ZIR ZEBRAFISH INTERNATIONAL RESOURCE CENTER

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$mef2ca^{b631}$

Nature of the mutation

The b631 allele contains a single A-to-C point mutation that changes the start methionine codon (ATG) into a leucine codon (CTG) (Miller et al., Developmental Biology 308: 144-157, 2007).

Genotyping assay

Genotyping of the b631 allele is based on the RFLP assay (Restriction Fragment Length Polymorphism; Botstein et al., Am. J. Hum. Genet. 32: 314-331, 1980). This method is used to detect a mutation that either creates or abolishes a site recognized by a specific restriction enzyme. In the RFLP assay, a sequence of interest is first PCR-amplified and then the PCR product is subjected to restriction enzyme digestion. The presence or absence of the mutation is determined by the resulting restriction pattern. The b631 mutation creates a site recognized by the BstNI restriction enzyme.

Primers:

HOO 03: 5' GGA AGG AGA AGG AGA CGA GTG T 3' HOO 02: 5' AAT TAC AAG TGC TTG ATG TTT GGA 3'

PCR program (53 30 30):

- 94°C for 3 min 1
- 2. 94°C for 30 sec
- 3. 53°C for 30 sec
- 72°C for **30** sec 4.
- 5. Go to step 2 (above) for 39 cycles
- 6. 72°C for 5 min
- 8.0°C hold 7.
- 8. **END**

Product size: 361 bp

Digestion of the PCR product with the BstNI restriction enzyme:

Product type	Product digestion	DNA fragments after digestion (bp)
PCR product derived from the WT template	unaffected	361 bp
PCR product containing the mutation	cleaved	290 bp and 71 bp