<table>
<thead>
<tr>
<th>Title</th>
<th>Sexual dimorphism of gonadal structure and gene expression in germ cell-deficient loach, a teleost fish</th>
</tr>
</thead>
<tbody>
<tr>
<td>Author(s)</td>
<td>Fujimoto, Takafumi; Nishimura, Toshiya; Goto-Kazeto, Rie; Kawakami, Yutaka; Yamaha, Etsuro; Arai, Katsutoshi</td>
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</tr>
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<td>2010-10-05</td>
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<td>Type</td>
<td>article (author version)</td>
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</tbody>
</table>

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Table S1. Survival rates and the number of PGCs in larvae injected with different doses of *dnd* MO.

<table>
<thead>
<tr>
<th>No. of eggs used</th>
<th>No. of normal larvae</th>
<th>No. of abnormal larvae</th>
<th>Survival rates</th>
<th>No. of observed larvae</th>
<th>Mean No. of PGCs s.d.</th>
<th>No. of PGCs observed in each larva</th>
</tr>
</thead>
<tbody>
<tr>
<td>Intact control</td>
<td>48</td>
<td>46</td>
<td>1</td>
<td>0.958</td>
<td>12</td>
<td>48.5 7.6</td>
</tr>
<tr>
<td>Control MO</td>
<td>48</td>
<td>44</td>
<td>3</td>
<td>0.917</td>
<td>11</td>
<td>50.5 13.0</td>
</tr>
<tr>
<td>(1000-2000 pg / embryo)</td>
<td>48</td>
<td>46</td>
<td>0</td>
<td>0.958</td>
<td>12</td>
<td>10.2 8.7</td>
</tr>
<tr>
<td><em>dnd</em> MO</td>
<td>48</td>
<td>46</td>
<td>2</td>
<td>0.938</td>
<td>12</td>
<td>7.8 14.5</td>
</tr>
<tr>
<td>(250-500 pg / embryo)</td>
<td>48</td>
<td>46</td>
<td>2</td>
<td>0.938</td>
<td>12</td>
<td>0.0 0.0</td>
</tr>
<tr>
<td><em>dnd</em> MO</td>
<td>48</td>
<td>46</td>
<td>0</td>
<td>0.958</td>
<td>12</td>
<td>0.0 0.0</td>
</tr>
<tr>
<td>(500-1000 pg / embryo)</td>
<td>48</td>
<td>46</td>
<td>2</td>
<td>0.875</td>
<td>12</td>
<td>0.0 0.0</td>
</tr>
<tr>
<td><em>dnd</em> MO</td>
<td>48</td>
<td>42</td>
<td>2</td>
<td>0.875</td>
<td>12</td>
<td>0.0 0.0</td>
</tr>
<tr>
<td>(1000-2000 pg / embryo)</td>
<td>48</td>
<td>42</td>
<td>2</td>
<td>0.875</td>
<td>12</td>
<td>0.0 0.0</td>
</tr>
<tr>
<td><em>dnd</em> MO</td>
<td>48</td>
<td>42</td>
<td>2</td>
<td>0.875</td>
<td>12</td>
<td>0.0 0.0</td>
</tr>
<tr>
<td>(2000-4000 pg / embryo)</td>
<td>48</td>
<td>42</td>
<td>2</td>
<td>0.875</td>
<td>12</td>
<td>0.0 0.0</td>
</tr>
</tbody>
</table>
Table S2. Classification of gonads in 13-month-old loach following injection of \textit{dnd} MO at the one- to two-cell stage.

<table>
<thead>
<tr>
<th>Sample size</th>
<th>Sample size</th>
<th>Morphological feature of gonads</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Ovary</td>
</tr>
<tr>
<td>Intact control</td>
<td>11</td>
<td>5</td>
</tr>
<tr>
<td>Control MO (1000-2000 pg / embryo)</td>
<td>11</td>
<td>1</td>
</tr>
<tr>
<td>\textit{dnd} MO (250-500 pg / embryo)</td>
<td>8</td>
<td>5</td>
</tr>
<tr>
<td>\textit{dnd} MO (500-1000 pg / embryo)</td>
<td>27</td>
<td>3</td>
</tr>
<tr>
<td>\textit{dnd} MO (1000-2000 pg / embryo)</td>
<td>22</td>
<td>0</td>
</tr>
<tr>
<td>\textit{dnd} MO (2000-4000 pg / embryo)</td>
<td>13</td>
<td>0</td>
</tr>
</tbody>
</table>
Table S3. Distribution patterns of *vasa*-positive cells of wild-type and *dnd* morphants at each stage.

<table>
<thead>
<tr>
<th>Stage</th>
<th>Wild-type</th>
<th><em>dnd</em> morphants</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>No. of <em>vasa</em>-positive individuals</td>
<td>Distribution of <em>vasa</em>-positive cells</td>
</tr>
<tr>
<td></td>
<td>N</td>
<td>Normal</td>
</tr>
<tr>
<td>Embryonic shield</td>
<td>18</td>
<td>18</td>
</tr>
<tr>
<td>2-4 somite</td>
<td>27</td>
<td>27</td>
</tr>
<tr>
<td>20 somite</td>
<td>27</td>
<td>27</td>
</tr>
<tr>
<td>30 somite</td>
<td>28</td>
<td>28</td>
</tr>
<tr>
<td>Larvae</td>
<td>14</td>
<td>14</td>
</tr>
<tr>
<td>Embryonic shield</td>
<td>15</td>
<td>15</td>
</tr>
<tr>
<td>2-4 somite</td>
<td>14</td>
<td>14</td>
</tr>
<tr>
<td>20 somite</td>
<td>15</td>
<td>15</td>
</tr>
<tr>
<td>30 somite</td>
<td>18</td>
<td>17</td>
</tr>
<tr>
<td>Larvae</td>
<td>18</td>
<td>0</td>
</tr>
</tbody>
</table>

*: A small number of *vasa*-positive cells were distributed in ectopic position, though most of *vasa*-positive cells were normal position.

**: Most of *vasa*-positive cells were distributed in ectopic position.

***: These embryos had a small number of *vasa*-positive cells distributed at normal position.
<table>
<thead>
<tr>
<th>Primer</th>
<th>Purpose</th>
<th>Sequence (5’-3’)</th>
</tr>
</thead>
<tbody>
<tr>
<td>dead end-degenerate-F</td>
<td>Partial cloning</td>
<td>ACGGCGGCCCTCC(GATC)CC(GATC)GG(GATC)TGG</td>
</tr>
<tr>
<td>dead end-degenerate-R</td>
<td>Partial cloning</td>
<td>CCGTTCGATGTACTTGGCC(GATC)AC(TG)GAG(TG)AA</td>
</tr>
<tr>
<td>dead end-5’ RACE-R1</td>
<td>RACE cloning</td>
<td>TCGTCGACCGCTGTCACACGGAGGGGACATAGC</td>
</tr>
<tr>
<td>dead end-5’ RACE-R2</td>
<td>RACE cloning</td>
<td>CCGTTCGATGTACTTGGCC(GATC)AC(TG)GAG(TG)AA</td>
</tr>
<tr>
<td>dead end-3’ RACE-F1</td>
<td>RACE cloning</td>
<td>TCGTCGACCGCTGTCACACGGAGGGGACATAGC</td>
</tr>
<tr>
<td>dead end-3’ RACE-F2</td>
<td>RACE cloning</td>
<td>TCGTCGACCGCTGTCACACGGAGGGGACATAGC</td>
</tr>
<tr>
<td>vasa-degenerate-F</td>
<td>Partial cloning</td>
<td>AGAGGAGAGAGATGCCTGTGGCC(GATC)GG(GATC)TGGCA</td>
</tr>
<tr>
<td>vasa-degenerate-R</td>
<td>Partial cloning</td>
<td>TGTCGACCGCTGTCACACGGAGGGGACATAGC</td>
</tr>
<tr>
<td>vasa-5’ RACE-R1</td>
<td>RACE cloning</td>
<td>TCGTCGACCGCTGTCACACGGAGGGGACATAGC</td>
</tr>
<tr>
<td>vasa-5’ RACE-R2</td>
<td>RACE cloning</td>
<td>TCGTCGACCGCTGTCACACGGAGGGGACATAGC</td>
</tr>
<tr>
<td>vasa-3’ RACE-F1</td>
<td>RACE cloning</td>
<td>TCGTCGACCGCTGTCACACGGAGGGGACATAGC</td>
</tr>
<tr>
<td>vasa-RT-F</td>
<td>RT-PCR</td>
<td>CTGCACTGCAATACGGGACATAGC</td>
</tr>
<tr>
<td>vasa-RT-R</td>
<td>RT-PCR</td>
<td>CTGCACTGCAATACGGGACATAGC</td>
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<tr>
<td>dmrt1-degenerate-F</td>
<td>Partial cloning</td>
<td>CGAGGCAGAGAGATGCCTGTGGCC(GATC)GG(GATC)TGGCA</td>
</tr>
<tr>
<td>dmrt1-degenerate-R</td>
<td>Partial cloning</td>
<td>TCGTCGACCGCTGTCACACGGAGGGGACATAGC</td>
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<td>RACE cloning</td>
<td>TCGTCGACCGCTGTCACACGGAGGGGACATAGC</td>
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<tr>
<td>dmrt1-3’ RACE-R2</td>
<td>RACE cloning</td>
<td>TCGTCGACCGCTGTCACACGGAGGGGACATAGC</td>
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<td>dmrt1-3’ RACE-F1</td>
<td>RACE cloning</td>
<td>TCGTCGACCGCTGTCACACGGAGGGGACATAGC</td>
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<tr>
<td>dmrt1-3’ RACE-F2</td>
<td>RACE cloning</td>
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<td>RACE cloning</td>
<td>TCGTCGACCGCTGTCACACGGAGGGGACATAGC</td>
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<tr>
<td>dmrt1-RT-F</td>
<td>RT-PCR</td>
<td>TCGTCGACCGCTGTCACACGGAGGGGACATAGC</td>
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<tr>
<td>dmrt1-RT-R</td>
<td>RT-PCR</td>
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<tr>
<td>foxl2-degenerate-F</td>
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<td>RACE cloning</td>
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<td>foxl2-5’ RACE-R2</td>
<td>RACE cloning</td>
<td>TCGTCGACCGCTGTCACACGGAGGGGACATAGC</td>
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<td>foxl2-3’ RACE-F3</td>
<td>RACE cloning</td>
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<tr>
<td>foxl2-RT-F</td>
<td>RT-PCR</td>
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<td>foxl2-RT-R</td>
<td>RT-PCR</td>
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<td>Partial cloning</td>
<td>TCGTCGACCGCTGTCACACGGAGGGGACATAGC</td>
</tr>
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<td>p450arom-5’ RACE-R1</td>
<td>RACE cloning</td>
<td>TCGTCGACCGCTGTCACACGGAGGGGACATAGC</td>
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<tr>
<td>p450arom-5’ RACE-R2</td>
<td>RACE cloning</td>
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<tr>
<td>p450arom-3’ RACE-F1</td>
<td>RACE cloning</td>
<td>TCGTCGACCGCTGTCACACGGAGGGGACATAGC</td>
</tr>
<tr>
<td>p450arom-3’ RACE-F2</td>
<td>RACE cloning</td>
<td>TCGTCGACCGCTGTCACACGGAGGGGACATAGC</td>
</tr>
<tr>
<td>p450arom-3’ RACE-F3</td>
<td>RACE cloning</td>
<td>TCGTCGACCGCTGTCACACGGAGGGGACATAGC</td>
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<tr>
<td>p450arom-RT-F</td>
<td>RT-PCR</td>
<td>TCGTCGACCGCTGTCACACGGAGGGGACATAGC</td>
</tr>
<tr>
<td>p450arom-RT-R</td>
<td>RT-PCR</td>
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<td>β-actin-RT-F</td>
<td>RT-PCR</td>
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<td>RT-PCR</td>
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</table>

Table S4. Sequences of primers used in the present study.