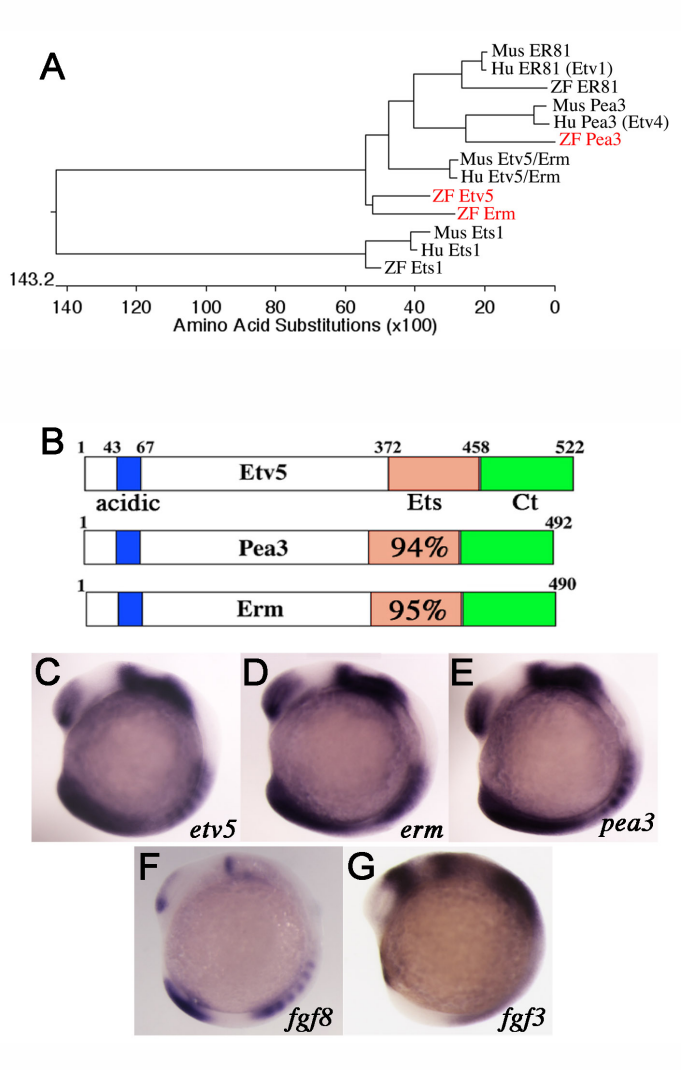
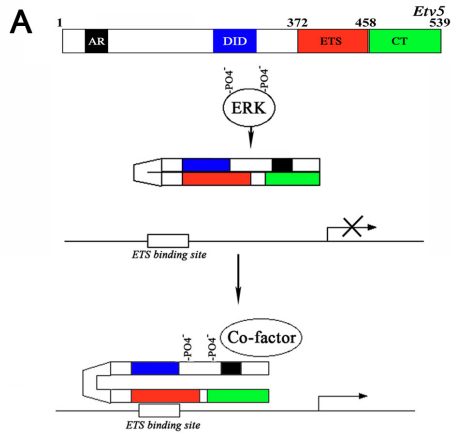
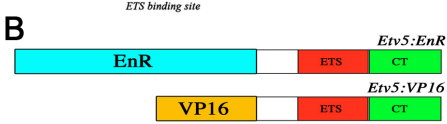
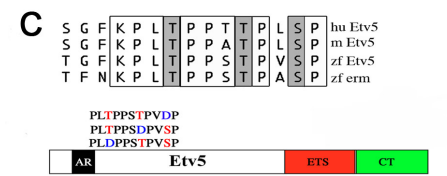
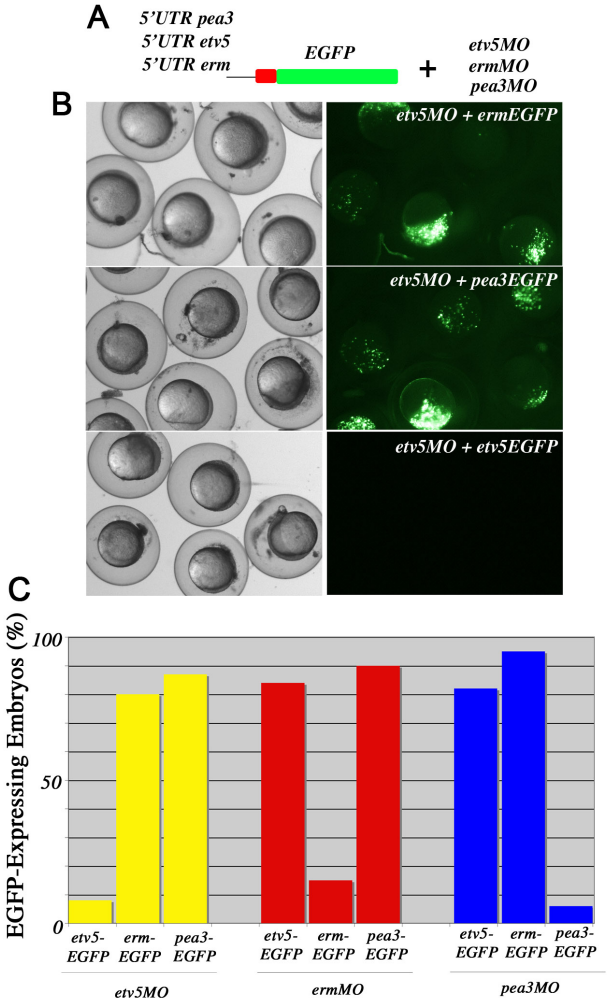
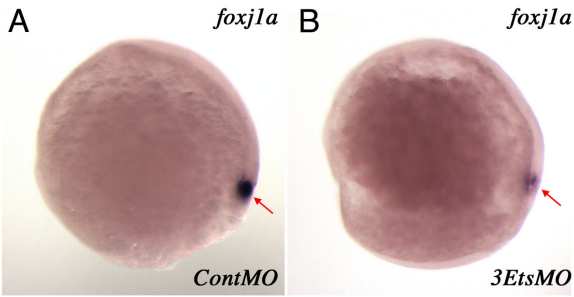

A
Mus ER81
Hu ER81 (Etv1)
ZF ER81
Mus Pea3
Hu Pea3 (Etv4)
ZF Pea3
Mus Etv5/Erm
Hu Etv5/Erm
ZF Etv5
ZF Erm
Mus Ets1
Hu Ets1
ZF Ets1
143.2
140 120 100 80 60 40 20 0
Amino Acid Substitutions (x100)
B
1 43 67 372 458 522
Etv5
acidic
Ets
Ct
1 492
Pea3
94%
1 490
Erm
95%
C
etv5
D
erm
E
pea3
F
fgf8
G
fgf3


A
Etv5
1
372
458
539
AR
DID
ETS
CT
PO4-
PO4-
ERK
ETS binding site
Co-factor
PO4-
PO4-
ETS binding site

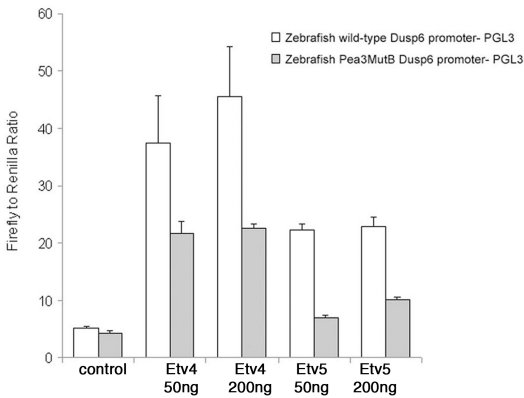

B
Etv5:EnR
EnR
ETS
CT
Etv5:VP16
VP16
ETS
CT


C
S G F K P L T P P T T P L S P hu Etv5
S G F K P L T P P A T P L S P m Etv5
T G F K P L T P P S T P V S P zf Etv5
T F N K P L T P P S T P A S P zf erm
PLTPPSTPVDP
PLTPPSDPVSP
PLDPPSTPVSP
AR
Etv5
ETS
CT


A
5'UTR pea3
5'UTR etv5
5'UTR erm
EGFP
+
etv5MO
ermMO
pea3MO
B
etv5MO + ermEGFP
etv5MO + pea3EGFP
etv5MO + etv5EGFP
C
EGFP-Expressing Embryos (%)
100
50
0
etv5-EGFP
erm-EGFP
pea3-EGFP
etv5-EGFP
erm-EGFP
pea3-EGFP
etv5-EGFP
erm-EGFP
pea3-EGFP
etv5MO
ermMO
pea3MO




Supplementary Figure 4

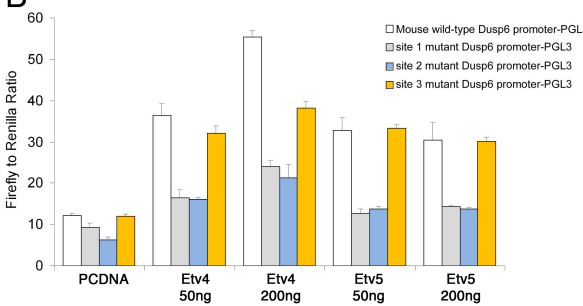



Supplementary Figure 5

**A** Alignment of highly conserved region in the Dusp6 promoter containing 3 putative Etv4/Etv5 binding motifs (bold)

```
mouse      ATCCGGAGCGGAAATTCCTTTCCGTTTTTCTCAATG
human      ATCCGGAGCGGAAATTCCTTTCCGTTTTTCTCAATG
zebrafish  ATCCGGAGCGGAAATTCCTTTCCGTTTTTCTCAATG
fugu       ATCCGGAGCGGAAATTCCTTTCCGTTTTTCTCAATG

Site 1 wt  ATCCGGAGCGGAAATTCCTTTCCGTTTTTGTGAATG
Site 1 mt  ATCCGGAGCGTTCATTCCTTTCCGTTTTTGTGAATG

Site 2 wt  ATCCGGAGCGGAAATTCCTTTCCGTTTTTGTGAATG
Site 2 mt  ATCCGGAGCGGAAAGAACTTTCCGTTTTTGTGAATG

Site 3 wt  ATCCGGAGCGGAAATTCCTTTCCGTTTTTGTGAATG
Site 3 mt  ATCCGGAGCGGAAATTCCTGAACGTTTTTGTGAATG

zebrafish  ATCCGGAGCGGAAATTCCTTTCCGTTTTTCTCAATG
Pea3B Mut  ATCCGGCCGCGGCCCCGTCCTTTCCGTTTTTCTCAATG
```

**B**




Supplementary Figure 6