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調査委員会　中間報告

論文1：　Obokata et al., Nature 505:641-647(2014)

- （1−1）Figure 1f の画像の不自然さ
  （1−2）Figure 1iの画像切り貼りの疑い
  （1−3）Methodの記載の一部の盗用の疑い
  （1−4）Methodの記載の一部の間違い
  （1−5）Figure 2d, 2eの画像の取り違えと、学位論文画像との酷似

論文2：　Obokata et al., Nature 505:676-680(2014)

- （2−1）Figure 1bとFig. 2g（下パネル）の画像 の酷似

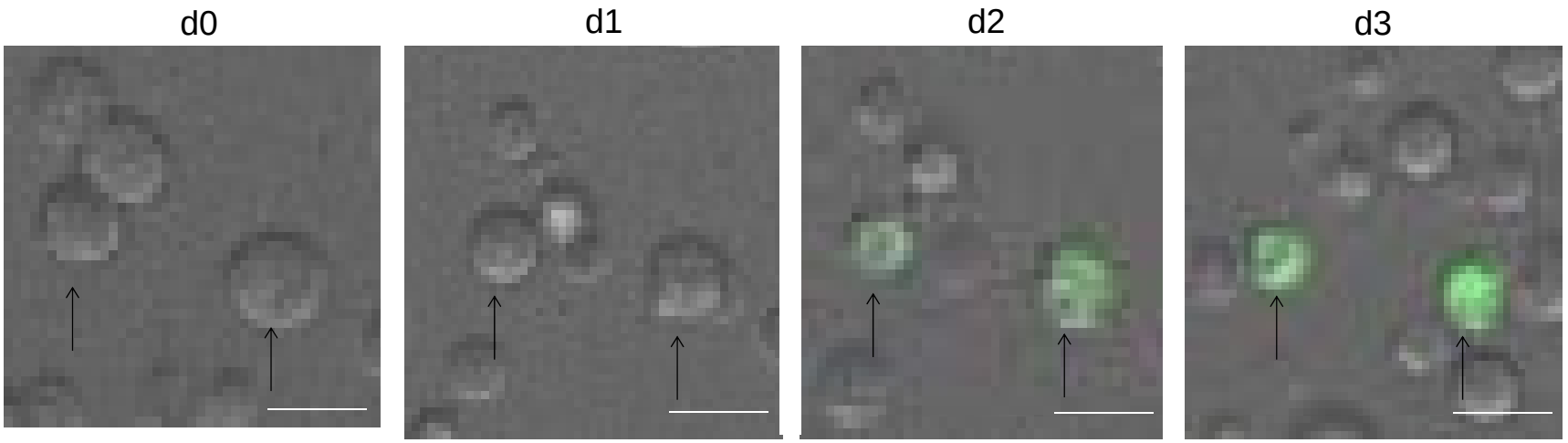
- 調査終了項目

調査対象者

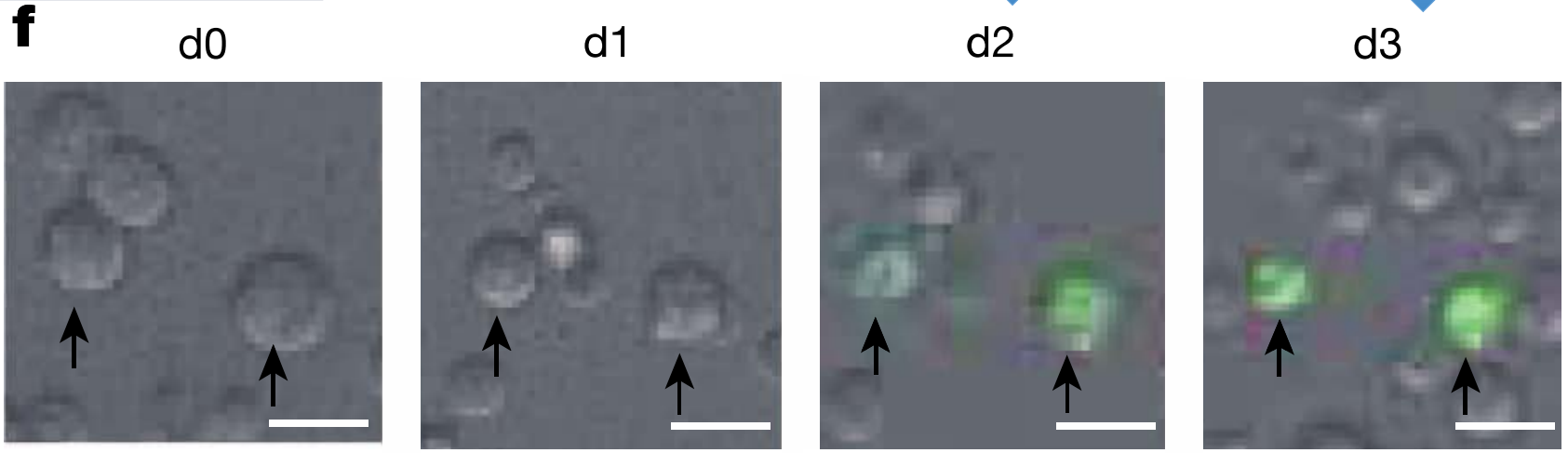
小保方晴子、笹井芳樹、若山照彦、丹羽仁史

1−1：　Fig. 1f の画像の不自然さ

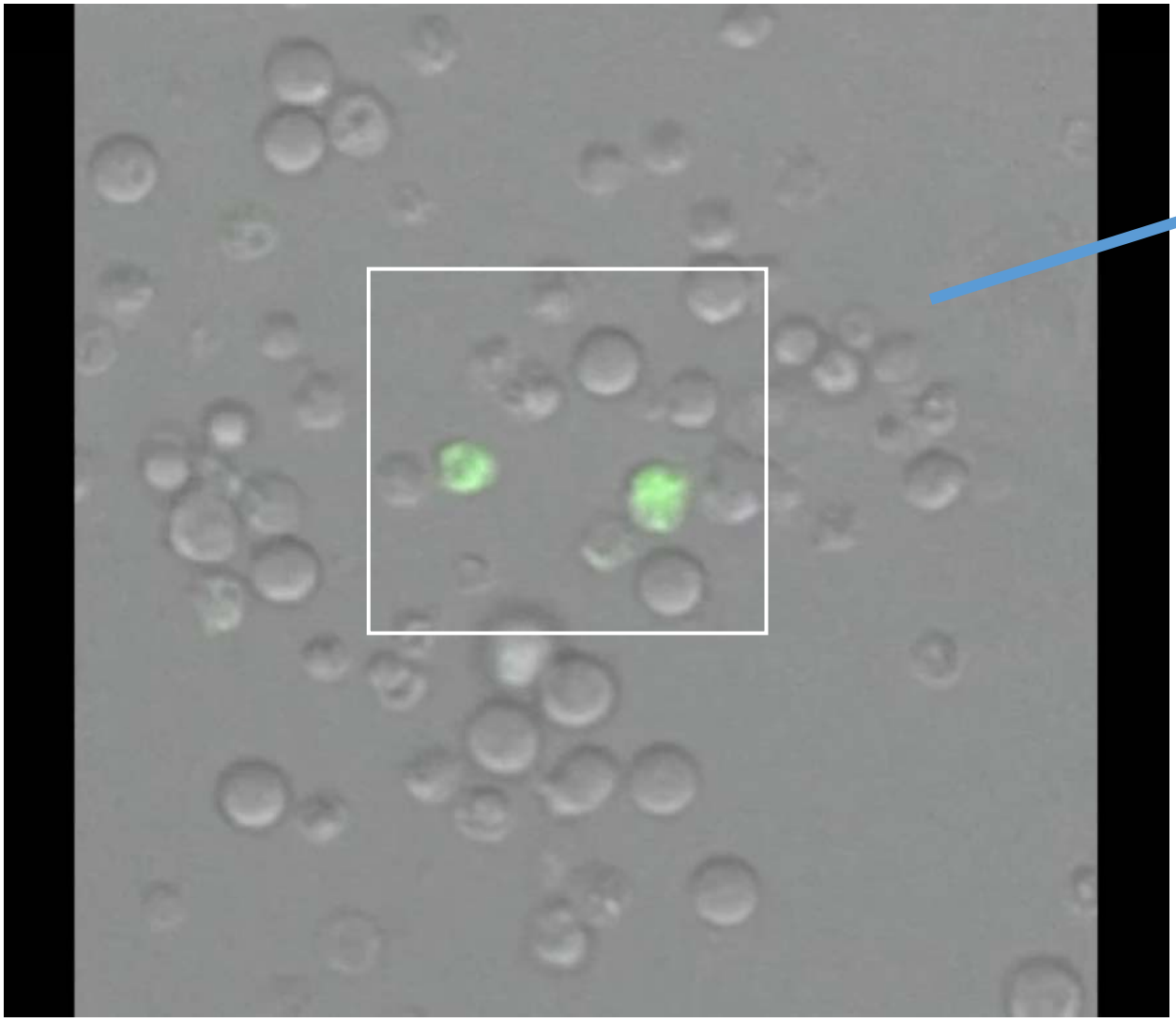
投稿論文の画像



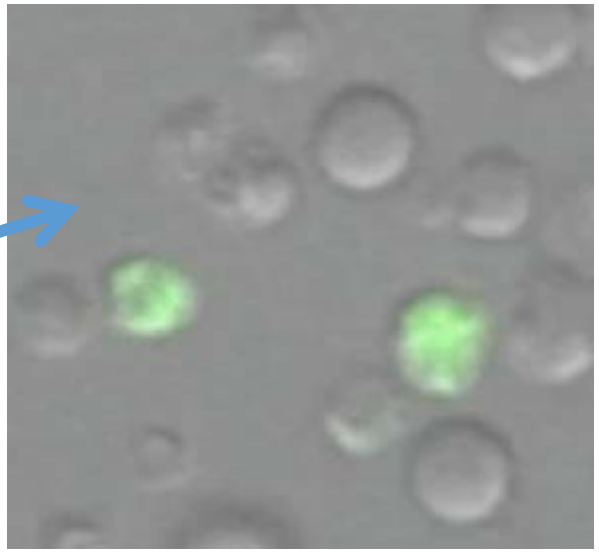
Nature誌掲載の画像



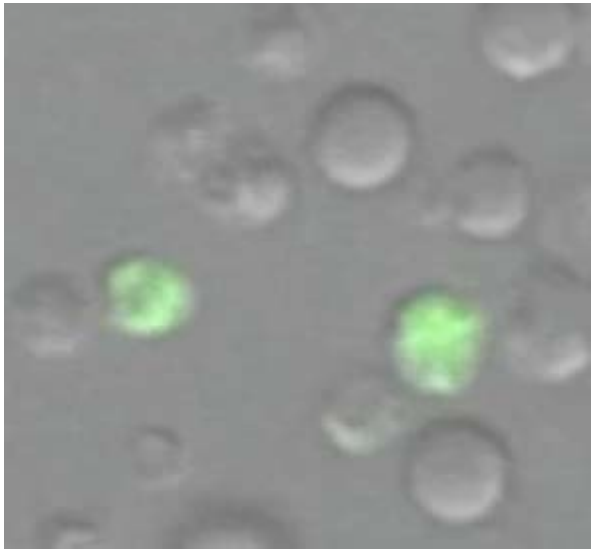
d3



切り出し



投稿論文の画像



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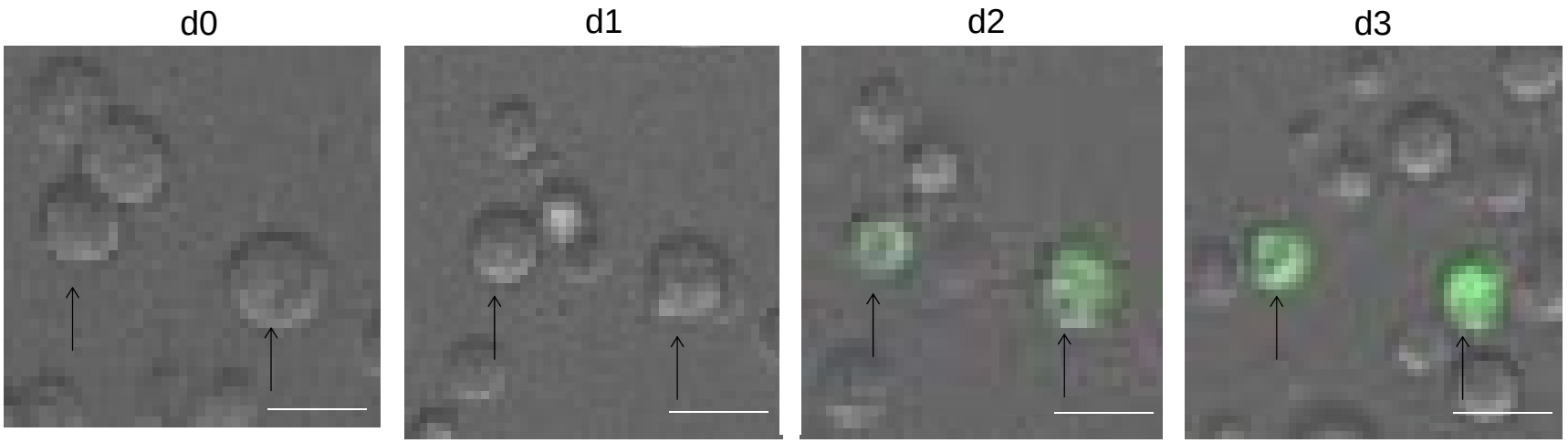
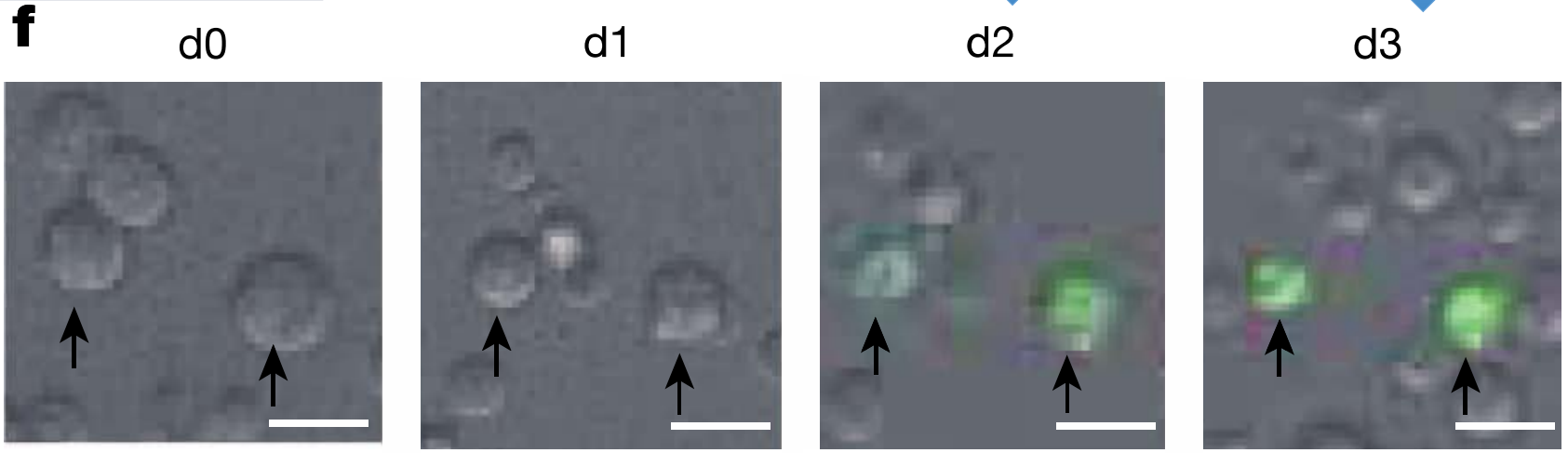


Nature誌掲載の画像



2−1： Fig. 1b と Fig. 2g の画像の酷似

Fig. 1b

STAP 細胞

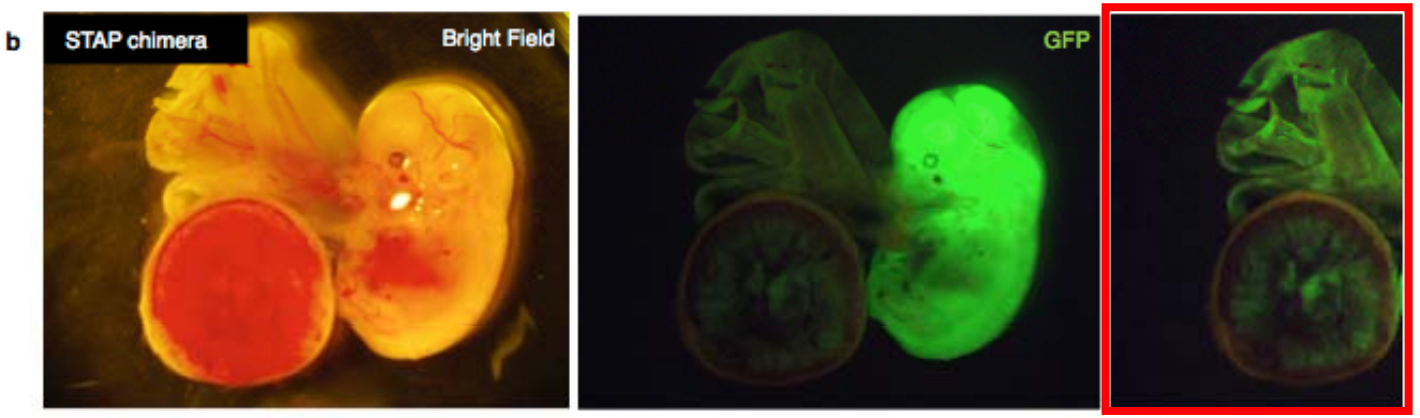
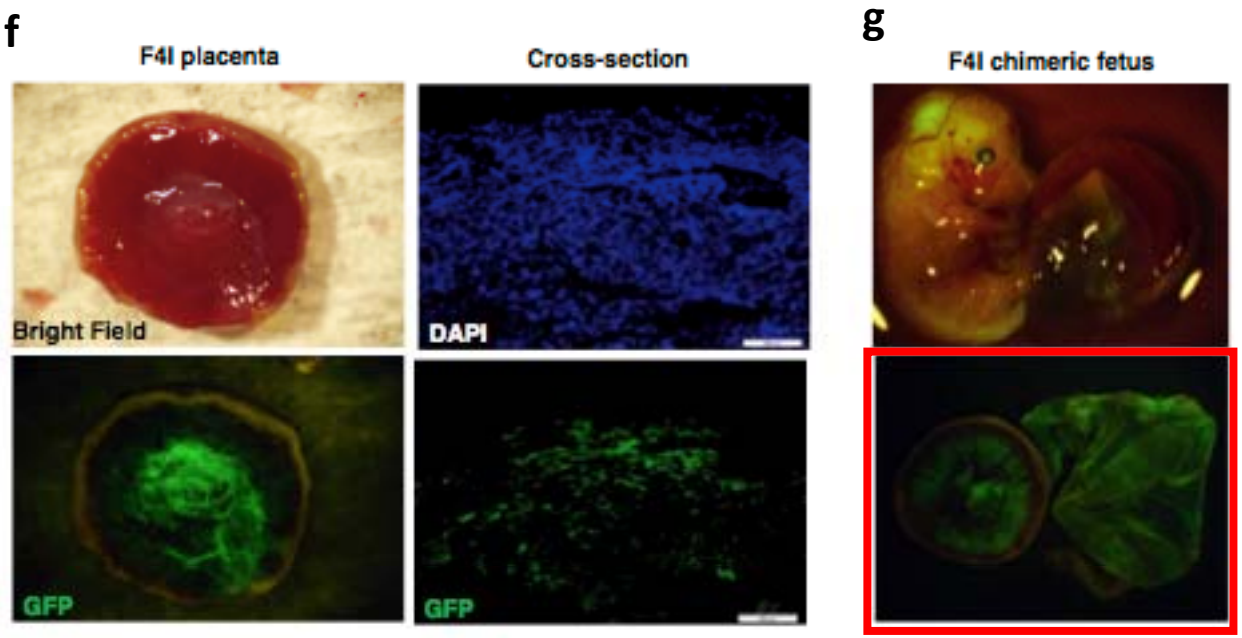


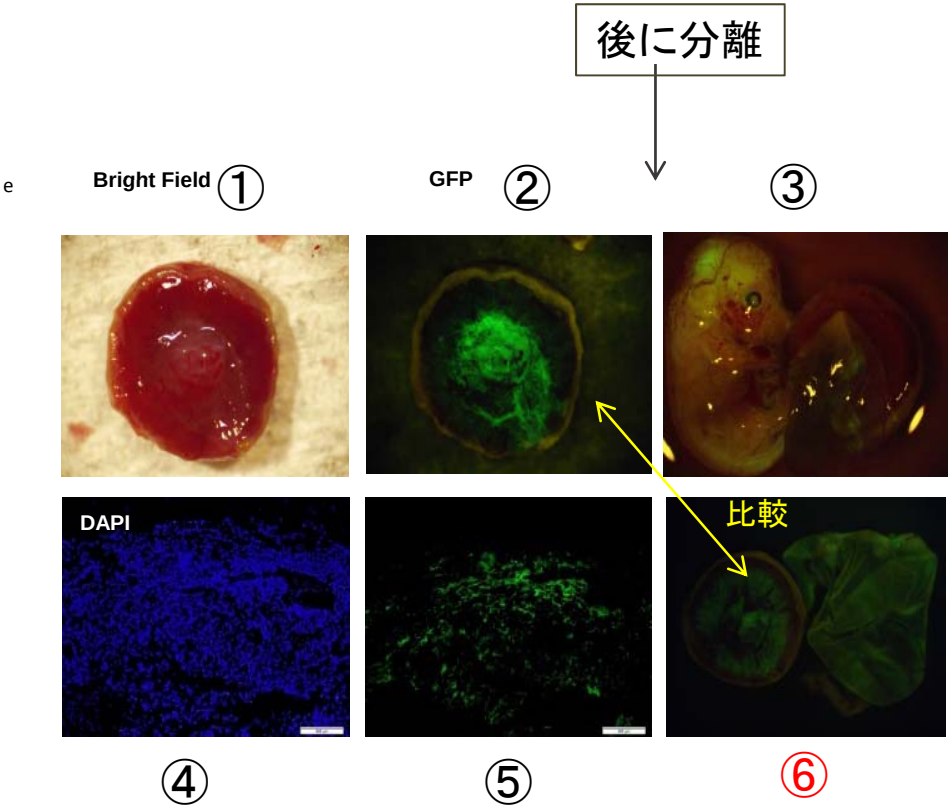
Fig. 2f, g

FGF-induced stem cell

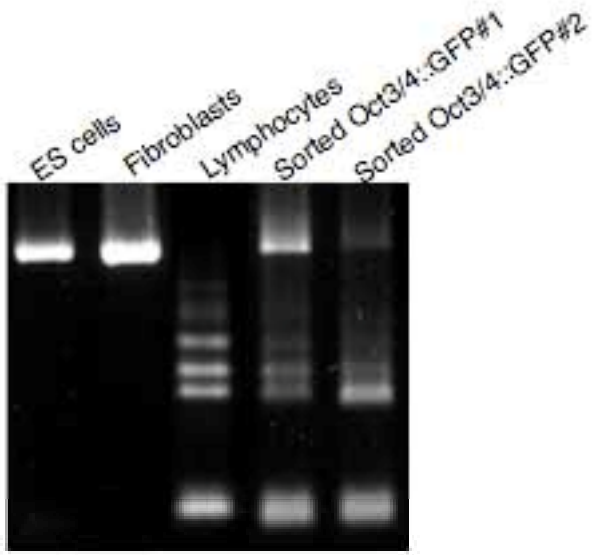


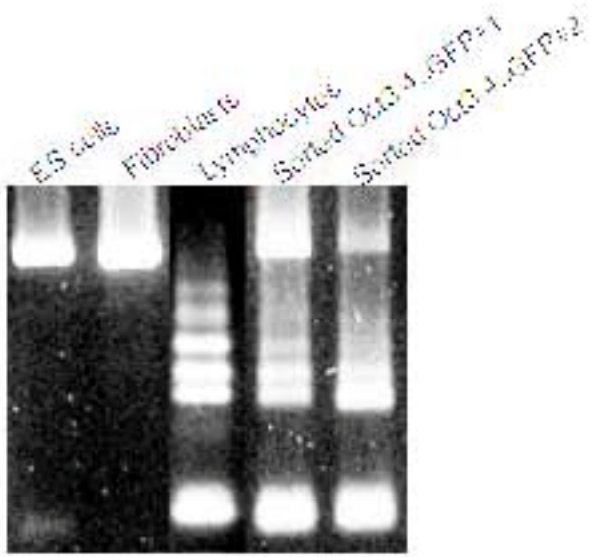
論文の構想検討段階の Figure のオプション

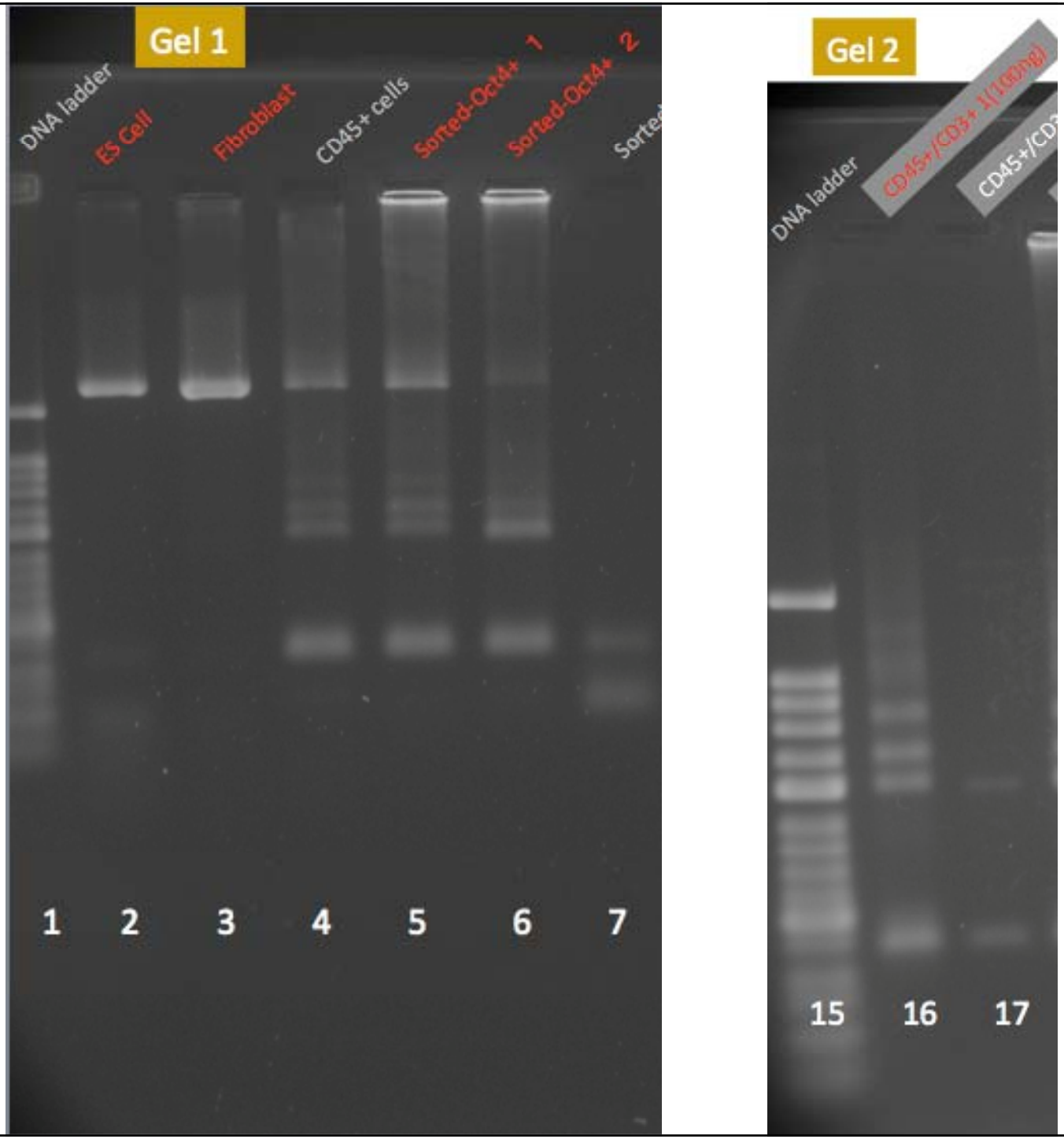
①–⑤は
今と違う配置



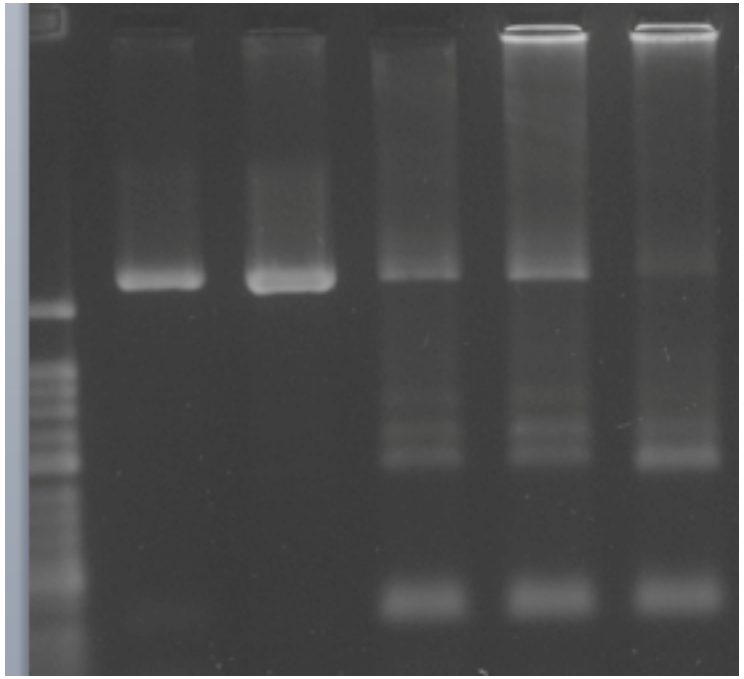
1−2： Fig. 1i の画像の切り貼りの疑い



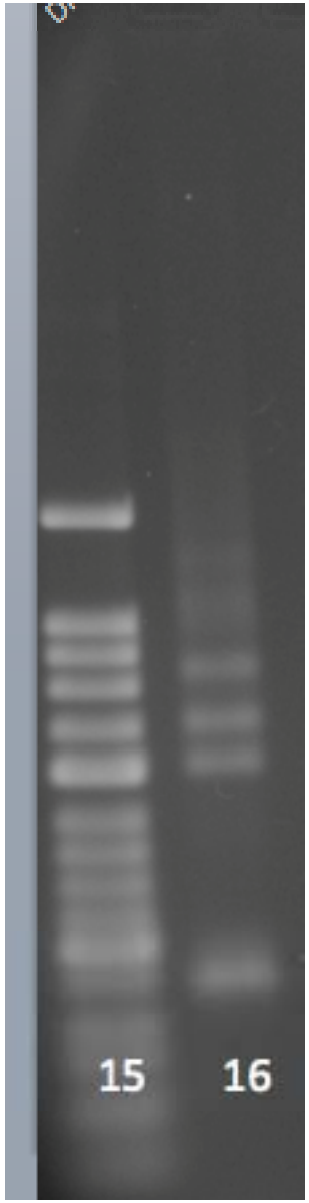



Gel 1
DNA ladder
ES Cell
Fibroblast
CD45+ cells
Sorted-Oct4+ 1
Sorted-Oct4+ 2
1
2
3
4
5
6
7
Gel 2
DNA ladder
15
16
17

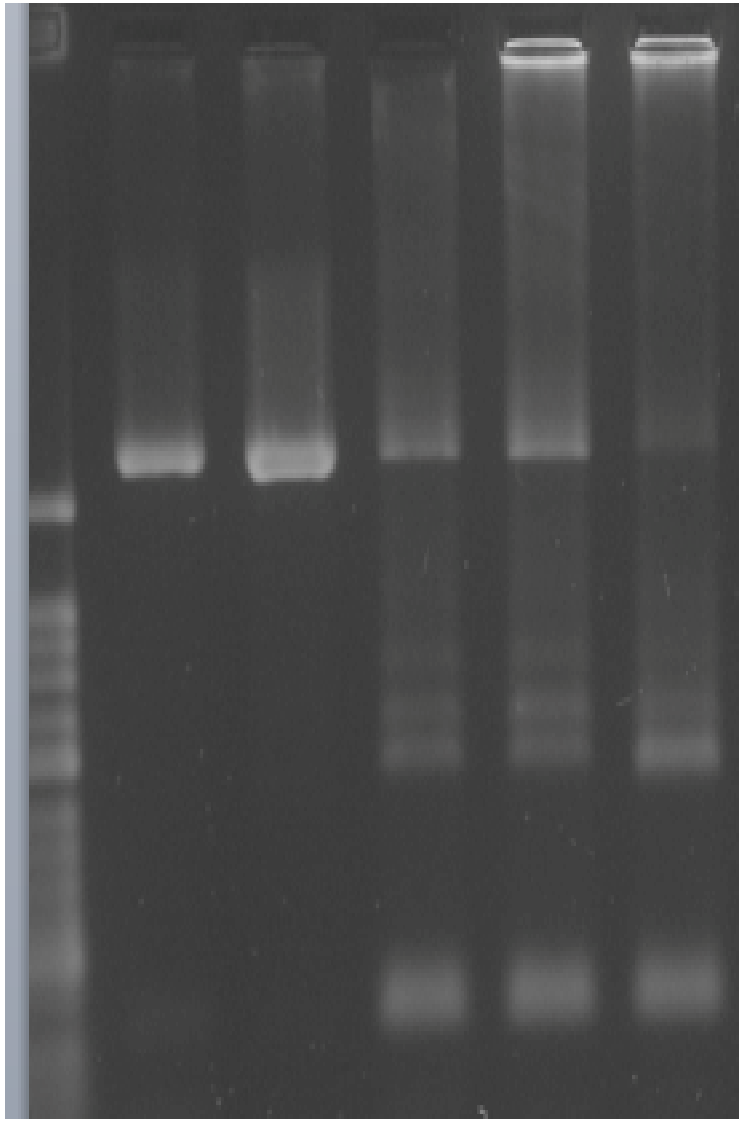
Gel 1



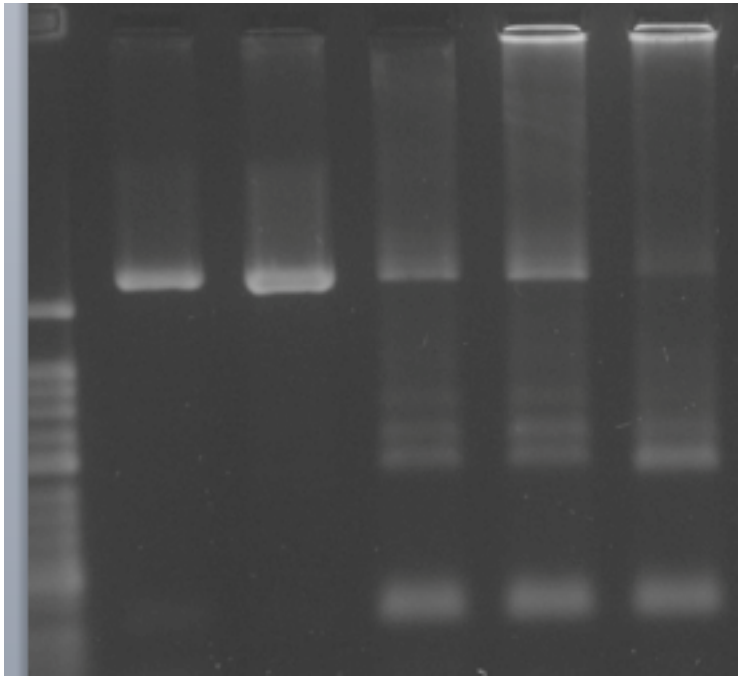
Gel 2



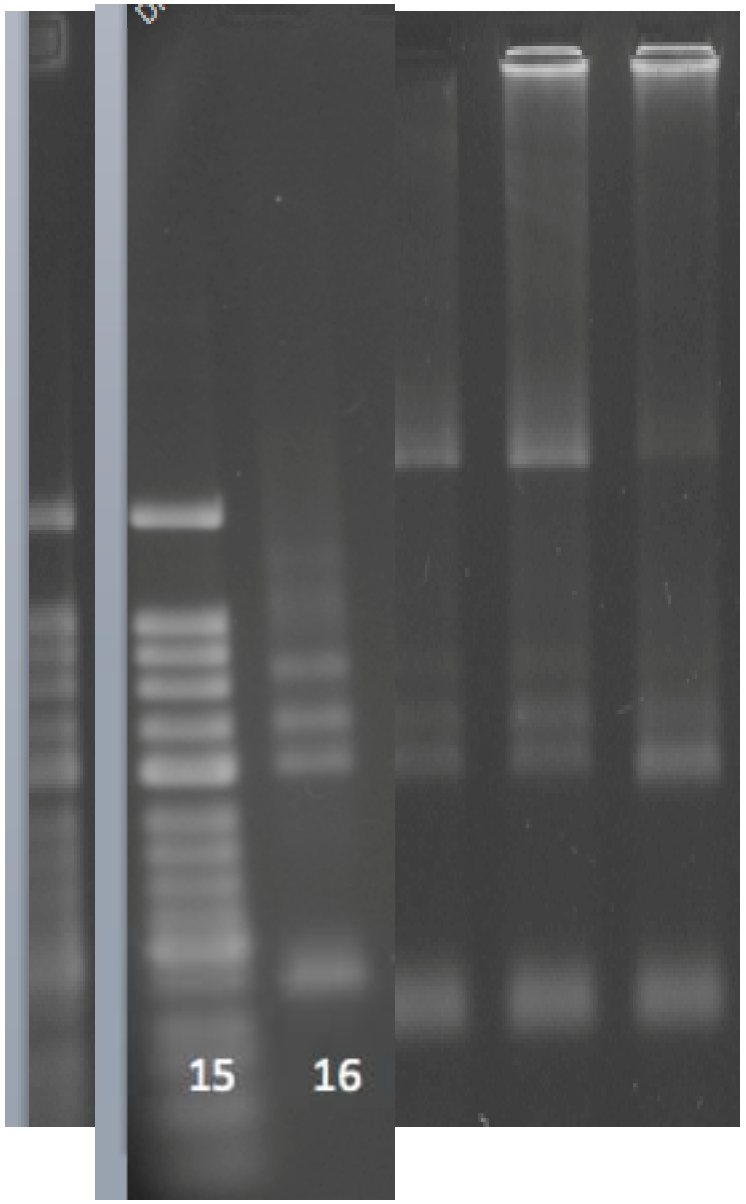
Gel 1 縦方向への拡大



Gel 1



Gel 1 縦方向への拡大



Gel 2

1-3： Method の記載の一部の盗用の疑い

Karyotype analysis. Karyotype analysis was performed by Multicolor FISH analysis (M-FISH). Subconfluent STAPS cells were arrested in metaphase by colcemid (final concentration 0.270 µg/ml) to the culture medium for 2.5 h at 37°C in 5% CO2. Cells were washed with PBS, treated with trypsin/ethylenediaminetetraacetic acid (EDTA), resuspended into cell medium and centrifuged for 5 min at 1200 rpm. To the cell pellet in 3 ml of PBS, 7 ml of a prewarmed hypotonic 0.0375 M KC1 solution was added. Cells were incubated for 20 min at 37°C. Cells were centrifuged for 5 min at 1200 rpm and the pellet was resuspended in 3-5 ml of 0.0375 M KC1 solution. The cells were fixed with methanol/acetic acid (3: 1; vol/vol) by gently pipetting. Fixation was performed four times prior to spreading the cells on glass slides. For the FISH procedure, mouse chromosome-specific painting probes were combinatorially labeled using seven different fluorochromes and hybridized as previously described (Jentsch et al, 2003). For each cell line, 9-15 metaphase spreads were acquired by using a Leica DM RXA RF8 epifluorescence microscope (Leica Mikrosysteme GmbH, Bensheim, Germany) equipped with a Sensys CCD camera (Photometries, Tucson, AZ). Camera and microscope were controlled by the Leica Q-FISH software (Leica Microsystems hanging solutions, Cambridge, United Kingdom). Metaphase spreads were processed on the basis of the Leica MCK software and presented as multicolor karyograms.

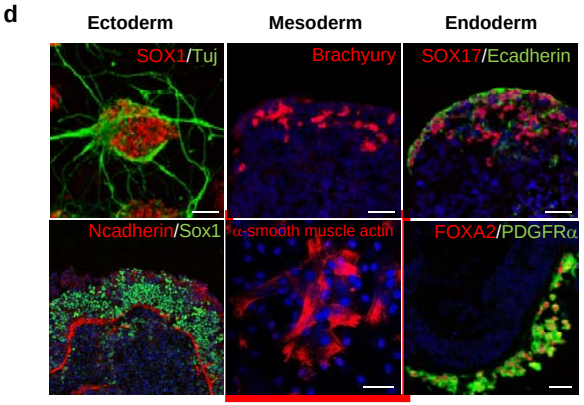
Guo J et.al.; Multicolor Karyotype Analyses Of Mouse embryonic stem cell. In Vitro Cell Dev Biol Anim 41(8-9), 278-283 (2005)

1–4： Method の記載の一部の間違い

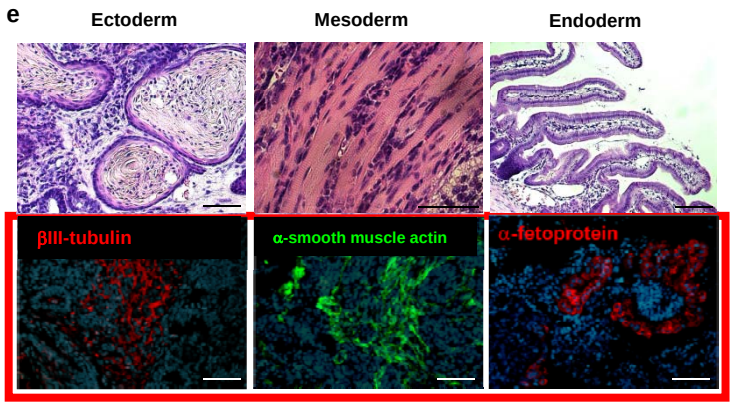
Karyotype analysis. Karyotype analysis was performed by Multicolor FISH analysis (M-FISH). Subconfluent STAPS cells were arrested in metaphase by colcemid (final concentration 0.270 µg/ml) to the culture medium for 2.5 h at 37°C in 5% CO2. Cells were washed with PBS, treated with trypsin/ethylenediaminetetraacetic acid (EDTA), resuspended into cell medium and centrifuged for 5 min at 1200 rpm. To the cell pellet in 3 ml of PBS, 7 ml of a prewarmed hypotonic 0.0375 M KC1 solution was added. Cells were incubated for 20 min at 37°C. Cells were centrifuged for 5 min at 1200 rpm and the pellet was resuspended in 3-5 ml of 0.0375 M KC1 solution. The cells were fixed with methanol/acetic acid (3: 1; vol/vol) by gently pipetting. Fixation was performed four times prior to spreading the cells on glass slides. For the FISH procedure, mouse chromosome-specific painting probes were combinatorially labeled using seven different fluorochromes and hybridized as previously described (Jentsch et al, 2003). For each cell line, 9-15 metaphase spreads were acquired by using a Leica DM RXA RF8 epifluorescence microscope (Leica Mikrosysteme GmbH, Bensheim, Germany) equipped with a Sensys CCD camera (Photometries, Tucson, AZ). Camera and microscope were controlled by the Leica Q-FISH software (Leica Microsystems hanging solutions, Cambridge, United Kingdom). Metaphase spreads were processed on the basis of the Leica MCK software and presented as multicolor karyograms.

1-5： Fig. 2d, 2e の画像の取り違え

In vitro 分化



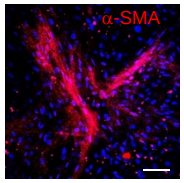
テラトーマ形成

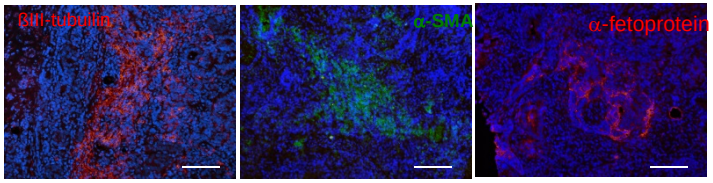


脾臓の血液系細胞から作成した
STAP細胞を使用

骨髄の血液系細胞から作成した
STAP 細胞を使用

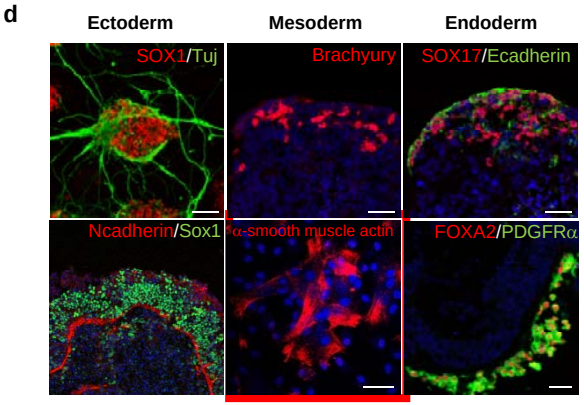
正しいデータ（脾臓血液細胞を用いた）に差し替えたい



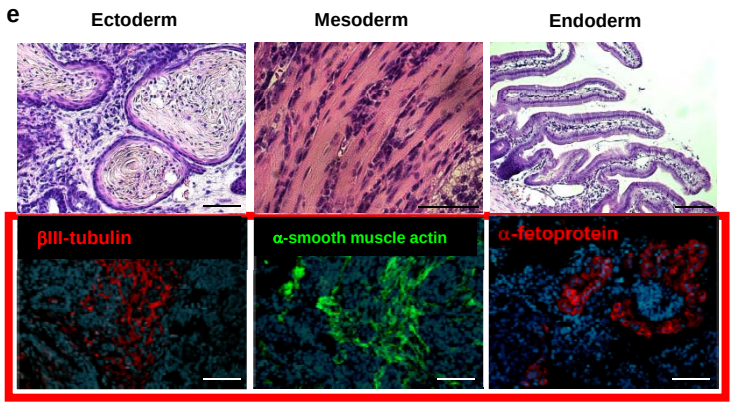


1–5： Fig. 2d, 2e 画像と学位論文の画像の酷似

In vitro 分化



テラトーマ形成



酸処理：STAP

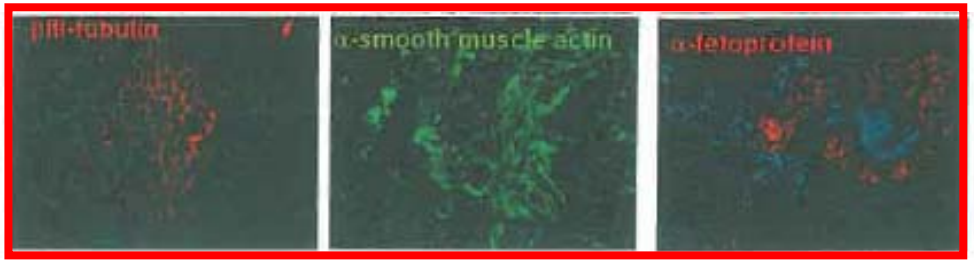
学位論文

骨髄の血液細胞

細いピペットを通過：スフェア

Fig. 11

Fig. 14



その他： Method の記載

Bisulphite sequencing

GFP-positive cells in STAP clusters were collected by FACS Aria. Genomic DNA was extracted from STAP cells and analysed. Bisulphite treatment of DNA was performed using the CpGenome DNA modification kit (Chemicon, http://www.chemicon.com), following the manufacturer's instructions. The resulting modified DNA was amplified by nested PCR using two forward (F) primers and one reverse (R) primer: Oct4 (F1, 5′ -GTTGTTTTGTTTTGGTTTTGGATAT-3′ ; F2, 5′ -ATGGGTTGAAATATTGGGTTTATTTA-3′ ; R, 5′ -CCACCCTCTAACCTTAACCTCTAAC-3′). And Nanog (F1, 5′ -GAGGATGTTTTTTAAGTTTTTTTT-3′ ; F2, 5′ -AATGTTTATGGTGGATTTTGTAGGT-3′ ; R, 5′ -CCCACACTCATATCAATATAATAAC-3′). PCR was done using TaKaKa Ex Taq Hot Start Version (RR030A). DNA sequencing was performed using a M13 primer at the Genome Resource and Analysis Unit, RIKEN CDB.