		PAIR1		*REC8*		*OSD1*	
T_0	WT	CAAGCAACCCAGTGCACCGCTGG	WT	CCGGAGAGCCTTAGTGCCATGGG	WT	CCTGCCGCCGACGAGCAACAAGG	WT
	#2	CAAGCAACCCAGTGCAC - GCTGG	-1bp	CCGGAGAGCCTTAGTGCACATGGG	+1bp	CCTGCCGCCGACGAGCATACAAGG	+1bp
		CAAGCAACCCAGTGCACTCGCTGG	+1bp	CCGGAGAGCCTTAGTGCGCATGGG	+1bp	CCTGCCGCCGACGAGCACACAAGG	+1bp
	#3	CAAGCAACCCAGTGCAC-CGCTGG	-1bp	CCGGA----------G	-17bp	CCTGCCGCCGACGAG - -AACAAGG	-2bp
		CAAGCAACCCAGTGCACTCGCTGG	+1bp	CCGGAGAGCCTTAGTGC - - TGGG	-2bp	CCTGCCGCCGACGAG - -AACAAGG	-2bp
	#6	CAAGCAACCCAGTGCAC-CGCTGG	-1bp	CCGGAGAGCCTTAGTGCTCATGGG	+1bp	CCTGCCGCCGACGAGCAAACAAGG	+1bp
		CAAGCAACCCAGTGCACACGCTGG	+1bp	CCGGAGAGCCTTAGT - - CATGGG	-2bp	CCTGCCGCCGACGAGC - ACAAGG	-1bp
	#7	CAAGCAACCCAGTGCACGCGCTGG	+1bp	CCGGAGAGCCTTAGTGCACATGGG	+1bp	CCTGCCGCCGACGAGCA - CAAGG	-1bp
		CAAGCAACCCAGTGCACCCGCTGG	+1bp	CCGGAGAGCCTTAGTGCTCATGGG	+1bp	CCTGCCGCCGACGAGCATACAAGG	+1bp
	#8	CAAGCAACCCAGTGCAC-CGCTGG	-1bp	CCGGAGAGCCTTAGTGCTCATGGG	+1bp	CCTGCCGCCGACGAGCAAACAAGG	+1bp
		CAAGCAACCCAGTGCACACGCTGG	+1bp	CCGGAGAGCCTTAGTGCGCATGGG	+1bp	CCTGCCGCCGACGAG - - ACAAGG	-2bp
	#13	CAAGCAACCCAGTGCACGCGCTGG	+1bp	CCGGAGAGCCTTAGTGCCCATGGG	+1bp	CCTGCCGCCGACGAG-----------	-27bp
		CAAGCAACCCAGTGCACTCGCTGG	+1bp	CCGGAGAGCCTTAGTTTGCCATGGG	+2bp	CCTGCCGCCGACGAG - -AACAAGG	-2bp
	#14	CAAGCAACCCAGTGCA - CGCTGG	-1bp	CCGGAGAGCCTTAGTGCCCATGGG	+1bp	CCTGCCGCCGACGAGCATACAAGG	+1bp
		CAAGCAACCCAGTGCACTCGCTGG	+1bp	CCGGAGAGCCTTAGTTTGCCATGGG	+2bp	CCTGCCGCCGACGAGCAAACAAGG	+1bp
	#15	CAAGCAACCCAGTGCACACGCTGG	+1bp	CCGGAGAGCCTTAGTGCACATGGG	+1bp	CCTGCCGCCGACGAGCAAACAAGG	+1bp
		CAAGCAACCCAGTGCACTCGCTGG	+1bp	CCGGAGAGCCTTAGTGCTCATGGG	+1bp	CCTGCCGCCGACGAGCAAACAAGG	+1bp
T_1	#2	CAAGCAACCCAGTGCAC - GCTGG	-1bp	CCGGAGAGCCTTAGTGCACATGGG	+1bp	CCTGCCGCCGACGAGCATACAAGG	+1bp
		CAAGCAACCCAGTGCACTCGCTGG	+1bp	CCGGAGAGCCTTAGTGCGCATGGG	+1bp	CCTGCCGCCGACGAGCACACAAGG	+1bp
	#6	CAAGCAACCCAGTGCAC-CGCTGG	-1bp	CCGGAGAGCCTTAGTGCTCATGGG	+1bp	CCTGCCGCCGACGAGCAAACAAGG	+1bp
		CAAGCAACCCAGTGCACACGCTGG	+1bp	CCGGAGAGCCTTAGT - - CATGGG	-2bp	CCTGCCGCCGACGAGC - ACAAGG	-1bp
	#7	CAAGCAACCCAGTGCACGCGCTGG	+1bp	CCGGAGAGCCTTAGTGCACATGGG	+1bp	CCTGCCGCCGACGAGCA - CAAGG	-1bp
		CAAGCAACCCAGTGCACCCGCTGG	+1bp	CCGGAGAGCCTTAGTGCTCATGGG	+1bp	CCTGCCGCCGACGAGCATACAAGG	+1bp

Fig. S3. Mutation detection of three *MiMe* genes of *Fix10* lines.

Sequence chromatograms showing detailed mutations at each target site.