## ZIR ZEBRAFISH INTERNATIONAL RESOURCE CENTER

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# $sp5l^{fh241}$

## **Nature of the mutation**

The *fh241* allele contains a single G-to-T point mutation that introduces a premature stop codon at amino acid 296, resulting in truncation of the Sp51 protein (Moens C., personal communication).

## Genotyping assay

Genotyping of the fh241 allele is based on the dCAPS assay (derived Cleaved Amplified Polymorphic Sequence; Neff et al., The Plant Journal 14(3): 387-392, 1998). In this assay, a restriction enzyme recognition site that includes the single nucleotide polymorphism (SNP) is introduced into the PCR product by a primer containing one or more mismatches to template DNA. The PCR product modified in this manner is then subjected to restriction enzyme digestion and the presence or absence of the SNP is determined by the resulting restriction pattern.

To genotype the *fh241* allele, a mismatch (marked in red) has been introduced into the forward primer. During PCR, this mismatch and the fh241 mutation create a Tsp509I restriction enzyme site in the amplified product. The Tsp509I site is not present in the PCR product derived from the WT DNA template.

#### **Primers:**

**fh241 03d:** 5' GAA GAG CTT CAC GCG TTC AAA T 3' **fh241 04:** 5'AGA GCA TCA GTC CCG CTG TG 3'

### PCR program (60 30 30):

- 1. 94°C for 3 min
- 2. 94°C for 30 sec
- 3. 60°C for 30 sec
- 4. 72°C for **30** sec
- 5. Go to step 2 (above) for 39 cycles
- 72°C for 5 min 6.
- 7. 8.0°C hold
- 8. **END**

## Product size: 186 bp

## Digestion of the PCR product with the Tsp509I restriction enzyme:

Product type	Product digestion	DNA fragments after digestion (bp)
PCR product derived from the WT template	unaffected	186 bp
PCR product containing the mutation	cleaved	167 bp and 19 bp