

**Publication**

[Kane, D.A., McFarland, K.N., and Warga, R.M. \(2005\) Mutations in half baked/E-cadherin block cell behaviors that are necessary for teleost epiboly Development](#)

Attribute Gene:   Attribute Feature:

**ZFIN Feature Builder - overview:**

Feature Type:  ▼

Name/Alele Designation:

- Point
- Insertional Construct
- Insertional Allele
- Translocation
- Inversion
- Deficiency
- Gene Family
- Special Feature
- Unknown

**ZFIN Feature Relationships:**

Feature	Type	Relationship	Target Feature
<input type="button" value="Add"/> <input type="text" value="Feature Names"/> ▼	[FYI text]	<input type="text" value="valid relationships"/> ▼ <small>(determined by type of selected feature)</small>	<input type="text" value="Feature Names"/> ▼
m134	point	is_allele_of	oep

**Create New Genotype in ZFIN:**

Genotype Handle:

Background:  ▼  ▼

Define Genotype:  ▼  ▼  ▼

**Genotypes Available for Curation:**

Genotype Handle	Display Name	Feature(s)	Zygosity	Background	
MZm134;AB	oep <sup>m134/m134</sup>	m134	Maternal Zygotic	AB	<input type="button" value="X"/>
m134Mat/MZb16;AB/WIK	oep <sup>m134/+;cyc<sup>b16/b16</sup></sup>	m134 b16	Maternal Maternal Zygotic	AB / WIK	<input type="button" value="X"/>

**Environment:**

Name
_Standard

Add Name:

- Chemical
- Morpholino (requires seq ID)
- Physical
- Physiological
- Salinity
- Temperature

**Define Environments:**

Env.	Condition
Add	<input type="text"/>

Value:  units  Comments

**Figure Caption or Text Description:**

Label	Caption
Fig. 3	Phenocopies of <i>hab</i> allele-specific traits by disruption of EC1 or EC4. (A) Injection of morpholino oligonucleotide MO1 into wild-type embryos at increasing doses mimics the epiboly arrest phenotype. (B) Phenotype of <i>hab</i> allele at equivalent stage. (C) Aberrant splice products caused by MO1 appear at doming, shortly after the beginning of zygotic transcription (Kane and Kimmel, 1993). Arrow indicates maternal product. (D) Splicing event caused by MO1 (black bar) and conceptual protein, inferred by sequencing RT-PCR product using the primers indicated by arrows in exon8 and exon11. (E) Injection of MO2 into wild-type

Add

**Image:**

Figure	Image
Upload	Fig. 3 

**Define Experiment:**

Add

Expressed Gene	Genotype Handle	Environment	Assay
Gene list	Handle list	Env. list	Assay list

(optional for PATO)

- Expression assays include: ISH, NB, IHC, WB, RTPCR, NPA, PX, DISH, CDNAC

**Experiments Available for Curation:**

Expressed Gene	Genotype Handle	Environment	Assay	
-	MZm134;AB	standard	Alcian staining	X
shh	m134Mat/MZb16;AB/WIK	morpholino	ISH	X

After defining all Experiments, the curator can go to either a Gene Expression or Phenotype annotation panel.

### ZFIN Gene Expression (FX) Curation - overview:

An Expression record is created by selecting a Figure, Experiment, and Developmental Stage range.

The Experiment list must contain only those defined experiments where an Expressed Gene has been specified.

Add Fig. 4 ▼

shh m134Mat/MZb16;AB/WIK morpholino ISH ▼

Start: 26+ somites (22.00h-24.00h) ▼

End: Prim-5 (24.00h-30.00h) ▼

The curator associates Anatomical Structures with Expression records, selecting from a list of AO terms that have been compiled specifically for this publication:

Update Structures for Expression(s)

Fig.4 shh m134Mat/MZb16;AB/WIK morpholino ISH 26+somites to Prim-5

$\Phi$			Modifier	Structure
<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>	not	<b>floor plate</b> (5-9 somites - Days 45-89)
<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>		<b>floor plate</b> (5-9 somites - Days 45-89)
<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>		<b>hypochord</b> (10-13 somites - Protruding-mouth)
<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>		neural keel (Bud - 10-13 somites)
<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>	not	<b>notochord</b> (Bud - Day 5)
<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>		<b>notochord</b> (Bud - Day 5)

## Phenotype Annotation:

(To reduce clutter below, we have omitted a Qualifier column, a second Stage column, and any additional Entities and Measurements)

Select from a list of *all* previously defined Experiments.

### Example 1

From the Experiment list, I select:

– MZm134;AB standard Alcian staining ▼

(no Expressed Gene is specified in this Experiment)

	Figure	Stage:	Entity:	Attribute:	Context:	
Add	Fig. list ▼				from context ontology ▼	
3		Prim-5	pigmentation	spotted	recessive ▼	X
4		Day 4	floor plate	malformed	recessive ▼	X

### Example 2

From the Experiment list, I select:

shh m134Mat/MZb16;AB/WIK morpholino ISH ▼

Because an Expressed Gene is specified in this Experiment, it is assumed that an alteration in its expression pattern is being described, thus the Entity is pre-filled with “expression pattern” and can not be modified:

	Figure	Stage:	Entity:	Attribute:	Context:	
Add	Fig. list ▼		expression pattern		from context ontology ▼	
3		Prim-5	expression pattern	ectopic	▼	X
4		Day 4	expression pattern	intense	▼	X