Figure S1


Figure S1. Nuclear positional changes in LMCs and MMCs between 4.0 and 4.7

## hpf

Angles between the center of the cell and the nucleus relative to the medial-lateral axis were measured (red line). $n=$ number of nuclei examined.

Figure S2


Figure S2. Expression of $\boldsymbol{n d r}$, mesoderm, and endoderm genes in

## C-syne2a-overexpressing embryos

(A-D) Expression of $n d r 1, n d r 2$, $t a$, and sox32 was examined by WISH in $n l a c Z$ or

C-syne $2 a$ mRNA overexpressing embryos at 5.3 hpf . The number of embryos
examined is shown at the lower right corner of each panel. Animal pole views. Scale
bars: $200 \mu \mathrm{~m}$. (E) Number of sox32-expressing endodermal cells in nlacZ- or C-syne2a-overexpressing embryos at $5.3 \mathrm{hpf} . \mathrm{n}=$ number of embryos examined. *** $p<0.001$. (F) Expression of $n d r 1, n d r 2, t a$, and sox 32 was examined by qPCR in nlac $Z$ or $C$-syne $2 a$ mRNA-overexpressing embryos at 5.3 hpf . Error bars represent standard deviations of three or four independent experiments. ${ }^{* * *} p<0.001$.

Figure S3


Figure S3. Expression of $\boldsymbol{n d r}$, mesoderm, and endoderm genes in SP600125-treated embryos
(A-D) Expression of $n d r 1$, $n d r 2$, ta, and sox32 was examined by whole-mount in situ hybridization in DMSO- or SP600125-treated embryos at 4.7 hpf. Number of embryos
examined is shown at the lower right corner of each panel. Animal pole views. Scale bars: $200 \mu \mathrm{~m}$. (E) Number of sox32-expressing endodermal cell was counted in DMSO-, or SP600125-treated embryos. $\mathrm{n}=$ number of embryos examined. ${ }^{* * *} p<$ 0.001. (F) Expression of $n d r 1$, $n d r 2$, $t a$, and sox32 was examined by qPCR in DMSOor SP600125-treated embryos at 4.7 hpf . Error bars represent standard deviations of three or four independent experiments. ${ }^{* * *} p<0.001 .{ }^{* *} p<0.05$.

Figure S4


Figure S4. MT formation was not affected by inhibition of Nodal or JNK signaling
(A-D) Cross sections of WT, SB505124-, and SP600125-treated embryos; MTs, cell membrane, and nuclei were visualized by $\alpha$-tubulin ( $\alpha$-tub), $\beta$-cat, and DAPI staining, respectively at 4.0 or 4.7 hpf . Number of nuclei examined is shown at the lower right corner of each panel. Scale bars: $10 \mu \mathrm{~m}$. (E) Percentage of cytoplasmic area occupied by MTs in LMCs of WT, SB505124-, and SP600125-treated embryos.

## Figure S5



Figure 8A-C
EGFP-smad2 mRNA (100 pg)
+smad4a mRNA (100 pg)
+mb-RFP mRNA (80 pg)
+H2B-mCherry mRNA (80 pg)
 (2880 pg each)
+dextran-Alexa Fluor® 594
$5.3 \mathrm{hpf} \sim 6.0 \mathrm{hpf}$

live imaging

Figure S5. Experimental design of work presented in Figure 8

A mixture of $E G F P-s m a d 2$, smad4a, $m b-R F P$, and $H 2 B-m C h e r r y$ mRNAs was injected into WT embryos at the one-cell stage. At $3 \mathrm{hpf}, n d r 1$ or nlacZ mRNA was injected with dextran-Alexa Fluor ${ }^{\circledR} 594$ into the YSL, and confocal live images were captured at 5.3-6.0 hpf.

Table S1. Primer sequences used for quantitative real-time PCR

Click here to Download Table S1


## Movie 1

Time-lapse image of the nucleus in LMC between 4.0 and 4.7 hpf . A white dotted line indicate the boundary between the blastoderm and the YSL. Thick white lines indicate DNBs.


Movie 2

Time-lapse image of the nucleus in MMC between 4.0 and 4.7 hpf . A white dotted line indicate the boundary between the blastoderm and the YSL. Thick white lines indicate DNBs.

