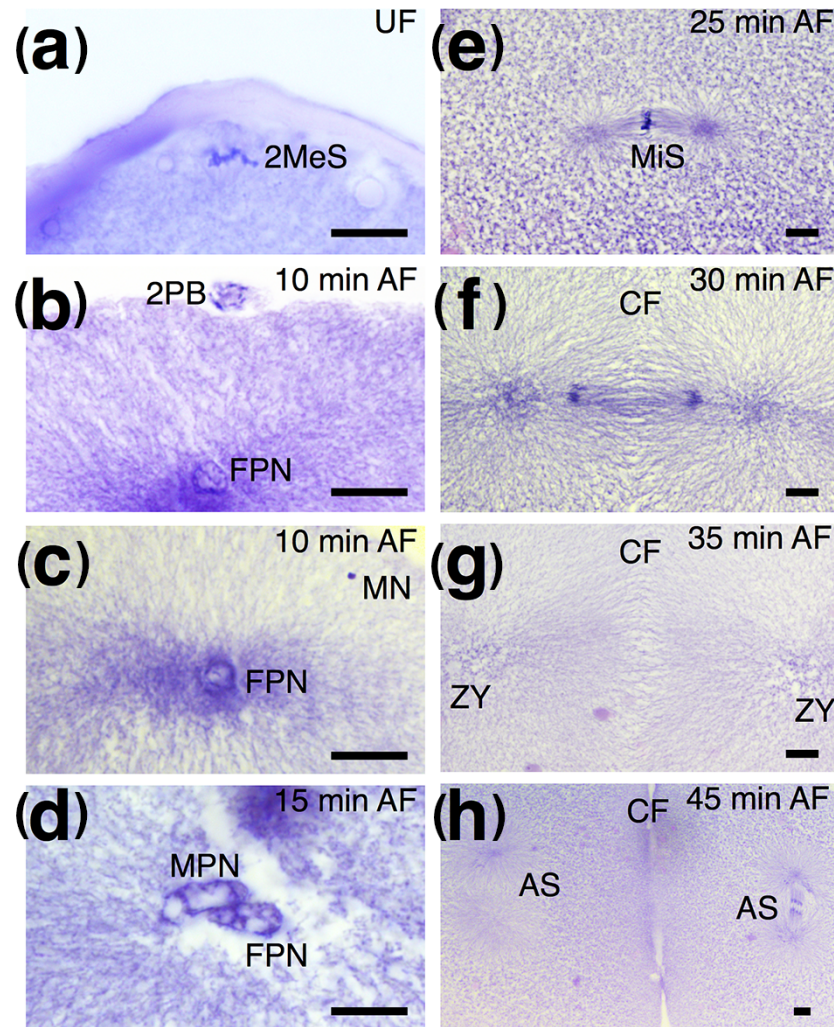


## **Supplemental Information**

Title: Generation of clonal zebrafish line by androgenesis without egg irradiation

Jilun Hou<sup>a</sup>, Takafumi Fujimoto<sup>b, \*</sup>, Taiju Saito<sup>c</sup>, Etsuro Yamaha<sup>d</sup>, Katsutoshi Arai<sup>b</sup>

Supplemental Figure



**Figure S1.** Histological sections of intact control eggs from zebrafish (*Danio rerio*). (a) Unfertilized eggs at metaphase of the second meiosis; (b) 10 min after fertilization (AF), second polar body was released, and the egg nucleus existed in the egg cytoplasm underneath the polar body; (c) 10 min AF, the condensed sperm nucleus and egg nucleus in the blastodisc; (d) 15 min AF, decondensed female and male pronuclei; (e) 25 min AF, metaphase of the first cleavage; (f) 30 min AF, anaphase of the first cleavage; (g) 35 min AF, prophase of the second cleavage; (h) 45 min AF, anaphase of the second cleavage. Scale bars denote 10 μm. Abbreviation: 2MeS, 2nd meiotic spindle; 2PB, 2nd polar body; FPN, female pronucleus; MN, male nucleus; MPN, male pronucleus; MiS, mitotic spindle; CF, cleavage furrow; ZY, zygote; AS, anaphase spindle.

## Supplemental Tables

**Table S1**

External appearance and ploidy status of progeny from groups subjected to different temperatures during cold-shock treatment (30 min) in zebrafish (*Danio rerio*).

Treatment	External appearance	Number of larvae	Ploidy status				
			1N	2N	3N	Hypo-2N	Hyper-2N
Intact control	Normal	80	0	80	0	0	0
	Abnormal	16	0	16	0	0	0
1°C, cold-shock	Normal	2	0	0	2	0	0
	Abnormal	3	1	0	0	0	2 <sup>a</sup>
4°C, cold-shock	Normal	0	0	0	0	0	0
	Abnormal	14	7	0	1	3 <sup>b</sup>	3 <sup>c</sup>
7°C, cold-shock	Normal	3	0	0	3	0	0
	Abnormal	47	39	0	1	6 <sup>d</sup>	1 <sup>e</sup>
10°C, cold-shock	Normal	30	0	6	23	0	1 <sup>f</sup>
	Abnormal	44	8	8	17	7 <sup>g</sup>	4 <sup>h</sup>

<sup>a</sup> 2.3N and 2.8N

<sup>b</sup> 1.2N, 1.3N and 1.6N

<sup>c</sup> 2.4N, 2.5N and 3.4N

<sup>d</sup> 1.2N (3), 1.3N (2), and 1.5N

<sup>e</sup> 2.6N

<sup>f</sup> 2.6N

<sup>g</sup> 1.2N, 1.4N, 1.6N (3), and 1.7N (2)

<sup>h</sup> 2.2N (2), 2.6N, and 2.7N

**Table S2**

External appearance and ploidy status of progeny from groups subjected to different durations of cold-shock treatment (7°C) in zebrafish (*Danio rerio*).

Treatment	External appearance	Number of larvae	Ploidy status				
			1N	2N	3N	Hypo-2N	Hyper-2N
Intact control	Normal	104	0	104	0	0	0
20 min cold-shock	Abnormal	0	0	0	0	0	0
	Normal	6	0	1	5	0	0
30 min cold-shock	Abnormal	61	34	12	1	10 <sup>a</sup>	4 <sup>b</sup>
	Normal	7	0	0	7	0	0
40 min cold-shock	Abnormal	46	33	2	2	5 <sup>c</sup>	4 <sup>d</sup>
	Normal	6	0	0	6	0	0
50 min cold-shock	Abnormal	43	29	3	4	2 <sup>e</sup>	5 <sup>f</sup>
	Normal	4	0	0	4	0	0
60 min cold-shock	Abnormal	19	16	0	1	2 <sup>g</sup>	0
	Normal	3	0	0	3	0	0
60 min cold-shock	Abnormal	21	16	0	2	0	3 <sup>h</sup>

<sup>a</sup> 1.2N (4), 1.3N (2), 1.5N, 1.6N (2), and 1.7N

<sup>b</sup> 2.3N, 2.4N, 2.6N, and 2.8N

<sup>c</sup> 1.3N, 1.4N, 1.6N (2), and 1.8N

<sup>d</sup> 2.4N (3) and 6N

<sup>e</sup> 1.2N and 1.5N

<sup>f</sup> 2.3N, 2.6N (2), and 2.7N (2)

<sup>g</sup> 1.3N and 1.5N

<sup>h</sup> 2.2N and 2.4N (2)

**Table S3**

Microsatellite genotypes at four loci in haploid, diploid, and triploid progeny following cold-shock treatment (7°C, 30 min) in zebrafish (*Danio rerio*).

Locus (LG) <sup>a</sup>	Female	Male	Progeny from cold shock treatment		
			Haploid	Diploid	Triploid
Z7576 (LG 12)	208/246	121/121	121: 10	208/121: 3 247/121: 7	208/246/121: 10
Z6010 (LG 17)	123/161	175/179	175: 7 179: 3	123/175: 3 123/179: 3 161/175: 2 161/179: 2	123/161/175: 6 123/161/179: 4
Z9708 (LG 20)	214/218	172/286	172: 5 286: 5	214/172: 1 218/172: 1 214/286: 5 218/286: 3	214/218/172: 4 214/218/286: 6
Z11786 (LG 25)	152/152	140/164	140: 7 164: 3	152/140: 5 152/164: 5	152/140: 4 152/164: 6

Abbreviation: LG, linkage group.

<sup>a</sup> See Shimoda *et al.*<sup>15</sup>.

**Table S4**

Microsatellite genotyping of putative androgenetic doubled haploids (DHs) with the golden phenotype in zebrafish (*Danio rerio*).

Locus (LG) <sup>a</sup>	DH1	DH2	DH3	DH4	DH5	DH6	DH7	DH8
Z1781 (LG 1)	200	200	200	200	200	200	200	200
Z8874 (LG 1)	150	150	150	150	150	150	150	150
Z644 (LG 2)	230	230	230	230	230	230	230	230
Z9408 (LG 3)	186	238	280	238	280	280	280	238
Z7629 (LG 4)	238	186	188	188	186	282	188	188
Z896 (LG 5)	228	205	205	228	228	228	205	228
Z3314 (LG 5)	126	126	126	126	126	126	126	126
Z740 (LG 6)	232	235	235	232	232	235	235	235
Z1050 (LG 6)	138	138	144	144	144	138	138	144
Z8495 (LG 7)	240	240	240	240	240	240	240	240
Z1402 (LG 8)	206	206	206	206	206	206	206	206
Z9637 (LG 8)	146	146	146	146	146	146	146	146
Z106 (LG 9)	188	188	188	188	188	188	188	188
Z1450 (LG 10)	238	238	258	238	238	238	238	238
Z10215 (LG 11)	118	118	118	118	118	118	118	118
Z7576 (LG 12)	121	378	376	121	378	378	206	206
Z6622 (LG 13)	154	154	154	274	154	274	274	274
Z1652 (LG 14)	140	98	98	98	140	140	98	140
Z3309 (LG 15)	104	118	174	176	118	118	176	118
Z992 (LG 16)	220	256	256	256	220	256	220	256
Z3127 (LG17)	138	140	138	140	140	140	140	140
Z1990 (LG17)	190	190	190	190	190	190	190	190
Z1136 (LG 18)	116	116	116	116	184	116	116	116
Z9331 (LG 19)	292	292	292	292	292	292	292	292
Z9708 (LG 20)	218	218	218	218	218	218	218	218
Z11113 (LG 21)	220	220	220	220	196	220	220	220
Z6613 (LG 22)	184	118	184	184	184	184	184	184
Z5265 (LG 23)	196	216	216	200	152	216	196	216
Z7349 (LG 24)	204	212	212	212	212	212	212	212
Z11786 (LG 25)	164	164	164	152	152	164	164	164

Abbreviation: LG, linkage group.

<sup>a</sup> See Shimoda *et al.*<sup>15</sup>.

**Table S5**

Summary of amplified fragment length polymorphism (AFLP) data.

	No. of fish	No. of primer sets	No. of bands	Frequency of polymorphisms (%)	BSI <sup>a</sup>
Clonal line	8	64	34–94	0.00	1
Intact control	8	31	52–103	50.00–92.42	0.76 ± 0.13

Abbreviation: BSI: band sharing index

<sup>a</sup>The data are shown as total means ± SDs for all primers. See Arai *et al.*<sup>32</sup>.

**Table S6**

Adaptors and primers used for amplified fragment length polymorphism (AFLP).

Adaptor or primer	Sequences (5' → 3')
<i>Eco</i> RI adaptor-1	CTCGTAGACTGCGTACC
<i>Eco</i> RI adaptor-2	AATTGGTACGCAGTCTAC
<i>Mse</i> I adaptor-1	GACGATGAGTCCTGAG
<i>Mse</i> I adaptor-2	TACTCAGGACTCAT
<i>Eco</i> RI preselective primer	GACTGCGTACCAATT <u>CA</u>
<i>Mse</i> I preselective primer	GATGAGTCCTGAGTAA <u>C</u>
Selective primer:	
E-AAC	GACTGCGTACCAATT <u>CAAC</u>
E-AAG	GACTGCGTACCAATT <u>CAAG</u>
E-ACA	GACTGCGTACCAATT <u>CACA</u>
E-ACC	GACTGCGTACCAATT <u>CACC</u>
E-ACG	GACTGCGTACCAATT <u>CACG</u>
E-ACT	GACTGCGTACCAATT <u>CACT</u>
E-AGC	GACTGCGTACCAATT <u>CAGC</u>
E-AGG	GACTGCGTACCAATT <u>CAGG</u>
M-CAA	GATGAGTCCTGAGTAA <u>CAA</u>
M-CAC	GATGAGTCCTGAGTAA <u>CAC</u>
M-CAG	GATGAGTCCTGAGTAA <u>CAG</u>
M-CAT	GATGAGTCCTGAGTAA <u>CAT</u>
M-CTA	GATGAGTCCTGAGTAA <u>CTA</u>
M-CTC	GATGAGTCCTGAGTAA <u>CTC</u>
M-CTG	GATGAGTCCTGAGTAA <u>CTG</u>
M-CTT	GATGAGTCCTGAGTAA <u>CTT</u>



**Table S7**

Primer combinations for selective amplification using amplified fragment length polymorphism (AFLP)<sup>a</sup>.

	M1 M-CAA	M2 M-CAC	M3 M-CAG	M4 M-CAT	M5 M-CTA	M6 M-CTC	M7 M-CTG	M8 M-CTT
E1 E-AAC	E1/M1*	E1/M2*	E1/M3*	E1/M4*	E1/M5*	E1/M6*	E1/M7*	E1/M8*
E2 E-AAG	E2/M1*	E2/M2*	E2/M3*	E2/M4*	E2/M5*	E2/M6*	E2/M7*	E2/M8*
E3 E-ACA	E3/M1	E3/M2	E3/M3	E3/M4	E3/M5	E3/M6	E3/M7	E3/M8
E4 E-ACC	E4/M1	E4/M2	E4/M3	E4/M4	E4/M5	E4/M6	E4/M7	E4/M8
E5 E-ACG	E5/M1	E5/M2	E5/M3	E5/M4	E5/M5	E5/M6	E5/M7	E5/M8
E6 E-ACT	E6/M1	E6/M2	E6/M3	E6/M4	E6/M5	E6/M6	E6/M7	E6/M8
E7 E-AGC	E7/M1	E7/M2*	E7/M3*	E7/M4*	E7/M5*	E7/M6*	E7/M7*	E7/M8*
E8 E-AGG	E8/M1*	E8/M2*	E8/M3*	E8/M4*	E8/M5*	E8/M6*	E8/M7*	E8/M8*

<sup>a</sup> For the clonal line, all of the combinations were used; for the intact control, the combinations with asterisk in the table were used.