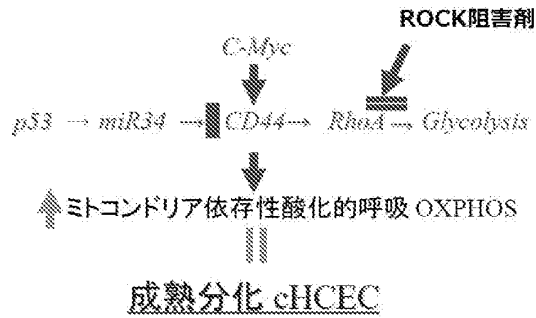


[図1]

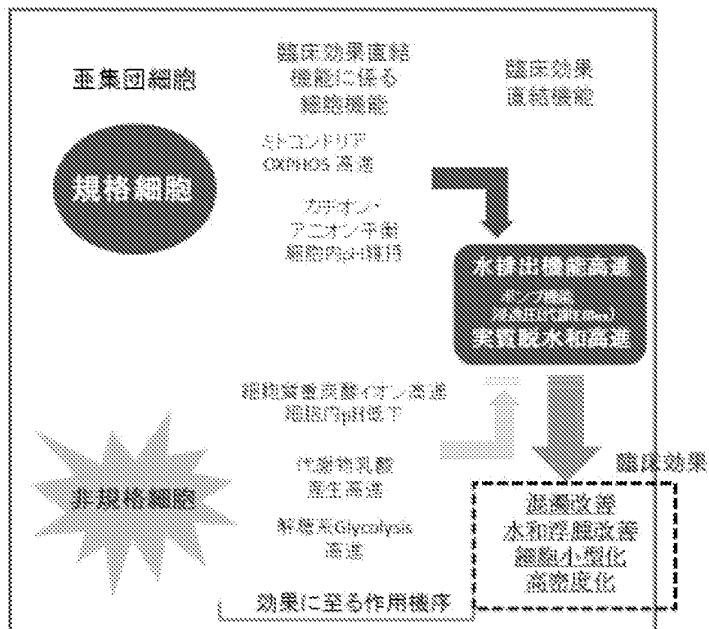
CD44を介するミトコンドリアのエネルギー代謝制御

Depression of CD44/RhoA Axis Skewed
the Energy Metabolism from Glycolysis to OXPHOS
in Differentiated Mature cHCECs

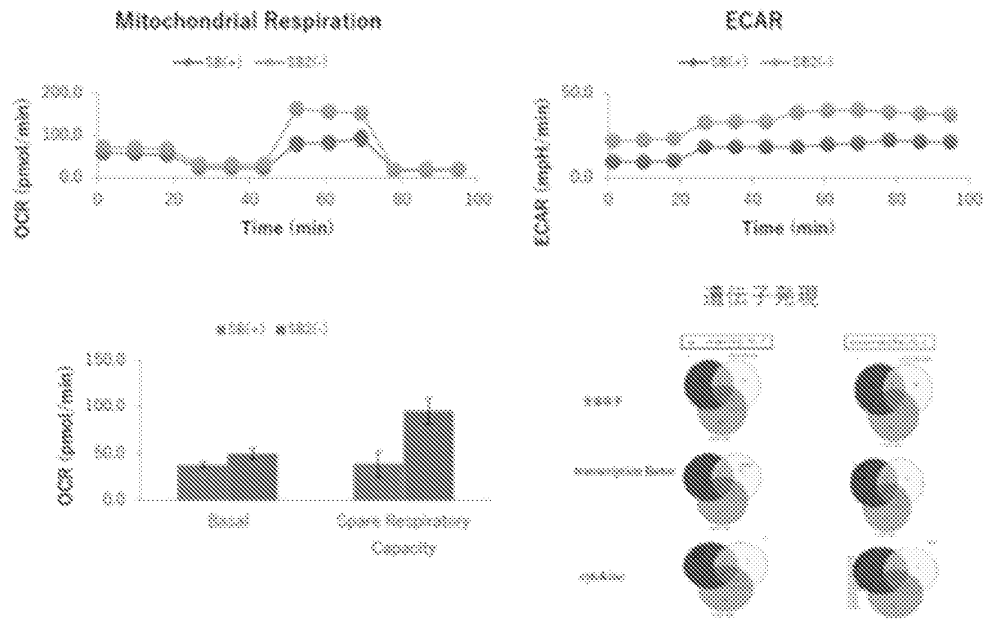


[図2]

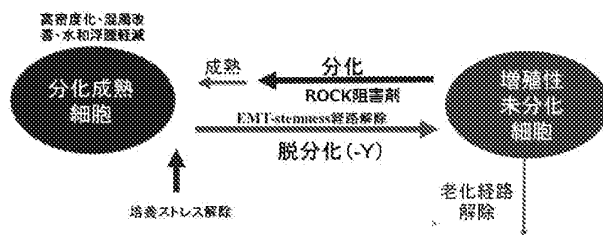
細胞注入再生医療



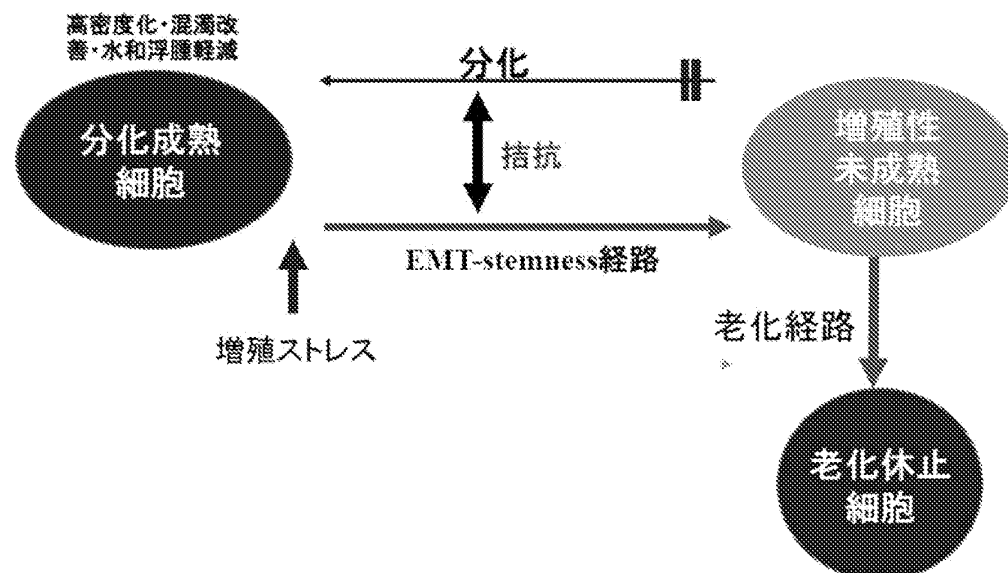
[図3]



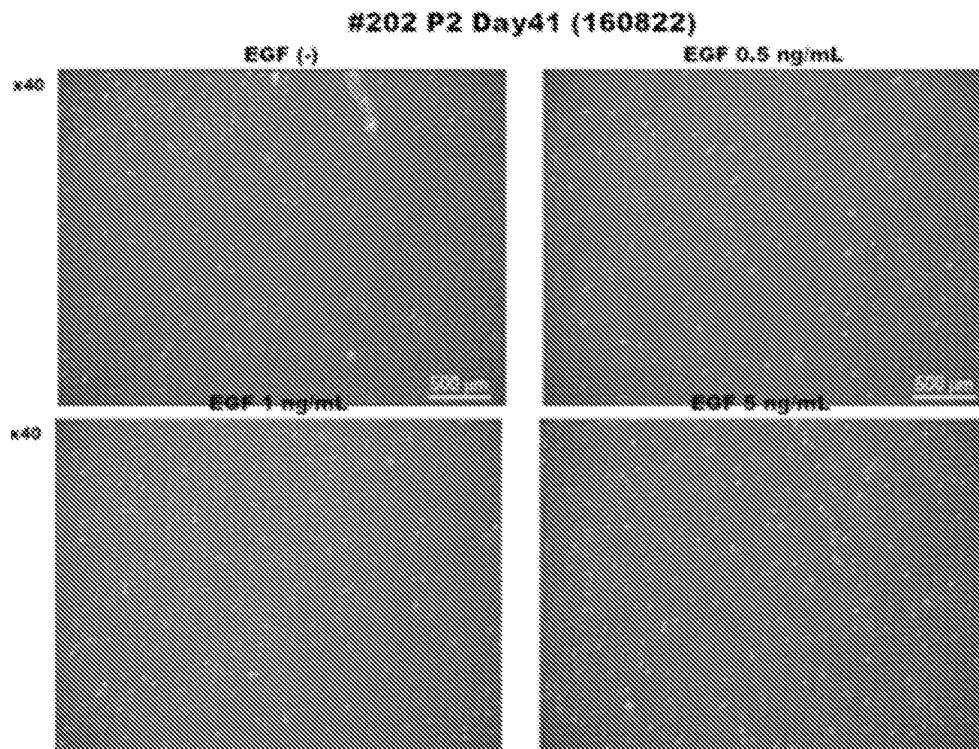
[図4]



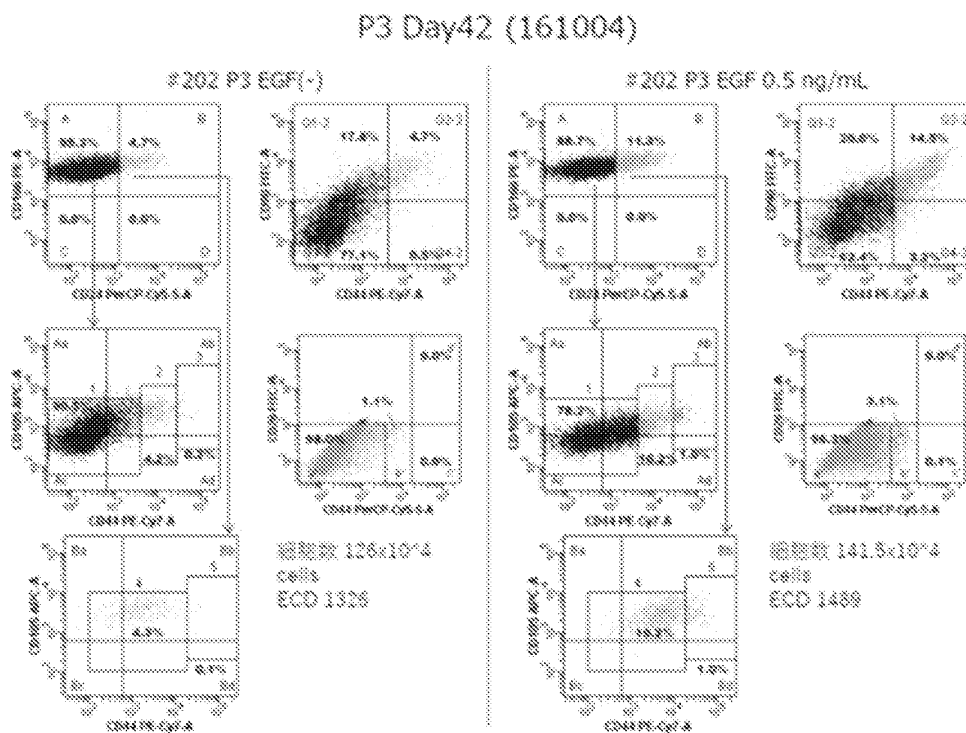
[図5]



[図6]

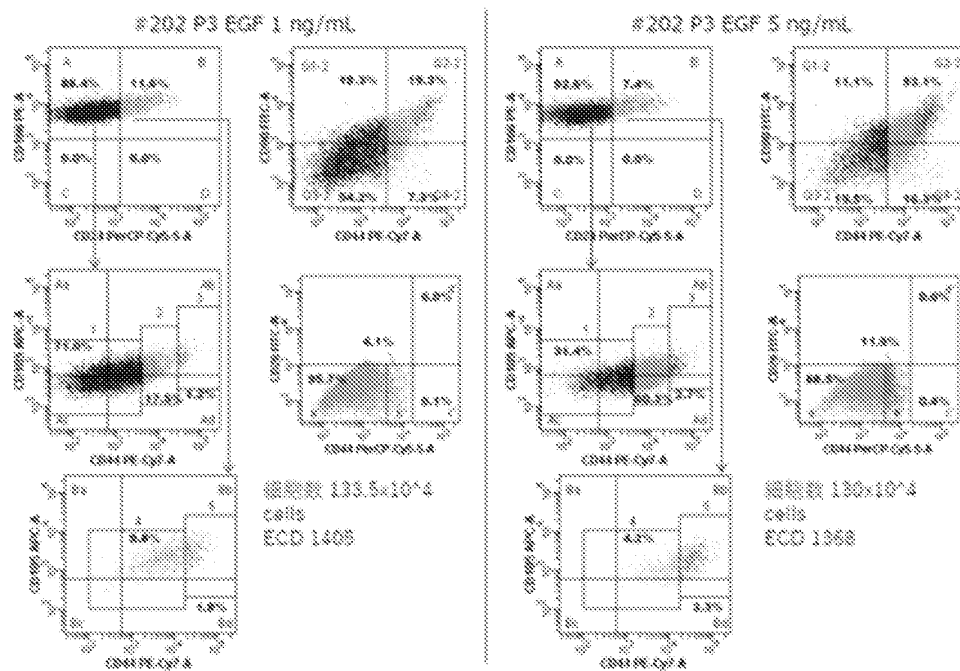


[図7]



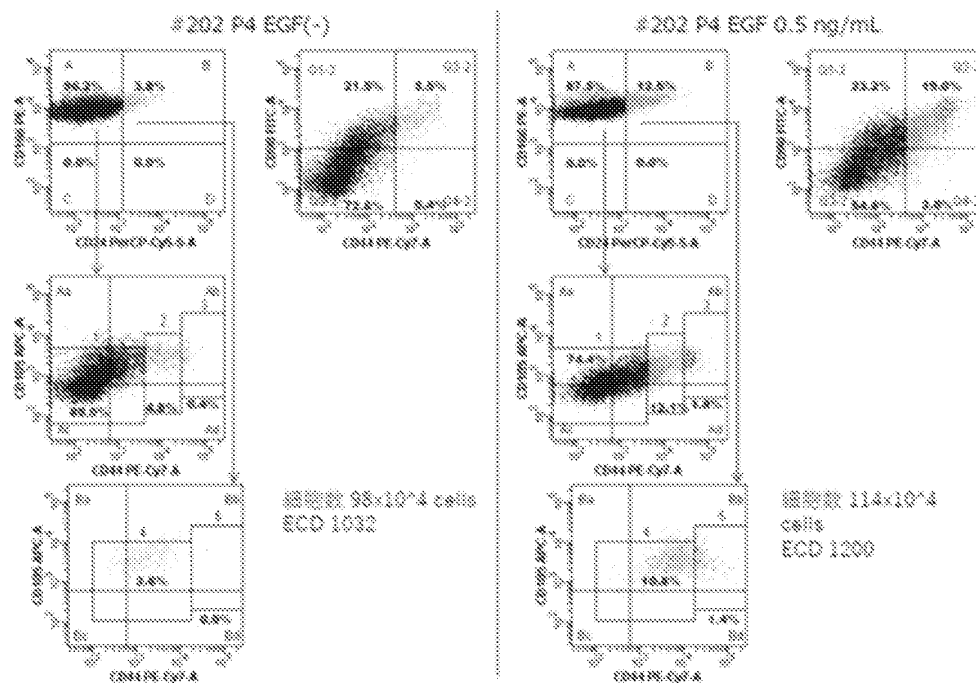
[図8]

P3Day42 (161004)



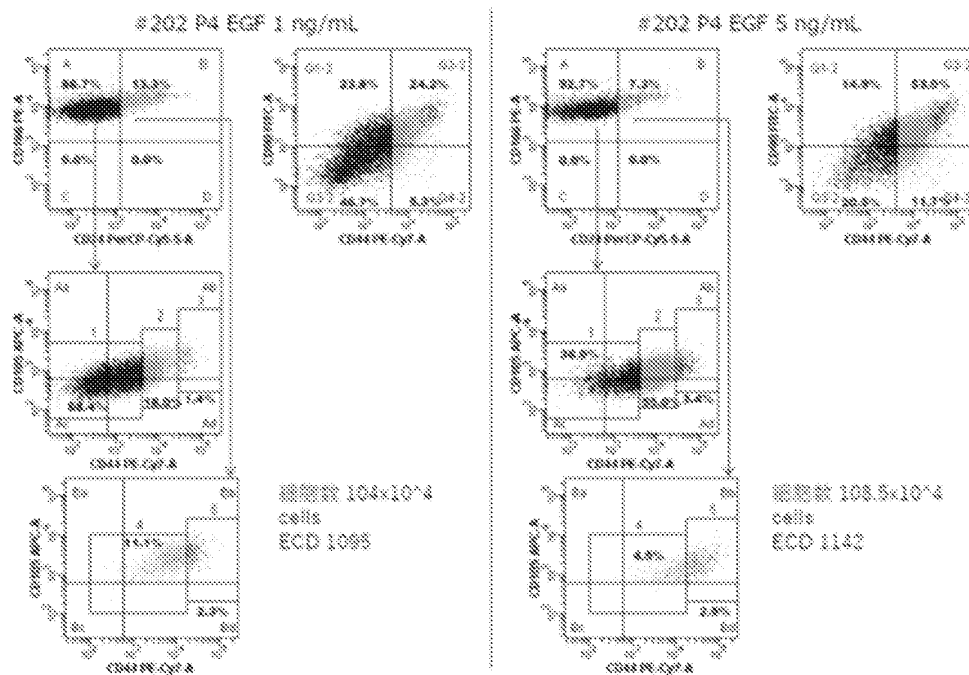
[図9]

P4Day42 (161115)



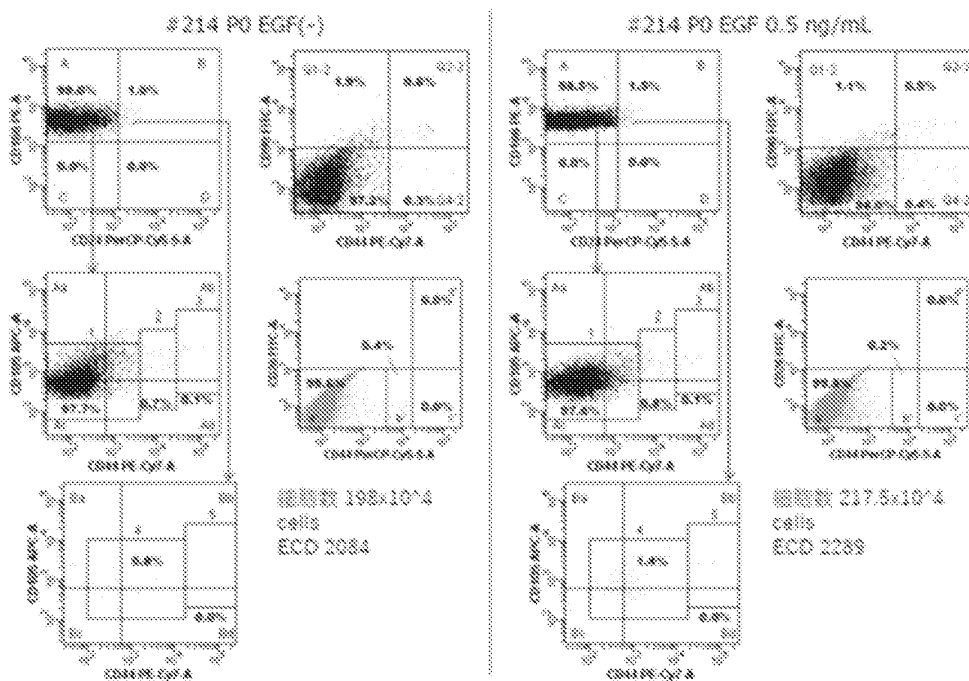
[図10]

P4Day42 (161115)



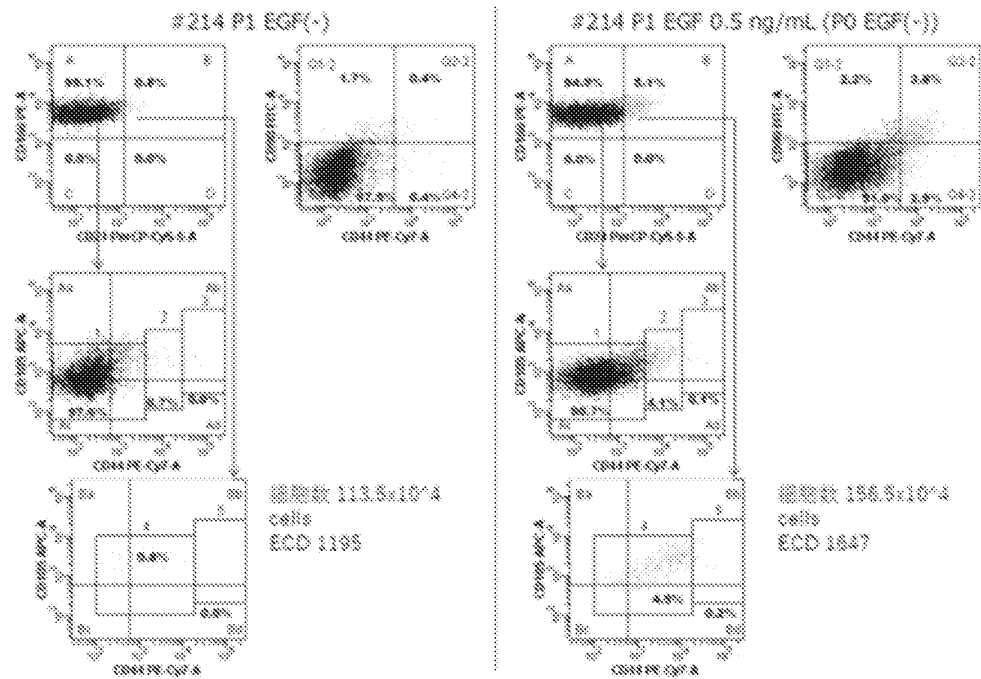
[図11]

Day41 (161014)



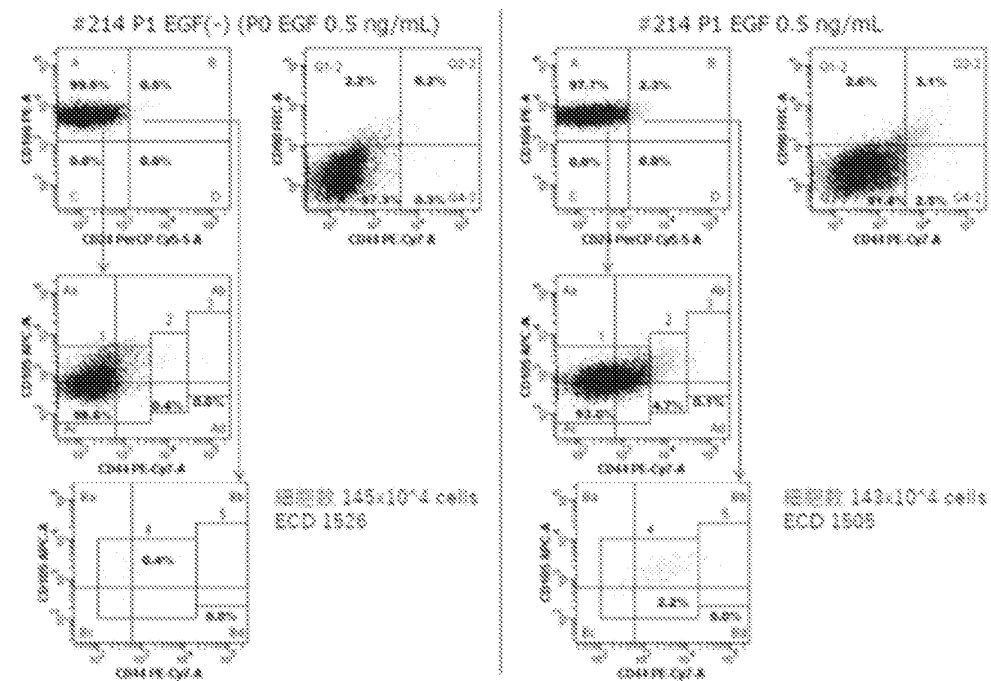
[図12]

Day42 (161125)

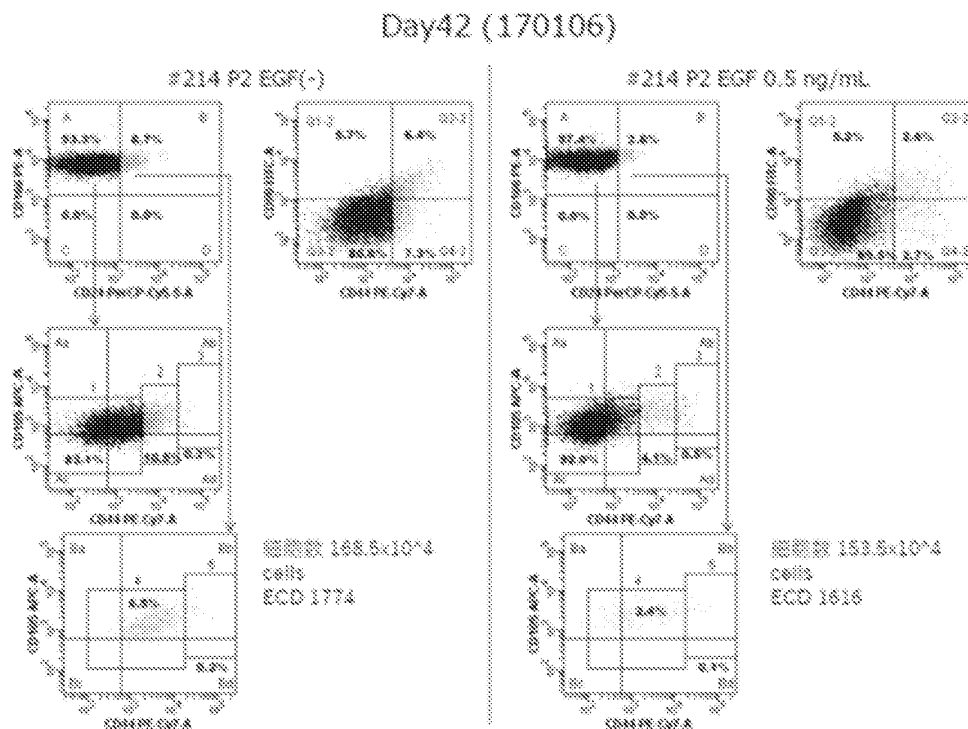


[図13]

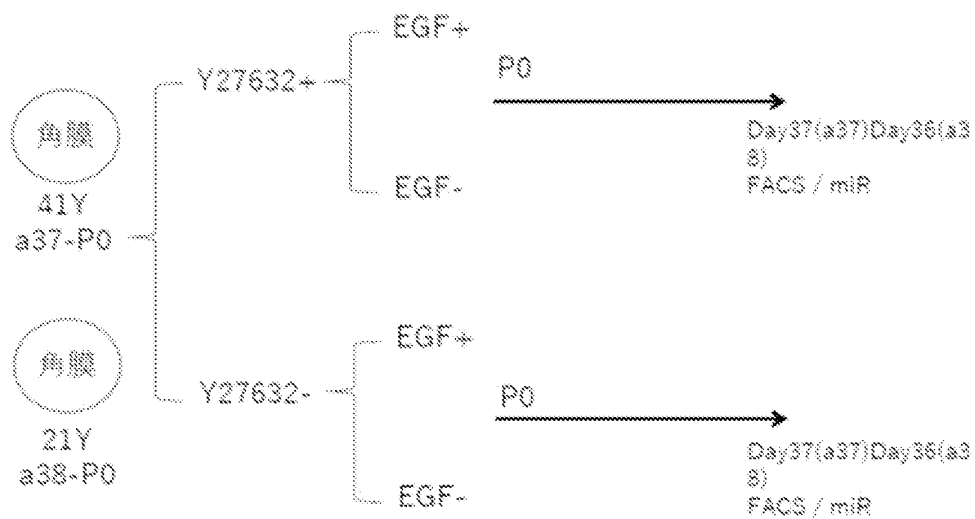
Day42 (161125)



[図14]



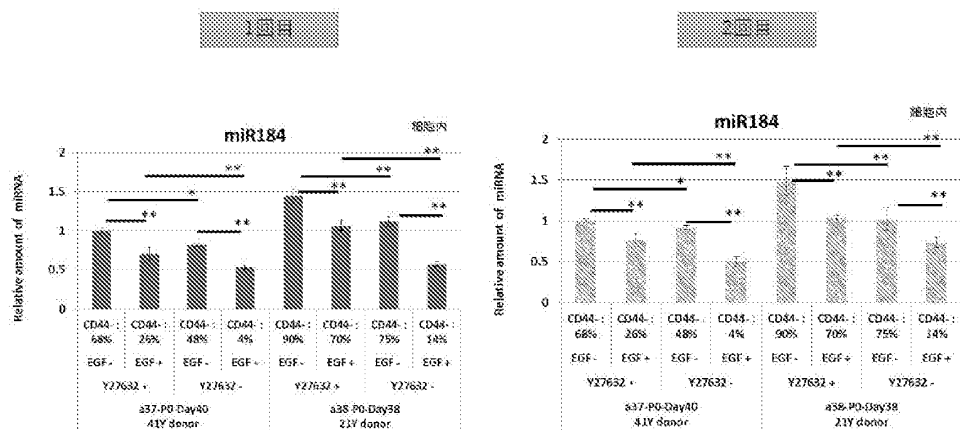
[図15]



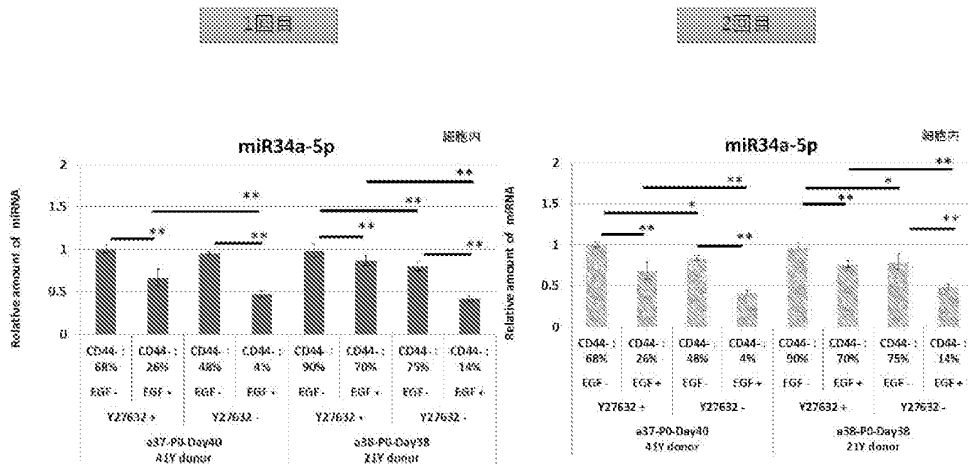
[図16]

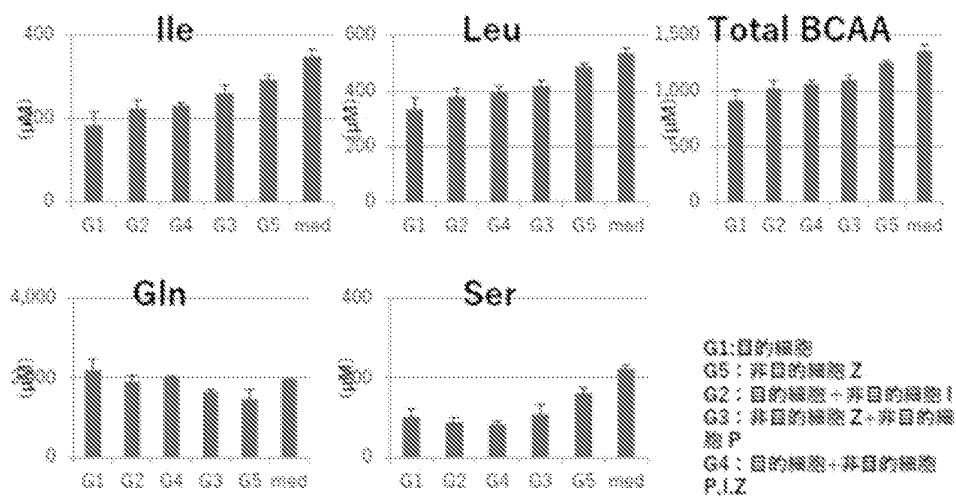
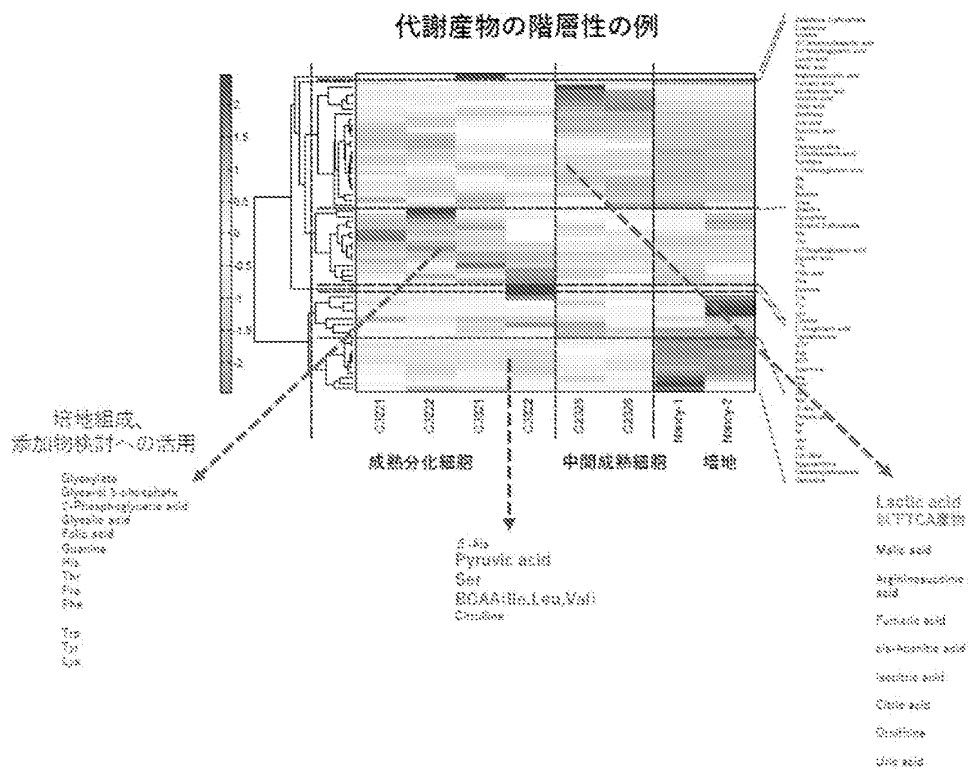
	Y27632+				Y27632-			
	EGF-		EGF+		EGF-		EGF+	
	41Y a37- P0	21Y a38- P0	41Y a37- P0	21Y a38- P0	41Y a37- P0	21Y a38- P0	41Y a37- P0	21Y a38- P0
CD44-	68%	90%	25%	70%	48%	75%	4%	14%
CD44+ / CD44++	22%	4%	43%	19%	32%	10%	32%	54%
CD44+++	4%	1%	9%	3%	11%	2%	35%	26%
CD24++ / CD44+++	1%	0%	10.3%	1%	2%	0%	27%	6%
CD44- / CD90-	61%	93%	25%	68%	43%	84%	4%	13%
写真評価								

[図17]

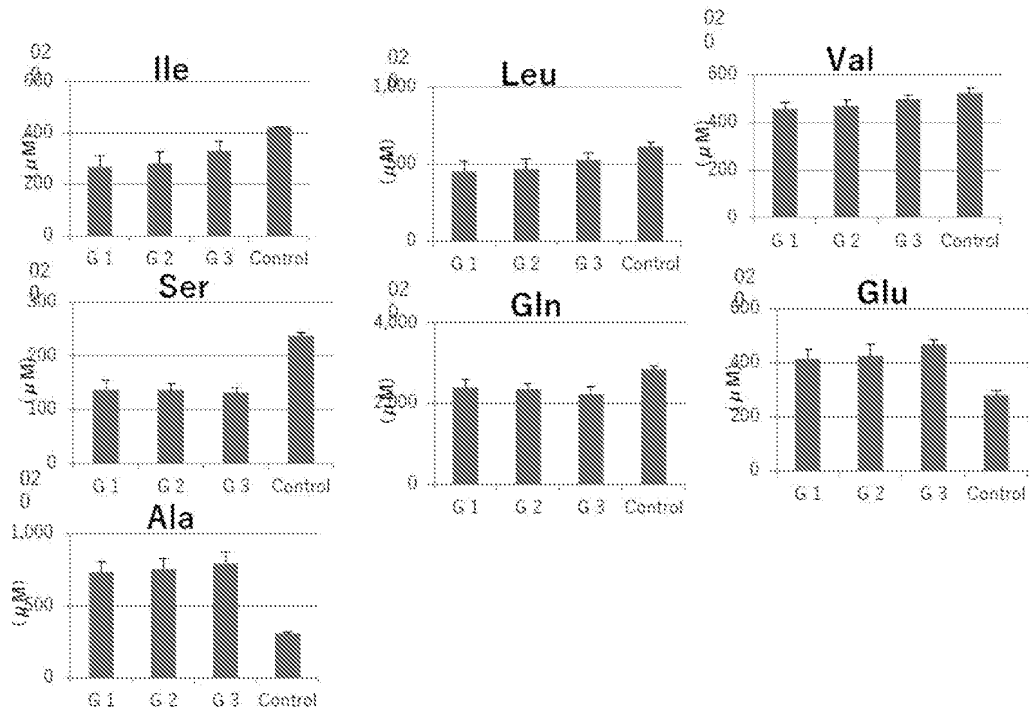


[図18]

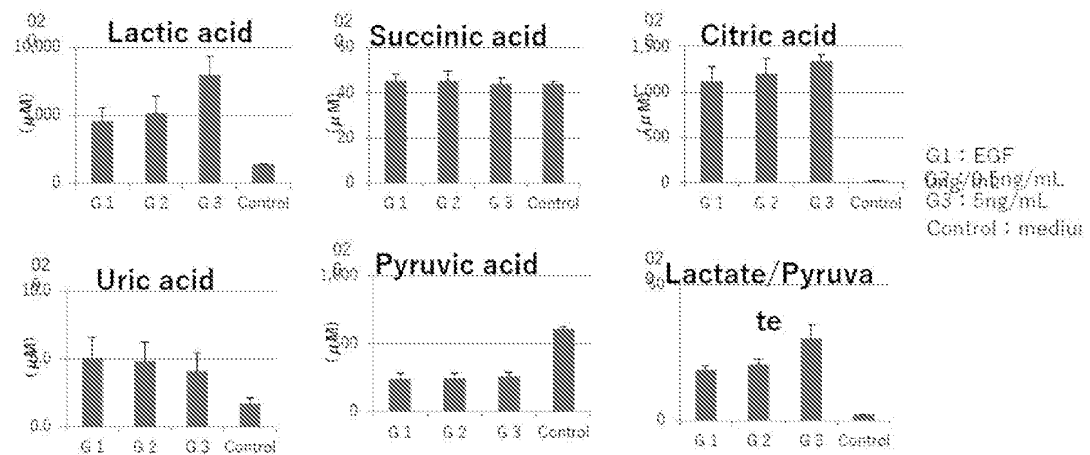




[図21]



[図22]



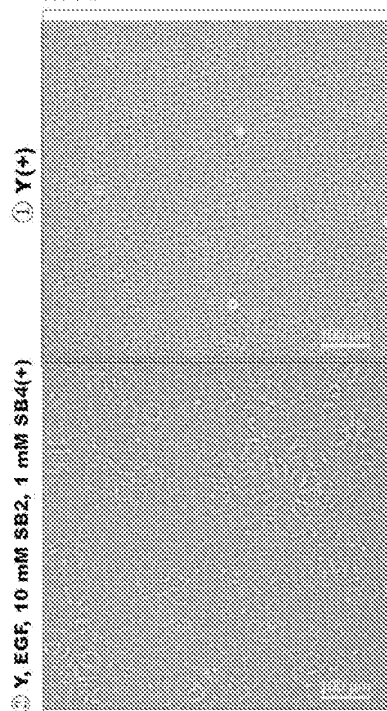
[図23]

添加試薬	①	②	③	④	⑤
Y27632	+	+	+	+	+
EGF	-	+	-	+	+
10 mM SB2	-	+	+	-	+
1 mM SB4	-	+	-	-	-

[図24]

CT09 P5 D34 (190122)

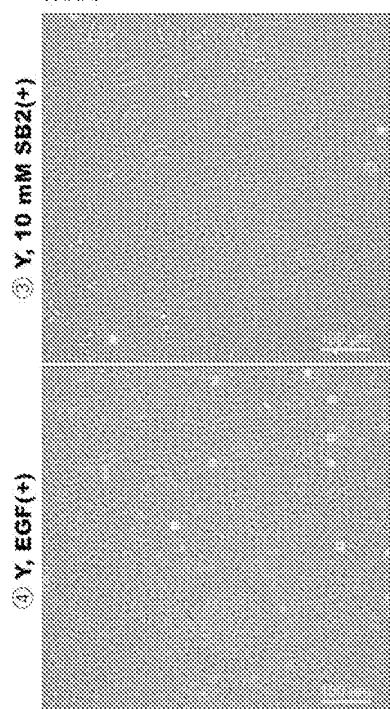
x100



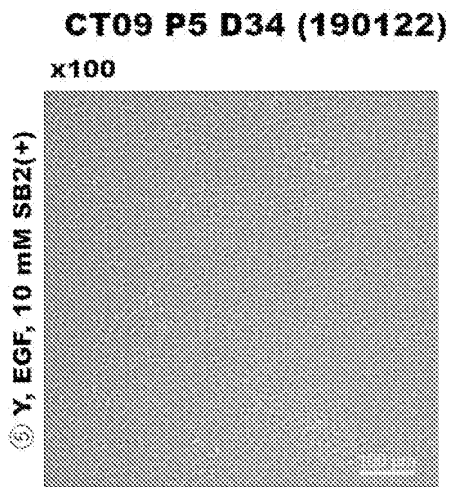
[図25]

CT09 P5 D34 (190122)

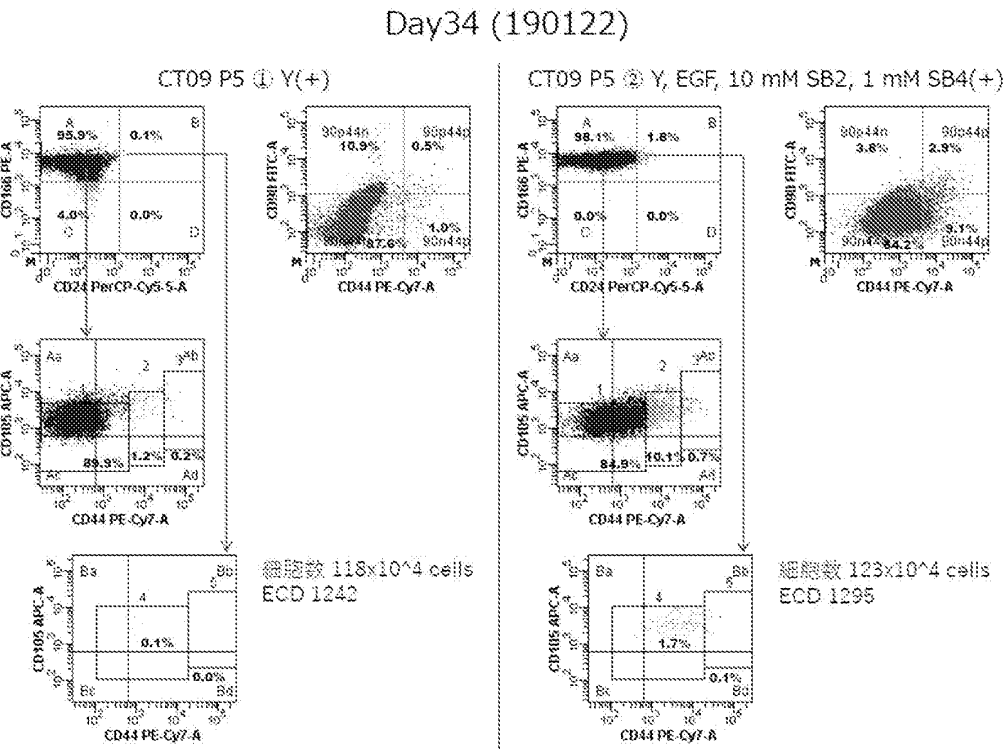
x100



[図26]

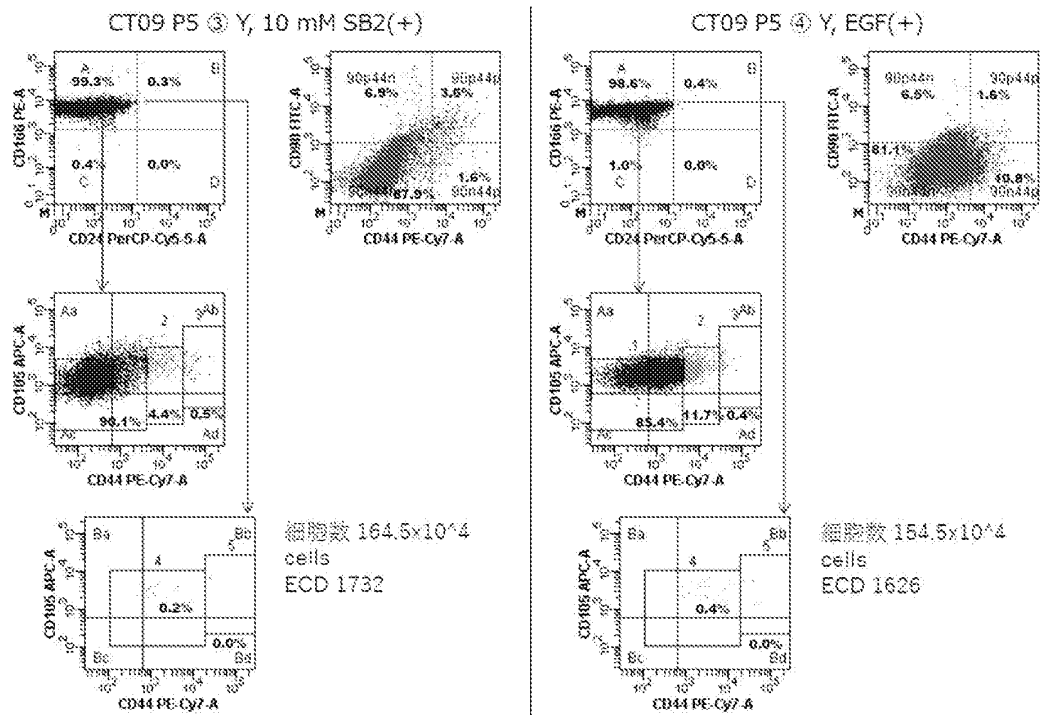


[図27]



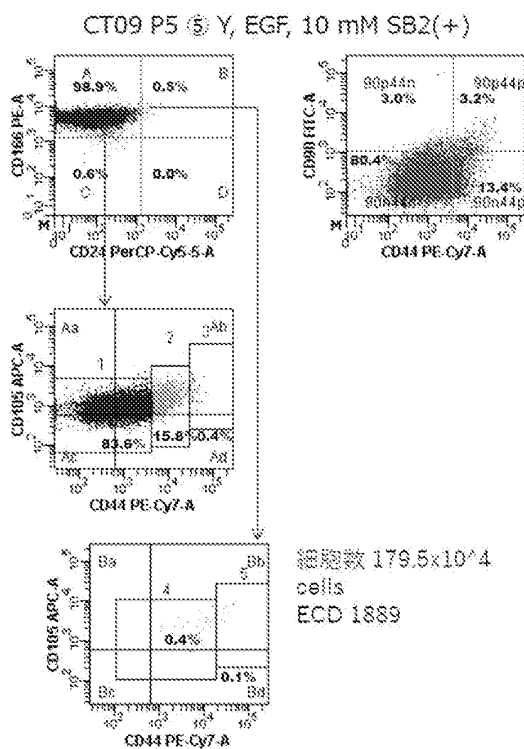
[図28]

Day34 (190122)



[図29]

Day34 (190122)

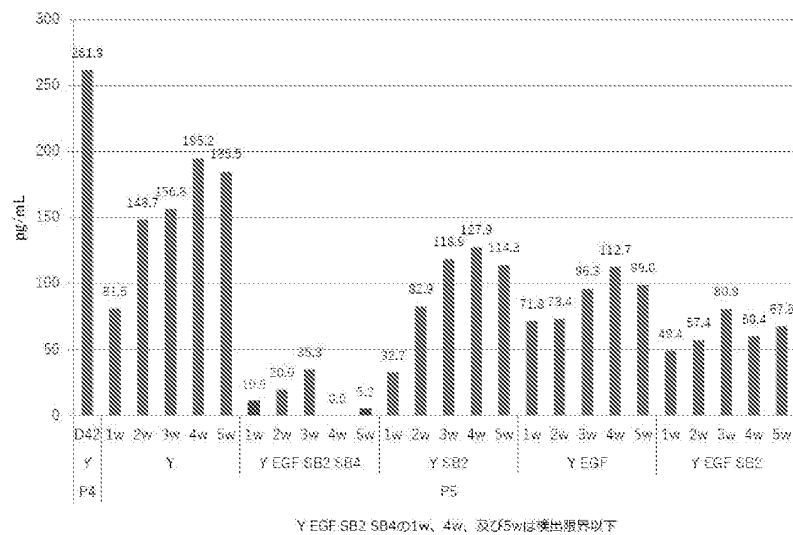


[図30]

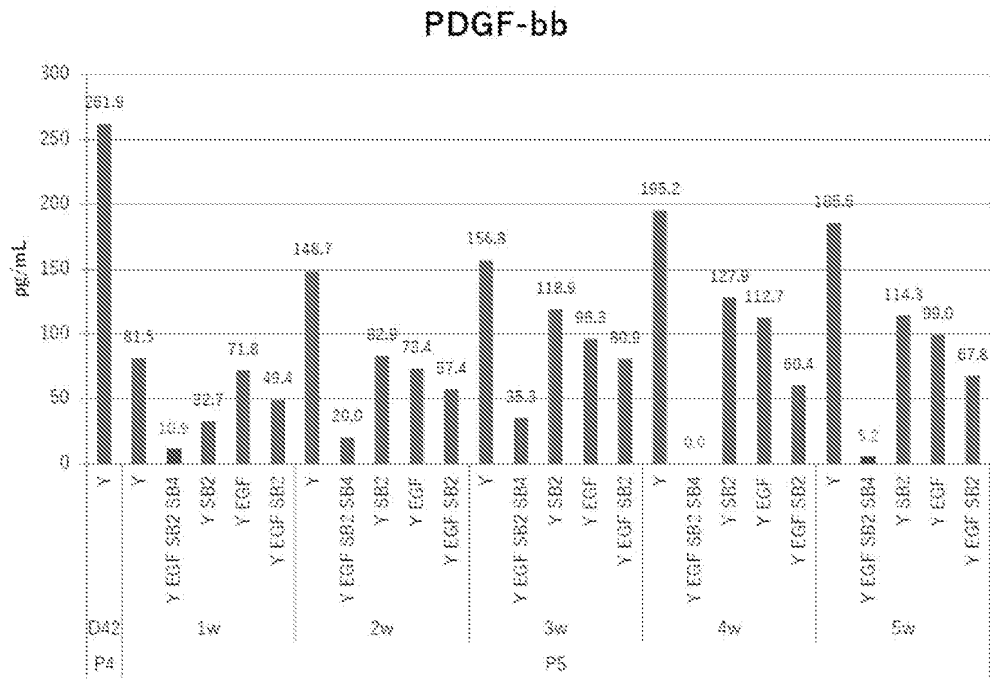
		添加試薬	培養上清
P4		Y	Day42
P5	①	Y	1w, 2w, 3w, 4w, 5w
	②	Y, EGF, 10 mM SB2, 1 mM SB4	1w, 2w, 3w, 4w, 5w
	③	Y, 10 mM SB2	1w, 2w, 3w, 4w, 5w
	④	Y, EGF	1w, 2w, 3w, 4w, 5w
	⑤	Y, EGF, 10 mM SB2	1w, 2w, 3w, 4w, 5w

[図31]

PDGF-bb

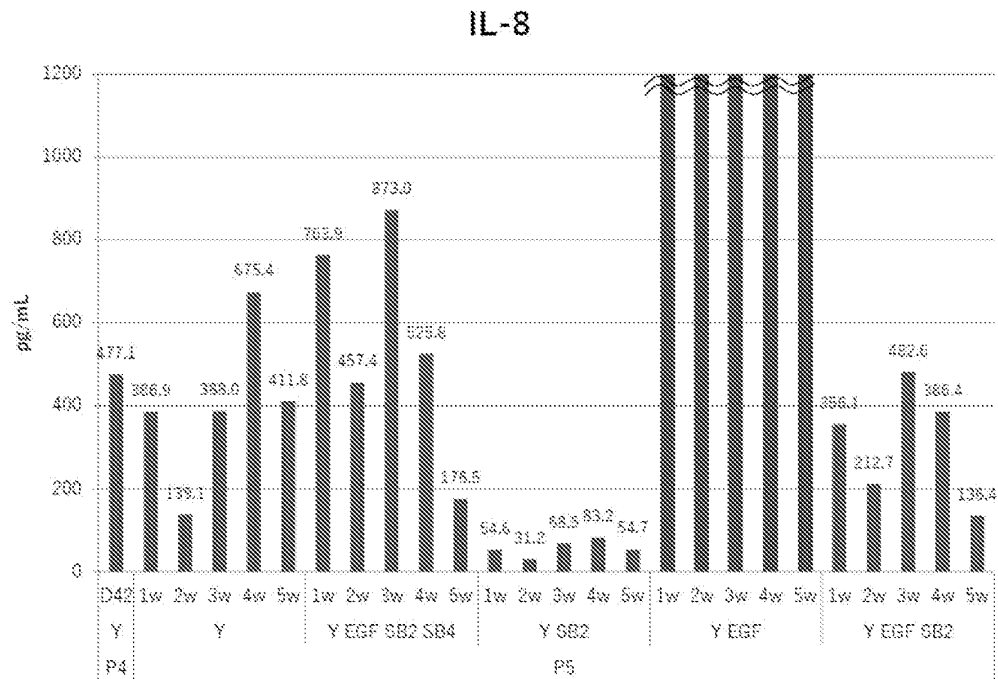


[図32]



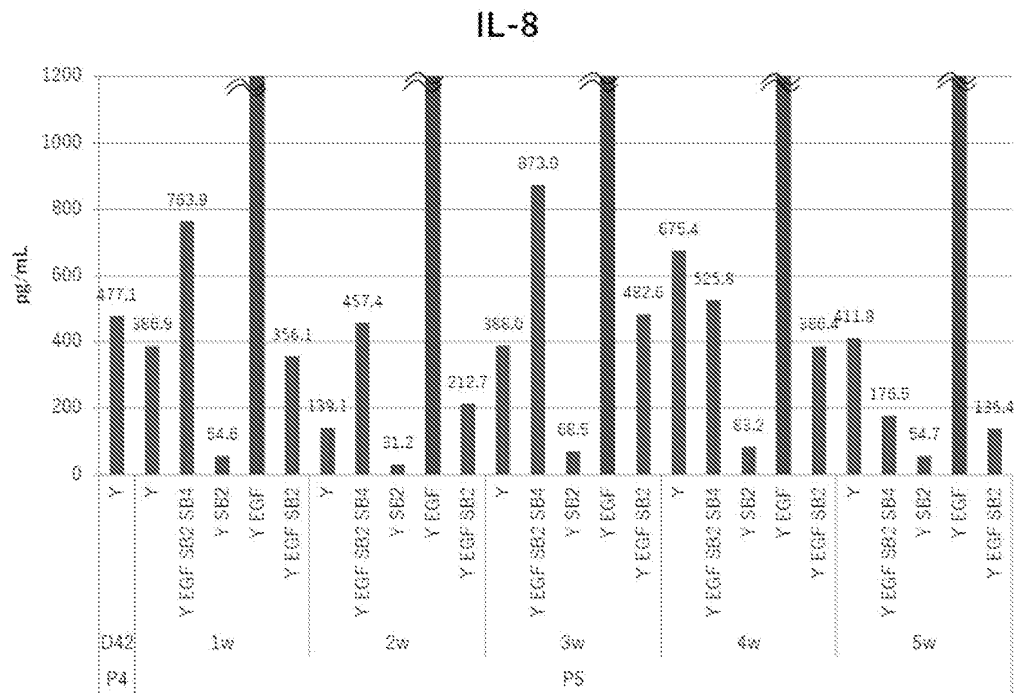
1wのY EGF SB2 SB4、4wのY EGF SB2 SB4、及び5wのY EGF SB2 SB4は検出限界以下

[図33]



Y EGF SB2の1w~5wは検出限界以上

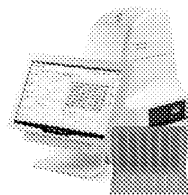
[図34]



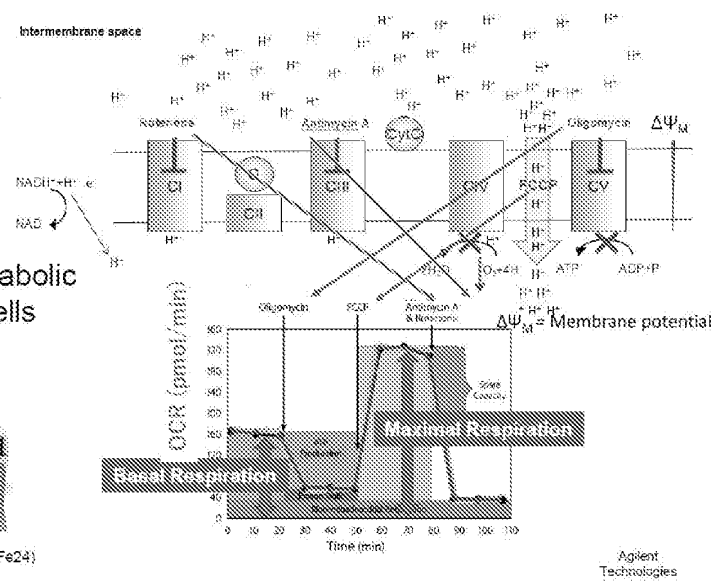
[図35]

Mito Stress Test

To measure the metabolic pathways in living cells

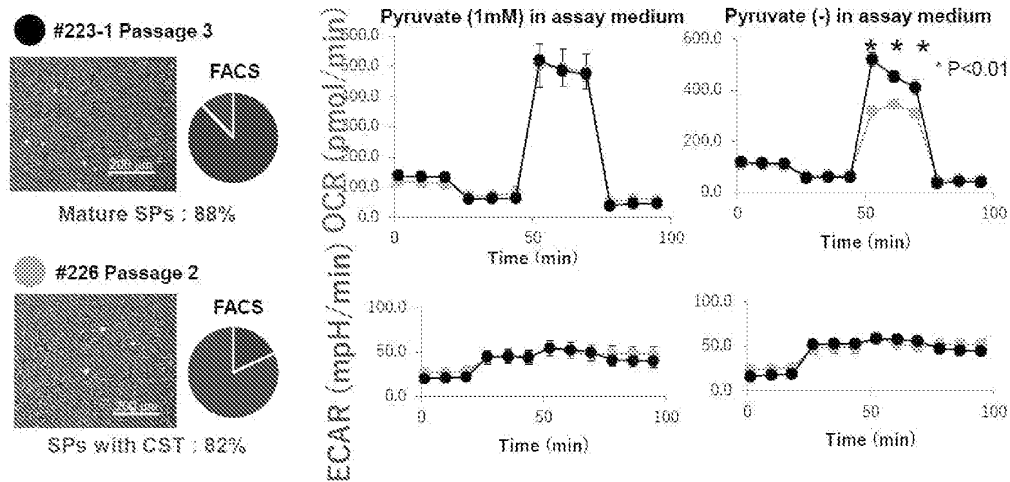


Extracellular flux analyzer (XFe24)



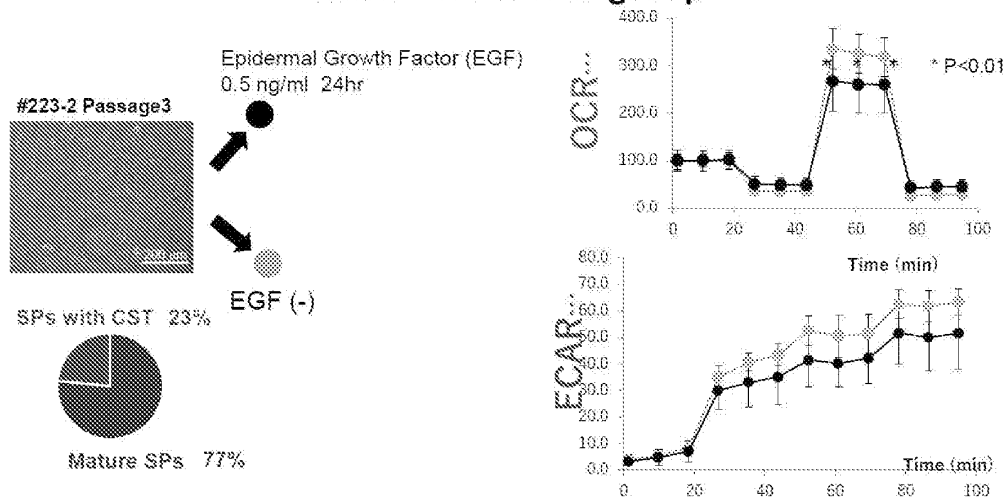
[図36]

In the absence of pyruvic acid, maximal respirations decreases only in SPs with CST



[図37]

The maximal respiration significantly decreased in the EGF added group



[図38]

培養No.	#190318	#190719	#190802
Donor No.	ACS-736 OSCN/ODCN	AEB-301 OSCN/ODCN	ACW-134 OSCN/ODCN
Age	73	40	28
Gender	Male	Male	Female
ECD	3040/3021	3448/3289	3003/3021
COD	Metastatic Prostate Cancer	Bleomycin Lung Toxicity 2/2 Chemo Treatments	ESRD
D-P	17:29	11:28	8:57
D-C	8D	8D	5D

[図39]

Y添加	Day0-3	Day4-9	Day10-19	Day20-	Day28-
①	+	+	+	+	+, SB2+
②	-	+	+	+	+, SB2+
③	-	-	+	+	+, SB2+
④	-	-	-	+	+, SB2+
⑤	+	-	-	-	-, SB2+
⑥	-	-	-	-	-, SB2+

[図40]

	添加物	上清回収
P1	-SB2	D37, D41
P2	+SB2	1w~6w
	-SB2	1w~6w

[図41]

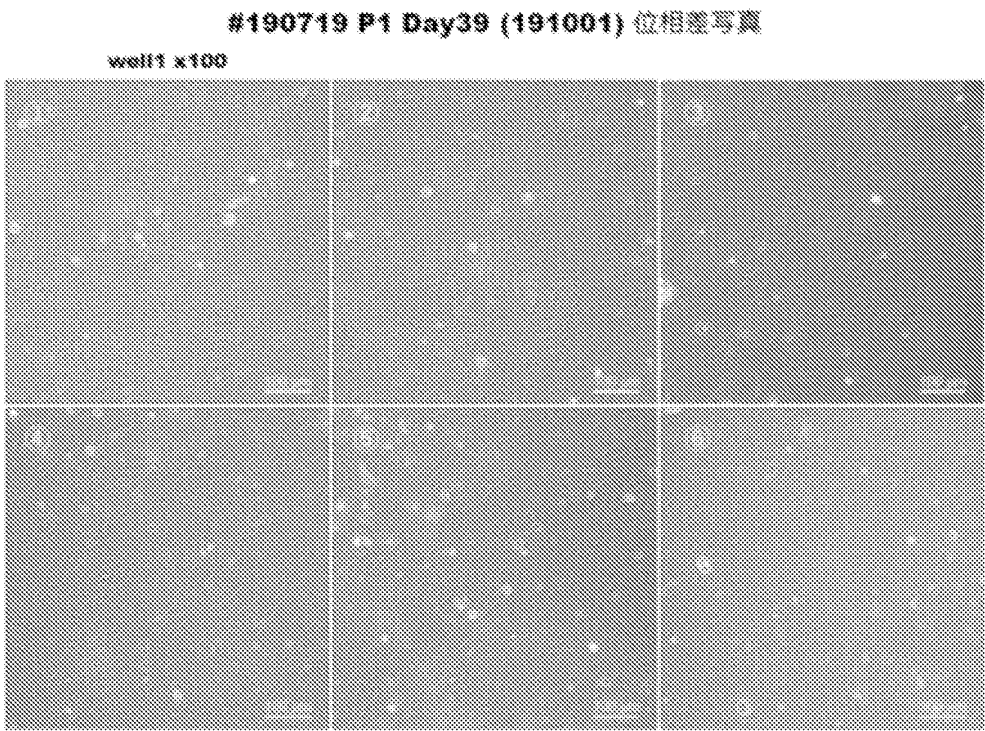
#190719 P1, P2のFACS結果

P1	Fluor-1 (%)	CD44+ (%)	CD44- (%)
1 well1	82.6	0.6	0.1
1 well2	73.4	0.7	0
2 well1	79.1	0.7	1.1
2 well2	82.2	0.6	0.1
3 well1	90.1	0.5	0.3
3 well2	94.2	0.3	0.1
4 well1	80.9	1.8	0.2
4 well2	84	1.9	0.4
5 well1	45.7	3	1.4
5 well2	49.3	2.5	0.4
6 well1	57.8	7.7	3.2
6 well2	54.6	9.4	5.6

#190802 P1のFACS結果

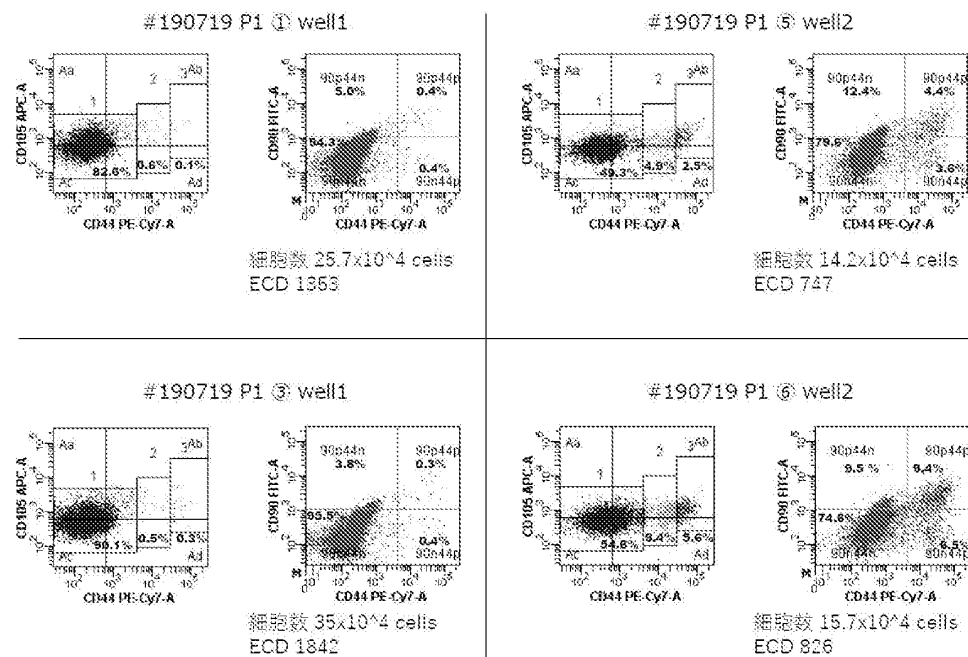
P1	Fluor-1 (%)	CD44+ (%)	CD44- (%)
1 well1	88.2	1	0.4
1 well2	90.1	0.7	0.1
2 well1	89.3	0.6	0.3
2 well2	87.2	0.9	0.4
3 well1	95	0.5	0.1
3 well2	88.2	0.9	0.1
4 well1	92.1	2.6	1.1
4 well2	92.7	2.5	0.4
5 well1	82.2	5.4	1.3
5 well2	84.8	5.9	1.3
6 well1	84.9	8	3.1
6 well2	84.6	8.2	1.6

[図42]



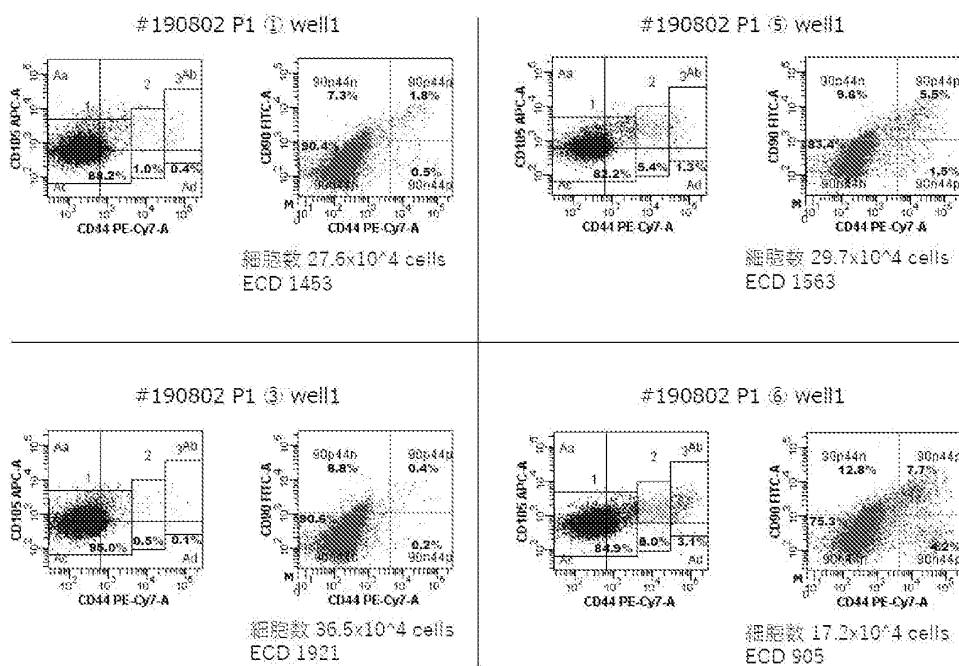
[図43]

#190719 P1 Day39 (191001) FACS結果



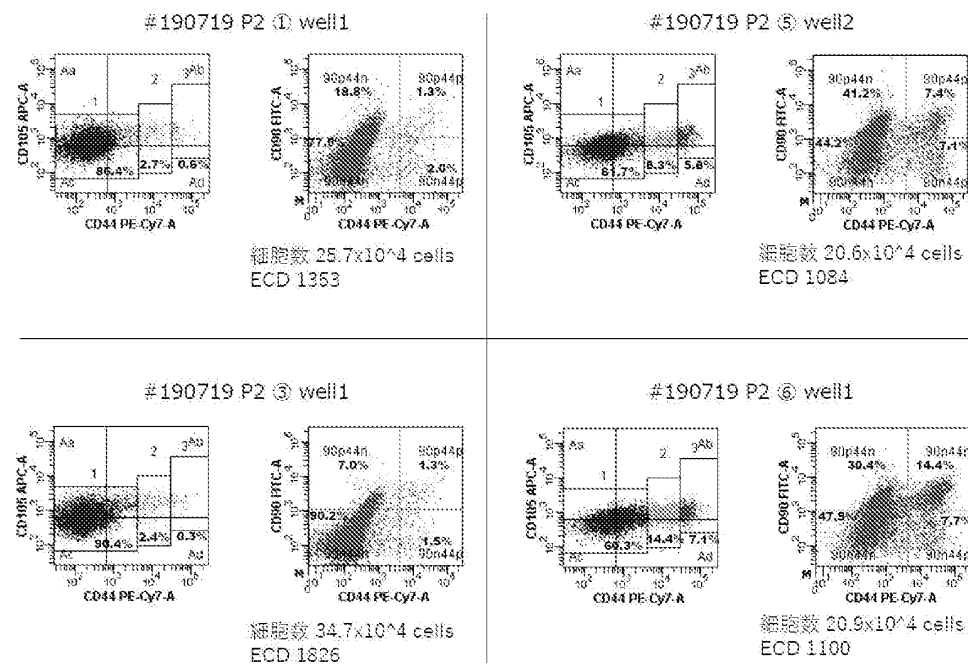
[図44]

#190802 P1 Day35 (191011) FACS結果



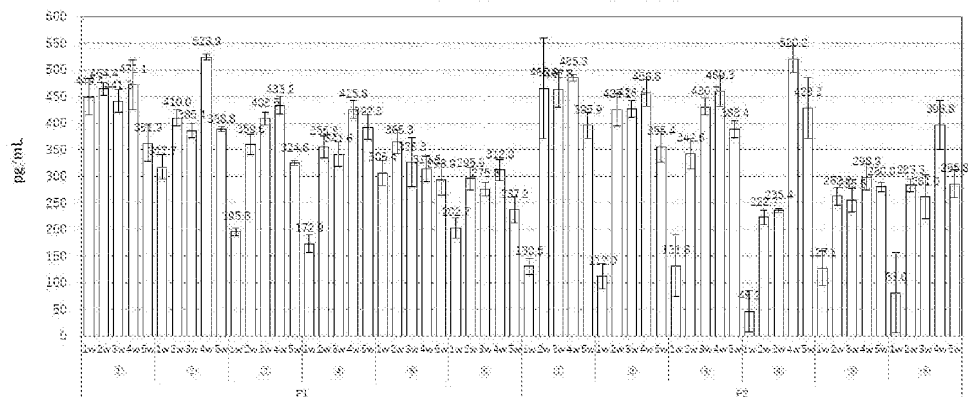
[図45]

#190719 P2 Day40 (191106) FACS結果

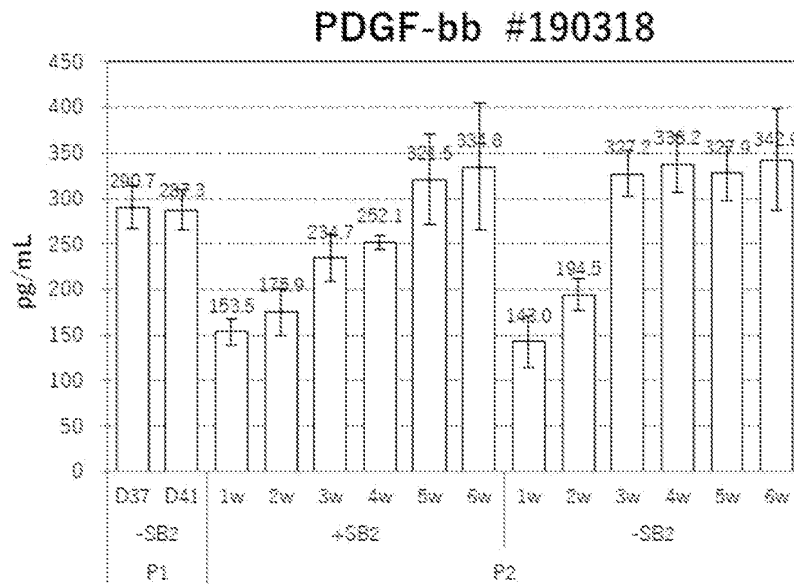


[図46]

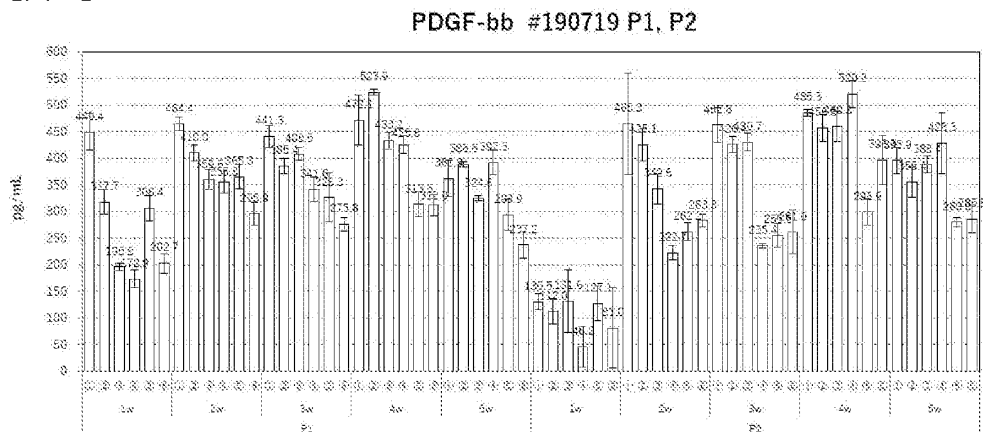
PDGF-bb #190719 P1, P2



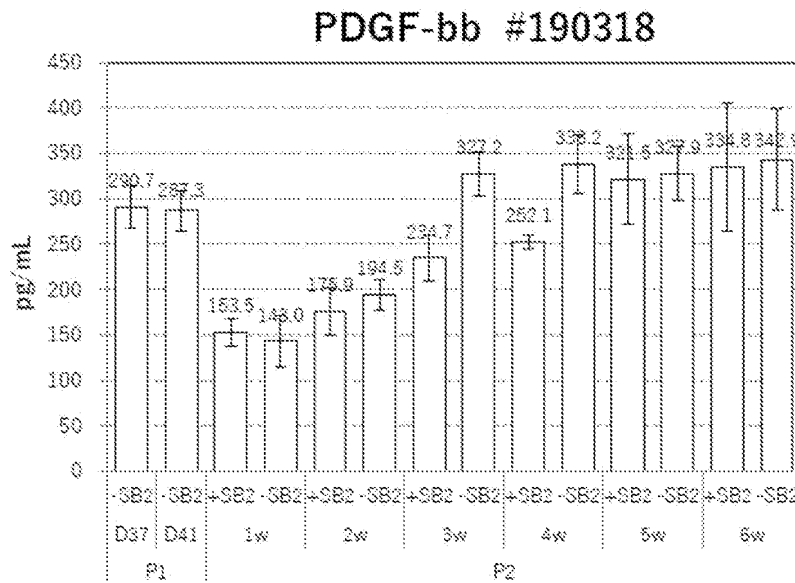
[図47]



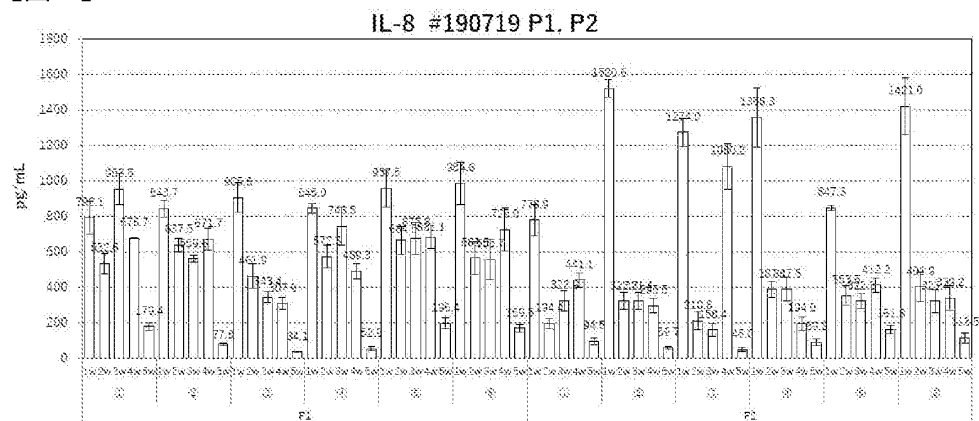
[図48]



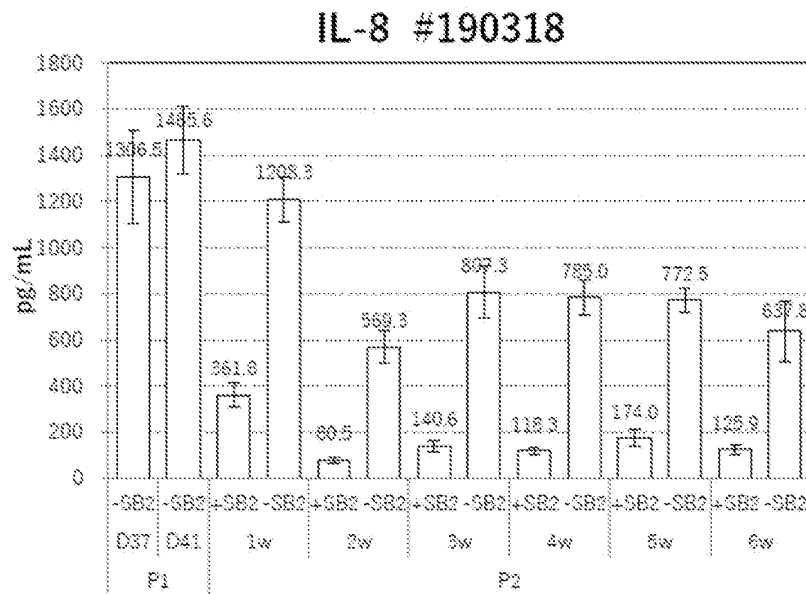
[図49]



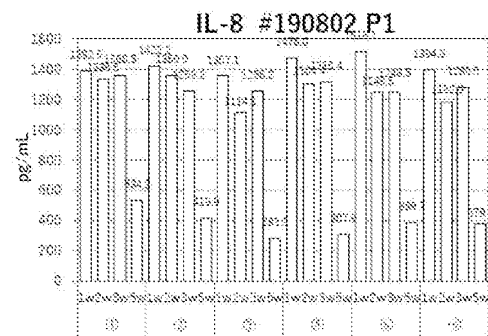
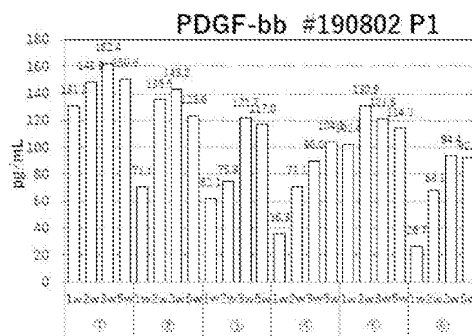
[図50]



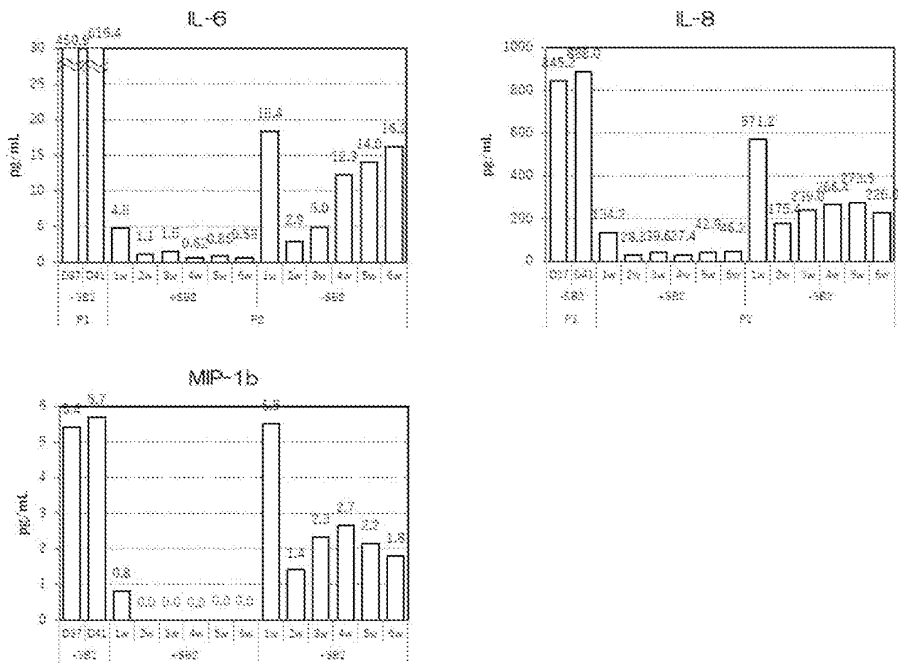
[図51]



[図52]



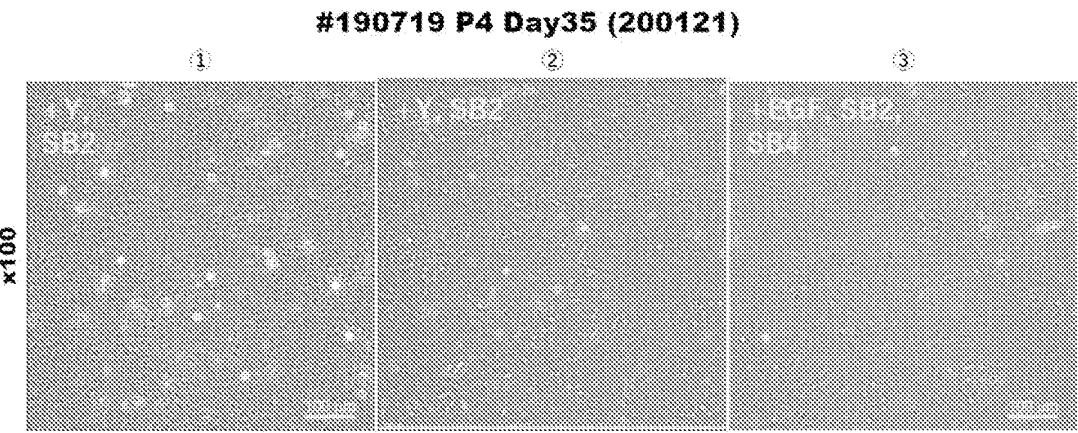
[図53]



[図54]

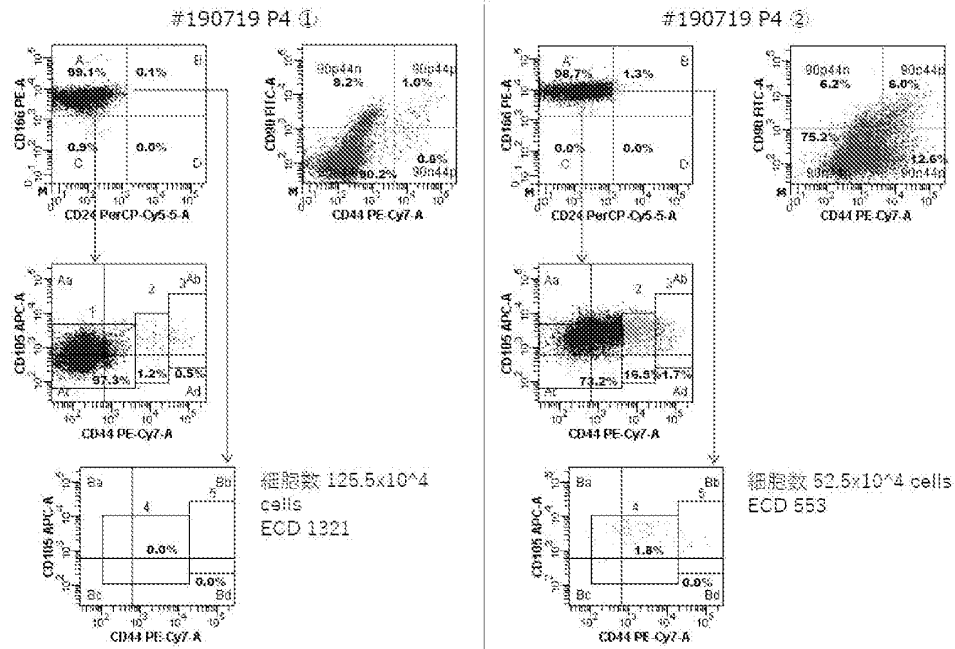
	Day0-3	Day4-	Day10-	Day28-
①	+Y, A			+Y, A, SB2
②	+A		+Y, A	+Y, A, SB2
③	+Y, A	+A, EGF, SB2, SB4		

[図55]



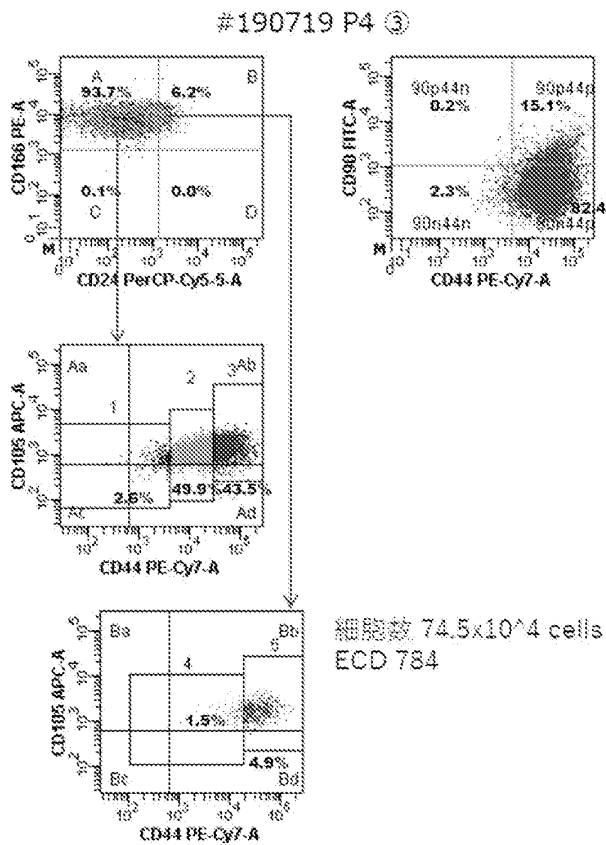
[図56]

Day35 (200121)

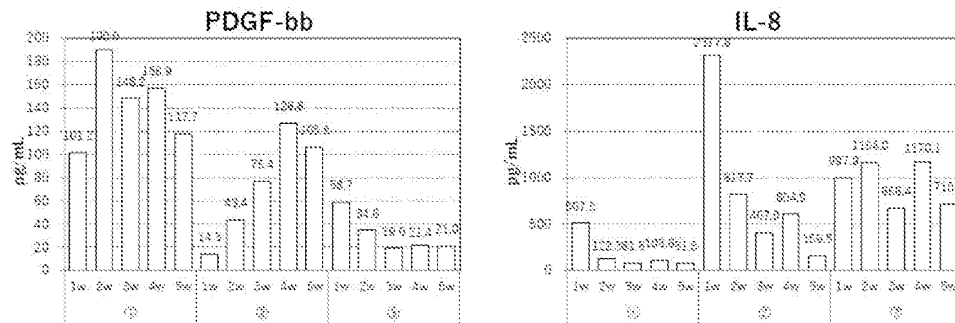


[図57]

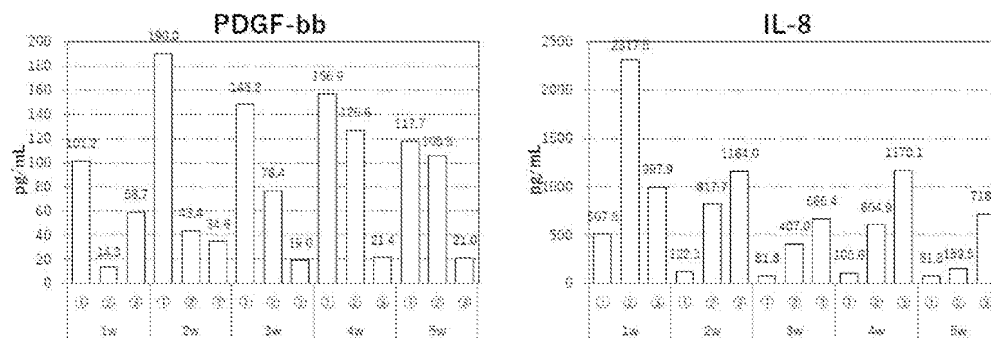
Day35 (200121)



[図58]



[図59]



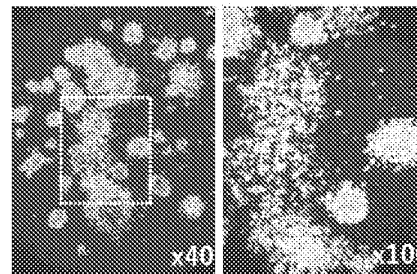
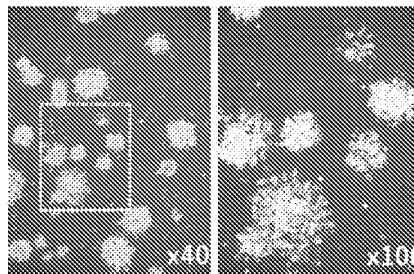
[図60]

Day 4

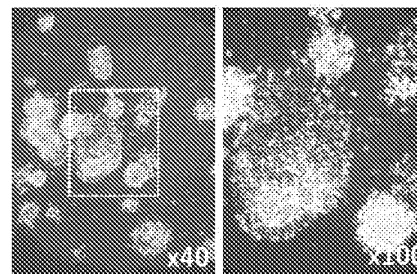
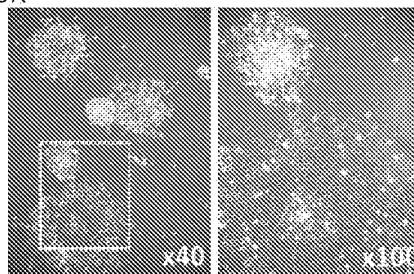
AEM-510DCN

視野 1

視野 2

Y-, A+

AEM-510OSCN

Y+, A+

Y-: 球状に近い。
Y+: 広がっている

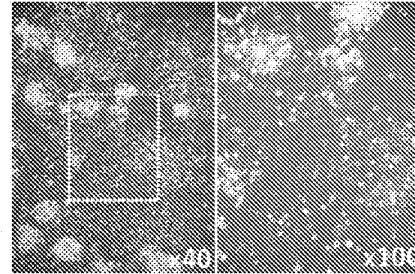
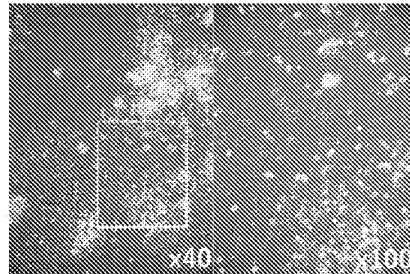
[図61]
Day 7

AEM-510DCN

視野 1

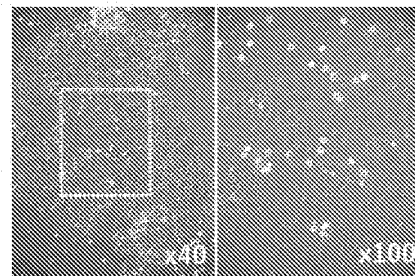
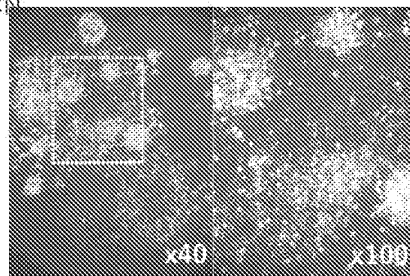
視野 2

Y-, A+
↓
Y+, A+



AEM-510OSCN

Y+, A+
↓
Y+, A+



Y- : 広がっている。
Y+ : より平坦になっている。

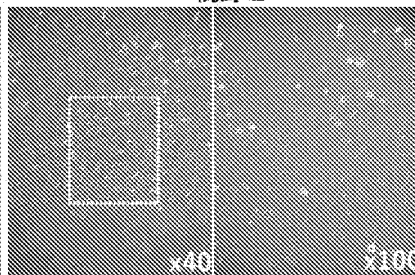
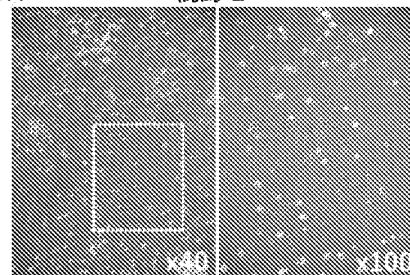
[図62]
Day 12

AEM-510DCN

視野 1

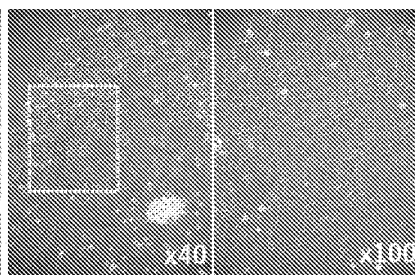
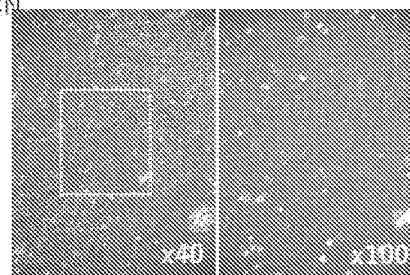
視野 2

Y-, A+
↓
Y+, A+



AEM-510OSCN

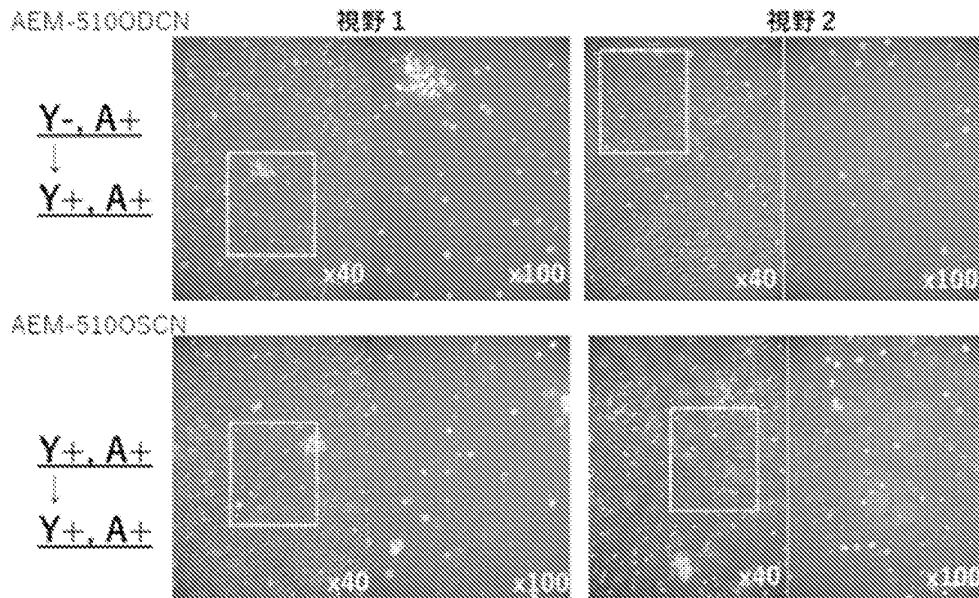
Y+, A+
↓
Y+, A+



Y- : より平坦になっている。
Y+ : より平坦になっている。

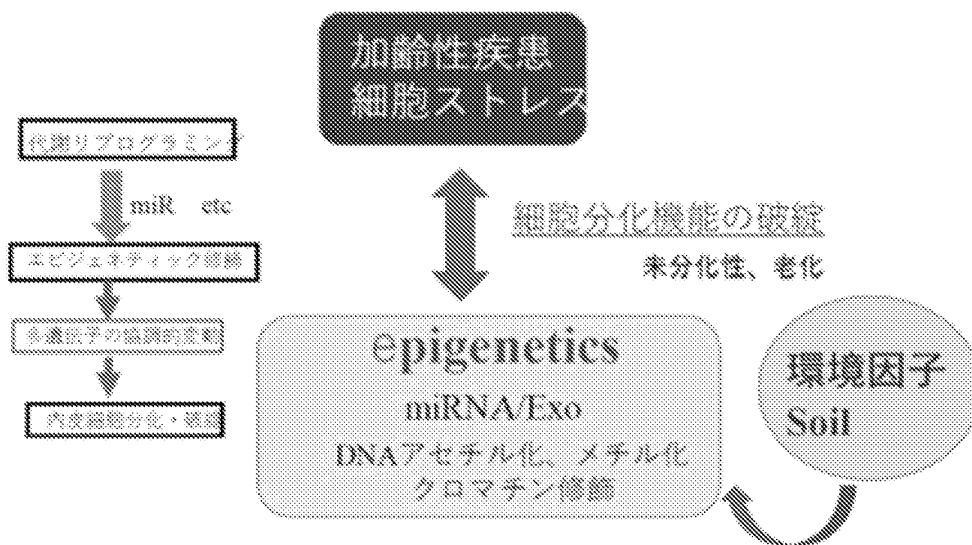
[図63]

Day 14



培養開始後2週目に至り違いは見られなくなった。

[図64]



[図65]

脱分化
前駆細胞分化
成熟細胞

ACLY vs
ACO1
IDH1
MDH1
ME1
ACSS2
ACAT2
LDH

CS
ACO2
IDH2
MDH2
ME3
ACSS1
ACAT1
PDH
BCAT2
BCKDH2

ACLY, ATP-citrate lyase, CS, citrate synthase
Aconitase 1/2
Isocitrate dehydrogenase 1/2
Malate dehydrogenase
Malic acid enzyme 1/3
Acetyl-CoA acetyltransferase 1/2
Lactate dehydrogenase, Pyruvate dehydrogenase
Branched-chain ketoacid dehydrogenase 2

細胞質・核

ミトコンドリア

[図66]

培養条件

Nancy Y(+) A(+)

#184非規格細胞

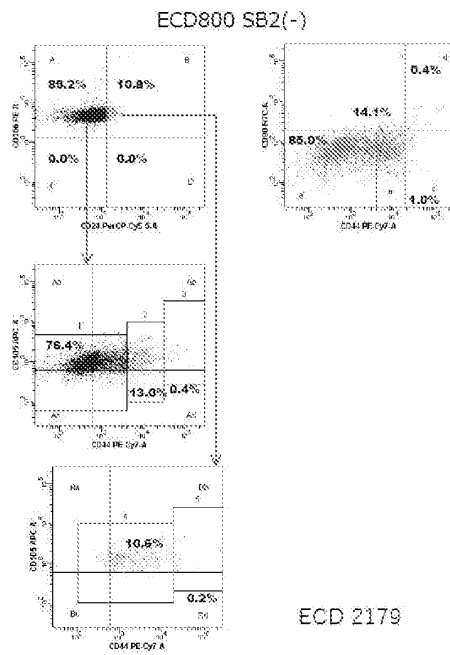
P0
SB2(-) 6wp_x2
↓
P1 : Day286 (160531)
SB2(-) ECD800
↓
P2 : Day134 (161012)
SB2(-) ECD800
↓
P3 : Day56 (161207)
SB2(+) ECD800
↓
P4 : D135 (170421)
SB2(+) ECD800

#225規格細胞

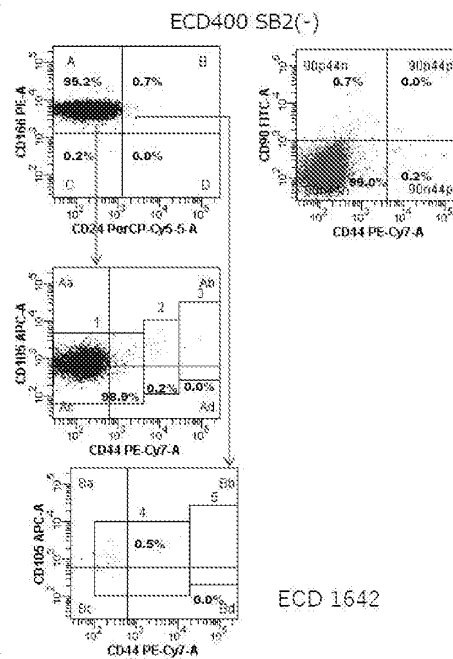
P0
SB2(-) 6wp_x1
↓
P1 : Day43 (170322)
SB2(-) ECD400
↓
P2 : Day78 (170606)
SB2(-) ECD400
↓
P3 : Day77 (170822)
SB2(-) ECD400
↓
P4 : D45 (171006)
SB2(-) ECD400

[図67]

#184 P1 Day286 (160531)

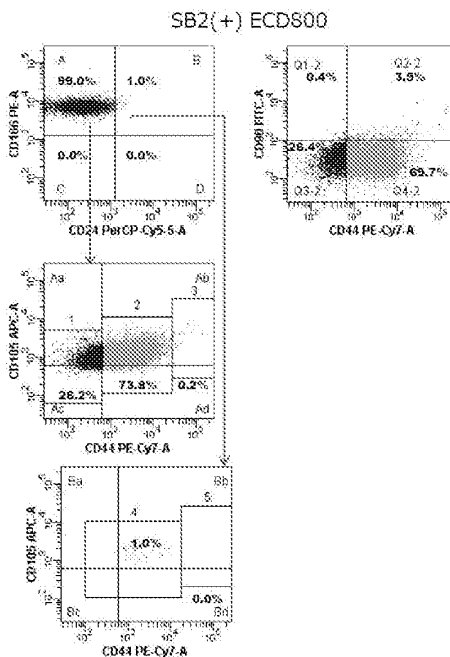


#225 P1 Day43 (170322)

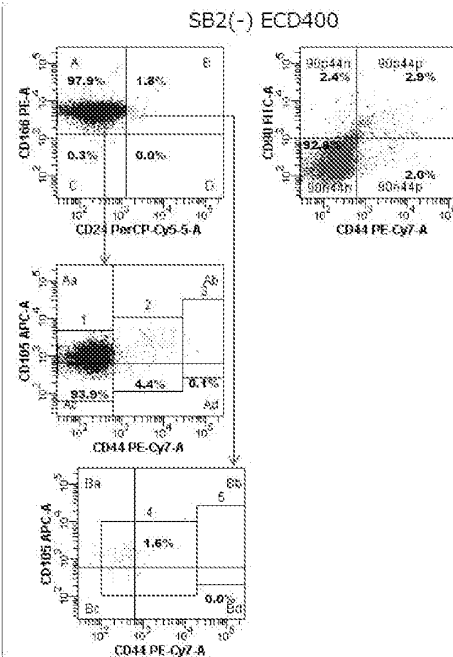


[図68]

#184 P4 D135 (170421)



#225 P4 D45 (171006)



```

graph TD
    A[LC/MS data set  
(with unique UniProt ID)] --> B[4,641]
    B --> C[323  
• abundance ratio calculation failed]
    B --> D[4,318]
    D --> E[3  
• DAVID ID conversion failed]
    D --> F[4,315]
    F --> G[Gene expression analysis]
    F --> H[Gene ontology analysis]
    G --> I[49  
• overlapped UniProt ID  
linked a single DAVID ID]
    G --> J[4,266]
    J --> K[484  
• missing ≥ 2  
data of 3  
aliquots in at  
least either  
LQ or HQ  
cell groups]
    J --> L[3,782]
    H --> M[assigned into three groups according to the  
range of Abundance Ratio (LQ / HQ)]
    M --> N["≤ 0.5"]
    M --> O["0.5 - 2.0"]
    M --> P["≥ 2.0"]
    N --> Q[507]
    Q --> R[3]
    Q --> S[504]
    O --> T[2,804]
    T --> U[15]
    T --> V[2,789]
    P --> W[1,004]
    W --> X[28]
    W --> Y[976]
    R --> Z[• exchange overlapped UniProt ID  
linked to a single DAVID ID]
    U --> Z
    X --> Z
    Z --> S
    Z --> V
    Z --> Y
  
```

LC/MS data set
(with unique UniProt ID)

4,641

323
• abundance ratio calculation failed

4,318

3
• DAVID ID conversion failed

4,315

Gene expression analysis

49
• overlapped UniProt ID linked a single DAVID ID

4,266

484
• missing ≥ 2 data of 3 aliquots in at least either LQ or HQ cell groups

3,782

Gene ontology analysis

assigned into three groups according to the range of Abundance Ratio (LQ / HQ)

≤ 0.5 0.5 - 2.0 ≥ 2.0

507 2,804 1,004

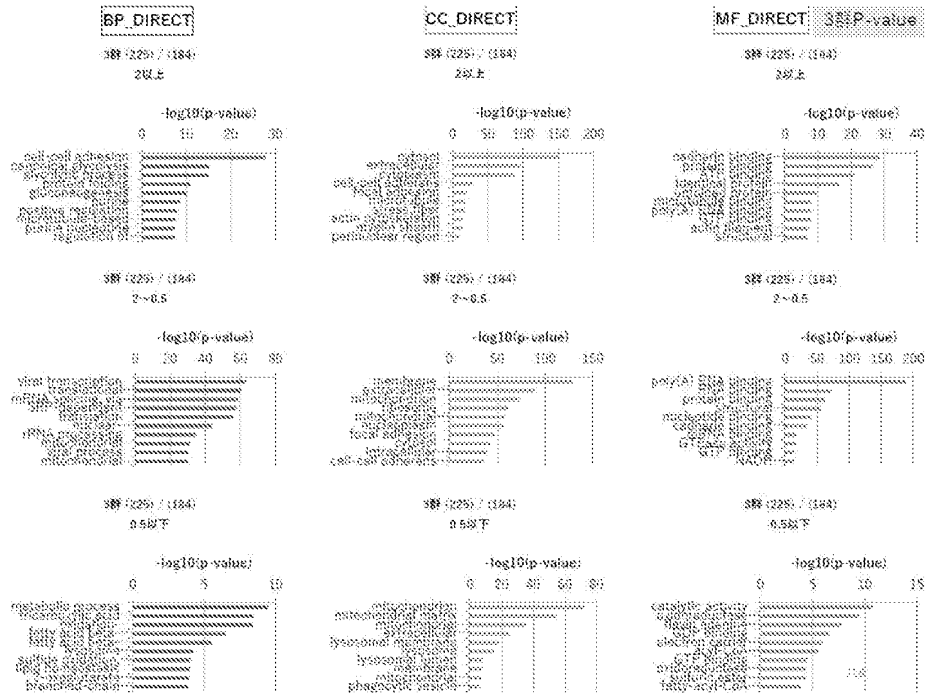
3 15 28

• exchange overlapped UniProt ID linked to a single DAVID ID

504 2,789 976

Accession	Description	# Unique Peptide s	Score Massot Massot	Score Seqres Seqres 1-H7	Abundanc ncs (155)	Abundanc ncs (155)	Abundanc ncs (155)	Abundanc ncs (155)	Abundanc ncs (155)	Abundanc ncs (155)	Abundanc ncs (155)	Abundanc ncs (155)	Abundanc ncs (155)	Abundanc ncs (155)	Abundanc ncs (155)	Abundanc ncs (155)	Abundanc ncs (155)	Abundanc ncs (155)	Abundanc ncs (155)
P00918	Carbonic anhydrase 2 OS=Homo sapiens GN=CA2 PE=1 SV=2	17	965	174.4	27.591	48316	35483	22978	76395	1.08E+	1.22E+	30210	27243	15768	65576	94710	1.22E+	1.22E+	1.22E+
						43	58	98	570	08	08	29	11	87	641	704	08	08	08
P07451	Carbonic anhydrase 3 OS=Homo sapiens GN=CA3 PE=1 SV=3	20	2913	374.2	27.567	18194	10257	10681	2.57E+	4.87E+	4.76E+	12129	78734	75305	2.21E+	4.27E+	4.76E+	4.76E+	4.76E+
						682	840	952	08	08	08	523	08	38	08	08	08	08	08

【図72】



【図73】

	Category	Term	Count	%	PValue	Genes
Annotation Cluster 1	Enrichment Score: 72.73354929082193	UP_KEYWORDS	Mitochondrion	154	38.79089	1.63E-95 P24752, P
		UP_KEYWORDS	Transit peptide	187	25.95214	1.63E-77 P24752, P
		GOTERM_CC_DIRECT	GO:0007399 mitochondrion	153	38.53904	1.08E-73 P24752, P
		UP_SEQ_FEATURE	transit peptide:Mitochondrion	97	24.43325	1.79E-68 P49748, P
		GOTERM_CC_DIRECT	GO:0005759 mitochondrial matrix	78	19.54736	4.07E-58 P24752, P
Annotation Cluster 2	Enrichment Score: 19.705645707316353	UP_KEYWORDS	Lysosome	43	10.83123	1.98E-26 Q8NCC3, I
		KEGG_PATHWAY	hsa04142:lysosome	39	7.556675	2.51E-19 Q8NCC3, I
		GOTERM_CC_DIRECT	GO:0005784 lysosome	31	7.808584	1.57E-15 Q8NCC3, I
Annotation Cluster 3	Enrichment Score: 12.884973261402643	UP_KEYWORDS	Oxidoreductase	56	14.10579	7.82E-23 P49748, P
		GOTERM_MF_DIRECT	GO:0016491 oxidoreductase activity	24	6.04534	7.94E-11 Q8W72, C
		GOTERM_BP_DIRECT	GO:0055114 oxidation-reduction process	35	8.836121	3.57E-07 P00367, Q
Annotation Cluster 4	Enrichment Score: 9.89201150504489	KEGG_PATHWAY	hsa01200:Carbon metabolism	24	6.04534	7.82E-14 P11628, P

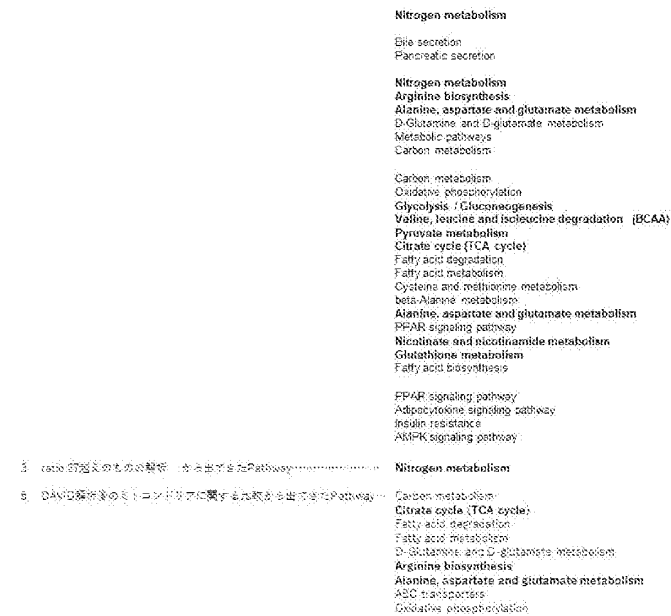
【図74】

	Category	Term	Count	%	PValue	Genes
Annotation Cluster 1	Enrichment Score: 9.402122000000000	UP_KEYWORDS	Mitochondrion	154	38.79089	1.63E-95 P24752, P
		UP_KEYWORDS	Transit peptide	187	25.95214	1.63E-77 P24752, P
		GOTERM_CC_DIRECT	GO:0007399 mitochondrion	153	38.53904	1.08E-73 P24752, P
		UP_SEQ_FEATURE	transit peptide:Mitochondrion	97	24.43325	1.79E-68 P49748, P
		GOTERM_CC_DIRECT	GO:0005759 mitochondrial matrix	78	19.54736	4.07E-58 P24752, P
Annotation Cluster 2	Enrichment Score: 9.277003662000000	UP_KEYWORDS	Lysosome	43	10.83123	1.98E-26 Q8NCC3, I
		KEGG_PATHWAY	hsa04142:lysosome	39	7.556675	2.51E-19 Q8NCC3, I
		GOTERM_CC_DIRECT	GO:0005784 lysosome	31	7.808584	1.57E-15 Q8NCC3, I
		UP_KEYWORDS	Oxidoreductase	56	14.10579	7.82E-23 P49748, P
		GOTERM_MF_DIRECT	GO:0016491 oxidoreductase activity	24	6.04534	7.94E-11 Q8W72, C
Annotation Cluster 3	Enrichment Score: 9.200115050000000	UP_KEYWORDS	Oxidoreductase	56	14.10579	7.82E-23 P49748, P
		GOTERM_MF_DIRECT	GO:0016491 oxidoreductase activity	24	6.04534	7.94E-11 Q8W72, C
		GOTERM_BP_DIRECT	GO:0055114 oxidation-reduction process	35	8.836121	3.57E-07 P00367, Q
		KEGG_PATHWAY	hsa01200:Carbon metabolism	24	6.04534	7.82E-14 P11628, P
		UP_KEYWORDS	Mitochondrion	154	38.79089	1.63E-95 P24752, P
Annotation Cluster 4	Enrichment Score: 9.200115050000000	UP_KEYWORDS	Mitochondrion	154	38.79089	1.63E-95 P24752, P
		UP_KEYWORDS	Transit peptide	187	25.95214	1.63E-77 P24752, P
		GOTERM_CC_DIRECT	GO:0007399 mitochondrion	153	38.53904	1.08E-73 P24752, P
		UP_SEQ_FEATURE	transit peptide:Mitochondrion	97	24.43325	1.79E-68 P49748, P
		GOTERM_CC_DIRECT	GO:0005759 mitochondrial matrix	78	19.54736	4.07E-58 P24752, P

[図75]

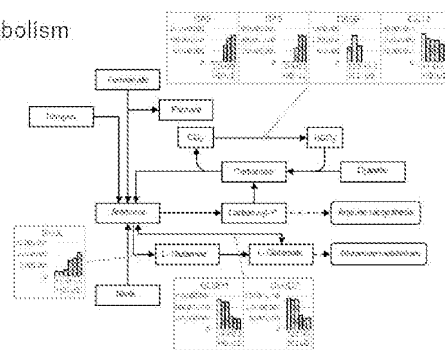
	Category	Term	Count	%	PValue	Genes
Annotation Cluster 1 Enrichment Score: 9.89201150604989	KEGG_PATHWAY	hsa01230:Carbon metabolism	24	6.04534	7.82E-14	81308
	KEGG_PATHWAY	hsa00020:Citrate cycle (TCA cycle)	11	2.770781	6.28E-09	71349
	KEGG_PATHWAY	hsa00071:Fatty acid degradation	9	2.267003	3.21E-05	748738
Annotation Cluster 4 Enrichment Score: 4.531021570326307	GO_BP_DIRECT	GO:0006635:fatty acid beta-oxidation	10	2.518892	3.99E-07	149748
	KEGG_PATHWAY	hsa01212:Fatty acid metabolism	9	2.267003	6.19E-05	748738
Annotation Cluster 7 Enrichment Score: 3.0657450355612973	KEGG_PATHWAY	hsa00471:D-Glutamine and D-glutamate metabolism	4	1.007557	9.49E-05	48448
	KEGG_PATHWAY	hsa00120:Arginine biosynthesis	5	1.258445	0.002334	748438
	KEGG_PATHWAY	hsa00020:Alanine, aspartate and glutamate metabolism	6	1.511335	0.00315	748438
	KEGG_PATHWAY	hsa02010:ABC transporters	6	1.511335	0.00363	834678
	KEGG_PATHWAY	hsa00190:Oxidative phosphorylation	9	2.267003	0.039548	806738

[図76]



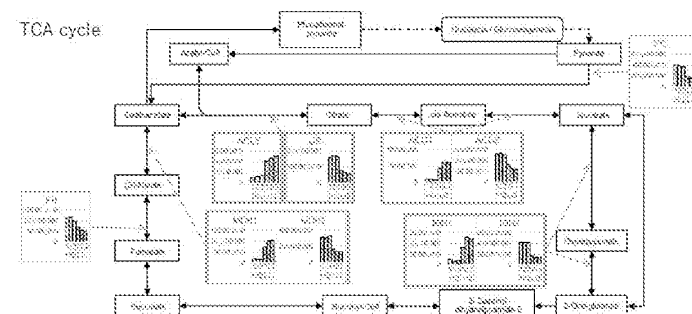
[図77]

Nitrogen metabolism

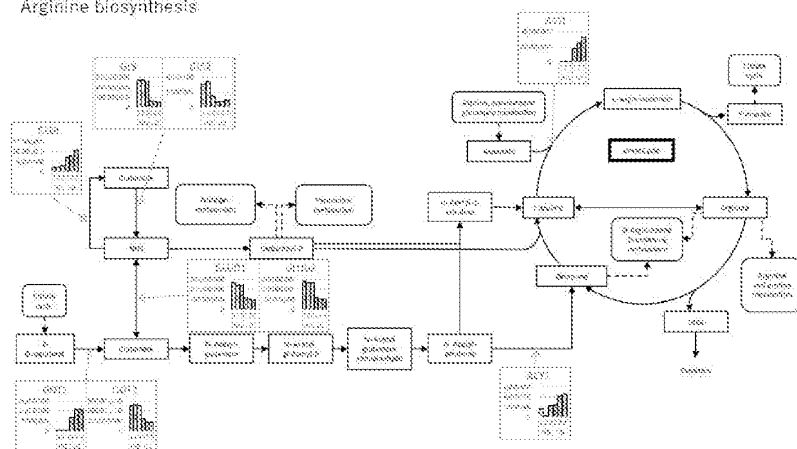


[図78]

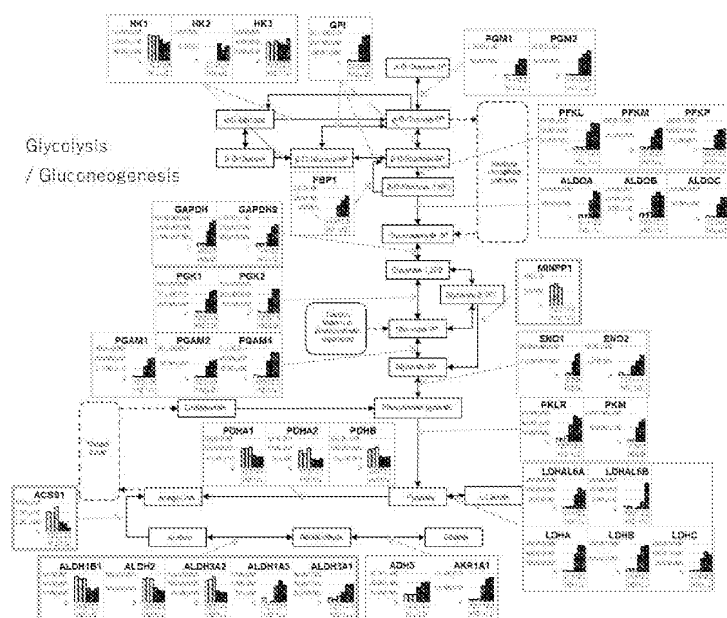
TCA cycle



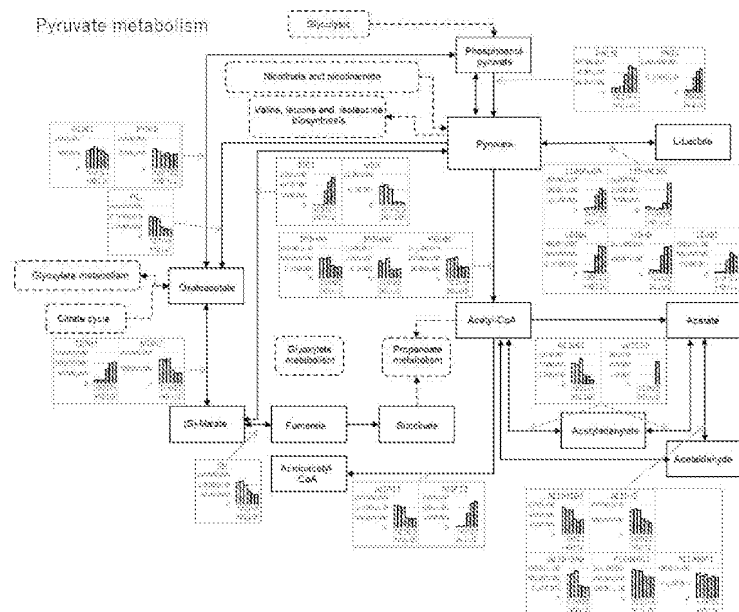
Arginine biosynthesis



Glycolysis
/ Gluconeogenesis

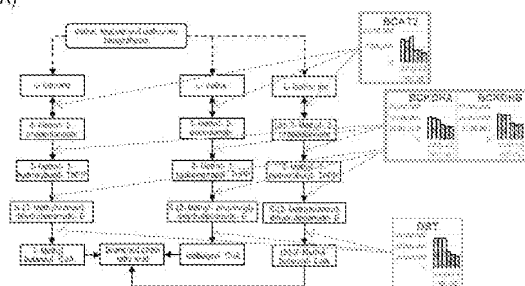


[圖81]



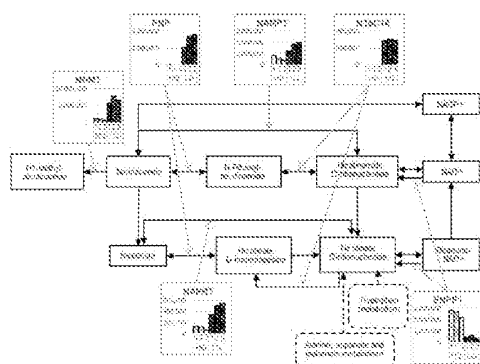
[图82]

Valine, leucine and isoleucine degradation (BCAA)



[图83]

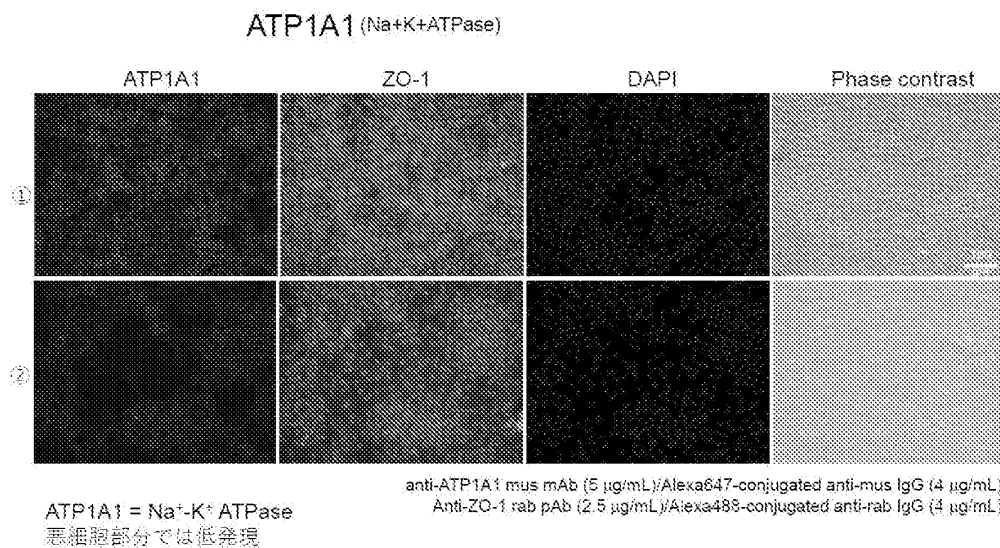
Nicotinate and nicotinamide metabolism



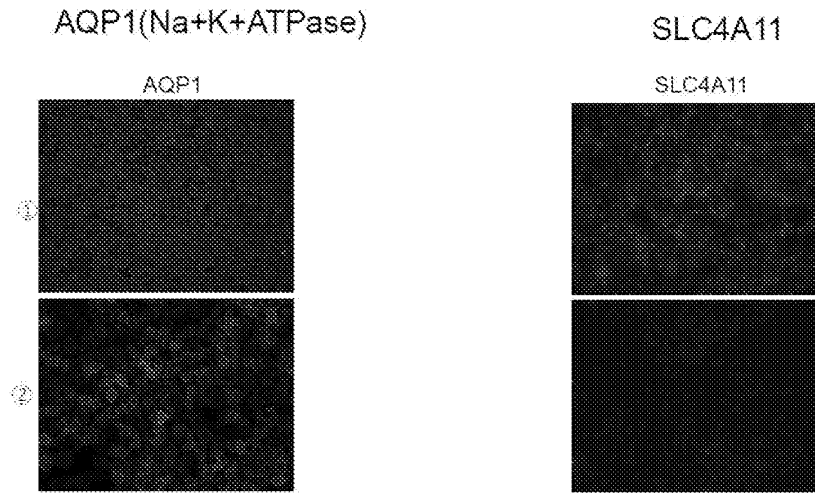
[図84]

Target	Antibody	Source
human ATP1A1 = Na ⁺ -K ⁺ -ATPase	anti-Na ⁺ -K ⁺ -ATPase α-1 Antibody, clone C404.9 G5-369	mouse
human ATP2B3	Anti-Calcium Pump PMCA3 ATPase IgG (ab223787)	abcam
human AQP1	Anti-Aquaporin 1 (AQP1) IgG (ab122307)	abcam
human AE1	Anti-Band 3 AE1 IgG (EPR1436) (ab196413)	abcam
human AE2	SLC4A2 Polyclonal Antibody (Catalog # PA5-32676)	mylogen
human NBC-e1	Anti-SLC4A4/NBC-e1 IgG (ab96218)	abcam
human SLC4A11	Anti-SLC4A11 Antibody (HPA015193)	coigen/Abcam Antibodies
human NHE1	Anti-Sodium/Hydrogen Exchanger 1/NHE-1 IgG (ab57513)	abcam
human MCT1	MCT1/SLC16A1 Antibody (ABP1-58656)	KODON (R&D)
human MCT6	Anti-SLC16A7 Antibody (HPA053363)	sigma/Abcam Antibodies
human MCT4	Anti-SLC16A3/MCT 4 antibody (ab124728)	Abcam
human CA2	Anti-Carbonic anhydrase 2/CA2 antibody (ab191343)	abcam
human CA3	Anti-Carbonic Anhydrase 3/CA3 IgG (ab175309)	abcam
human CA8	Anti-Carbonic Anhydrase 8/CA8 antibody (ab126635)	abcam
human CA12	Anti-Carbonic Anhydrase 12/CA12 IgG (ab66190)	abcam
human ZO-1	ZO-1 Monoclonal Antibody (ZO1-1A12) (P93-9130)	mylogen
	ZO-1 Polyclonal Antibody (P-61-7300)	mylogen
DAPI	D923 - CellStain [®] DAPI solution (stock code 340-07871)	Dynabead
2nd Abs: anti-rab IgG dye-conjugated	mylogen	Donkey anti-Rabbit IgG (H+L) Highly Cross-Adsorbed Secondary Antibody, Alexa Fluor Plus 488 (# A32789)
	mylogen	Donkey anti-Rabbit IgG (H+L) Highly Cross-Adsorbed Secondary Antibody, Alexa Fluor Plus 568 (# A32789)
2nd Abs: anti-mus IgG dye-conjugated	mylogen	Donkey anti-Mouse IgG (H+L) Highly Cross-Adsorbed Secondary Antibody, Alexa Fluor Plus 488 (# A32756)
	mylogen	Donkey anti-Mouse IgG (H+L) Highly Cross-Adsorbed Secondary Antibody, Alexa Fluor Plus 647 (# A32757)

[図85]



[図86]



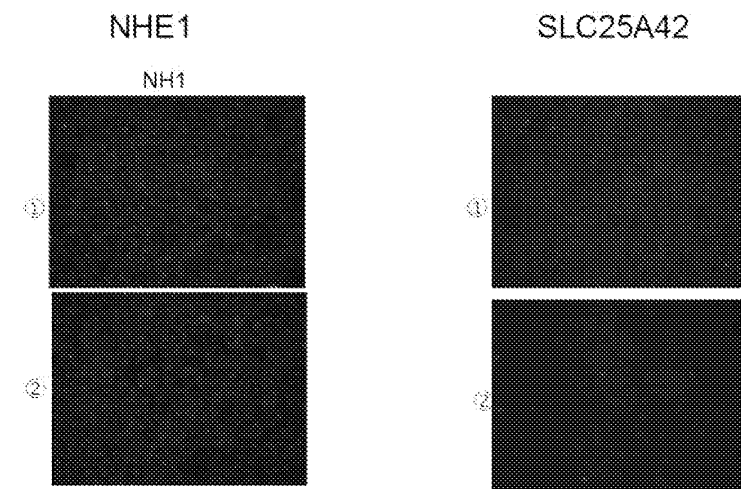
**AQP1：規格細胞で細胞膜に高発現
相転移細胞では非発現**

SLC4A11：規格細胞で高発現

anti-AQP1 rab pAb (0.87 µg/mL)/Alexa647-conjugated anti-rab IgG (4 µg/mL)
Anti-ZO-1 mus mAb (2.5 µg/mL)/Alexa488-conjugated anti-mus IgG (4 µg/mL)

anti-SLC4A11 rab pAb (3 µg/mL)/Alexa647-conjugated anti-rab IgG (4 µg/mL)
Anti-ZO-1 mus mAb (2.5 µg/mL)/Alexa488-conjugated anti-mus IgG (4 µg/mL)

[図87]



NHE1：規格細胞で高発現

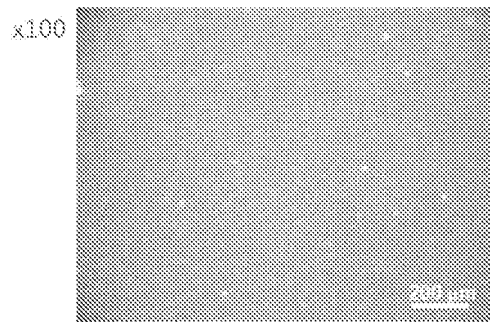
SLC25A42：規格細胞で発現

anti-NHE1 rab pAb (2 µg/mL)/Alexa647-conjugated anti-rab IgG (4 µg/mL)
Anti-ZO-1 mus mAb (2.5 µg/mL)/Alexa488-conjugated anti-mus IgG (4 µg/mL)

anti-SLC25A42 rab pAb (2 µg/mL)/Alexa647-conjugated anti-rab IgG (4 µg/mL)
Anti-ZO-1 mus mAb (2.5 µg/mL)/Alexa488-conjugated anti-mus IgG (4 µg/mL)

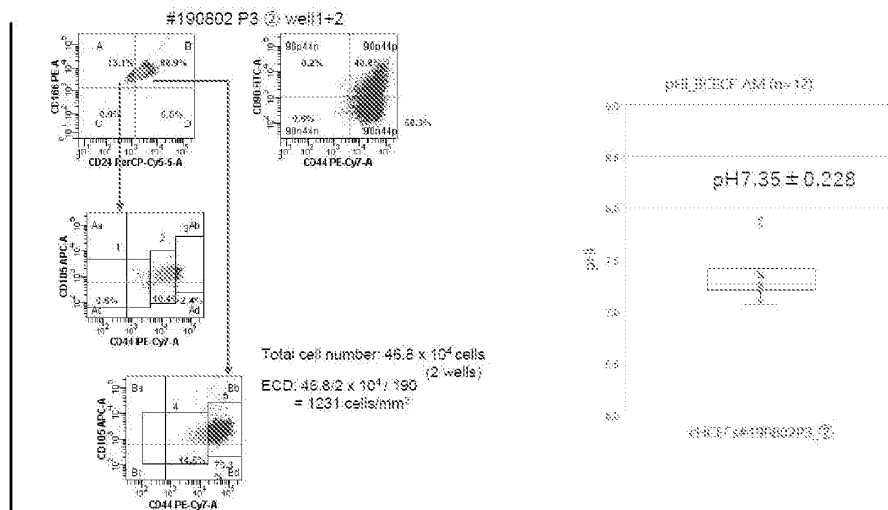
[図90]

#190719P2 (Day40)_① (Nancy A+Y)well#2



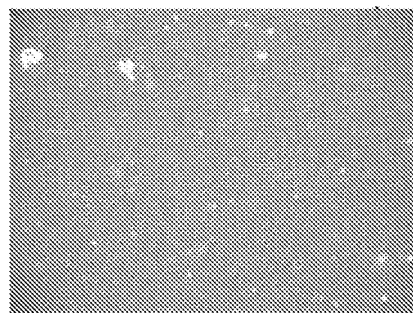
[図91]

#190802P3 Day40 (200115)

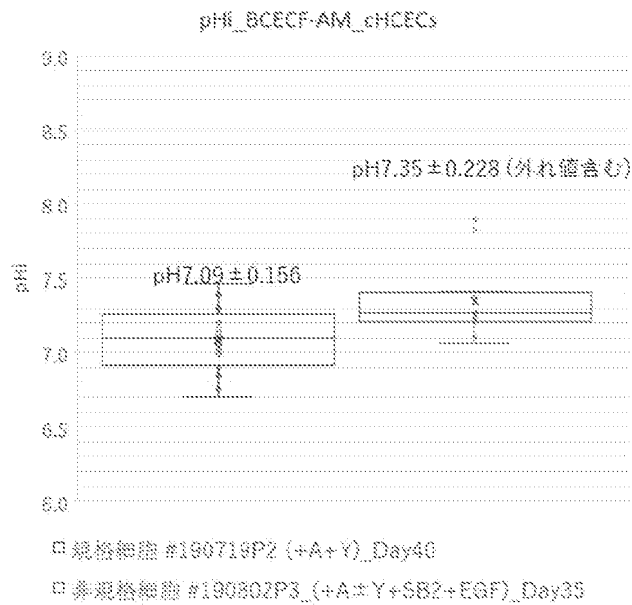


[図92]

#190802P3 Day40 Nancy A(+) Y(+) : 200115 ① well#1+2



【図93】

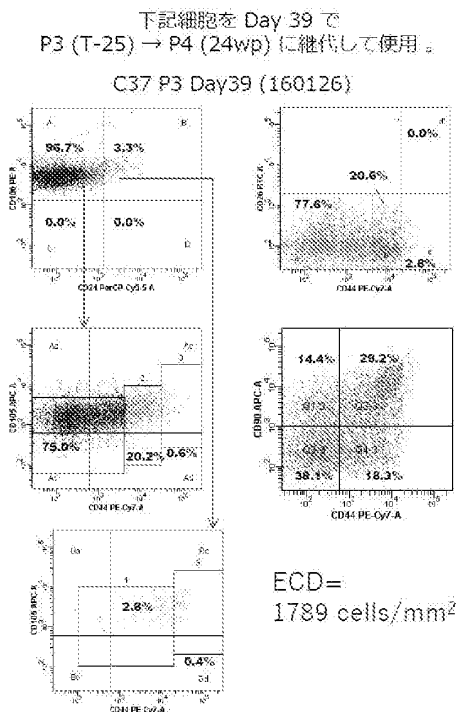


【
【統計処理_中央値比較時】

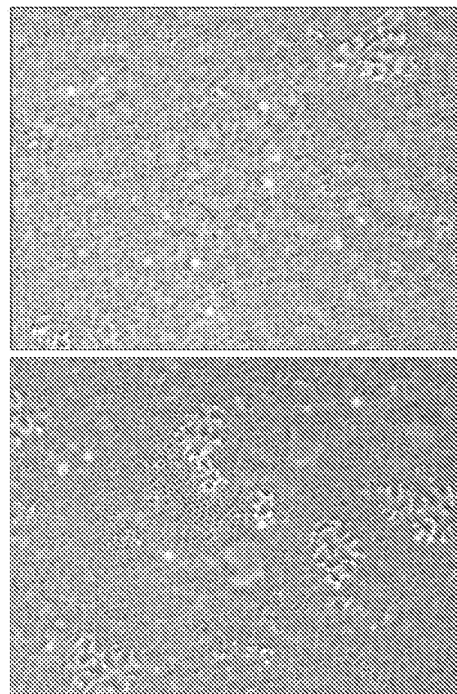
外れ値含む場合

Mann-Whitney U-test: $p = 0.003966$

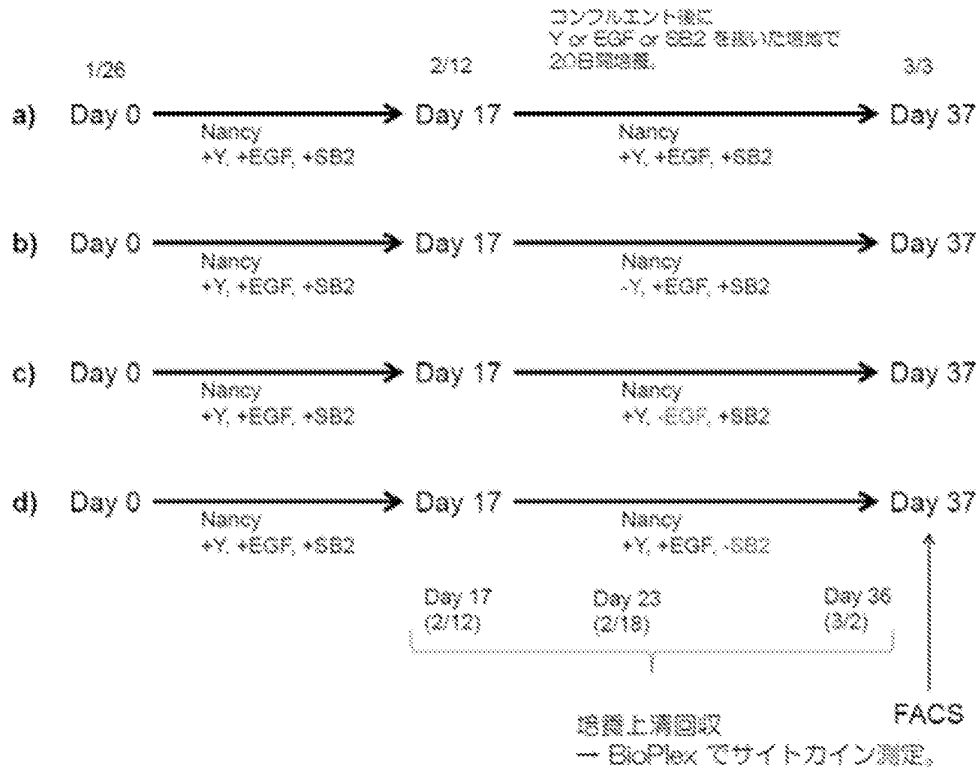
【図94】



Day38 (160125) CPCで撮影 x200

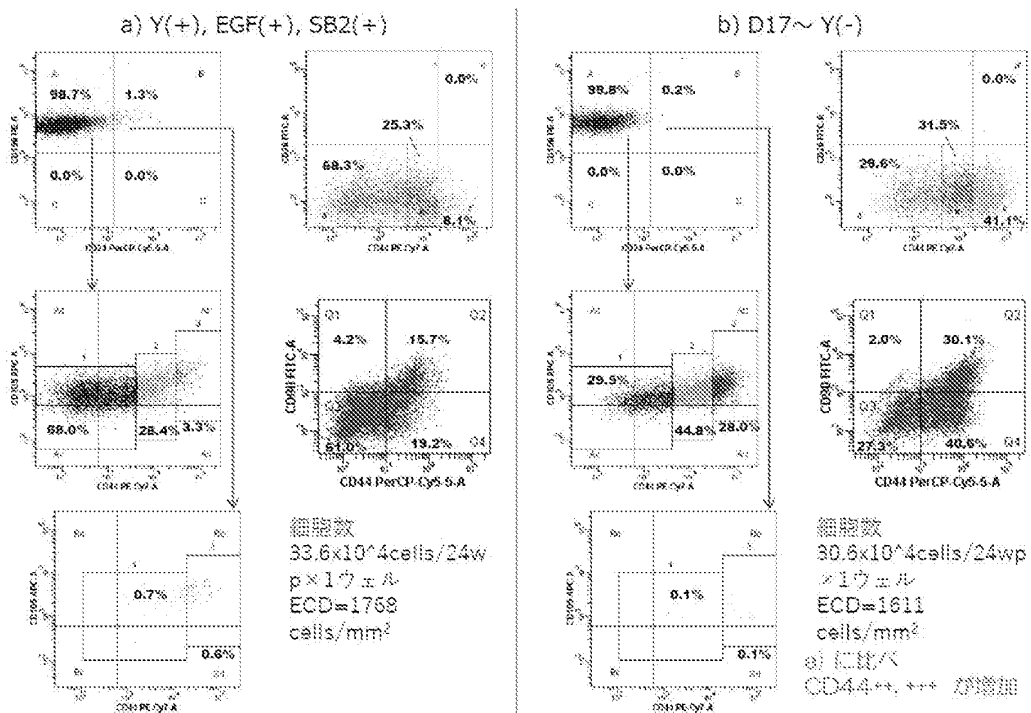


[図95]



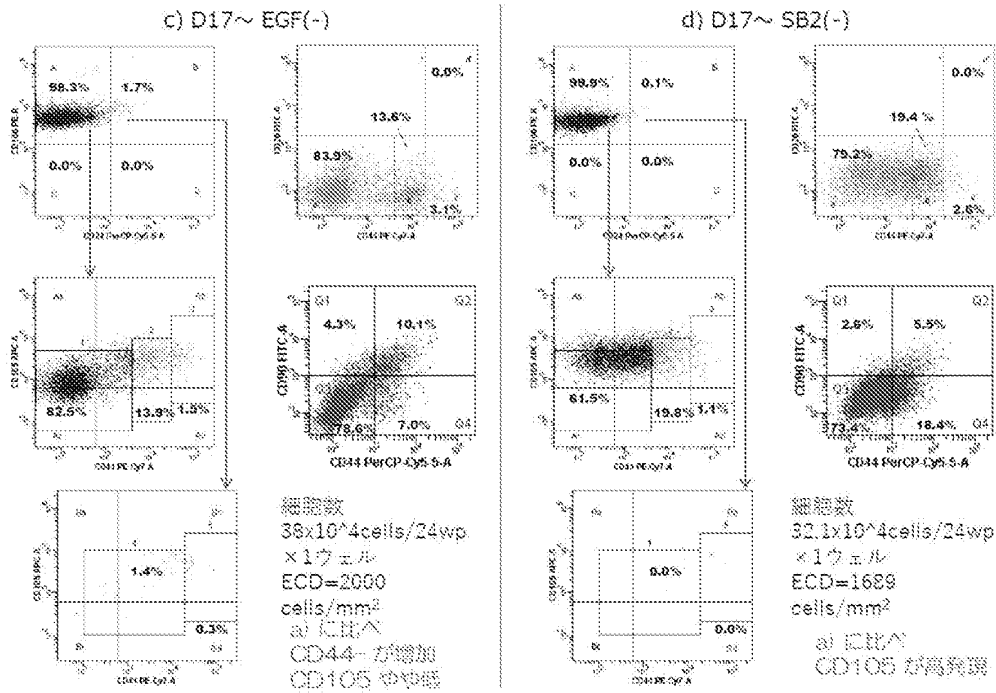
[図96]

Day37 (20160303)



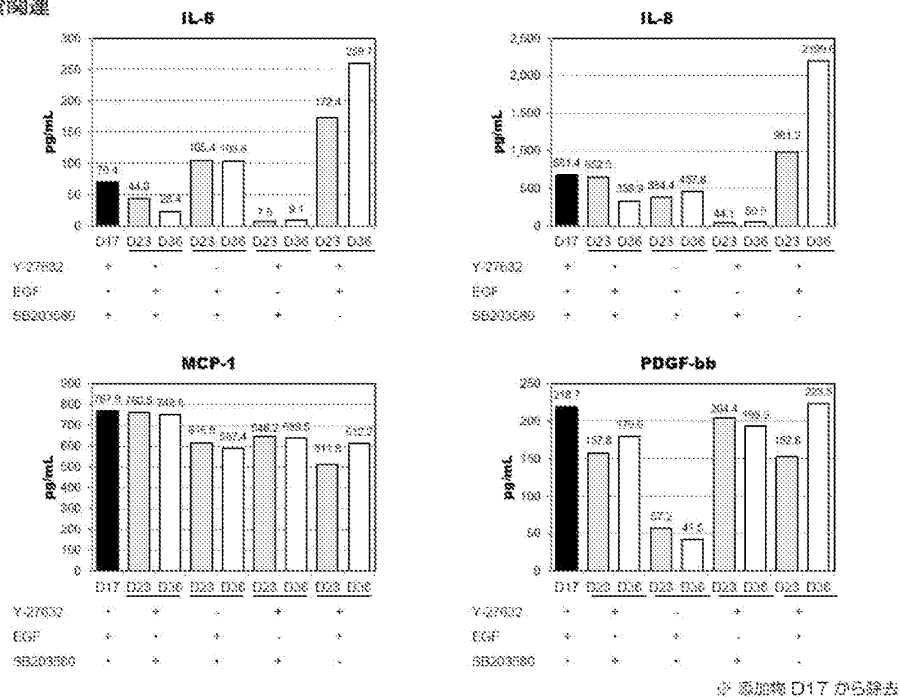
[図97]

Day 37 (20160303)



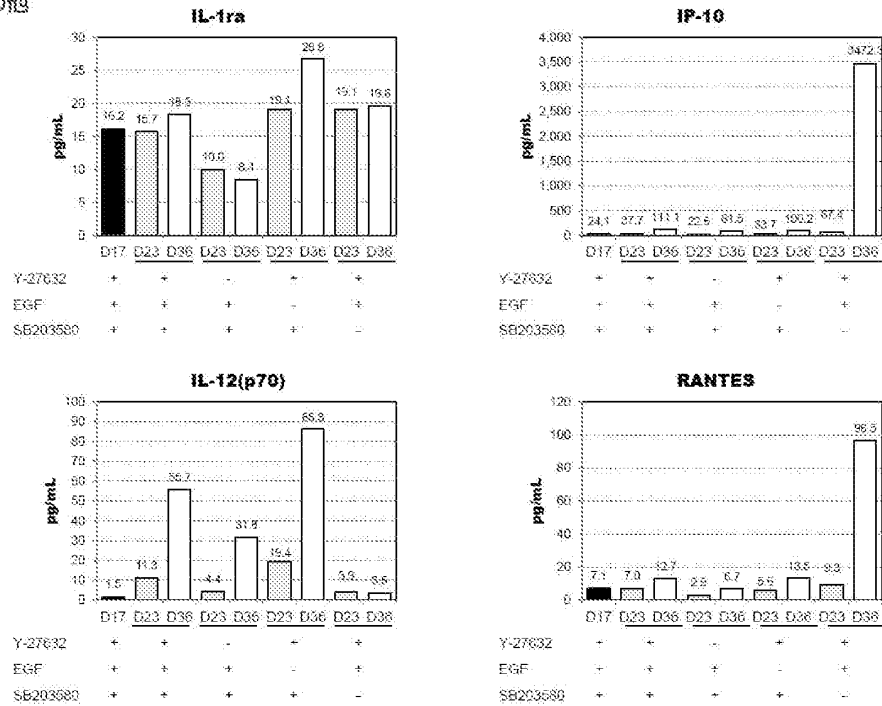
[図98]

品管関連



[図99]

その他

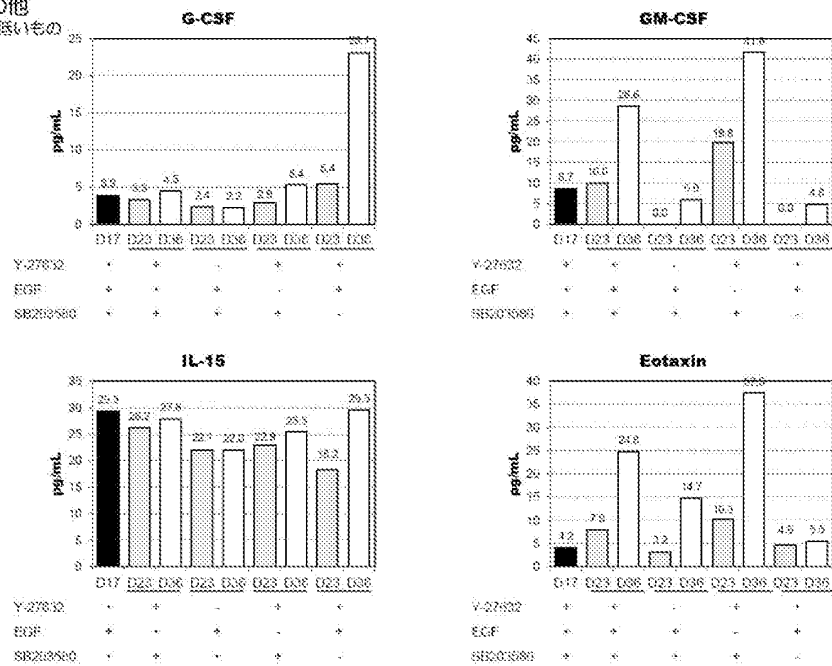


※ 添加物 D17 から除去

[図100]

その他

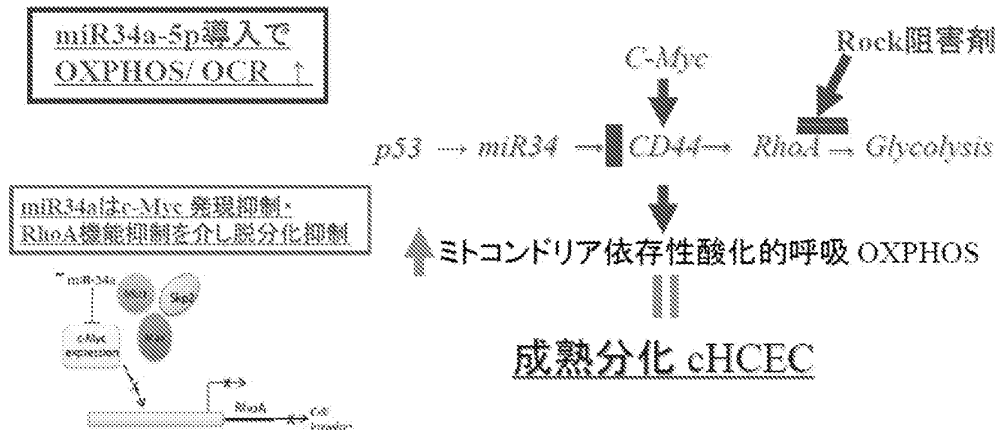
値の低いもの



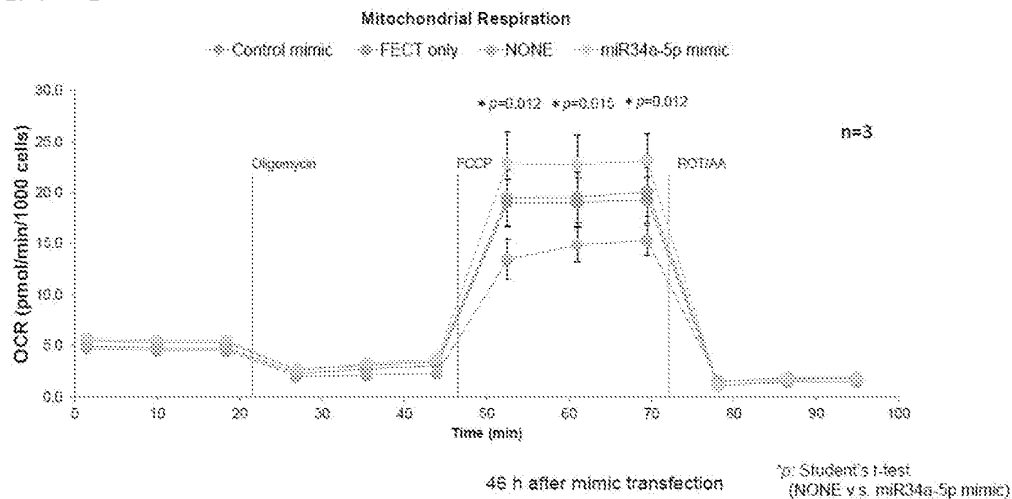
※ 添加物 D17 から除去

[図101]

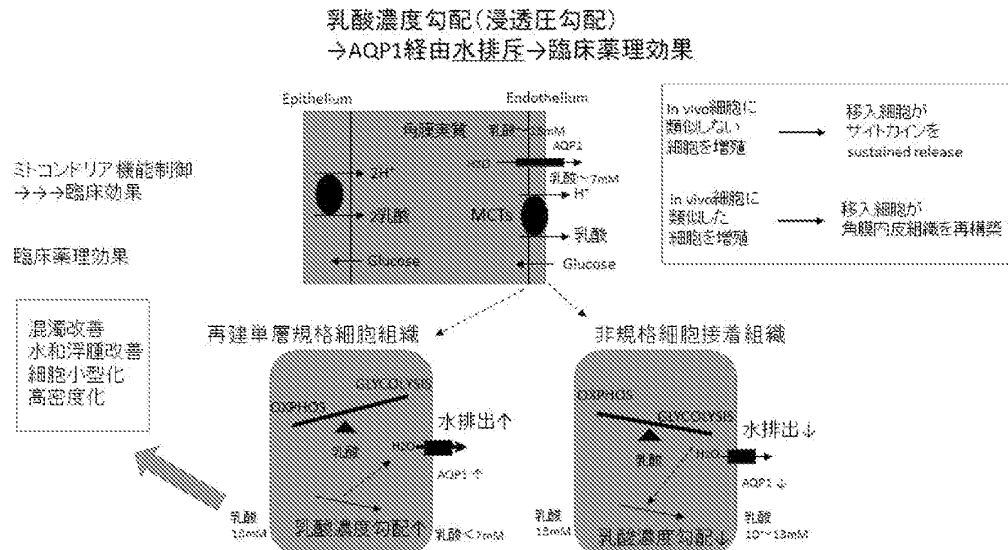
MiR34aとCD44発現の係りと ミトコンドリアのエネルギー代謝制御経路



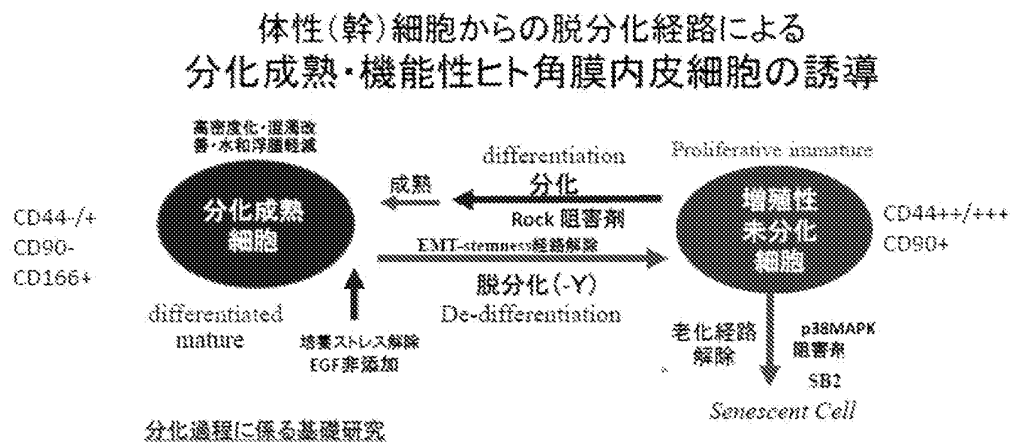
[図102]



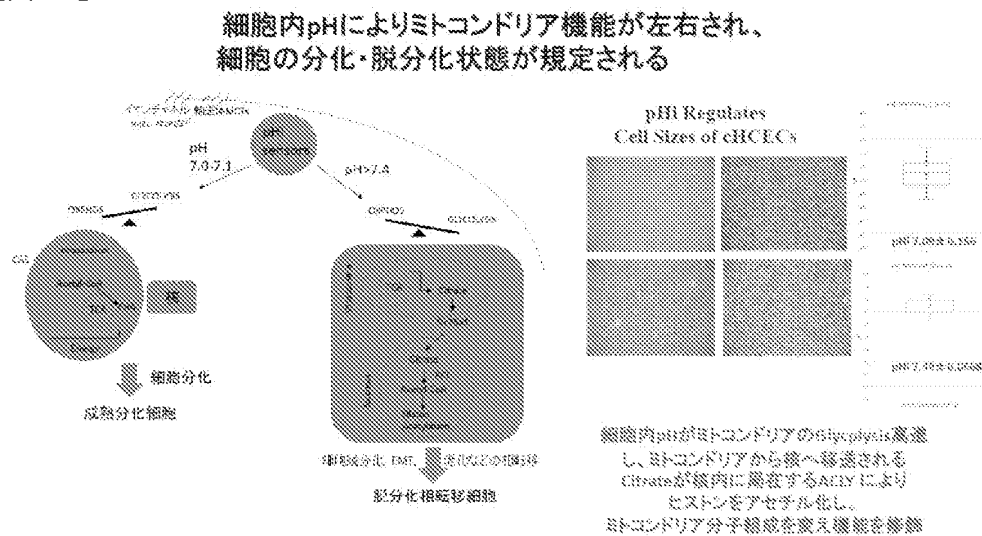
[図103]



[図104]

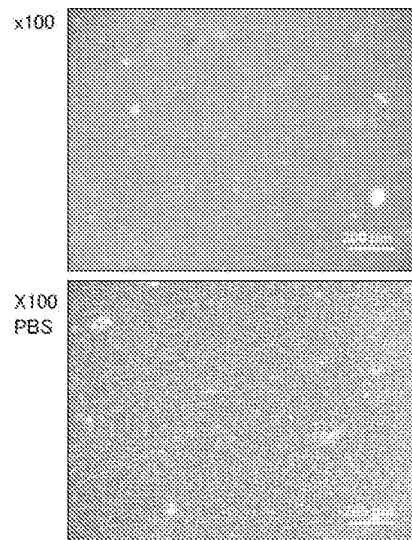


[図105]

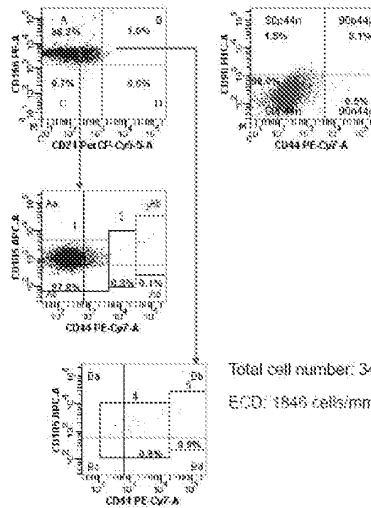


[図106]

cHCECs_#CR04 P3_Day41 (Nancy+Y)



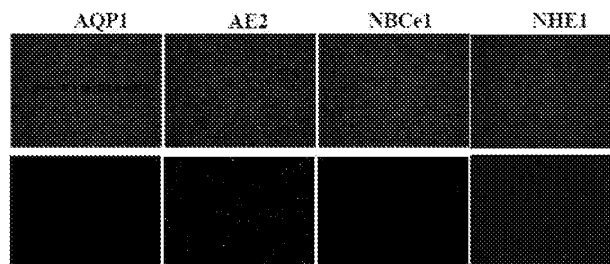
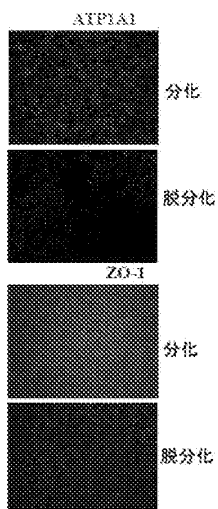
【規格細胞用として培養】
#CR04 P3 Day41 (+Y)



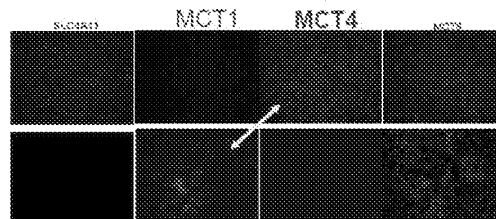
Total cell number: 34.7×10^4 cells
ECDF: 1846 cells/mm²

[図107]

規格・非規格細胞におけるイオンチャネル・単カルボン酸輸送体発現

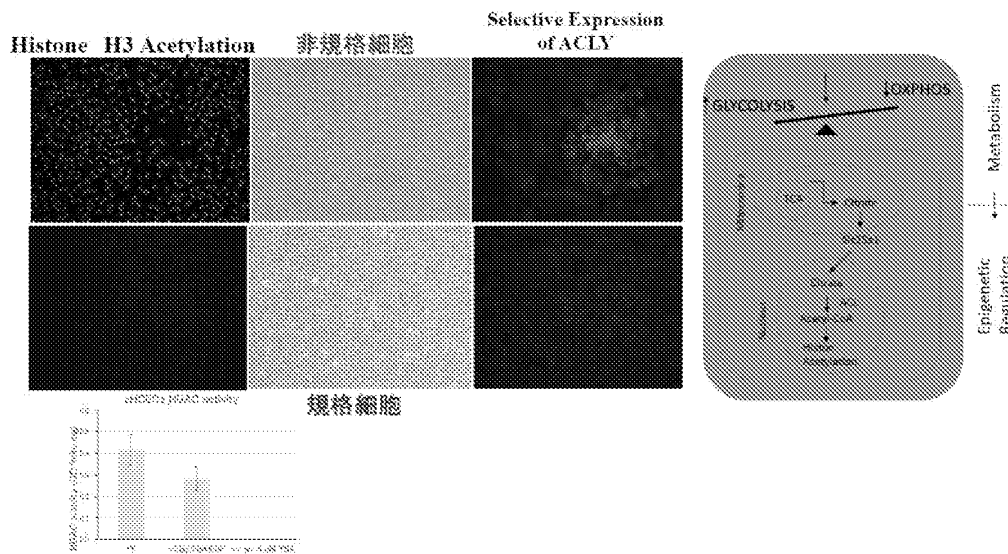
Na⁺-K⁺ATPase & ZO-1

Monocarboxic Acid Transporters



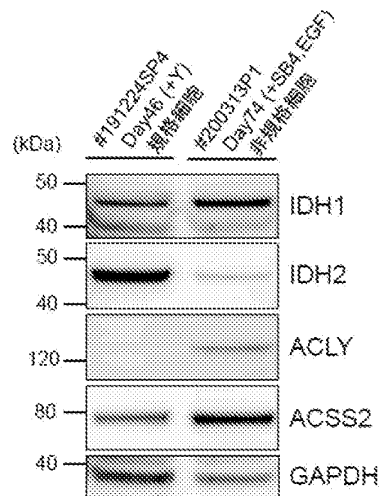
[図108]

非規格細胞におけるヒストンのアセチル化亢進



[図109]

Immunoblotting: #191224S P4 Day46 & #200313 P1 Day74



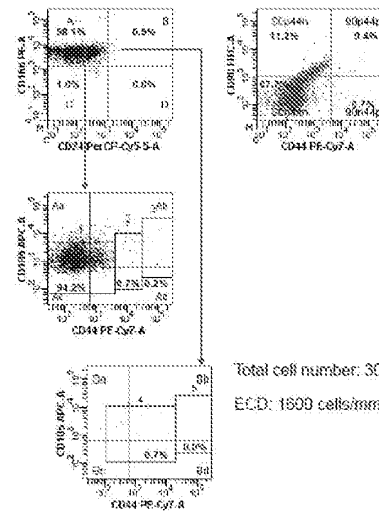
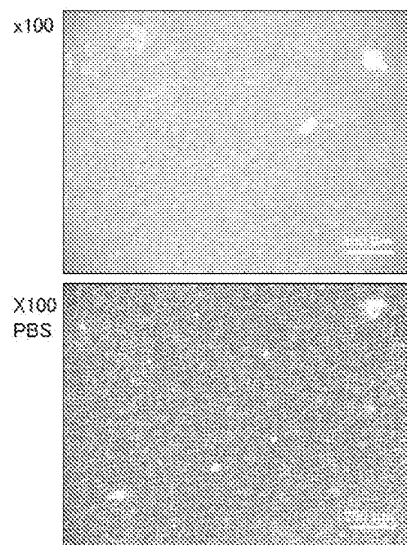
anti-IDH1 rab pAb (1:180 dilution, 5 µg/mL)
 anti-IDH2 rab pAb (1:120 dilution, 5 µg/mL)
 anti-ATP citrate lyase rab pAb (1:2000 dilution, 0.119 µg/mL)
 anti-ACSS2 rab pAb (1:200 dilution, 5 µg/mL)
 anti-GAPDH rab pAb (1:2000 dilution, 15 µg/mL)

[図110]

cHCECs_#191224SP4 (Day46)_① (Nancy+Y)

【規格細胞用として培養】

#191224S P4 Day46 (+Y)



Total cell number: 30.4×10^4 cells
 ECD: 1800 cells/mm²

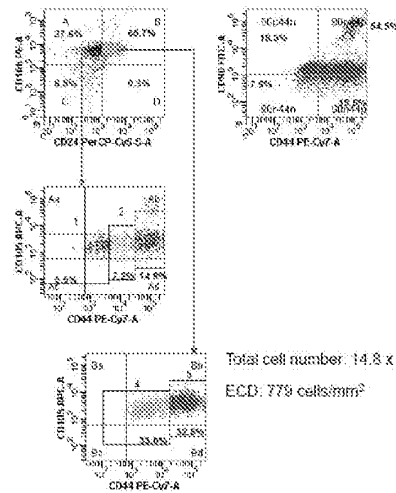
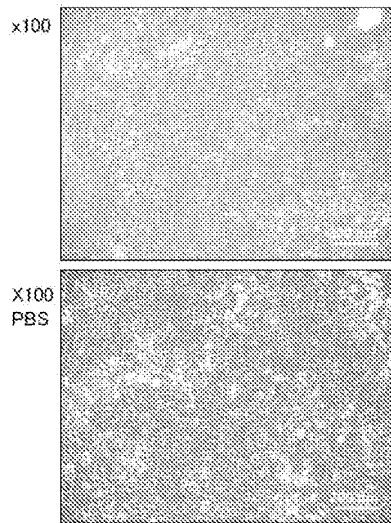
Nancy + 10 μ M Y-27632 + 20 μ g/mL ascorbic acid

[図111]

cHCECs_#200313 (Day74)_② (Nancy+SB4+EGF)

【非規格細胞用として培養】

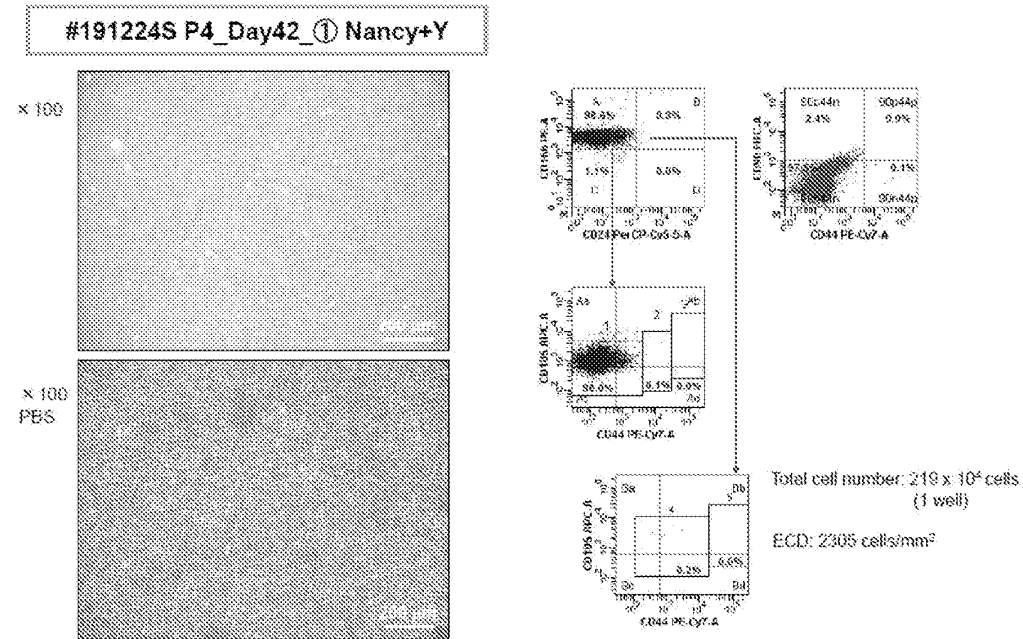
#200313 P1 Day74 (+SB4,EGF)



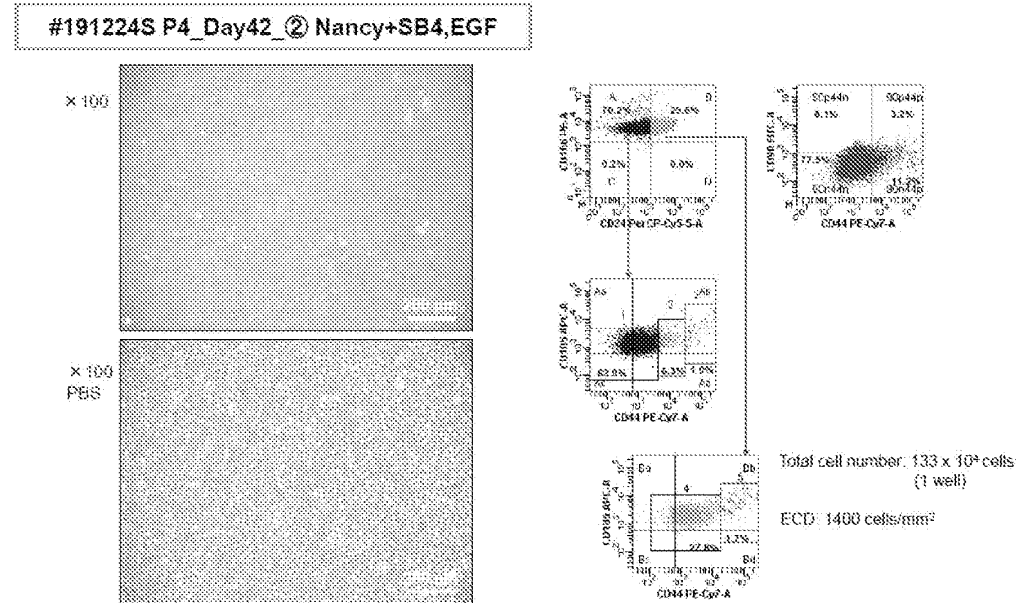
Total cell number: 14.8×10^4 cells
 ECD: 779 cells/mm²

Nancy + 1 μ M SB431542 + 5 ng/mL EGF + 20 μ g/mL ascorbic acid

[図112]



[図113]



[図114]

HAT/HDAC活性測定結果

