAGGACACGAGT	GAAGGCTGTAAGGGTGAGGAGACTG	GACTGAGGCCTGGCCCGACGCCCGTCGGCGGCGAACGCCCTCCCTTGAGTGGCGCTAACAGGGCGC
JSGyLOS_161	108	ACAGGACACGAGT	GAAGGCTGTAAGGGTGAGGAGACTG	GACTGAGGCCTGGCCCGACGCCCGTCGGCGGCGAACGCCCTCCCTTGAGTGGCGCTAACAGGGCGC
JKS_316_Site6	108	ACAGGACACGAGT	GAAGGCTGTAAGGGTGAGGAGACTG	GACTGAGGCCTGGCCCGACGCCCGTCGGCGGCGAACGCCCTCCCTTGAGTGGCGCTAACAGGGCGC
JSGyLOS_130	111	ACAGGACACGAGT	GAAGGCTGTAAGGGTGAGGAGACTG	GACTGAGGCCTGGCCCGACGCCCGTCGGCGGCGAACGCCCTCCCTTGAGTGGCGCTAACAGGGCGC
JSGyLOS_119	111	ACAGGACACGAGT	GAAGGCTGTAAGGGTGAGGAGACTG	GACTGAGGCCTGGCCCGACGCCCGTCGGCGGCGAACGCCCTCCCTTGAGTGGCGCTAACAGGGCGC
CIMMYT_8783	111	ACAGGACACGAGT	GAAGGCTGTAAGGGTGAGGAGACTG	GACTGAGGCCTGGCCCGACGCCCGTCGGCGGCGAACGCCCTCCCTTGAGTGGCGCTAACAGGGCGC
JSG_197	111	ACAGGACACGAGT	GAAGGCTGTAAGGGTGAGGAGACTG	GACTGAGGCCTGGCCCGACGCCCGTCGGCGGCGAACGCCCTCCCTTGAGTGGCGCTAACAGGGCGC
JSGyMAS_109	108	ACAGGACACGAGT	GAAGGCTGTAAGGGTGAGGAGACTG	GACTGAGGCCTGGCCCGACGCCCGTCGGCGGCGAACGCCCTCCCTTGAGTGGCGCTAACAGGGCGC
JSG_378	111	ACAGGACACGAGT	GAAGGCTGTAAGGGTGAGGAGACTG	GACTGAGGCCTGGCCCGACGCCCGTCGGCGGCGAACGCCCTCCCTTGAGTGGCGCTAACAGGGCGC
CIMMYT_11355	108	ACAGGACACGAGT	GAAGGCTGTAAGGGTGAGGAGACTG	GACTGAGGCCTGGCCCGACGCCCGTCGGCGGCGAACGCCCTCCCTTGAGTGGCGCTAACAGGGCGC
JSGyMAS_264	111	ACAGGACACGAGT	GAAGGCTGTAAGGGTGAGGAGACTG	GACTGAGGCCTGGCCCGACGCCCGTCGGCGGCGAACGCCCTCCCTTGAGTGGCGCTAACAGGGCGC
USDA_P1566686	111	ACAGGACACGAGT	GAAGGCTGTAAGGGTGAGGAGACTG	GACTGAGGCCTGGCCCGACGCCCGTCGGCGGCGAACGCCCTCCCTTGAGTGGCGCTAACAGGGCGC
Benz_967	111	ACAGGACACGAGT	GAAGGCTGTAAGGGTGAGGAGACTG	GACTGAGGCCTGGCCCGACGCCCGTCGGCGGCGAACGCCCTCCCTTGAGTGGCGCTAACAGGGCGC
Beadle_Kato_Si	111	ACAGGACACGAGT	GAAGGCTGTAAGGGTGAGGAGACTG	GACTGAGGCCTGGCCCGACGCCCGTCGGCGGCGAACGCCCTCCCTTGAGTGGCGCTAACAGGGCGC
JSG_374	108	ACAGGACACGAGT	GAAGGCTGTAAGGGTGAGGAGACTG	GACTGAGGCCTGGCCCGACGCCCGTCGGCGGCGAACGCCCTCCCTTGAGTGGCGCTAACAGGGCGC
CIMMYT_11374	111	ACAGGACACGAGT	GAAGGCTGTAAGGGTGAGGAGACTG	GACTGAGGCCTGGCCCGACGCCCGTCGGCGGCGAACGCCCTCCCTTGAGTGGCGCTAACAGGGCGC
Puga_11066	111	ACAGGACACGAGT	GAAGGCTGTAAGGGTGAGGAGACTG	GACTGAGGCCTGGCCCGACGCCCGTCGGCGGCGAACGCCCTCCCTTGAGTGGCGCTAACAGGGCGC

P1213793	215	CC TGG CCG CCG CA CGC GG CCCC CTG GAG G CCCC CA CGC CG CGG AGT AAC GC ACT CG CTG TG CTA GCG CGC CT CTC TCCC CT GACT CGT TG CTG GGG
OAX68	234	CC TGG CCG CCG CA CGC GG CCCC CTG GAG G CCCC CA CGC GG CGG AGT AAC GC ACT CG CTG TG CTA GCG CGC CT CTC TCCC CT GACT CGT TG CTG GGG
URG_II	179	CC TGG CCG CCG CA CGC GG CCCC CTG GAG G CCCC CA CGC GG CGG AGT AAC GC ACT CG CTG TG CTA GCG CGC CT CTC TCCC CT GACT CGT TG CTG GGG
MEX48	217	CC TGG CCG CCG CA CGC GG CCCC CTG GAG G CCCC CA CGC GG CGG AGT AAC GC ACT CG CTG TG CTA GCG CGC CT CTC TCCC CT GACT CGT TG CTG GGG
SIM2	213	CC TGG CCG CCG CA CGC GG CCCC CTG GAG G CCCC CA CGC GG CGG AGT AAC GC ACT CG CTG TG CTA GCG CGC CT CTC TCCC CT GACT CGT TG CTG GGG
VEN453	210	CC TGG CCG CCG CA CGC GG CCCC CTG GAG G CCCC CA CGC GG CGG AGT AAC GC ACT CG CTG TG CTA GCG CGC CT CTC TCCC CT GACT CGT TG CTG GGG
GUAN131	210	CC TGG CCG CCG CA CGC GG CCCC CTG GAG G CCCC CA CGC GG CGG AGT AAC GC ACT CG CTG TG CTA GCG CGC CT CTC TCCC CT GACT CGT TG CTG GGG
GHG160	215	CC TGG CCG CCG CA CGC GG CCCC CTG GAG G CCCC CA CGC GG CGG AGT AAC GC ACT CG CTG TG CTA GCG CGC CT CTC TCCC CT GACT CGT TG CTG GGG
MAG450	215	CC TGG CCG CCG CA CGC GG CCCC CTG GAG G CCCC CA CGC GG CGG AGT AAC GC ACT CG CTG TG CTA GCG CGC CT CTC TCCC CT GACT CGT TG CTG GGG
XHG17	215	CC TGG CCG CCG CA CGC GG CCCC CTG GAG G CCCC CA CGC GG CGG AGT AAC GC ACT CG CTG TG CTA GCG CGC CT CTC TCCC CT GACT CGT TG CTG GGG

APC1	218	CC	TGGCCCGCCAGCGGCCGCCCCCTGGAGGCCGCCCCCACGGCGCGAGATGAAACAGCACTCCGCTGGCTGAGCGCGCGCTTCTCCCGCTTGCACTGTGTTCTGTGGCG
SAN329	218	CC	TGGCCCGCCAGCGGCCGCCCCCTGGAGGCCGCCCCCACGGCGCGAGATGAAACAGCACTCCGCTGGCTGAGCGCGCGCTTCTCCCGCTTGCACTGTGTTCTGTGGCG
OAX70	218	CC	TGGCCCGCCAGCGGCCGCCCCCTGGAGGCCGCCCCCACGGCGCGAGATGAAACAGCACTCCGCTGGCTGAGCGCGCGCTTCTCCCGCTTGCACTGTGTTCTGTGGCG
GU14	215	CC	TGGCCCGCCAGCGGCCGCCCCCTGGAGGCCGCCCCCACGGCGCGAGATGAAACAGCACTCCGCTGGCTGAGCGCGCGCTTCTCCCGCTTGCACTGTGTTCTGTGGCG
JSGyMAS_401	215	CC	TGGCCCGCCAGCGGCCGCCCCCTGGAGGCCGCCCCCACGGCGCGAGATGAAACAGCACTCCGCTGGCTGAGCGCGCGCTTCTCCCGCTTGCACTGTGTTCTGTGGCG
JSGyLOS_161	215	CC	TGGCCCGCCAGCGGCCGCCCCCTGGAGGCCGCCCCCACGGCGCGAGATGAAACAGCACTCCGCTGGCTGAGCGCGCGCTTCTCCCGCTTGCACTGTGTTCTGTGGCG
Wilkes_Site6	215	CC	TGGCCCGCCAGCGGCCGCCCCCTGGAGGCCGCCCCCACGGCGCGAGATGAAACAGCACTCCGCTGGCTGAGCGCGCGCTTCTCCCGCTTGCACTGTGTTCTGTGGCG
JSGyLOS_130	215	CC	TGGCCCGCCAGCGGCCGCCCCCTGGAGGCCGCCCCCACGGCGCGAGATGAAACAGCACTCCGCTGGCTGAGCGCGCGCTTCTCCCGCTTGCACTGTGTTCTGTGGCG
JSGyLOS_119	146	-	
CIMMYT_8783	137	-	
JSG_197	137	-	
JSGyLOS_109	131	-	
JSG_378	140	-	
CIMMYT_11355	143	-	
JSGyMAS_264	146	-	
USDA_PI566686	129	-	
Benz_967	146	-	
<u>Beadle_Kato_Si</u>	138	-	
JSG_374	144	-	
CIMMYT_11374	144	-	
Puga_11066	146	-	

	Zea mays cultvar	Z. mays ssp. parviglumis	Zea mays ssp. mexicana	Hopscotch	
CHI349	2581	TCTTGTGATGGAGTCGGGAGC	GGAAGGAGCACACGACAC	GGCCACCGG	TGGGGCTCCGATGCC
P1213793	2580	CTGTAACARACAGAAGTAAAGCATCTTCGGAGA	TAAAGATAAGGATATTCTG	GTAACTAGAATTCCTC	TAGTTGTRACGATCCTGTA
OAX68	2584	CTGTAACARACAGAAGTAAAGCATCTTCGGAGA	TAAAGATAAGGATATTCTG	GTAACTAGAATTCCTC	TAGTTGTRACGATCCTGTA
URG II	2543	CTGTAACARACAGAAGTAAAGCATCTTCGGAGA	TAAAGATAAGGATATTCTG	GTAACTAGAATTCCTC	TAGTTGTRACGATCCTGTA
MEX48	2581	CTGTAACARACAGAAGTAAAGCATCTTCGGAGA	TAAAGATAAGGATATTCTG	GTAACTAGAATTCCTC	TAGTTGTRACGATCCTGTA
SIN2	2566	CTGTAACARACAGAAGTAAAGCATCTTCGGAGA	TAAAGATAAGGATATTCTG	GTAACTAGAATTCCTC	TAGTTGTRACGATCCTGTA
PUE32	2574	CTGTAACARACAGAAGTAAAGCATCTTCGGAGA	TAAAGATAAGGATATTCTG	GTAACTAGAATTCCTC	TAGTTGTRACGATCCTGCGG
VEN453	2588	CTGTAACARACAGAAGTAAAGCATCTTCGGAGA	TAAAGATAAGGATATTCTG	GTAACTAGAATTCCTC	TAGTTGTRACGATCCTGCGG
GUAI131	2581	CTGTAACARACAGAAGTAAAGCATCTTCGGAGA	TAAAGATAAGGATATTCTG	GTAACTAGAATTCCTC	TAGTTGTRACGATCCTGCGG
CHH160	2579	CTGTAACARACAGAAGTAAAGCATCTTCGGAGA	TAAAGATAAGGATATTCTG	GTAACTAGAATTCCTC	TAGTTGTRACGATCCTGCGG
MAG450	2583	CTGTAACARACAGAAGTAAAGCATCTTCGGAGA	TAAAGATAAGGATATTCTG	GTAACTAGAATTCCTC	TAGTTGTRACGATCCTGCGG
YUC7	2584	CTGTAACARACAGAAGTAAAGCATCTTCGGAGA	TAAAGATAAGGATATTCTG	GTAACTAGAATTCCTC	TAGTTGTRACGATCCTGCGG
APC13	2583	CTGTAACARACAGAAGTAAAGCATCTTCGGAGA	TAAAGATAAGGATATTCTG	GTAACTAGAATTCCTC	TAGTTGTRACGATCCTGCGG
SAN329	2582	CTGTAACARACAGAAGTAAAGCATCTTCGGAGA	TAAAGATAAGGATATTCTG	GTAACTAGAATTCCTC	TAGTTGTRACGATCCTGCGG
OAX70	2584	CTGTAACARACAGAAGTAAAGCATCTTCGGAGA	TAAAGATAAGGATATTCTG	GTAACTAGAATTCCTC	TAGTTGTRACGATCCTGCGG
GUAI14	1242				
JSGyNAS_401	2580	CCTAACACAAAGAGTAAAGCATCTTCGGAGA	TAAAGATAAGGATATTCTG	GTAACTAGAATTCCTC	AGACGATCCTGTA
JSGyLOS_161	2579	CCTAACACAAAGAGTAAAGCATCTTCGGAGA	TAAAGATAAGGATATTCTG	GTAACTAGAATTCCTC	AGACGATCCTGTA
Wilkes_Site6	2580	CCTAACACAAAGAGTAAAGCATCTTCGGAGA	TAAAGATAAGGATATTCTG	GTAACTAGAATTCCTC	AGACGATCCTGTA
JSGyLOS_130	852				
JSGyLOS_119	821				
CIMMYT_8783	842				
JSG_197	849				
JSGyLOS_109	843				
JSG_378	806				
CIMMYT_11355	858				
JSGyNAS_264	836				
USDA_P1566686	830				
Benz_967	1181				
Beadle_Kato_Si	859				
JSG_374	866				
CIMMYT_11374	862				
Puga_11066	839				
Puga_11066	1	CGGCGCTACAGAGGACACACGCTAGACAGTAGAGCAGACAGCGGGGGAGACGATGACAGACCCAGCAAGCAGAAGAAATAATIGCTCTGGAGGTCCA			
CHI349	2691	ATGTTGTTATGCGTATATAACATGATGGGGGCC	CTTCAAGAGGAGCACACCTTAACTTTCCTC	ATTTACACACTCGTCCATGAATCATACTGTT	
P1213793	2690	ATGTTGTTATGCGTATATAACATGATGGGGGCC	CTTCAAGAGGAGCACCTTAACTTTCCTC	ATTTACACACTCGTCCATGAATCATACTGTT	
OAX68	2694	ATGTTGTTATGCGTATATAACATGATGGGGGCC	CTTCAAGAGGAGCACCTTAACTTTCCTC	ATTTACACACTCGTCCATGAATCATACTGTT	
URG II	2653	ATGTTGTTATGCGTATATAACATGATGGGGGCC	CTTCAAGAGGAGCACCTTAACTTTCCTC	ATTTACACACTCGTCCATGAATCATACTGTT	
MEX48	2691	ATGTTGTTATGCGTATATAACATGATGGGGGCC	CTTCAAGAGGAGCACCTTAACTTTCCTC	ATTTACACACTCGTCCATGAATCATACTGTT	
SIN2	2676	ATGTTGTTATGCGTATATAACATGATGGGGGCC	CTTCAAGAGGAGCACCTTAACTTTCCTC	ATTTACACACTCGTCCATGAATCATACTGTT	
PUE32	2684	ATGTTGTTATGCGTATATAACATGATGGGGGCC	CTTCAAGAGGAGCACCTTAACTTTCCTC	ATTTACACACTCGTCCATGAATCATACTGTT	
VEN453	2688	ATGTTGTTATGCGTATATAACATGATGGGGGCC	CTTCAAGAGGAGCACCTTAACTTTCCTC	ATTTACACACTCGTCCATGAATCATACTGTT	
GUAI131	2691	ATGTTGTTATGCGTATATAACATGATGGGGGCC	CTTCAAGAGGAGCACCTTAACTTTCCTC	ATTTACACACTCGTCCATGAATCATACTGTT	
CHH160	2689	ATGTTGTTATGCGTATATAACATGATGGGGGCC	CTTCAAGAGGAGCACCTTAACTTTCCTC	ATTTACACACTCGTCCATGAATCATACTGTT	
MAG450	2693	ATGTTGTTATGCGTATATAACATGATGGGGGCC	CTTCAAGAGGAGCACCTTAACTTTCCTC	ATTTACACACTCGTCCATGAATCATACTGTT	
YUC7	2694	ATGTTGTTATGCGTATATAACATGATGGGGGCC	CTTCAAGAGGAGCACCTTAACTTTCCTC	ATTTACACACTCGTCCATGAATCATACTGTT	
APC13	2693	ATGTTGTTATGCGTATATAACATGATGGGGGCC	CTTCAAGAGGAGCACCTTAACTTTCCTC	ATTTACACACTCGTCCATGAATCATACTGTT	
SAN329	2692	ATGTTGTTATGCGTATATAACATGATGGGGGCC	CTTCAAGAGGAGCACCTTAACTTTCCTC	ATTTACACACTCGTCCATGAATCATACTGTT	
OAX70	2694	ATGTTGTTATGCGTATATAACATGATGGGGGCC	CTTCAAGAGGAGCACCTTAACTTTCCTC	ATTTACACACTCGTCCATGAATCATACTGTT	
GUAI14	1242				
JSGyNAS_401	2690	ATGTTGTTATGCGTATATAACATGATGGGGGCC	CTTCAAGAGGAGCACCTTAACTTTCCTC	ATTTACACACTCGTCCATGAATCATACTGTT	
JSGyLOS_161	2689	ATGTTGTTATGCGTATATAACATGATGGGGGCC	CTTCAAGAGGAGCACCTTAACTTTCCTC	ATTTACACACTCGTCCATGAATCATACTGTT	
Wilkes_Site6	2690	ATGTTGTTATGCGTATATAACATGATGGGGGCC	CTTCAAGAGGAGCACCTTAACTTTCCTC	ATTTACACACTCGTCCATGAATCATACTGTT	
JSGyLOS_130	852				
JSGyLOS_119	821				
CIMMYT_8783	842				
JSG_197	849				
JSGyLOS_109	843				
JSG_378	806				
CIMMYT_11355	858				
JSGyNAS_264	836				
USDA_P1566686	830				
Benz_967	1181				
Beadle_Kato_Si	859				
JSG_374	866				
CIMMYT_11374	862				
Puga_11066	839				
Puga_11066	111	ATGTTGTTATGCGTATATAACATGATGGGGGCC	CTTCAAGAGGAGCACCTTAACTTTCCTC	ATTTACACACTCGTCCATGAATCATACTGTT	
CHI349	2801	CTTTTCTCCCCGGTGTGGGTGTGGTGTGGTGT	TATACCGGAATTTACCGGAA	TATACCGGAATTTACCGGAA	
P1213793	2800	CTTTTCTCCCCGGTGTGGGTGTGGTGTGGTGT	TATACCGGAATTTACCGGAA	TATACCGGAATTTACCGGAA	
OAX68	2804	CTTTTCTCCCCGGTGTGGGTGTGGTGTGGTGT	TATACCGGAATTTACCGGAA	TATACCGGAATTTACCGGAA	
URG II	2763	CTTTTCTCCCCGGTGTGGGTGTGGTGTGGTGT	TATACCGGAATTTACCGGAA	TATACCGGAATTTACCGGAA	
MEX48	2801	CTTTTCTCCCCGGTGTGGGTGTGGTGTGGTGT	TATACCGGAATTTACCGGAA	TATACCGGAATTTACCGGAA	
SIN2	2786	CTTTTCTCCCCGGTGTGGGTGTGGTGTGGTGT	TATACCGGAATTTACCGGAA	TATACCGGAATTTACCGGAA	
PUE32	2794	CTTTTCTCCCCGGTGTGGGTGTGGTGTGGTGT	TATACCGGAATTTACCGGAA	TATACCGGAATTTACCGGAA	
VEN453	2808	CTTTTCTCCCCGGTGTGGGTGTGGTGTGGTGT	TATACCGGAATTTACCGGAA	TATACCGGAATTTACCGGAA	
GUAI131	2801	CTTTTCTCCCCGGTGTGGGTGTGGTGTGGTGT	TATACCGGAATTTACCGGAA	TATACCGGAATTTACCGGAA	
CHH160	2799	CTTTTCTCCCCGGTGTGGGTGTGGTGTGGTGT	TATACCGGAATTTACCGGAA	TATACCGGAATTTACCGGAA	
MAG450	2803	CTTTTCTCCCCGGTGTGGGTGTGGTGTGGTGT	TATACCGGAATTTACCGGAA	TATACCGGAATTTACCGGAA	
YUC7	2804	CTTTTCTCCCCGGTGTGGGTGTGGTGTGGTGT	TATACCGGAATTTACCGGAA	TATACCGGAATTTACCGGAA	
APC13	2803	CTTTTCTCCCCGGTGTGGGTGTGGTGTGGTGT	TATACCGGAATTTACCGGAA	TATACCGGAATTTACCGGAA	
SAN329	2802	CTTTTCTCCCCGGTGTGGGTGTGGTGTGGTGT	TATACCGGAATTTACCGGAA	TATACCGGAATTTACCGGAA	
OAX70	2804	CTTTTCTCCCCGGTGTGGGTGTGGTGTGGTGT	TATACCGGAATTTACCGGAA	TATACCGGAATTTACCGGAA	
GUAI14	1269				
JSGyNAS_401	2800	CTTTTCTCCCCGGTGTGGGTGTGGTGTGGTGT	TATACCGGAATTTACCGGAA	TATACCGGAATTTACCGGAA	
JSGyLOS_161	2799	CTTTTCTCCCCGGTGTGGGTGTGGTGTGGTGT	TATACCGGAATTTACCGGAA	TATACCGGAATTTACCGGAA	
Wilkes_Site6	2800	CTTTTCTCCCCGGTGTGGGTGTGGTGTGGTGT	TATACCGGAATTTACCGGAA	TATACCGGAATTTACCGGAA	
JSGyLOS_130	879				
JSGyLOS_119	851				
CIMMYT_8783	871				
JSG_197	876				
JSGyLOS_109	872				
JSG_378	843				
CIMMYT_11355	888				
JSGyNAS_264	864				
USDA_P1566686	857				
Benz_967	1220				
Beadle_Kato_Si	889				
JSG_374	896				
CIMMYT_11374	892				
Puga_11066	869				
Puga_11066	146				
CHI349	2900	TGTGTTGATGGAGTCGGGAGC	GGAAAGGAGCACACGACAC	GGGCCACCGG	TGGGGCTTCGATGCC
P1213793	2901	TGTGTTGATGGAGTCGGGAGC	GGAAAGGAGCACACGACAC	GGGCCACCGG	TGGGGCTTCGATGCC
OAX68	2904	TGTGTTGATGGAGTCGGGAGC	GGAAAGGAGCACACGACAC	GGGCCACCGG	TGGGGCTTCGATGCC
URG II	2864	TGTGTTGATGGAGTCGGGAGC	GGAAAGGAGCACACGACAC	GGGCCACCGG	TGGGGCTTCGATGCC
MEX48	2902	TGTGTTGATGGAGTCGGGAGC	GGAAAGGAGCACACGACAC	GGGCCACCGG	TGGGGCTTCGATGCC
SIN2	2887	TGTGTTGATGGAGTCGGGAGC	GGAAAGGAGCACACGACAC	GGGCCACCGG	TGGGGCTTCGATGCC
PUE32	2897	TGTGTTGATGGAGTCGGGAGC	GGAAAGGAGCACACGACAC	GGGCCACCGG	TGGGGCTTCGATGCC
VEN453	2907	TGTGTTGATGGAGTCGGGAGC	GGAAAGGAGCACACGACAC	GGGCCACCGG	TGGGGCTTCGATGCC
GUAI131	2902	TGTGTTGATGGAGTCGGGAGC	GGAAAGGAGCACACGACAC	GGGCCACCGG	TGGGGCTTCGATGCC
CHH160	2900	TGTGTTGATGGAGTCGGGAGC	GGAAAGGAGCACACGACAC	GGGCCACCGG	TGGGGCTTCGATGCC
MAG450	2904	TGTGTTGATGGAGTCGGGAGC	GGAAAGGAGCACACGACAC	GGGCCACCGG	TGGGGCTTCGATGCC
YUC7	2903	TGTGTTGATGGAGTCGGGAGC	GGAAAGGAGCACACGACAC	GGGCCACCGG	TGGGGCTTCGATGCC
APC13	2902	TGTGTTGATGGAGTCGGGAGC	GGAAAGGAGCACACGACAC	GGGCCACCGG	TGGGGCTTCGATGCC
SAN329	2901	TGTGTTGATGGAGTCGGGAGC	GGAAAGGAGCACACGACAC	GGGCCACCGG	TGGGGCTTCGATGCC
OAX70	2905	TGTGTTGATGGAGTCGGGAGC	GGAAAGGAGCACACGACAC	GGGCCACCGG	TGGGGCTTCGATGCC
GUAI14	1363				
JSGyNAS_401	2901	TGTGTTGATGGAGTCGGGAGC	GGAAAGGAGCACACGACAC	GGGCCACCGG	TGGGGCTTCGATGCC
JSGyLOS_161	2901	TGTGTTGATGGAGTCGGGAGC	GGAAAGGAGCACACGACAC	GGGCCACCGG	TGGGGCTTCGATGCC
Wilkes_Site6	2901	TGTGTTGATGGAGTCGGGAGC	GGAAAGGAGCACACGACAC	GGGCCACCGG	TGGGGCTTCGATGCC
JSGyLOS_130	967				
JSGyLOS_119	958				
CIMMYT_8783	968				
JSG_197	975				
JSGyLOS_109	962				
JSG_378	939				
CIMMYT_11355	987				
JSGyNAS_264	962				
USDA_P1566686	964				
Benz_967	1327				
Beadle_Kato_Si	986				
JSG_374	993				
CIMMYT_11374	987				
Puga_11066	972				
Puga_11066	146				

PUE32	3279	CG-CGCCGG-CGGCTG-GA	TAATTCGCGAACATCAGC	TAGCCTACTTGAGAAGTAAACACACACACACA-C	CTACAGTCGCA	CCCATG
VEN453	3285	CG-CGCCGG-CGGCTG-GA	GAATTAACTCGCGAACATCAGC	TAGCCTACTTGAGAAGTAAACACACACACACA-C	CTACAGTCGCA	CCCATG
GUAI131	3280	CG-CGCCGG-CGGCTG-GA	GAATTAACTCGCGAACATCAGC	TAGCCTACTTGAGAAGTAAACACACACACACA-C	CTACAGTCGCA	CCCATG
CHH160	3282	CG-CGCCGG-CGGCTG-GA	GAATTAACTCGCGAACATCAGC	TAGCCTACTTGAGAAGTAAACACACACACACA-C	CTACAGTCGCA	CCCATG
MAG450	3282	CG-CGCCGG-CGGCTG-GA	GAATTAACTCGCGAACATCAGC	TAGCCTACTTGAGAAGTAAACACACACACACA-C	CTACAGTCGCA	CCCATG
YUC7	3281	CG-CGCCGG-CGGCTG-GA	GAATTAACTCGCGAACATCAGC	TAGCCTACTTGAGAAGTAAACACACACACACA-C	CTACAGTCGCA	CCCATG
APC13	3280	CG-CGCCGG-CGGCTG-GA	GAATTAACTCGCGAACATCAGC	TAGCCTACTTGAGAAGTAAACACACACACACA-C	CTACAGTCGCA	CCCATG
SAN329	3279	CG-CGCCGG-CGGCTG-GA	GAATTAACTCGCGAACATCAGC	TAGCCTACTTGAGAAGTAAACACACACACACA-C	CTACAGTCGCA	CCCATG
OAX70	3287	CG-CGCCGG-CGGCTG-GA	GAATTAACTCGCGAACATCAGC	TAGCCTACTTGAGAAGTAAACACACACACACA-C	CTACAGTCGCA	CCCATG
GUAI14	1742	CG-----GGCGCTGCGA	GAATTAACTCGCGAACATCAGC	TAGCCTACTTGAGAAGTAAACACACACACACA-C	CTACAGTCGCA	CCCATG
JSGYMAS_401	3283	CG-CGCCGG-CGGCTG-GA	GAATTAACTCGCGAACATCAGC	TAGCCTACTTGAGAAGTAAACACACACACACA-C	CTACAGTCGCA	CCCATG
JSGYLOS_161	3281	CG-CGCCGG-CGGCTG-GA	GAATTAACTCGCGAACATCAGC	TAGCCTACTTGAGAAGTAAACACACACACACA-C	CTACAGTCGCA	CCCATG
Wilkes_Site6	3283	CG-CGCCGG-CGGCTG-GA	GAATTAACTCGCGAACATCAGC	TAGCCTACTTGAGAAGTAAACACACACACACA-C	CTACAGTCGCA	CCCATG
JSGYLOS_130	1353	---GCCCGGG-CGGCTG-GA	GAATTAACTCGCGAACATCAGC	TAGCCTACTTGAGAAGTAAACACACACACACA-C	CTACAGTCGCA	CCCATG
JSGYLOS_119	1335	GWGCGCCGG-CGGCTG-GA	GAATTAACTCGCGAACATCAGC	TAGCCTACTTGAGAAGTAAACACACACACACA-C	CTACAGTCGCA	CCCATG
CIMMYT_8783	1335	-----AATTAACTCGCGAACATCAGC	AATTAACTCGCGAACATCAGC	TAGCCTACTTGAGAAGTAAACACACACACACA-C	CTACAGTCGCA	CCCATG
JSG_197	1365	GCGCCGG-CGGCTG-GA	GAATTAACTCGCGAACATCAGC	TAGCCTACTTGAGAAGTAAACACACACACACA-C	CTACAGTCGCA	CCCATG
JSGYLOS_109	1348	GCGCCGG-CGGCTG-GA	GAATTAACTCGCGAACATCAGC	TAGCCTACTTGAGAAGTAAACACACACACACA-C	CTACAGTCGCA	CCCATG
JSG_378	1323	GCGCCGG-CGGCTG-GA	GAATTAACTCGCGAACATCAGC	TAGCCTACTTGAGAAGTAAACACACACACACA-C	CTACAGTCGCA	CCCATG
CIMMYT_11355	1364	GCGCCGG-CGGCTG-GA	GAATTAACTCGCGAACATCAGC	TAGCCTACTTGAGAAGTAAACACACACACACA-C	CTACAGTCGCA	CCCATG
JSGYMAS_264	1340	GCGCCGG-CGGCTG-GA	GAATTAACTCGCGAACATCAGC	TAGCCTACTTGAGAAGTAAACACACACACACA-C	CTACAGTCGCA	CCCATG
USAID_P1566668	1334	GCG-----GGCGCTG-GA	GAATTAACTCGCGAACATCAGC	TAGCCTACTTGAGAAGTAAACACACACACACA-C	CTACAGTCGCA	CCCATG
Benz_967	1703	GCGCCGG-CGGCTG-GA	GAATTAACTCGCGAACATCAGC	TAGCCTACTTGAGAAGTAAACACACACACACA-C	CTACAGTCGCA	CCCATG
Beadle_Kato_Si	1359	GCG-----GGCGCTG-GA	GAATTAACTCGCGAACATCAGC	TAGCCTACTTGAGAAGTAAACACACACACACA-C	CTACAGTCGCA	CCCATG
JSG_374	1370	GCGGCCGCCG-CGGCTG-GA	GAATTAACTCGCGAACATCAGC	TAGGCCACTTCTGAAAGGAGTAAA-C	CACACACACACACACTCTGCGCA	CCCATGCA
CIMMYT_11374	1359	-----GGCAATTAACTCGCGAACATCAGC	GGCAATTAACTCGCGAACATCAGC	TAGGCCACTTCTGAAAGGAGTAAA-C	CACACACACACACACTCTGCGCA	CCCATGCA
Puga_11066	1352	-----GGCAATTAACTCGCGAACATCAGC	GGCAATTAACTCGCGAACATCAGC	TAGGCCACTTCTGAAAGGAGTAAA-C	CACACACACACACACTCTGCGCA	CCCATGCA
Puga_11000	146	-----GGCAATTAACTCGCGAACATCAGC	GGCAATTAACTCGCGAACATCAGC	TAGGCCACTTCTGAAAGGAGTAAA-C	GGG----WGA-TGAG-WGCA-WGCA-WGCA	CCCATGCA

Zea mays cultivar	Z. mays ssp. parviglumis	Zea mays ssp. mexicana	TB1 binding
CHI349	3377	CGCGAGCTCAAGACACAGGGC	CAGACTG
P1213793	3378	GCAGAGCTCAAGACACAGGGC	CAGACTG
OAX68	3379	GCAGAGCTCAAGACACAGGGC	CAGACTG
URG_II	3380	GCAGAGCTCAAGACACAGGGC	CAGACTG
MEX46	3383	GCAGAGCTCAAGACACAGGGC	CAGACTG
SIN2	3382	GCAGAGCTCAAGACACAGGGC	CAGACTG
PUE32	3376	GCAGAGCTCAAGACACAGGGC	CAGACTG
VEN453	3382	GCAGAGCTCAAGACACAGGGC	CAGACTG
GUAI131	3377	GCAGAGCTCAAGACACAGGGC	CAGACTG
CHH160	3381	GCAGAGCTCAAGACACAGGGC	CAGACTG
MAG450	3381	GCAGAGCTCAAGACACAGGGC	CAGACTG
YUC7	3380	GCAGAGCTCAAGACACAGGGC	CAGACTG
APC13	3379	GCAGAGCTCAAGACACAGGGC	CAGACTG
SAN329	3378	GCAGAGCTCAAGACACAGGGC	CAGACTG
OAX70	3386	GCAGAGCTCAAGACACAGGGC	CAGACTG
GUAI14	1829	GCAGAGCTCAAGACACAGGGC	CAGACTG
JSGyMAS_401	3380	GCAGAGCTCAAGACACAGGGC	CAGACTG
JSGyLOS_161	3378	-CAGAGCTCAAGACACAGGGC	CAGACTG
Wilkes_Site6	3380	GCAGAGCTCAAGACACAGGGC	CAGACTG
JSGyLOS_130	1443	GCAGAGCTCAAGACACAGGGC	CAGACTG
JSGyLOS_119	1433	GCAGAGCTCAAGACACAGGGC	CAGACTG
CIMMYT_8783	1415	GCAGAGCTCAAGACACAGGGC	CAGACTG
JSG_197	1463	-CAGAGCTCAAGACACAGGGC	-CAGACTG
JSGyLOS_109	1442	-CAGAGCTCAAGACACAGGGC	-CAGACTG
JSG_378	1423	-CAGAGCTCAAGACACAGGGC	-CAGACTG
CIMMYT_11355	1461	-CAGAGCTCAAGACACAGGGC	-CAGACTG
JSGyMAS_264	1436	-CAGAGCTCAAGACACAGGGC	-CAGACTG
USDA_PI566686	1428	GCAGAGCTCAAGACACAGGGC	-CAGACTG
Benz_967	1790	GCAGAGCTCAAGACACAGGGC	-CAGACTG
Beadle_Kato_Si	1455	GCAGAGCTCAAGACACAGGGC	-CAGACTG
JSG_374	1467	GCAGAGCTCAAGACACAGGGC	-CAGACTG
CIMMYT_11374	1441	GCAGAGCTCAAGACACAGGGC	-CAGACTG
Puga_11066	1451	GCAGAGCTCAAGACACAGGGC	-CAGACTG
Puga_11066	1	CGGGCGTACAGAGGTACACAGTACAGA	TAGAGTCAGCAGCAGCAGCGGGGGGGAGCATGACAGCACAGAACGAAGAAATAATTCTCCCTTTGGAGGCTTCCA
CHI349	3104	-ATGATCATAGCGCTGTG	CTGGCTCAGC
P1213793	3105	TGGC	-ATGATCATAGCGCTGTG
OAX68	3115	TGGC	-ATGATCATAGCGCTGTG
URG_II	3068	TGGC	-ATGATCATAGCGCTGTG
MEX46	3110	TGGC	-ATGATCATAGCGCTGTG
SIN2	3083	TGGC	-ATGATCATAGCGCTGTG
PUE32	3105	TGGC	-ATGATCATAGCGCTGTG
VEN453	3111	TGGC	-ATGATCATAGCGCTGTG
GUAI131	3106	TGGC	-ATGATCATAGCGCTGTG
CHH160	3108	TGGC	-ATGATCATAGCGCTGTG
MAG450	3108	TGGC	-ATGATCATAGCGCTGTG
YUC7	3107	TGGC	-ATGATCATAGCGCTGTG
APC13	3106	TGGC	-ATGATCATAGCGCTGTG
SAN329	3105	TGGC	-ATGATCATAGCGCTGTG
OAX70	3113	TGGC	-ATGATCATAGCGCTGTG
GUAI14	1576	TGGC	-ATGATCATAGCGCTGTG
JSGyMAS_401	3109	TGGC	-ATGATCATAGCGCTGTG
JSGyLOS_161	3107	TGGC	-ATGATCATAGCGCTGTG
Wilkes_Site6	3109	TGGC	-ATGATCATAGCGCTGTG
JSGyLOS_130	1179	TGGC	-ATGATCATAGCGCTGTG
JSGyLOS_119	1165	-	-ATGATCATAGCGCTGTG
CIMMYT_8783	1176	-	-ATGATCATAGCGCTGTG
JSG_197	1183	-	-ATGATCATAGCGCTGTG
JSGyLOS_109	1166	ATGATCATAGCGCTGTG	CCCTGTG
JSG_378	1143	TGGCTG	-ATGATCATAGCGCTGTG
CIMMYT_11355	1195	-	-ATGATCATAGCGCTGTG
JSGyMAS_264	1174	-	-ATGATCATAGCGCTGTG
USDA_PI566686	1168	TGGC	-ATGATCATAGCGCTGTG
Benz_967	1535	TGGCTG	-ATGATCATAGCGCTGTG
Beadle_Kato_Si	1187	-	-ATGATCATAGCGCTGTG
JSG_374	1201	-	-ATGATCATAGCGCTGTG
CIMMYT_11374	1194	-	-ATGATCATAGCGCTGTG
Puga_11066	1180	-	-ATGATCATAGCGCTGTG
Puga_11066	111	ACAGAACACGACT	-GAAGGGTAAGGTGAGAGAC
CHI349	3174	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCGCG
P1213793	3175	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
OAX68	3185	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
URG_II	3173	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
MEX46	3100	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
SIN2	3194	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
PUE32	3175	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
VEN453	3181	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
GUAI131	3176	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
CHH160	3178	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
MAG450	3178	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
YUC7	3177	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
APC13	3176	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
SAN329	3175	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
OAX70	3183	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
GUAI14	1642	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
JSGyMAS_401	3179	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
JSGyLOS_161	3177	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
Wilkes_Site6	3179	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
JSGyLOS_130	1179	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
JSGyLOS_119	1165	-	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
CIMMYT_8783	1176	-	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
JSG_197	1183	-	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
JSGyLOS_109	1166	ATGATCATAGCGCTGTG	CCCTGTG
JSG_378	1143	TGGCTG	-ATGATCATAGCGCTGTG
CIMMYT_11355	1195	-	-ATGATCATAGCGCTGTG
JSGyMAS_264	1174	-	-ATGATCATAGCGCTGTG
USDA_PI566686	1168	TGGC	-ATGATCATAGCGCTGTG
Benz_967	1535	TGGCTG	-ATGATCATAGCGCTGTG
Beadle_Kato_Si	1187	-	-ATGATCATAGCGCTGTG
JSG_374	1201	-	-ATGATCATAGCGCTGTG
CIMMYT_11374	1194	-	-ATGATCATAGCGCTGTG
Puga_11066	1180	-	-ATGATCATAGCGCTGTG
Puga_11066	111	ACAGAACACGACT	-GAAGGGTAAGGTGAGAGAC
CHI349	3174	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
P1213793	3175	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
OAX68	3185	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
URG_II	3173	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
MEX46	3100	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
SIN2	3194	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
PUE32	3175	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
VEN453	3181	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
GUAI131	3176	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
CHH160	3178	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
MAG450	3178	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
YUC7	3177	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
APC13	3176	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
SAN329	3175	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
OAX70	3183	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
GUAI14	1642	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
JSGyMAS_401	3179	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
JSGyLOS_161	3177	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
Wilkes_Site6	3179	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
JSGyLOS_130	1251	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
JSGyLOS_119	1231	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
CIMMYT_8783	1238	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
JSG_197	1261	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
JSGyLOS_109	1244	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
CIMMYT_11355	1260	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
JSGyMAS_264	1240	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
USDA_PI566686	1234	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
Benz_967	1609	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
Beadle_Kato_Si	1266	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
JSG_374	1259	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
CIMMYT_11374	1266	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
Puga_11066	1248	GGCCGCC	-GGCCCCGCGCTTACCATCTGATCACACACAGCAGCACCTTAGCTTCTTCCCACAAATTAAACGGATCACAGATCGACCGCGCG
Puga_11066	146	-	-GGAG

BKN32	833	GCCAAAGCGCAGAAGACTGGCACTGTCCTCGACCCGACACTGCACTGCCTT	--	GCATGCTGTTCTACGCCGCCAACACGCCGTGACGACGGGC
BKN29	821	GCCAAAGCGCAGAAGACTGGCACTGTCCTCGACCCGACACTGCACTGCCTT	--	GCATGCTGTTCTACGCCGCCAACACGCCGTGACGACGGGC
BKN27	821	GCCAAAGCGCAGAAGACTGGCACTGTCCTCGACCCGACACTGCACTGCCTT	--	GCATGCTGTTCTACGCCGCCAACACGCCGTGACGACGGGC
BKN22	821	GCCAAAGCGCAGAAGACTGGCACTGTCCTCGACCCGACACTGCACTGCCTT	--	GCATGCTGTTCTACGCCGCCAACACGCCGTGACGACGGGC
BKN20	832	GCCAAAGCGCAGAAGACTGGCACTGTCCTCGACCCGACACTGCACTGCCTT	--	GCATGCTGTTCTACGCCGCCAACACGCCGTGACGACGGGC
BKN19	821	GCCAAAGCGCAGAAGACTGGCACTGTCCTCGACCCGACACTGCACTGCCTT	--	GCATGCTGTTCTACGCCGCCAACACGCCGTGACGACGGGC
BKN17	803	GCCAAAGCGCAGAAGACTGGCACTGTCCTCGACCCGACACTGCACTGCCTT	--	GCATGCTGTTCTACGCCGCCAACACGCCGTGACGACGGGC
BKN16	815	GCCAAAGCGCAGAAGACTGGCACTGTCCTCGACCCGACACTGCACTGCCTT	--	GCATGCTGTTCTACGCCGCCAACACGCCGTGACGACGGGC
BKN15	810	GCCAAAGCGCAGAAGACTGGCACTGTCCTCGACCCGACACTGCACTGCCTT	--	GCATGCTGTTCTACGCCGCCAACACGCCGTGACGACGGGC
BKN14	811	GCCAAAGCGCAGAAGACTGGCACTGTCCTCGACCCGACACTGCACTGCCTT	--	GCATGCTGTTCTACGCCGCCAACACGCCGTGACGACGGGC
BKN12	811	GCCAAAGCGCAGAAGACTGGCACTGTCCTCGACCCGACACTGCACTGCCTT	--	GCATGCTGTTCTACGCCGCCAACACGCCGTGACGACGGGC
BKN10	823	GCCAAAGCGCAGAAGACTGGCACTGTCCTCGACCCGACACTGCACTGCCTT	--	GCATGCTGTTCTACGCCGCCAACACGCCGTGACGACGGGC
BKN09	821	GCCAAAGCGCAGAAGACTGGCACTGTCCTCGACCCGACACTGCACTGCCTT	--	GCATGCTGTTCTACGCCGCCAACACGCCGTGACGACGGGC
W22	821	GCCAAAGCGCAGAAGACTGGCACTGTCCTCGACCCGACACTGCACTGCCTT	--	GCATGCTGTTCTACGCCGCCAACACGCCGTGACGACGGGC
B73	820	GCCAAAGCGCAGAAGACTGGCACTGTCCTCGACCCGACACTGCACTGCCTT	--	GCATGCTGTTCTACGCCGCCAACACGCCGTGACGACGGGC
TIP534	909	TG-----CGGTGCG-----AGGGCATCTCTTGAG-----CCCCGGCTCGGCCCACTCCCAATCTCTCTCTCT-----ATCTCTCTCTCCATG-CATGCA-		
TIP517	917	TG-----CGGTGCGG-TGAGGGCATCTCTTGAG-----CCCCGGCGC-----ATCTCCCAATCTCTCTCT-----TCTC-TCTCTCCATG-CATGCA-ATGCGAT-		
TIP508	884	TG-----CGGTGCG-----AGGGCATCTCTTGAG-----CCCCGGCGC-----CGGCCCACTCTCTCT-----ATCTCTCTCTCT-----TCTC-TCTCTCCATG-CATGCA-----		

TIP469	955	TG	CGGCTGC	AAGGGCATCCTTGAG	CCCCCGCCCGCCGCCAACATCCC-TCTCTCTC-TTCTCTC-CATGCGAT-----GAT		
TIP466	898	TG	CGGCTGC	AAGGGCATCCTTGAG	CCCCCGCCCGCCGCCAACATCCC-TCTCTCTC-TTCTCTC-CATGCGAT-----GAT		
TIP462	925	TG	CGGCTGC	AAGGGCATCCTTGAG	CCCCCGCCCGCCGCCAACATCCC-TCTCTCTC-TTCTCTC-CATGCGAT-----GAT		
TIP458	923	TG	TGGGGCTCG	AAGGGCATCCTTGAG	CCCCGGCCCGCCGCCAACATCCC-TCTCTCTC-TTCTCTC-CATGCGAT-----GAT		
TIP454	932	TG	CGGCTGC	AAGGGCATCCTTGAG	CCCCGGCCCGCCGCCAACATCCC-TCTCTCTC-TTCTCTC-CATGCGAT-----GAT		
Crosses							
BNK31	925	TG	CGGCTGC	AAGGGCATCCTTGAG	CCCCGGCCCGCCGCCAACATCCC-TCTCTCTC-TTCTCTC-CATGCGAT-----GAT		
BNK32	923	TG	CGGCTGC	AAGGGCATCCTTGAG	CCCCGGCCCGCCGCCAACATCCC-TCTCTCTC-TTCTCTC-CATGCGAT-----GAT		
BNK33	909	TG	CGGCTGC	AAGGGCATCCTTGAG	CCCCGGCCCGCCGCCAACATCCC-TCTCTCTC-TTCTCTC-CATGCGAT-----GAT		
BNK32	929	TG	CGGCTGC	AAGGGCATCCTTGAG	CCCCGGCCCGCCGCCAACATCCC-TCTCTCTC-TTCTCTC-CATGCGAT-----GAT		
BNK29	927	TG	CGGCTGC	AAGGGCATCCTTGAG	CCCCGGCCCGCCGCCAACATCCC-TCTCTCTC-TTCTCTC-CATGCGAT-----GAT		
BNK27	927	TG	CGGCTGC	AAGGGCATCCTTGAG	CCCCGGCCCGCCGCCAACATCCC-TCTCTCTC-TTCTCTC-CATGCGAT-----GAT		
BNK22	927	TG	CGGCTGC	AAGGGCATCCTTGAG	CCCCGGCCCGCCGCCAACATCCC-TCTCTCTC-TTCTCTC-CATGCGAT-----GAT		
BNK20	938	TG	CGGCTGC	AAGGGCATCCTTGAG	CCCCGGCCCGCCGCCAACATCCC-TCTCTCTC-TTCTCTC-CATGCGAT-----GAT		
BNK19	927	TG	CGGCTGC	AAGGGCATCCTTGAG	CCCCGGCCCGCCGCCAACATCCC-TCTCTCTC-TTCTCTC-CATGCGAT-----GAT		
BNK17	909	TG	CGGCTGC	AAGGGCATCCTTGAG	CCCCGGCCCGCCGCCAACATCCC-TCTCTCTC-TTCTCTC-CATGCGAT-----GAT		
BNK16	921	TG	CGGCTGC	AAGGGCATCCTTGAG	CCCCGGCCCGCCGCCAACATCCC-TCTCTCTC-TTCTCTC-CATGCGAT-----GAT		
BNK15	916	TG	CGGCTGC	AAGGGCATCCTTGAG	CCCCGGCCCGCCGCCAACATCCC-TCTCTCTC-TTCTCTC-CATGCGAT-----GAT		
BNK14	917	TG	CGGCTGC	AAGGGCATCCTTGAG	CCCCGGCCCGCCGCCAACATCCC-TCTCTCTC-TTCTCTC-CATGCGAT-----GAT		
BNK12	917	TG	CGGCTGC	AAGGGCATCCTTGAG	CCCCGGCCCGCCGCCAACATCCC-TCTCTCTC-TTCTCTC-CATGCGAT-----GAT		
BNK10	929	TG	CGGCTGC	AAGGGCATCCTTGAG	CCCCGGCCCGCCGCCAACATCCC-TCTCTCTC-TTCTCTC-CATGCGAT-----GAT		
BNK09	927	TG	CGGCTGC	AAGGGCATCCTTGAG	CCCCGGCCCGCCGCCAACATCCC-TCTCTCTC-TTCTCTC-CATGCGAT-----GAT		
W22	927	TG	CGGCTGC	AAGGGCATCCTTGAG	CCCCGGCCCGCCGCCAACATCCC-TCTCTCTC-TTCTCTC-CATGCGAT-----GAT		
E73	926	TG	CGGCTGC	AAGGGCATCCTTGAG	CCCCGGCCCGCCGCCAACATCCC-TCTCTCTC-TTCTCTC-CATGCGAT-----GAT		

BNK20	832	GCCAAAGCGCAGAGACTGGCTGCTCGACCTCCCTCGCGAACGACTCTGCGACTGCTTTT	-- GCAATGCTTCTTACAGGCCGCCCCCACACGGCGTGACGACGGGC
B21	821	GCCAAAGCGCAGAGACTGGCTGCTCGACCTCCCTCGCGAACGACTCTGCGACTGCTTTT	-- GCAATGCTTCTTACAGGCCGCCCCCACACGGCGTGACGACGGGC
BKN17	803	GCCAAAGCGCAGAGACTGGCTGCTCGACCTCCCTCGCGAACGACTCTGCGACTGCTTTT	-- GCAATGCTTCTTACAGGCCGCCCCCACACGGCGTGACGACGGGC
BKN16	815	GCCAAAGCGCAGAGACTGGCTGCTCGACCTCCCTCGCGAACGACTCTGCGACTGCTTTT	-- GCAATGCTTCTTACAGGCCGCCCCCACACGGCGTGACGACGGGC
BKN15	810	GCCAAAGCGCAGAGACTGGCTGCTCGACCTCCCTCGCGAACGACTCTGCGACTGCTTTT	-- GCAATGCTTCTTACAGGCCGCCCCCACACGGCGTGACGACGGGC
BKN14	811	GCCAAAGCGCAGAGACTGGCTGCTCGACCTCCCTCGCGAACGACTCTGCGACTGCTTTT	-- GCAATGCTTCTTACAGGCCGCCCCCACACGGCGTGACGACGGGC
BKN12	811	GCCAAAGCGCAGAGACTGGCTGCTCGACCTCCCTCGCGAACGACTCTGCGACTGCTTTT	-- GCAATGCTTCTTACAGGCCGCCCCCACACGGCGTGACGACGGGC
BKN10	823	GCCAAAGCGCAGAGACTGGCTGCTCGACCTCCCTCGCGAACGACTCTGCGACTGCTTTT	-- GCAATGCTTCTTACAGGCCGCCCCCACACGGCGTGACGACGGGC
BW009	821	GCCAAAGCGCAGAGACTGGCTGCTCGACCTCCCTCGCGAACGACTCTGCGACTGCTTTT	-- GCAATGCTTCTTACAGGCCGCCCCCACACGGCGTGACGACGGGC
W22	821	GCCAAAGCGCAGAGACTGGCTGCTCGACCTCCCTCGCGAACGACTCTGCGACTGCTTTT	-- GCAATGCTTCTTACAGGCCGCCCCCACACGGCGTGACGACGGGC
B73	820	GCCAAAGCGCAGAGACTGGCTGCTCGACCTCCCTCGCGAACGACTCTGCGACTGCTTTT	-- GCAATGCTTCTTACAGGCCGCCCCCACACGGCGTGACGACGGGC
TIP534	909	TG-----CGCGCAGC-----AAGGCCATCCCTGTAG-----CCCCGGCTTCGCCCCACTCCAAATTCCTCTCTCT-----ATCTCTCATCTCCCATG-----ATGCGAT-----	
TIP517	917	TG-----CGGGCTGC-----TGGGAGCATCTCTTGTAG-----CCCCGGCC-----ACTCCAAATCTCTCTCT-----TCTCTCCATGCGAT-----ATGCGAT-----	
TIP508	884	TG-----CGGGCTGC-----AAGGGGACATCTCTTGTAG-----CCCCGGCC-----ACTCCAAATCTCTCTCT-----TCTCTCCATGCGAT-------GCGAT-----	
TIP485	913	TG-----CGGGCTGC-----AGCGCTGAGGGGACATCTCTTGTAG-----CCCCGGCC-----CCTCCCACTCCAAATCTCTCTCT-----TCTCTCCATGCGAT-----	
TIP469	955	TG-----CGGGCTGC-----AGGGCATCTCTTGTAG-----CCCCGGCC-----CCTCCCACTCCAAATCTCTCTCT-----TCTCTCCATGCGAT-----	
TIP466	988	TG-----CGGGCTGC-----AGGGCATCTCTTGTAG-----CCCCGGCC-----CCTCCCACTCCAAATCTCTCTCT-----TCTCTCCATGCGAT-----	
TIP462	925	TG-----CGGGCTGC-----AGGGCATCTCTTGTAG-----CCCCGGCC-----CCTCCCACTCCAAATCTCTCTCT-----TCTCTCCATGCGAT-----	
TIP458	923	TG-----CGGGCTGC-----AGGGCATCTCTTGTAG-----CCCCGGCC-----CCTCCCACTCCAAATCTCTCTCT-----TCTCTCCATGCGAT-----	

Iltis et al 125	129	-
INIFAP-JSG 378	149	
INIFAP-JSG 374	149	
CIMMYT-11355	149	
TAK-Kato Site_4	149	
BFB-Beno 967	149	
HGW-Wilkes Site	149	
INIFAP-JSG y LO	157	
INIFAP-JSG y MA	149	
GWB-BeadleKato	149	
INIFAP-JSG y LO	149	
NCRPIS-PI213793	150	
CIMMYT-CHH160	150	
NCRGP-MAG450	150	
INIFAP-YUC7	150	
PCIM-APC13	150	
NRC-SAN329	150	
INIFAP-GUA14	150	
CIMMYT-OAX70	150	
INIFAP-OAX68	150	
CIMMYT-URGII	150	
INIFAP-MEX48	433	TCTGGTGGGTGGTCGCCGTGACGCCGTGCCGTCGCTGCTCAACCGCTGG-CTGGTGCATCACGTTG-CCTGGGACTAGCTGC CGCCGCGCTGCCACCCTGAC
INIFAP-PUE32	433	TCTGGTGGGTGGTCGCCGTGACGCCGTGCCGTCGCTGCTCAACCGCTGGCTGGTGCATCACGTTG-CGGGACTAGCTGC CGCCGCGCTGCCACCCTGAC
INIFAP-SIN2	150	
NCRGP-CHI349	150	
CIMMYT-GUA131	150	
ICA-VEN453	150	
B73	149	
Iltis et al 125	129	-
INIFAP-JSG 378	149	
INIFAP-JSG 374	149	
CIMMYT-11355	149	
TAK-Kato Site_4	149	
BFB-Beno 967	149	
HGW-Wilkes Site	149	
INIFAP-JSG y LO	157	
INIFAP-JSG y MA	149	
GWB-BeadleKato	149	
INIFAP-JSG y LO	149	
NCRPIS-PI213793	150	
CIMMYT-CHH160	150	
NCRGP-MAG450	150	
INIFAP-YUC7	150	
PCIM-APC13	150	
NRC-SAN329	150	
INIFAP-GUA14	150	
CIMMYT-OAX70	150	
INIFAP-OAX68	150	
CIMMYT-URGII	150	
INIFAP-MEX48	541	CGCGACTATGGCGTCC-TCAACCGCGTGTCCACACATCACGGACACGGCACGGCTTCAACCGTCTTGAGGCTATGACTTATACGGATTGGCTTGC GG
INIFAP-PUE32	543	CGCGACTATGGCGTCCCTCAACCGCGTGTTCACACATCACGGACACGGTACCGTACGGCACACCTTTCACCTGTGAGGCTATGACTTATACGGATTGGCTTGC GG
INIFAP-SIN2	150	
NCRGP-CHI349	150	
CIMMYT-GUA131	150	
ICA-VEN453	150	
B73	149	
Iltis et al 125	129	-
INIFAP-JSG 378	149	
INIFAP-JSG 374	149	
CIMMYT-11355	149	
TAK-Kato Site_4	149	
BFB-Beno 967	149	
HGW-Wilkes Site	149	
INIFAP-JSG y LO	157	
INIFAP-JSG y MA	149	
GWB-BeadleKato	149	
INIFAP-JSG y LO	149	
NCRPIS-PI213793	150	
CIMMYT-CHH160	150	
NCRGP-MAG450	150	
INIFAP-YUC7	150	
PCIM-APC13	150	
NRC-SAN329	150	
INIFAP-GUA14	150	
CIMMYT-OAX70	150	
INIFAP-OAX68	150	
CIMMYT-URGII	150	
INIFAP-MEX48	650	CACTAGTTGGCGTCCCGCGTGCATAGCGAGCGTTAGCTAAGCAGTCAGGTAAATTGTTGAACGGACCGTTAAAAGCCCGCTGATAACGGCCGTGCTCGGGCT
INIFAP-PUE32	653	CACTAGTTGGCGTCCCGCGTGCATAGCGAGCGTTAGCTAAGCAGTCAGGTAAATTGTTGAACGGACCGTTAAAAGCCCGCTGATAACGGCCGTGCTCGGGCT
INIFAP-SIN2	150	
NCRGP-CHI349	150	
CIMMYT-GUA131	150	
ICA-VEN453	150	
B73	149	
Iltis et al 125	129	-
INIFAP-JSG 378	149	
INIFAP-JSG 374	149	
CIMMYT-11355	149	
TAK-Kato Site_4	149	
BFB-Beno 967	149	
HGW-Wilkes Site	149	
INIFAP-JSG y LO	157	
INIFAP-JSG y MA	149	
GWB-BeadleKato	149	
INIFAP-JSG y LO	149	
NCRPIS-PI213793	150	
CIMMYT-CHH160	150	
NCRGP-MAG450	150	
INIFAP-YUC7	150	
PCIM-APC13	150	
NRC-SAN329	150	
INIFAP-GUA14	150	
CIMMYT-OAX70	150	
INIFAP-OAX68	150	
CIMMYT-URGII	150	
INIFAP-MEX48	760	AGCCCAAAGGGCTAAATTCTGTGAGGCCGGCACGCTATCCGGGCCGGCTAACGCCGGGCCGCTTCATCCGTGCCGGCGGGCTGTGCTCGTGTAAAAATCG
INIFAP-PUE32	763	AGCCCAAAGGGCTAAATTCTGTGAGGCCGGCACGCTATCCGGGCCGGCTAACGCCGGGCCGCTTCATCCGTGCCGGCGGGCTGTGCTCGTGTAAAAATCG
INIFAP-SIN2	150	
NCRGP-CHI349	150	
CIMMYT-GUA131	150	
ICA-VEN453	150	
B73	149	

Supplementary Data 17. Sequence alignment of the TB1 binding region in the *tb1* *Hopscotch* region (A), prolificacy locus (B) and *tga1* promoter (C). Pink square frames represent the GGNCCC TB1 binding motif at the summit of each peak. The sequence of *Zea mays* landraces, *Zea mays* ssp. *parviglumis* and *Zea mays* ssp. *mexicana* in (A) are downloaded from Studer *et al.*, 2011; the sequence of *Zea mays* cultivars and *Zea mays* ssp. *parviglumis* in (B) are downloaded from Wills *et al.*, 2013; and the sequence of *Zea diploperennis*, *Z. mays* ssp. *parviglumis* and *Zea mays* cultivars in (C) are downloaded from Wang *et al.*, 2005.