

Supplementary Material

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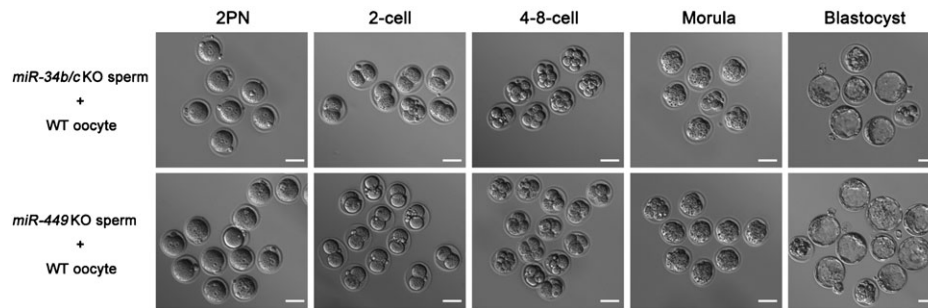


Fig. S1. Morphology of embryos at 2-pronucleus (PN), 2-cell, 4–8-cell, morula and blastocyst stages of development. Sperm and oocyte genotypes are labeled to the left. Scale bars = 100 μm .



Fig. S2. Pups born through ROSI using WT oocytes and *miR-34b/c* and *miR-449* double knockout round spermatids. Scale bar = 1 cm.

Table S1. Fertility of *miR-34b/c* KO, *miR-449* KO and miR-dKO mice

Male genotype	Female genotype	No. of litters	No. of pups	Average of litter size	Average of litter interval (days)
WT	WT	26	215	8.27 ± 0.66	23.04 ± 0.12
<i>miR-34b/c</i> KO	WT	20	149	7.45 ± 1.05	24.35 ± 0.21
<i>miR-34b/c</i> KO	<i>miR-34b/c</i> KO	15	109	7.26 ± 1.33	23.26 ± 0.22
<i>miR-449</i> KO	WT	18	145	8.06 ± 0.78	24.24 ± 0.34
<i>miR-449</i> KO	<i>miR-449</i> KO	24	170	7.08 ± 1.49	23.82 ± 0.83
miR-dKO	WT	0	0	0	0

Table S2. Development of WT oocytes or *miR-34b/c* KO oocytes injected with *miR-34b/c* KO spermatozoa

Oocyte genotype	Total No. of surviving oocytes (no. of exp.)	No. of oocytes with 2PN (% of Total)	No. of 2-cell (% of 2PN)	No. of 4-cell (% of 4-cell/2-cell)	No. of morula (% of 2-cell)	No. of Blastocyst (% of Blastocyst/2-cell)
WT	38 (2)	31 (81.58)	29 (93.55)	28 (96.55)	26 (89.66)	16 (55.17)
<i>miR-34b/c</i> KO	70 (2)	59 (84.29)	52 (88.13)	49 (94.23)	43 (82.69)	28 (53.85)
Parthenogenetic control	30 (2)	3	1	0	0	0

exp., experiment.

Table S3. Development of WT oocytes or *miR-449* KO oocytes injected with *miR-449* KO spermatozoa

Oocyte genotype	Total No. of surviving oocytes (no. of exp.)	No. of oocytes with 2PN (% of Total)	No. of 2-cell (% of 2PN)	No. of 4-cell (% of 4-cell/2-cell)	No. of morula (% of 2-cell)	No. of Blastocyst (% of Blastocyst/2-cell)
WT	124 (3)	108 (87.10)	102 (94.44)	95 (93.14)	87 (85.29)	59 (57.84)
<i>miR-449</i> KO	137 (4)	116 (84.67)	110 (94.83)	101 (91.82)	91 (82.73)	57 (51.82)
Parthenogenetic control	30 (2)	3	1	0	0	0

exp., experiment.

Tables S4–S6: See supplementary webpage

Table S7. Primer sequences for qPCR validation of RNA-Seq data

Gene symbol	Forward (5'→3')	Reverse (5'→3')
<i>Tekt3</i>	GTGCAGGGATATGGCTCAGT	TTCACAGCCAAGTCATGCTC
<i>Zpbp2</i>	TTTCCTGGAGCCGTTATCTG	ATCAGGTTCCCGATATGCAA
<i>Adam2</i>	CTTGACCACAGGCGATGCTAA	TGATAGGTAGCGCCAACATAATC
<i>Tekt4</i>	GCAAGTGAAGTCCGGCTTTCTC	TGGTCTGTGATCTCCGTCAG
<i>Nphp1</i>	GATAGTTTGGTGAAGGCA	CCCACAGGTGCAGCTTCAT
<i>Tekt2</i>	TTGAAGCCACCAAGAAGGTC	CCGGTGGTCAGAGTTGAGTT
<i>Cplx1</i>	AGTTCGTGATGAAACAAGCCC	TCTTCCTCCTTCTTAGCAGCA
<i>Pebp1</i>	GAGCTGGGCAAAGTGCTAAC	GTCTGTGAGGACCAGGGTGT
<i>Adam3</i>	TTGCGTGACAAGTTGGGAACA	GGGCTCAATCCATAAGTGATGT
<i>Gamt</i>	CACGCACCTGCAAATCCTG	TACCGAAGCCCCTTCCAAGA
<i>Sepp1</i>	AGCCATTAAGATCGCTTACTGTG	GAGGGCTCCGCAGTTTTATTG
<i>Prnd</i>	TCTCCACGGTCAAGGCAAG	CGGTTCTCAGCTACCCGAG
<i>Wipf3</i>	ACACCCCAGCTTAAGGAAG	CCTTTTGAACCCTCGATCTG
<i>Mfge8</i>	ATCTACTGCCTCTGCCCTGA	CCAGACATTTGGCATCATTG
<i>Gapdh</i>	AACTTTGGCATTGTGGAAGG	ACACATTGGGGGTAGGAACA