



Supplemental Material to:

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**Microtubule-associated protein 9 (Map9/Asap) is required
for the early steps of zebrafish development**

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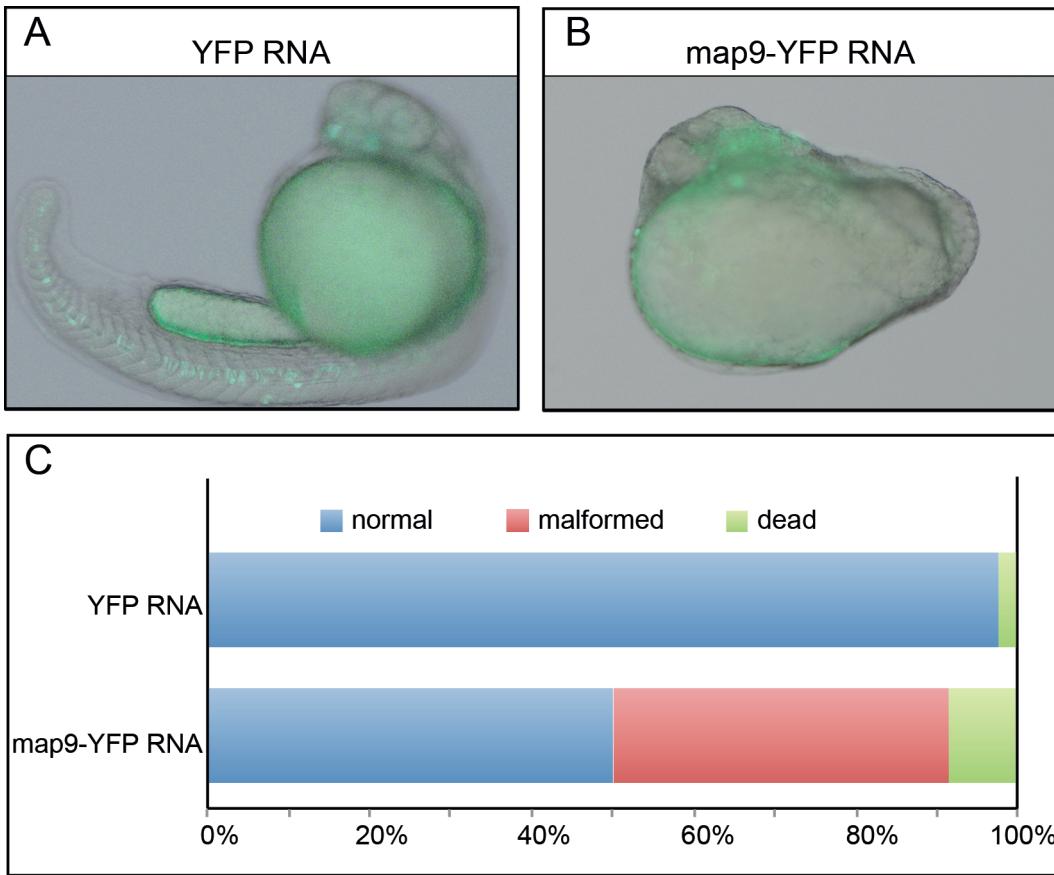


Figure S1

Map9 overexpression is associated with developmental defects and embryo death. (A-B) Embryos were injected with 400 pg YFP RNA, n=42 (A) or *map9*-YFP mRNA, n=36 (B) at the 1-cell stage and imaged at 24 hpf. Scale bars, 200 μ m. (C) Percentages of normal, malformed and dead embryos at 24 hpf.

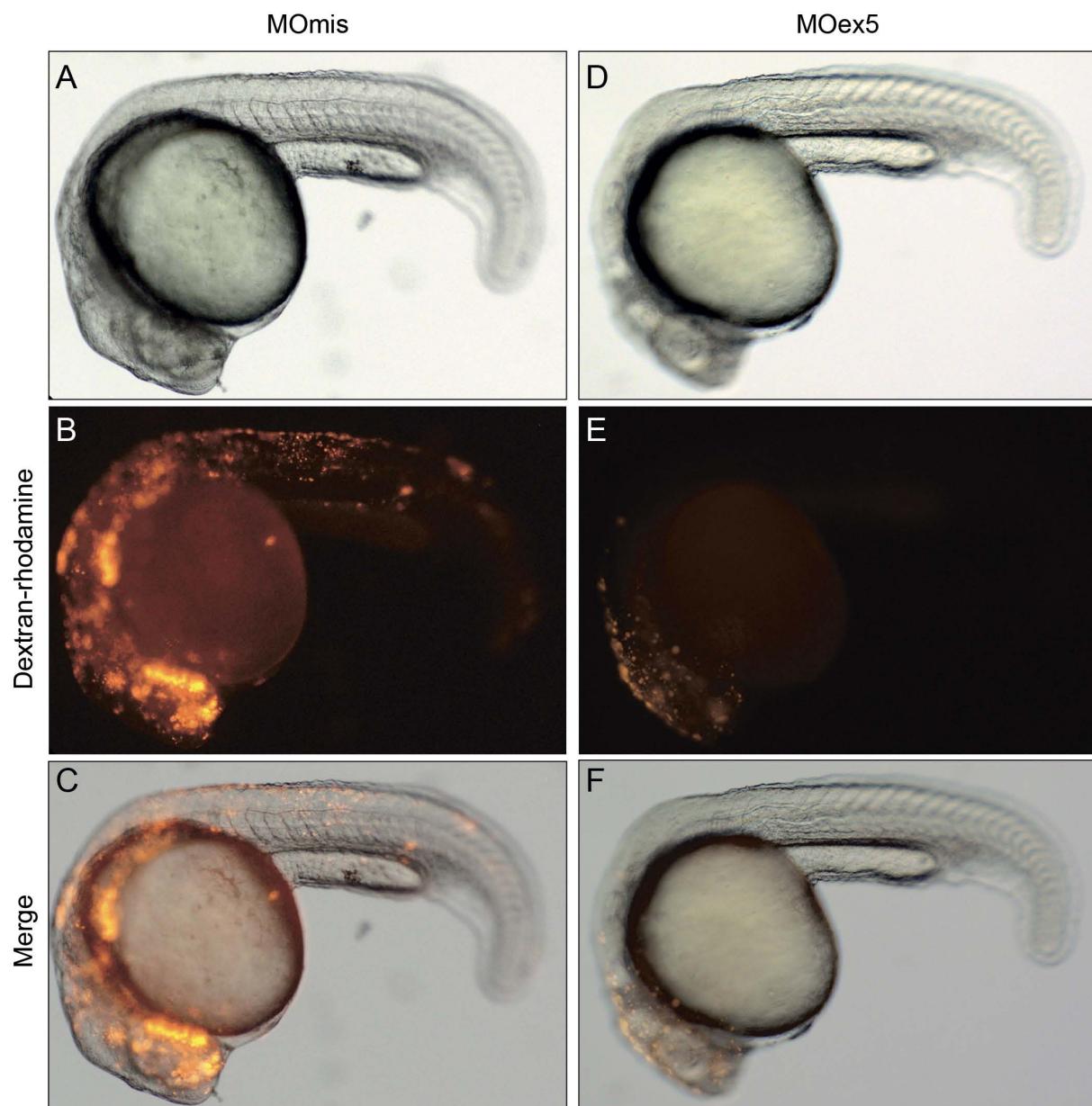


Figure S2

Morpholino-dependent depletion of *map9* in a random group of cells does not affect epiboly. One μg of MOex5 or control MOmis was co-injected with dextran-rhodamine (red) in a group of cells of 64-cell stage embryos. In contrast to embryos injected at the 1-cell stage (Figure 2) or injected directly in the YSL (Figure 6), these embryos do not exhibit developmental defects at 24 hpf.

Primer name	5' - 3' sequence
map9_ZF1_fwd	ATGATGACGACGATACTCA
map9_ZF2_rev	TTAGTGGCAGTGGAGATT
map9_ZF8_rev	GCCCTCCTAGTAATTCCAAG
map9_ZF18F	TCCAGTGCCATTGCCTTCAG
map9_ZFjctR	TTCTGTGGCAGCTGCTGACGAT
map9_ZFovF	TCTGTGGCAGCACTGCCAG
map9_ZFdelR1	TCTAACTGGCCAGTGTACAC
aurka_fwd	ATTGCAGATTGGCTGGTC
aurka_rev	TTCTCATCATGTGTTAACCTCAA
plk1_fwd	GCCATTACAAAAGTCTG
plk1_rev	GCCCTCCTAGTAATTCCAAG
plk4_fwd	AGGCCTCATTCTCGCTACC
plk4_rev	CTGCTGTGACCGCTATGTCT
shha_fwd	GCAGAAGAAGACATCCGAAGA
shha_rev	GGCCAGTGGTCATTACAGA
smo_fwd	AATTGGCCATGGTCTG
smo_rev	CTTCATTCTGGCAACCCTAG
igu_fwd	TCAATGCGGTGACGTTCTGT
igu_rev	AAGGCCTTTACAATGTTGG
gsc_fwd	AGAGACGACACCGAACCATTT
gsc_rev	GATT CCTCTGACGACGACCTT
oep_fwd	TTCGTTGGACTGACCGGAGTT
oep_rev	ATCCCTGAGGC GTTCATCGTA
sqt_fwd	CCGGACACTCTGACTGGA
sqt_rev	TCGCTTGCTGATATGGAGGAC
cyc_fwd	CTGCTCGGAGTGTGAAAG
cyc_rev	GTCAAAGATGCCACGTAG
mezzo_fwd	GCTCACGCTGCTCCAGAGAG
mezzo_rev	TGTGGCCAGGGATTCAAGAG
ntla_fwd	CCTCGGGTTCGTACTGTGAG
ntla_rev	TCCGGAAGAGTTGTCCATGT
sox17_fwd	TCCGCTCTCAGACTCCAAAT
sox17_rev	AATCGCTTGTTCGTTTCACC
sox32_fwd	ACGAAAGAGGAGCGCAGA
sox32_rev	CATTGCTTCCATGTCCTGC
tarama_fwd	TCAACCTCCAGATTCCAAT
tarama_rev	CTACCGGACCCCAACTACCT
charon_fwd	CACAAAAGCGAGCGAAAAAA
charon_rev	AGCCCTCCTCCGTTATGC
dnah9_fwd	CGCTTCAGGTCTGGAACACT
dnah9_rev	TGAGCCTCGGCTGCTATC
lefty1_fwd	CCAAGTGTGTCACCTCACAA
lefty1_rev	TCACGGTCTTGTGTTTCA
lefty2_fwd	CCACACAGGATCCAAAGGA
lefty2_rev	GCTGGAGTTACAGTTGCC
spaw_fwd	GTCCTGAGCTGATTGCACA
spaw_rev	CGTCTGGATGCAGAAAAC
foxa2_fwd	CAAAATGGAGGGACACGAAC
foxa2_rev	TGTTGCTGACCGAGGTGTAA
nipblA_fwd	GAGGCTCCAGTCCCAAGAAT
nipblA_rev	CCGGTTCTCCTTGACTTCC
nipblB_fwd	GCTGACGGAGCAGTACACGA
nipblB_rev	TGATCACCCCTTCTCCTCACA
bon_fwd	TTTTTCCAAACGCGGATATG
bon_rev	TCCTGAAGCGCATAACTGA
gata5_fwd	GGACGCCAGGGAACTCTAC
gata5_rev	ACACGGCAGGTACCCAG
eomesa_fwd	CAAAAGGCTTCAGGGACAAT
eomesa_rev	AGTAGGAGAGGGCGTCAGTCT
eomesb_fwd	CGCGAACATCAACACTTCA
eomesb_rev	GTCGTCCGACACCTCCAC

Table S1

Sequences of the primer pairs used to quantify gene expression by qPCR.