

Table S1. Primer sequences of the genes for ddPCR, genotyping and sequencing used in this study

Primer name	Primer sequence (5'-3')
ddPCR primers	
<i>ZmLOX5gsp-L</i>	CTCCATATGAGCCTGGGCAGATTG
<i>ZmLOX5gsp-R</i>	CAAGCGTGGACTCCTCTCTC
<i>α-Tubulin-F</i>	GCTATCCTGTGATCTGCCCTG
<i>α-Tubulin-R</i>	CGCCAAACTTAATAACCCAGTA
Genotyping primers	
9242	AGAGAAGCCAACGCCAWCGCCTCYA
<i>lox5-3F</i>	TGCCGGACCAGTCAAGCCCATAT
<i>lox5-3R</i>	GGCCCCCTCCGGTTCTTCAAGTC
Sequencing primers	
<i>ZmLOX5gDL-L</i>	GCGGTGATCGAGCCGTTTCGTAATC
<i>ZmLOX5gDL-R</i>	CAAGCGTGGACTCCTCTCTC
B73 ZmLOX5 specific primers	
<i>B73-8th intron-F</i>	ACTGAGGTGAGCAGCACTAAAC
<i>B73-8th intron-R</i>	GTTTAGTGCTGCTCACCTCAG
Yu796 ZmLOX5 specific primers	
<i>Yu796-8th intron-F</i>	TAGACAATACATAGATCGACTACAC
<i>Yu796-8th intron-R</i>	TATAGGCACCTCAGTACGTGTA

Table S2. Primer sequences for qRT-PCR tests in this study

Primer name	Primer (5'-3')	Tm (°C)	Product size (bp)
<i>ZmLOX5-F</i>	GGGCAGATTGTGTCTCGTAGTA	62	140
<i>ZmLOX5-R</i>	ATATTCAAGCGTGGACTCCTCT	60	140
<i>ZmLOX8-F</i>	CAGTACCGACAGACAGCCAT	60	163
<i>ZmLOX8-R</i>	GTTTCGGACCACCAAATCAA	57	163
<i>ZmLOX10-F</i>	ATCCTCAGCATGCATTAGTCC	59	139
<i>ZmLOX10-R</i>	AGTCTCAAACGTGCCTCTTGT	59	139
<i>ZmJAR1a-F</i>	TCTATCCGCCAAGCTGTTTC	58	150
<i>ZmJAR1a-R</i>	CCCCGTCATAATGCCATAGATG	61	150
<i>Zmα-Tubulin-F</i>	GCTATCCTGTGATCTGCCCTG	62	139
<i>Zmα-Tubulin-R</i>	CGCCAAACTTAATAACCCAGTA	59	139

Table S3. Sequencing results of *LOX5-CNV1* and *LOX5-CNV2* showing several SNPs found in Exons 9 and 10 relative to the reference sequence of *ZmLOX5* (Zm00001eb216870) of B73-REFERENCE-NAM-5.0 genome)

gDNA position at B73	B73	Yu796-CNV1	Percentage (%)	Yu796-CNV2	Percentage (%)	AA position at B73	B73	Yu796-CNV1	Yu796-CNV2
3810	<u>A</u> A <u>G</u>	<u>A</u> A <u>G</u>	61.5	<u>G</u> <u>T</u> <u>G</u>	38.5	391	K	K	<u>V</u>
3963	<u>A</u> A <u>C</u>	<u>A</u> A <u>C</u>	69.2	<u>G</u> A <u>C</u>	30.8	442	N	N	<u>D</u>
3984	<u>G</u> A <u>T</u>	<u>G</u> A <u>T</u>	69.2	<u>T</u> A <u>T</u>	30.8	449	D	D	<u>Y</u>
4216	A <u>T</u> <u>C</u>	A <u>T</u> <u>C</u>	38.5	A <u>T</u> <u>A</u>	61.5	496	I	I	I
4323	<u>C</u> <u>C</u> <u>C</u>	<u>C</u> <u>C</u> <u>C</u>	46.2	<u>C</u> <u>G</u> <u>C</u>	53.8	532	P	P	<u>R</u>
4326	A <u>G</u> <u>G</u>	A <u>G</u> <u>G</u>	46.2	A <u>T</u> <u>G</u>	53.8	533	R	R	<u>M</u>
4354	A <u>G</u> <u>G</u>	A <u>G</u> <u>G</u>	61.5	A <u>G</u> <u>C</u>	38.5	542	R	R	<u>S</u>
4365	A <u>C</u> <u>C</u>	A <u>C</u> <u>C</u>	69.2	A <u>G</u> <u>C</u>	30.8	546	T	T	<u>S</u>
4404	A <u>A</u> <u>C</u>	A <u>A</u> <u>C</u>	69.2	A <u>T</u> <u>C</u>	30.8	559	N	N	<u>I</u>
4410	<u>G</u> <u>G</u> <u>G</u>	<u>G</u> <u>G</u> <u>G</u>	30.8	<u>G</u> A <u>G</u>	69.2	561	G	G	<u>E</u>
4596	T <u>C</u> <u>C</u>	T <u>C</u> <u>C</u>	69.2	<u>T</u> <u>T</u> <u>C</u>	30.8	623	S	S	<u>F</u>

The Table presents the SNPs found in the coding sequence of Yu796 -2×*LOX5* compared to the B73-*LOX5* locus and the respective changes on the amino acid (AA) sequences. % represents the frequency of specific SNP occurrence in the sequenced PCR amplification products (n=13).