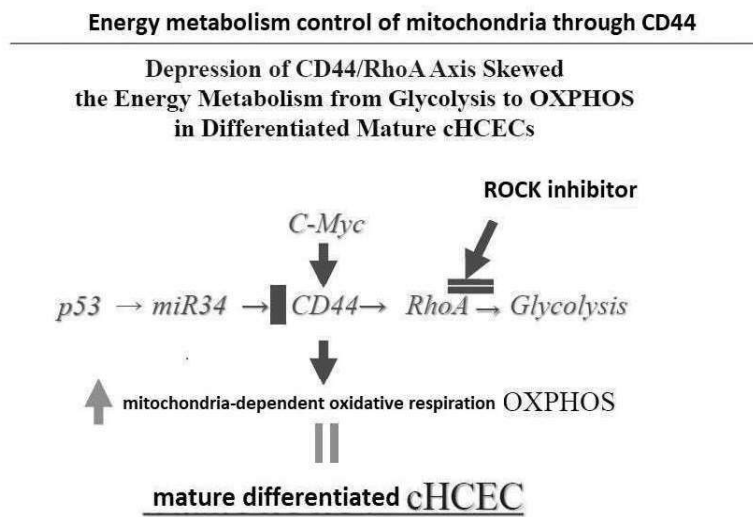
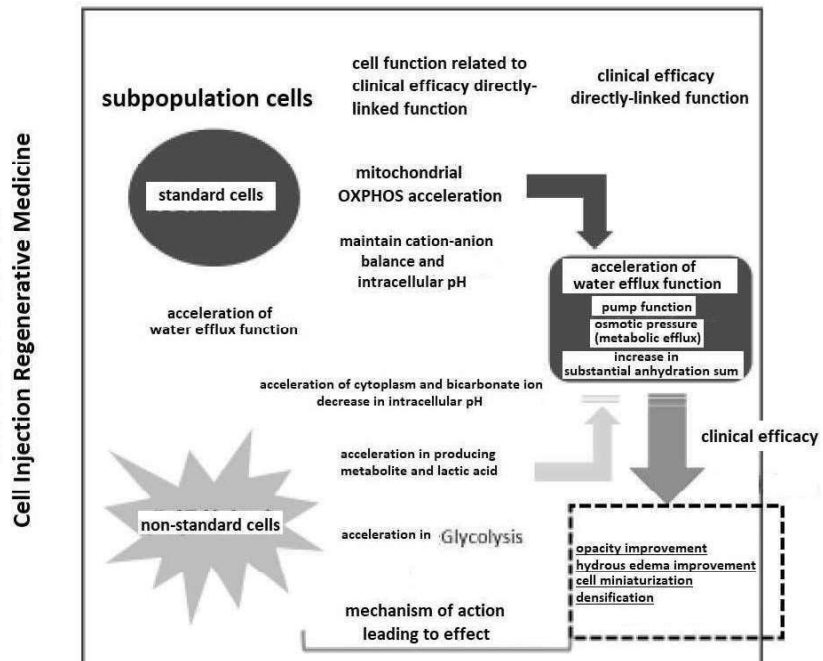
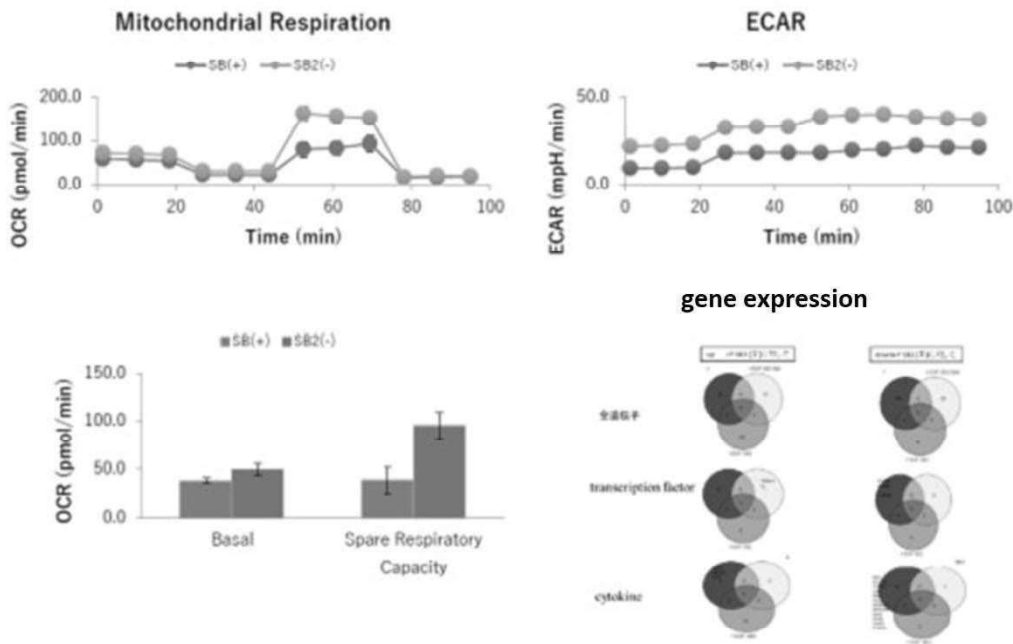


[Fig. 1]



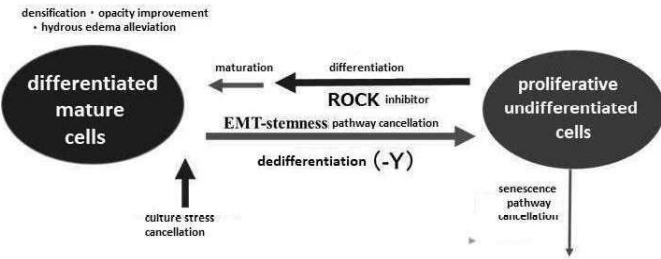


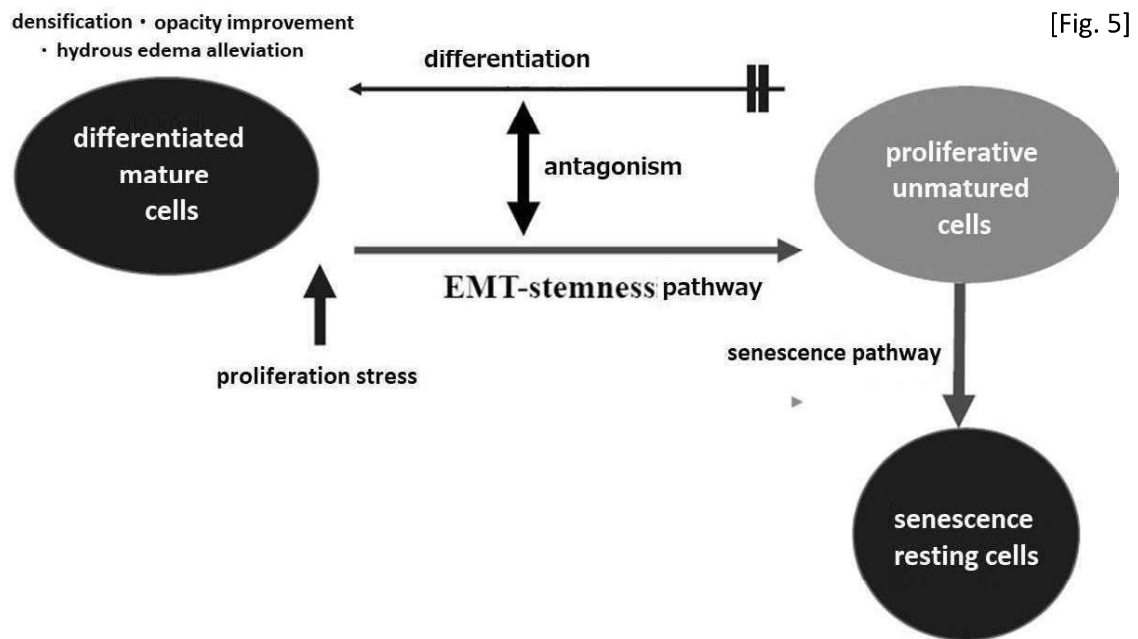
[Fig. 2]

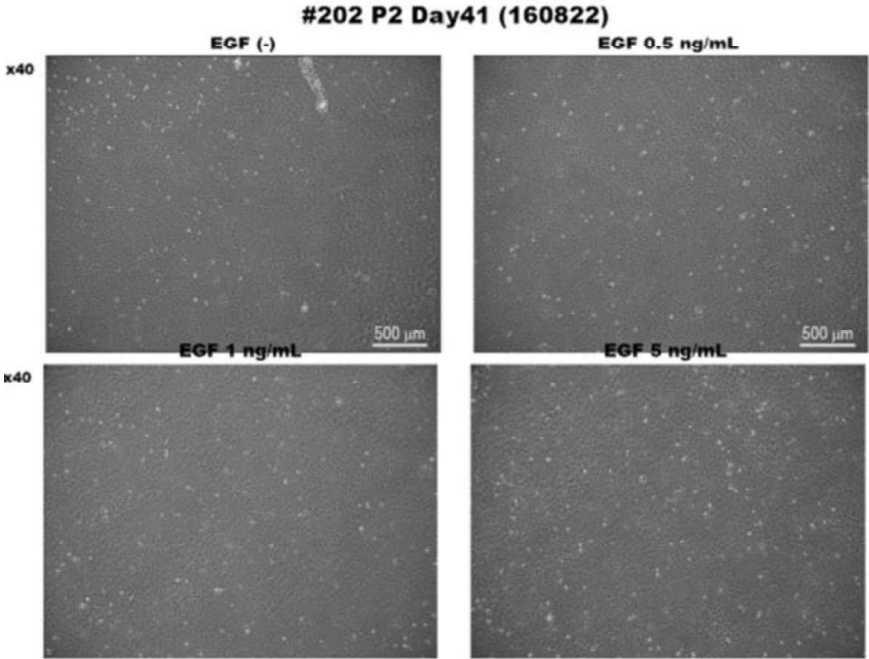


[Fig. 3]

[Fig. 4]



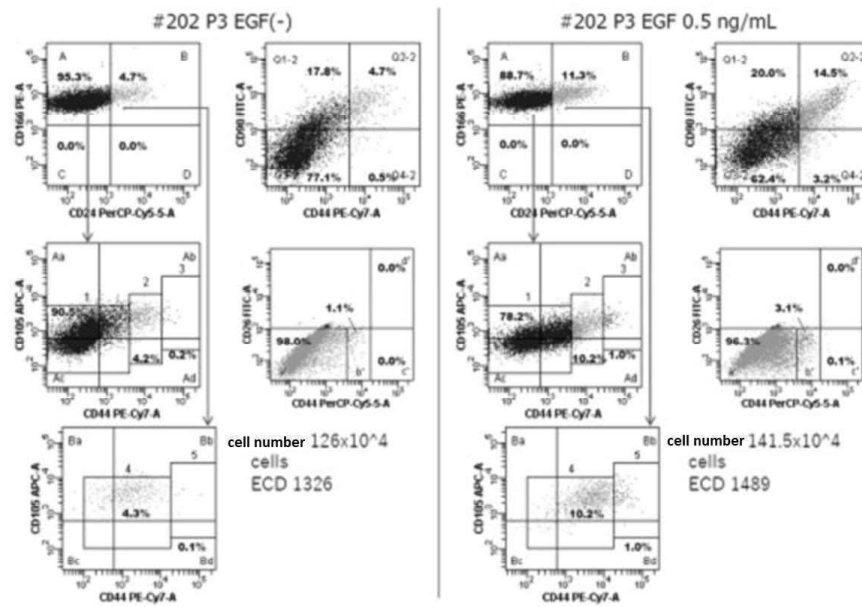




[Fig. 6]

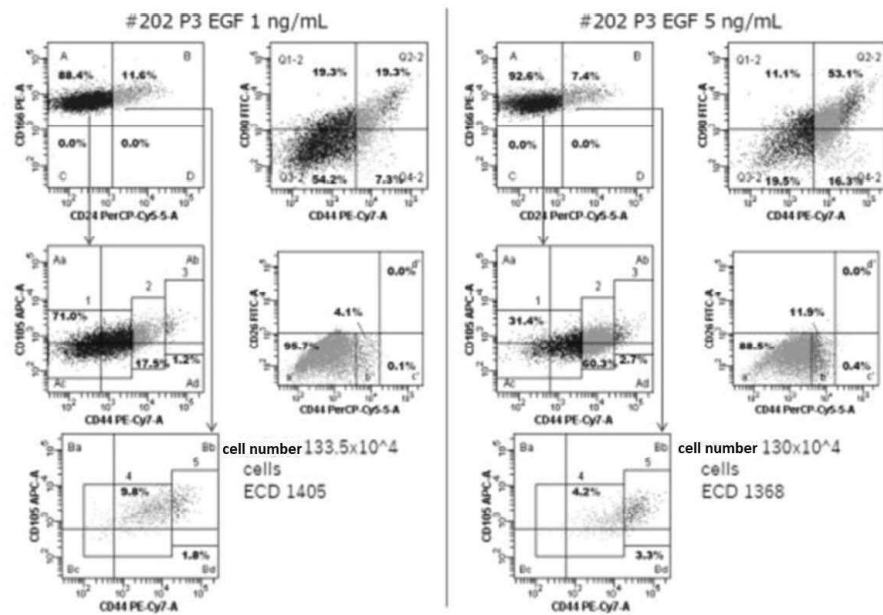
P3 Day42 (161004)

[Fig. 7]



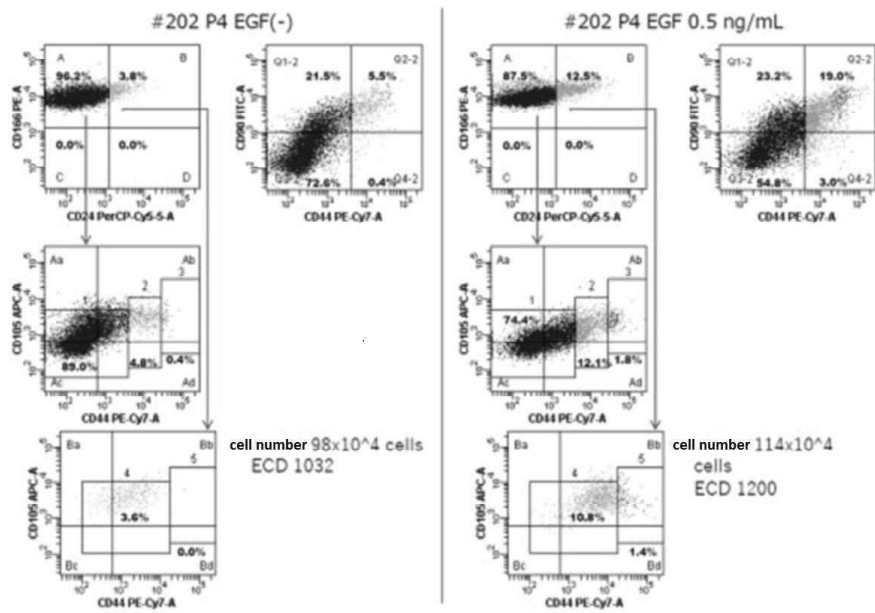
P3Day42 (161004)

[Fig. 8]



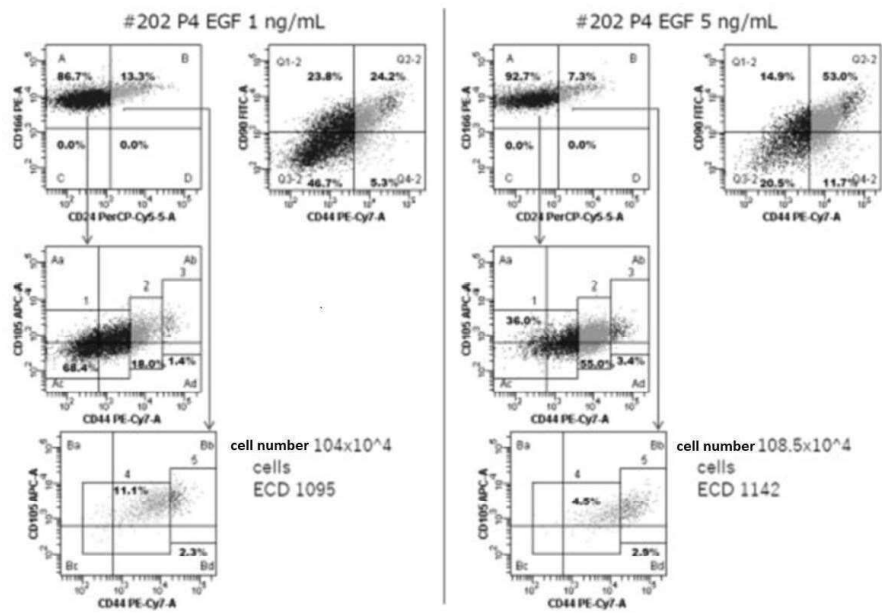
P4Day42 (161115)

[Fig. 9]



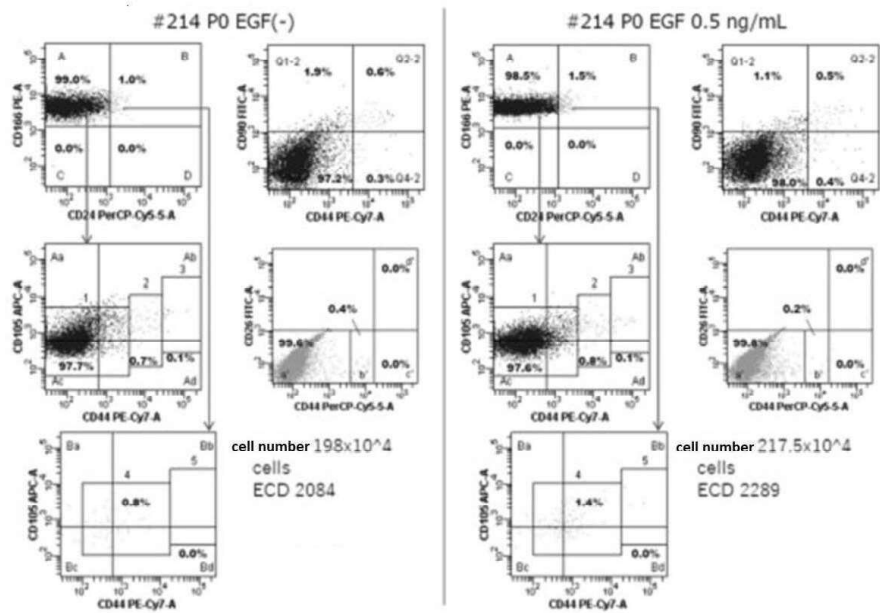
P4Day42 (161115)

[Fig. 10]



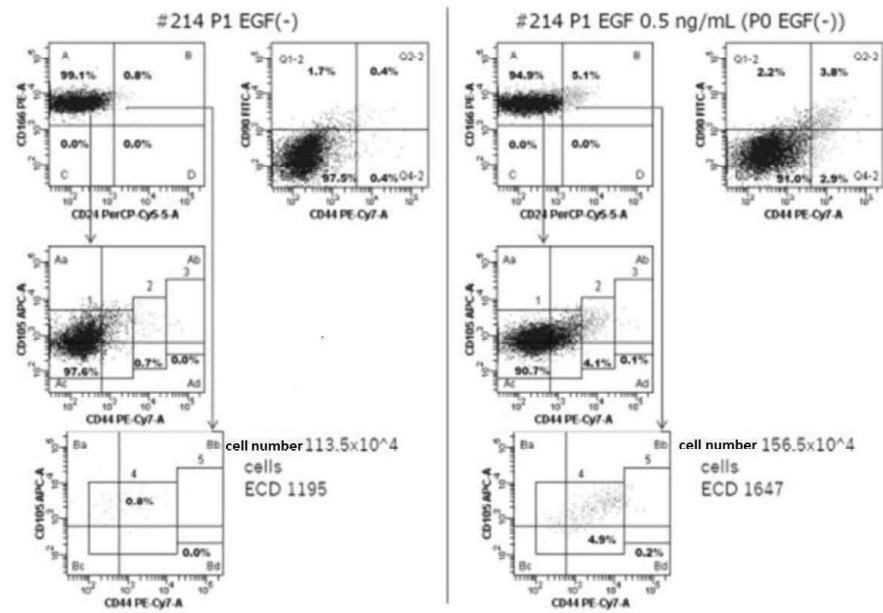
Day41 (161014)

[Fig. 11]



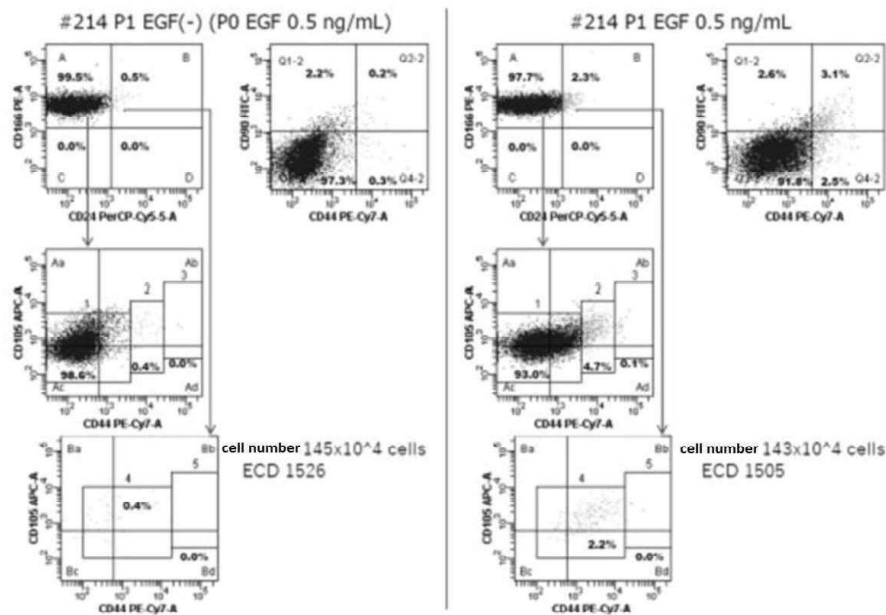
Day42 (161125)

[Fig. 12]



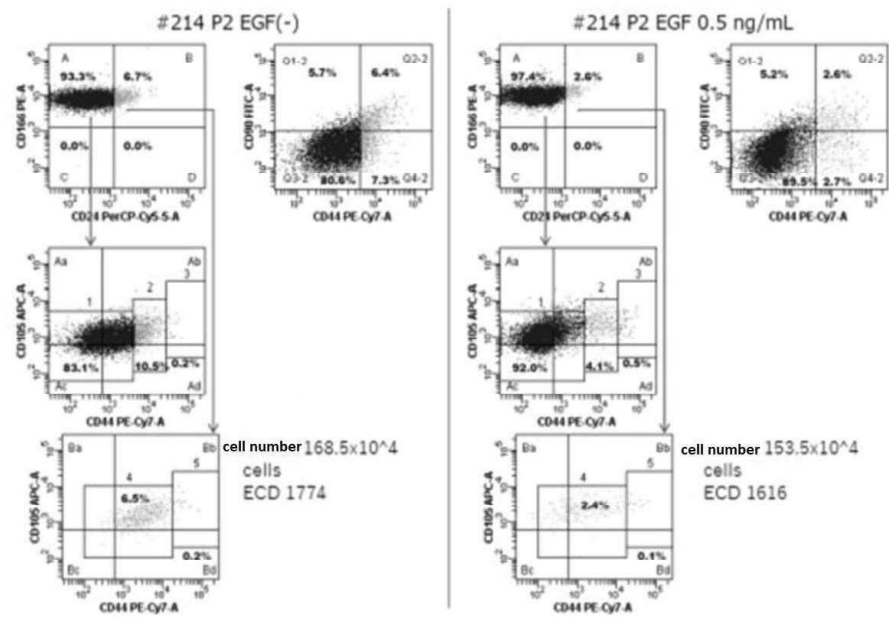
Day42 (161125)

[Fig. 13]



Day42 (170106)

[Fig. 14]



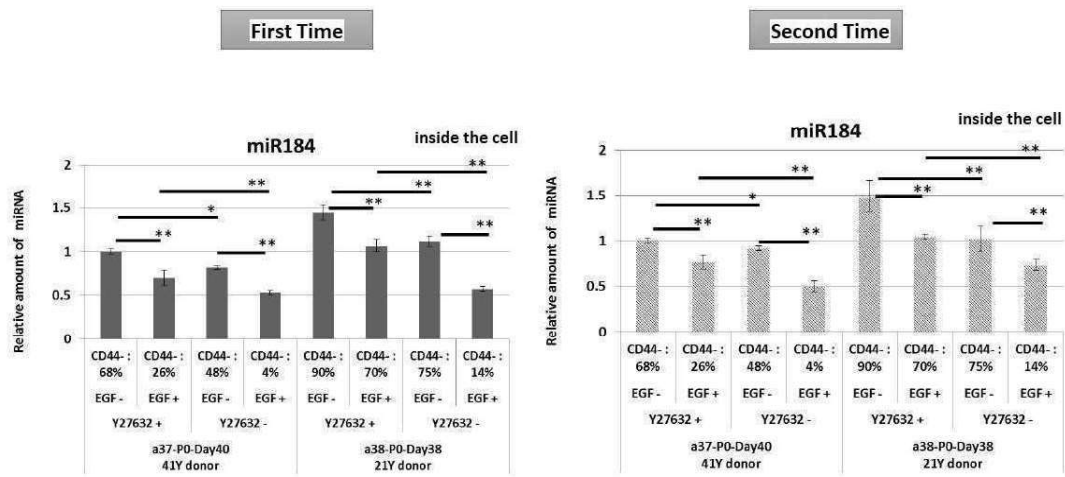
[Fig. 15]



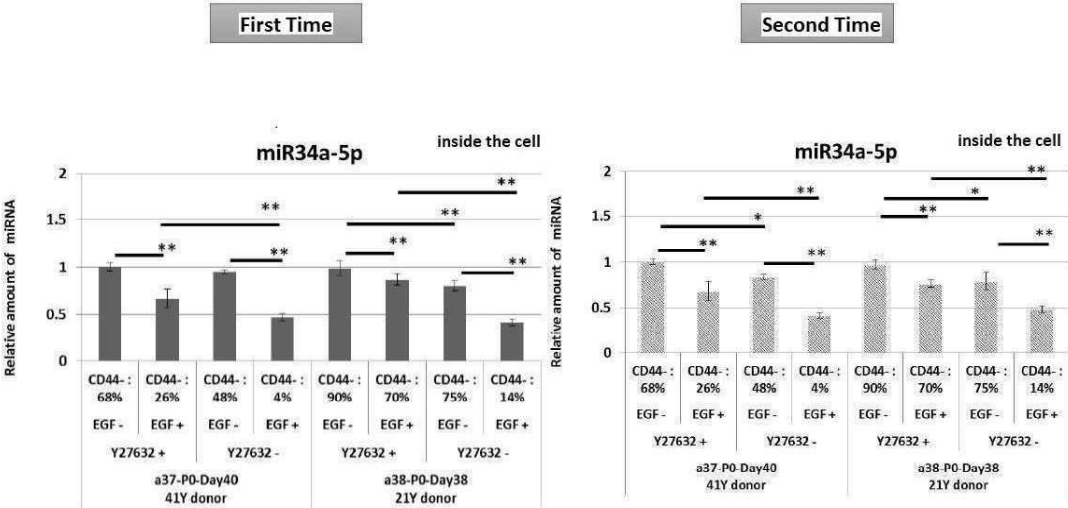
[Fig. 16]

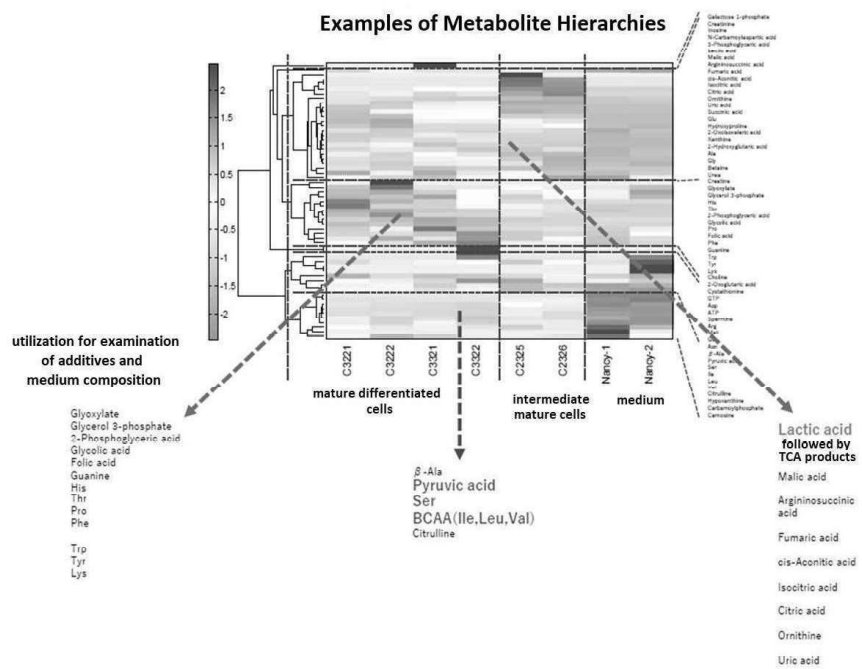
	Y27632+				Y27632-			
	EGF-		EGF+		EGF-		EGF+	
	41Y a37- P0	21Y a38- P0	41Y a37- P0	21Y a38- P0	41Y a37- P0	21Y a38- P0	41Y a37- P0	21Y a38- P0
CD44-	68%	90%	26%	70%	48%	75%	4%	14%
CD44+ / CD44++	22%	4%	43%	19%	32%	10%	32%	54%
CD44+++	4%	1%	9%	3%	11%	2%	35%	26%
CD24++ / CD44+++	1%	0%	10.3%	1%	2%	0%	27%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

[Fig. 17]

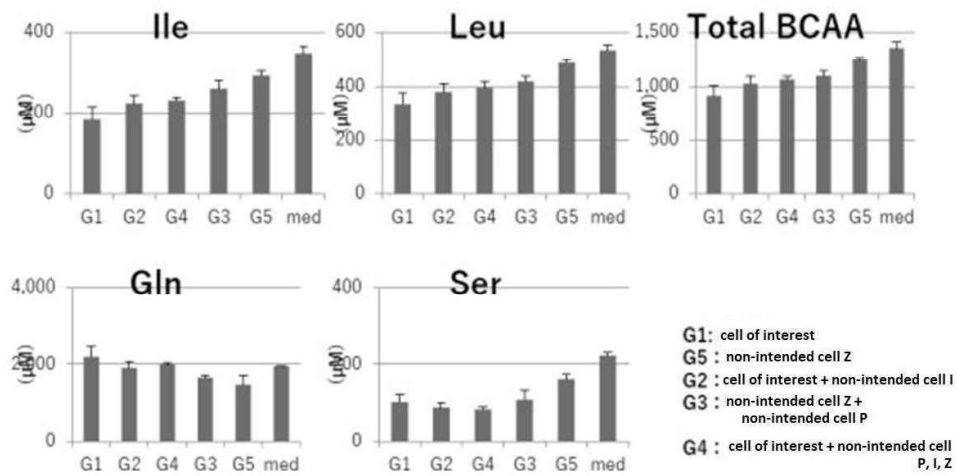


[Fig. 18]

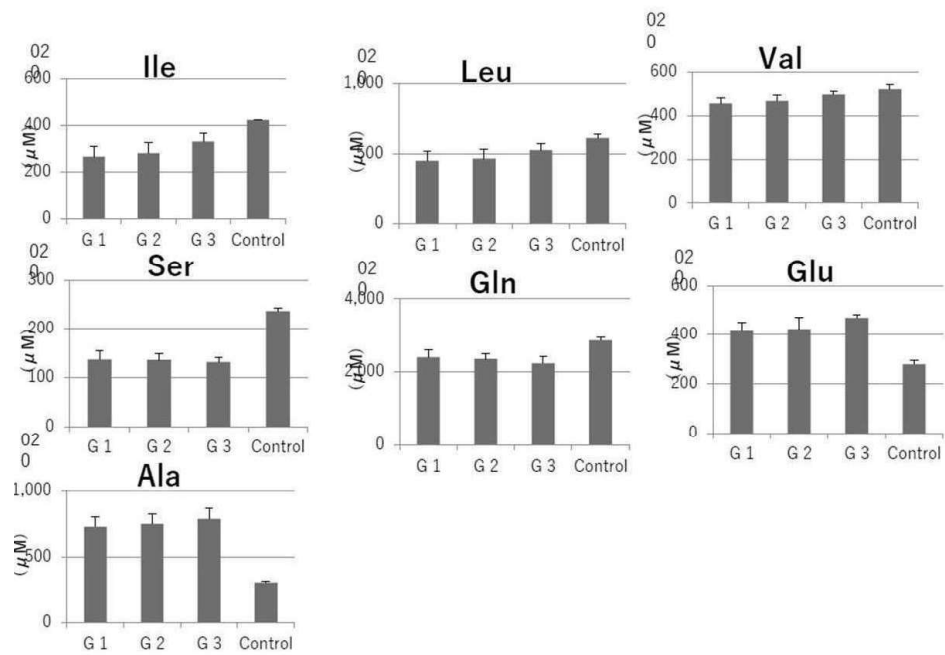




[Fig. 19]

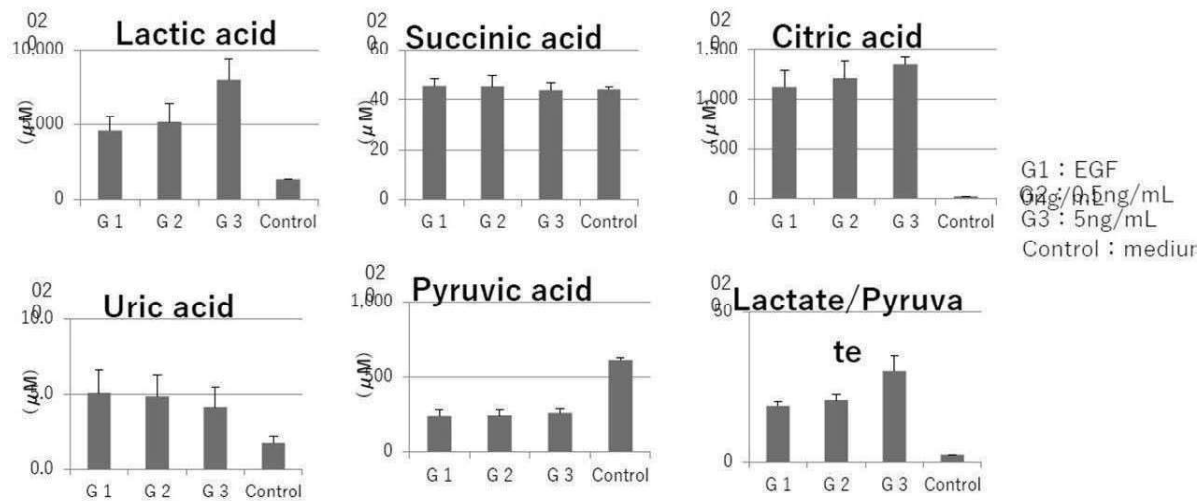


[Fig. 20]



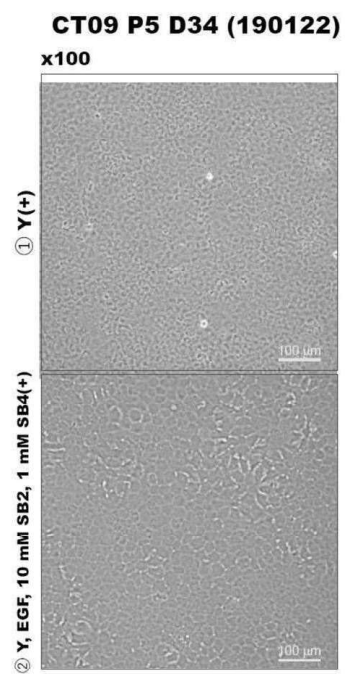
[Fig. 21]

[Fig. 22]

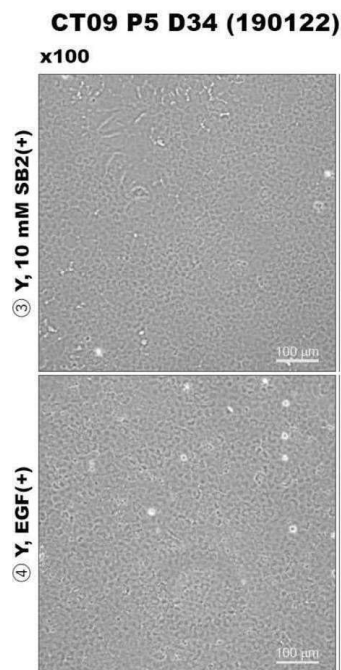


[Fig. 23]

Additive Reagent	①	②	③	④	⑤
Y27632	+	+	+	+	+
EGF	-	+	-	+	+
10 mM SB2	-	+	+	-	+
1 mM SB4	-	+	-	-	-

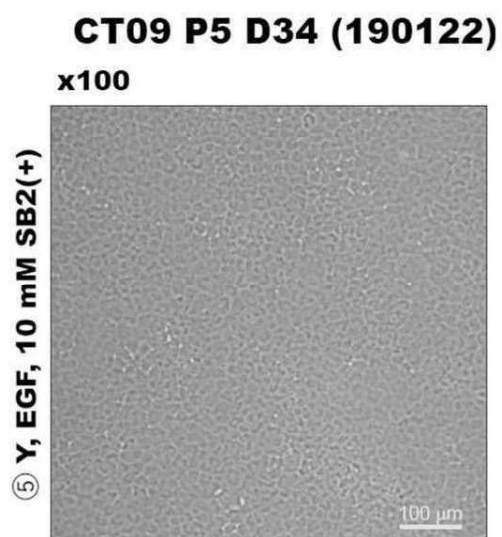


[Fig. 24]



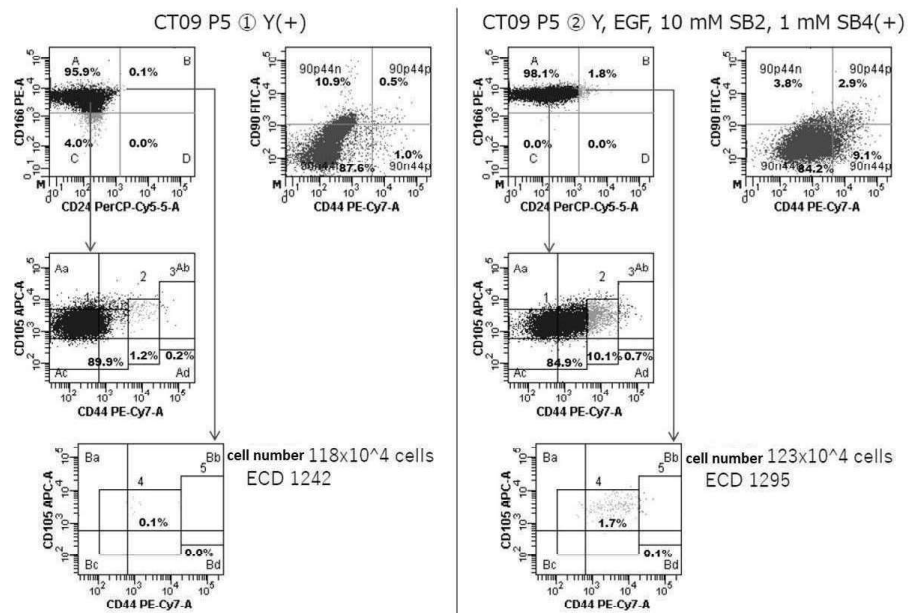
[Fig. 25]

[Fig. 26]



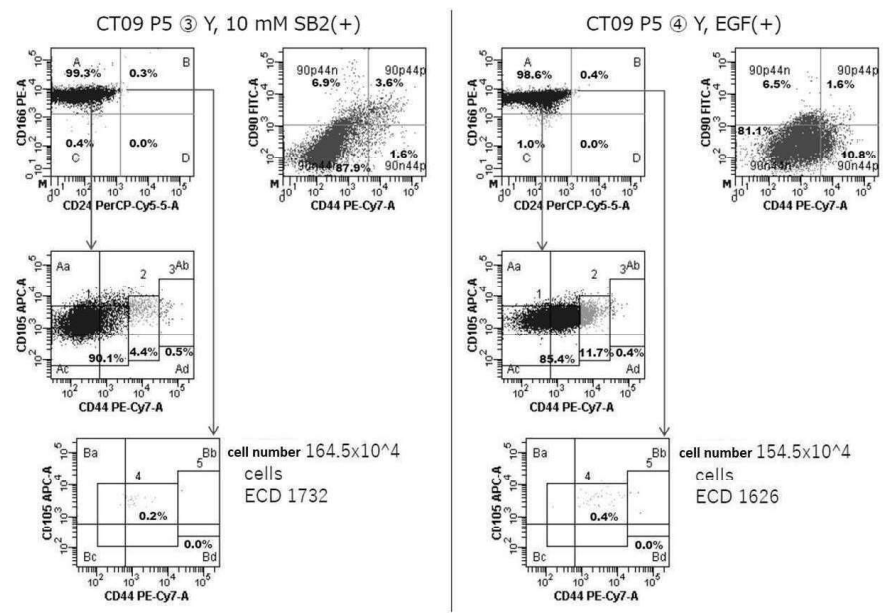
Day34 (190122)

[Fig. 27]



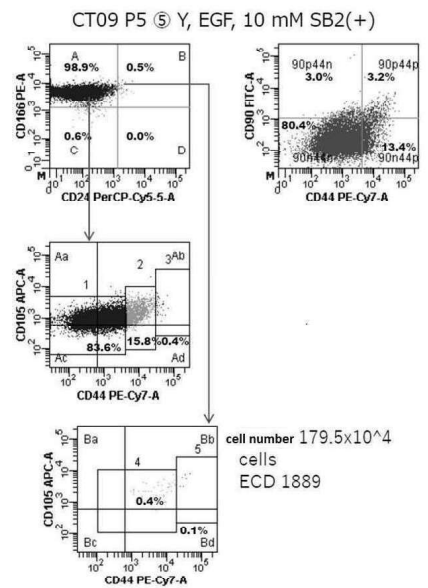
Day34 (190122)

[Fig. 28]



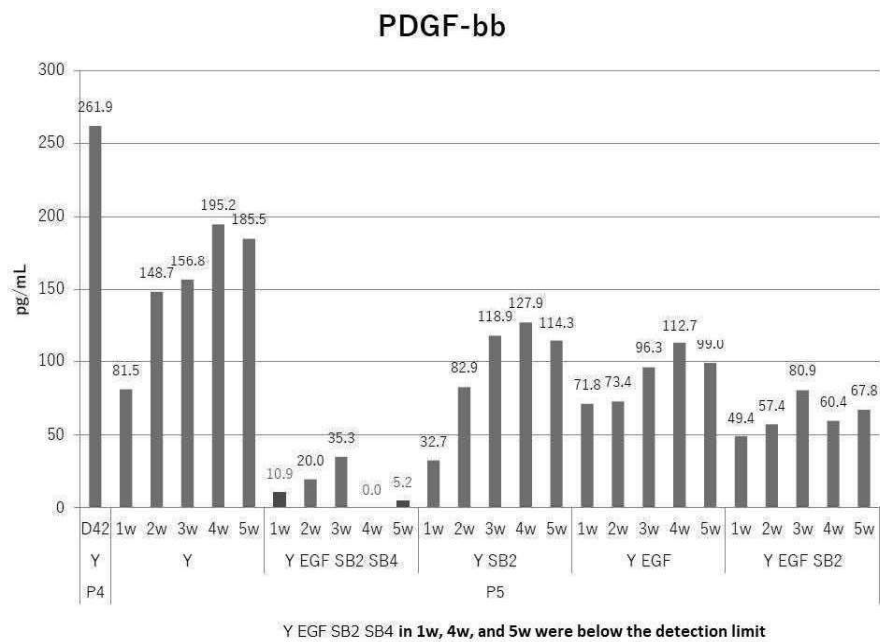
Day34 (190122)

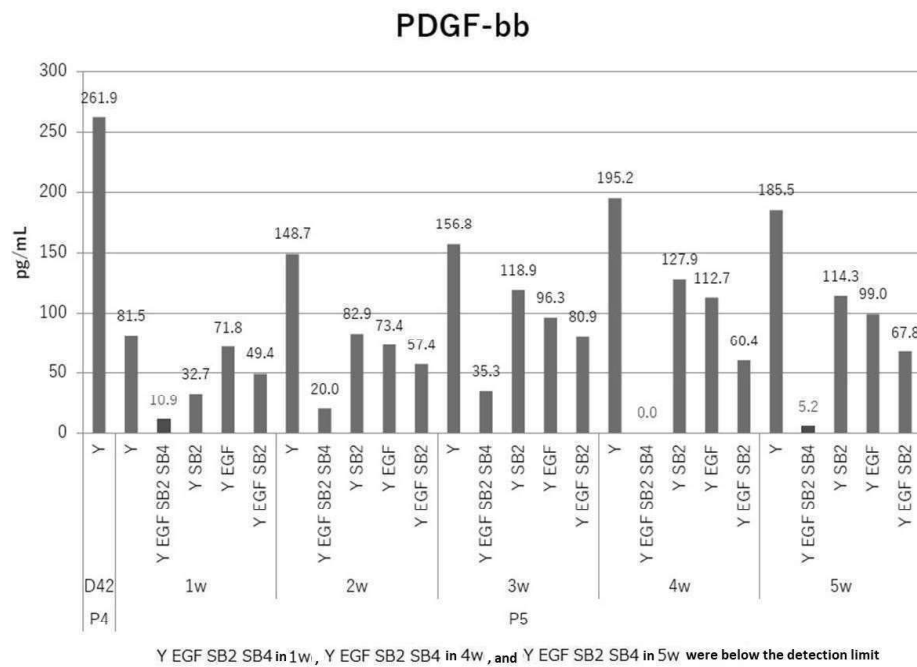
[Fig. 29]

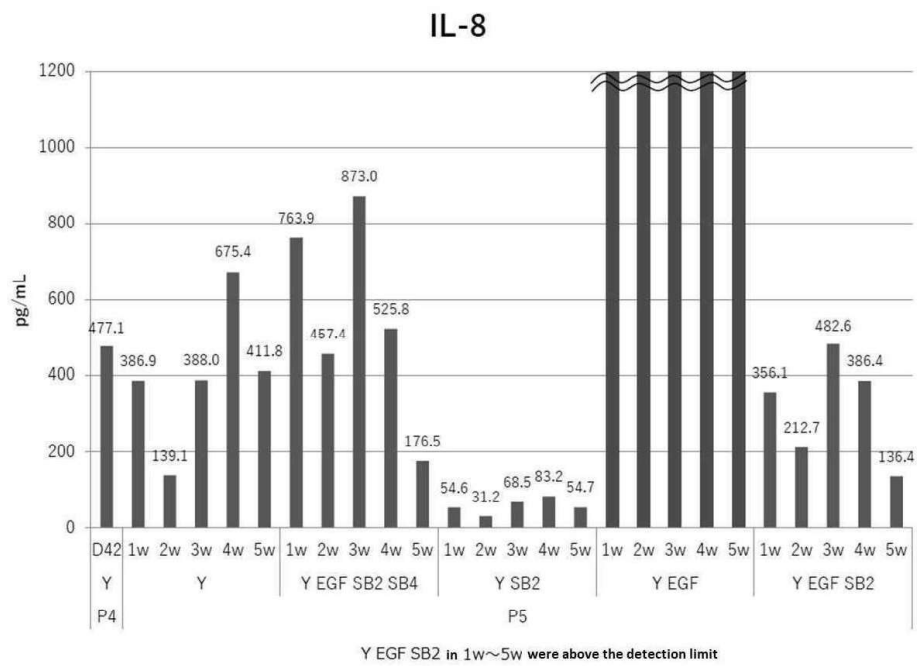


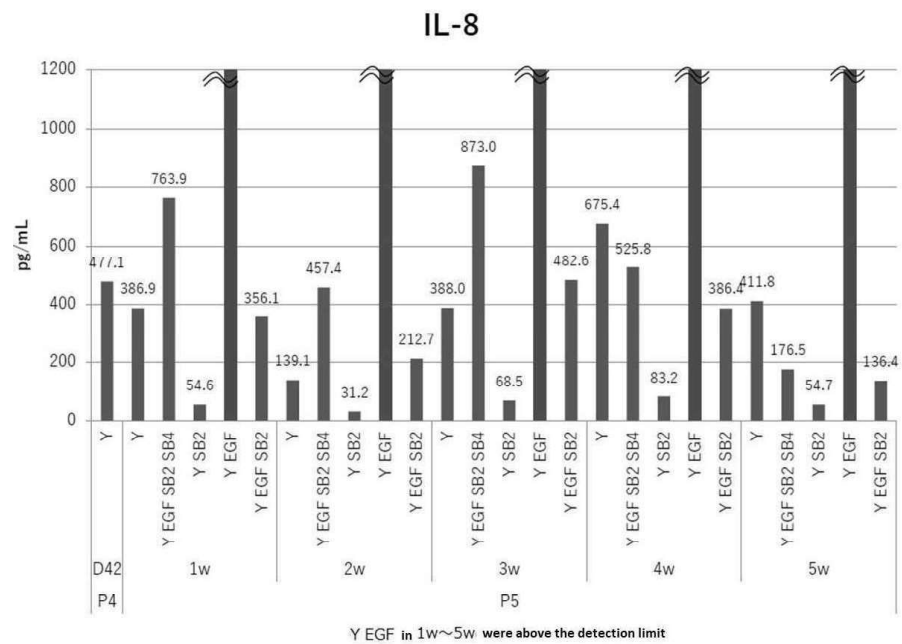
[Fig. 30]

		Additive Reagent	Culture Supernatant
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









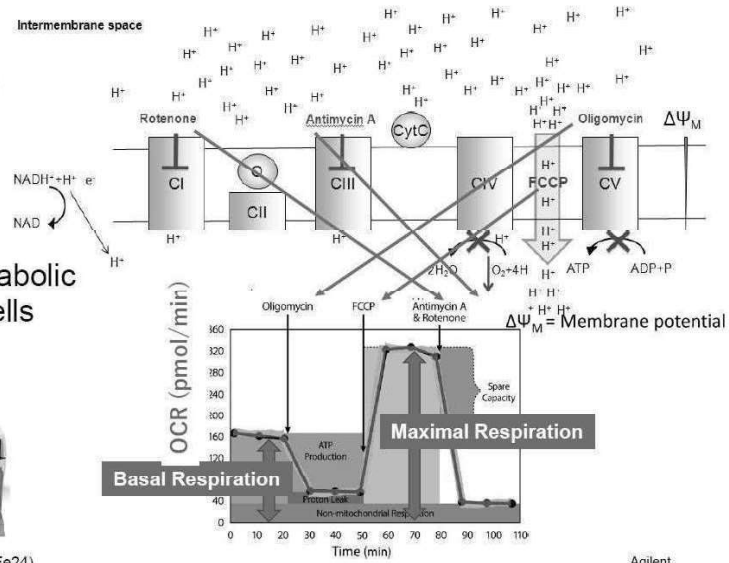
[Fig. 35]

Mito Stress Test

To measure the metabolic pathways in living cells



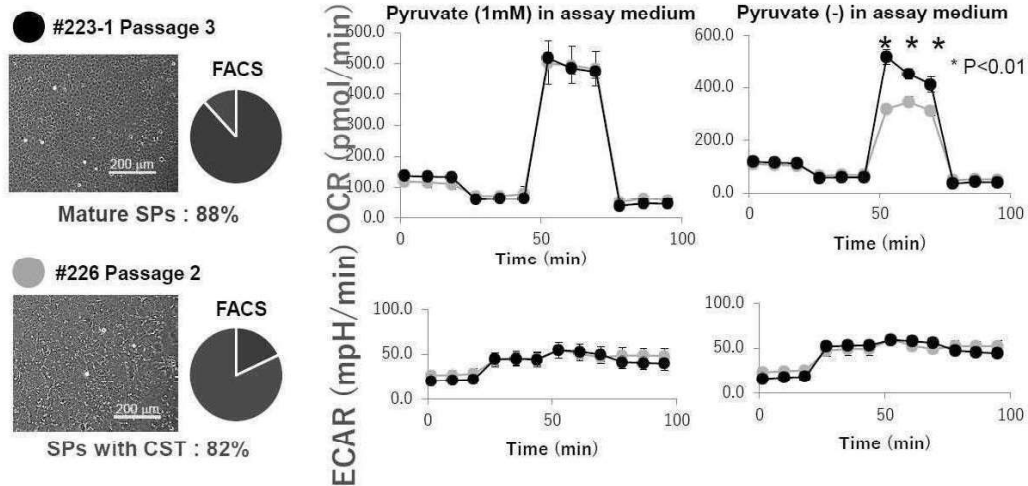
Extracellular flux analyzer (XFe24)



Agilent
Technologies

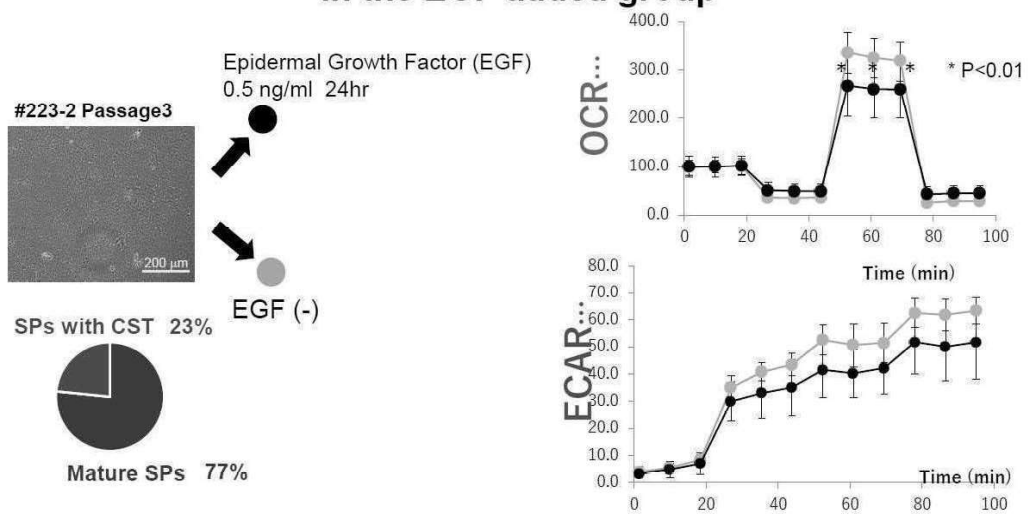
[Fig. 36]

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



[Fig. 37]

**The maximal respiration significantly decreased
in the EGF added group**



[Fig. 38]

Culture 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

[Fig. 39]

Y _{addition}	Day0-3	Day4-9	Day10-19	Day20-	Day28-
①	+	+	+	+	+, SB2+
②	-	+	+	+	+, SB2+
③	-	-	+	+	+, SB2+
④	-	-	-	+	+, SB2+
⑤	+	-	-	-	-, SB2+
⑥	-	-	-	-	-, SB2+

[Fig. 40]

	Additive	Supernatant Collection
P1	-SB2	D37, D41
P2	+SB2	1w~6w
	-SB2	1w~6w

FACS results of #190719 P1, P2

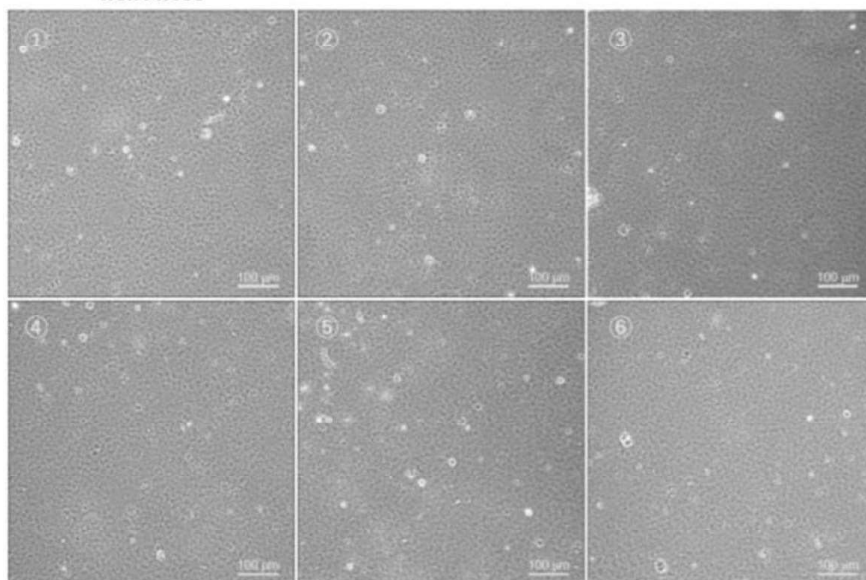
P1	Effector (%)	CD44+ (%)	CD44++ (%)	P2	Effector (%)	CD44+ (%)	CD44++ (%)
① well1	82.6	0.6	0.1	① well1	86.4	2.7	0.6
① well2	73.4	0.7	0	① well2	85.7	2.5	0.5
② well1	79.1	0.7	1.1	② well1	81.7	2.2	0.6
② well2	82.2	0.6	0.1	② well2	76.4	1.8	0.5
③ well1	90.1	0.5	0.3	③ well1	90.4	2.4	0.3
③ well2	94.2	0.3	0.1	③ well2	89.5	3.5	0.7
④ well1	80.9	1.8	0.2	④ well1	86.5	3.5	0.6
④ well2	84	1.9	0.4	④ well2	83.6	3.5	0.8
⑤ well1	45.7	3	1.4	⑤ well1	71.1	8	5.6
⑤ well2	49.3	2.5	0.4	⑤ well2	61.7	8.3	5.8
⑥ well1	57.8	7.7	3.2	⑥ well1	60.3	14.4	7.1
⑥ well2	54.8	9.4	5.6	⑥ well2	59.9	14.3	9.8

FACS results of #190802 P1 [Fig. 41]

P1	Effector (%)	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

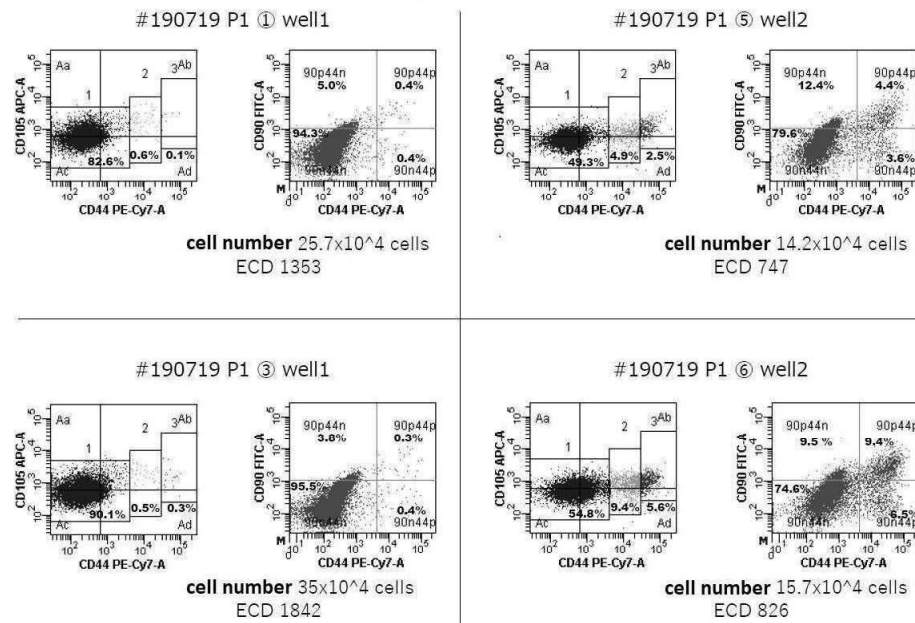
#190719 P1 Day39 (191001) phase-contrast photos
well1 x100

[Fig. 42]



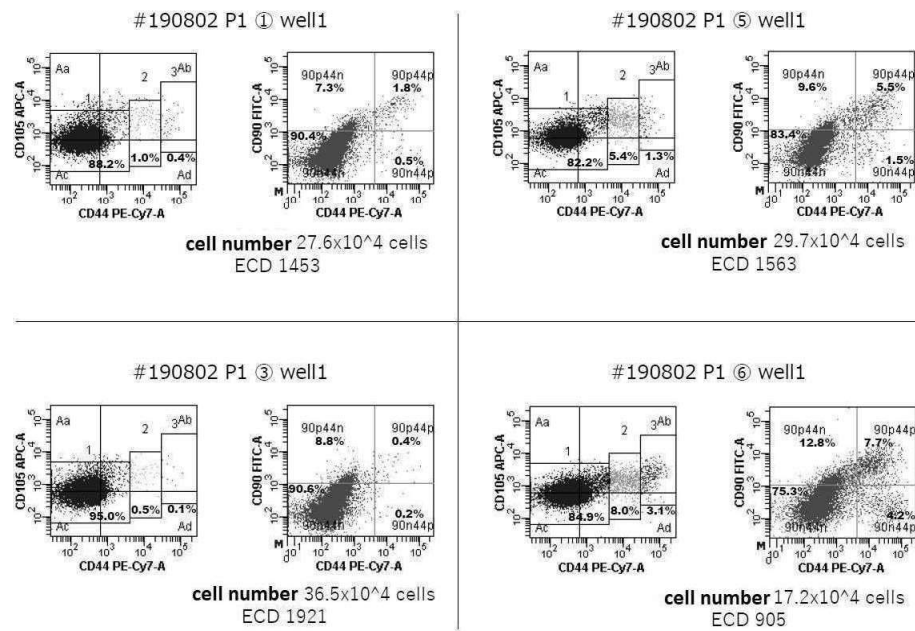
#190719 P1 Day39 (191001) FACSResults

[Fig. 43]



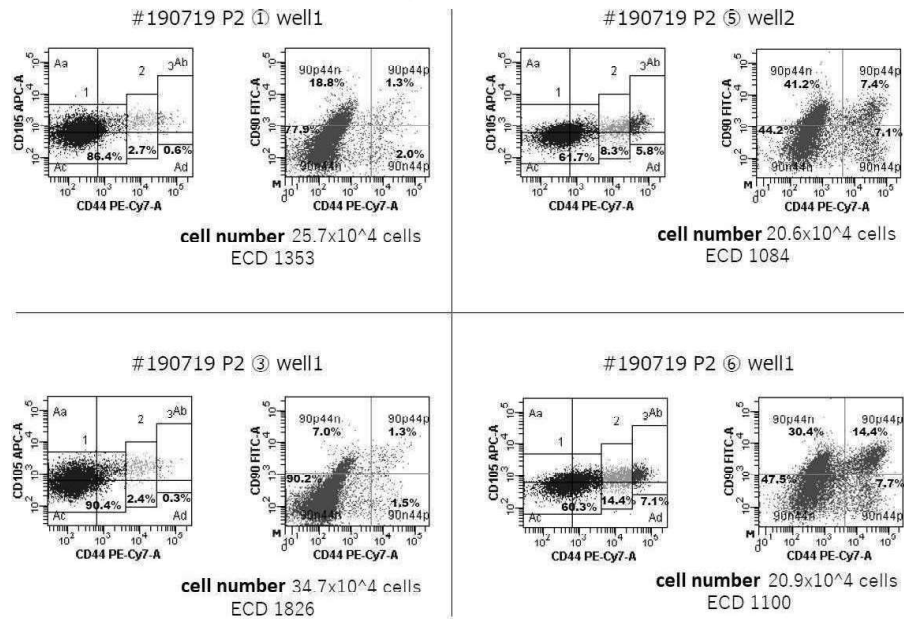
#190802 P1 Day35 (191011) FACSResults

[Fig. 44]

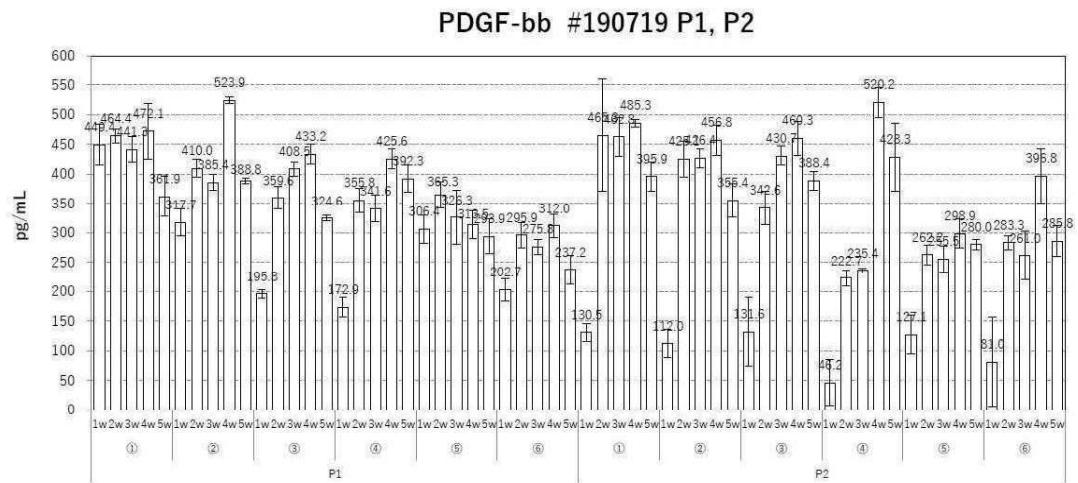


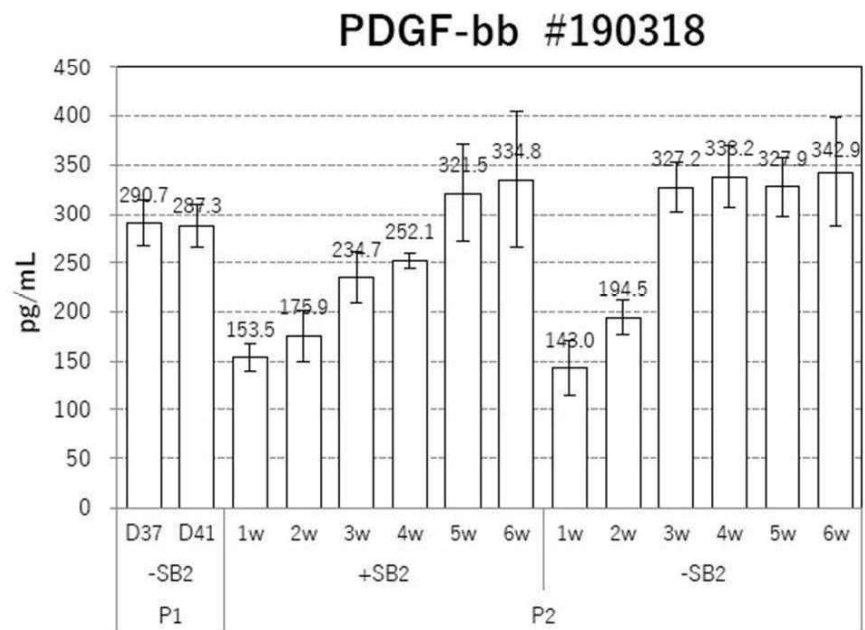
#190719 P2 Day40 (191106) FACS Results

[Fig. 45]

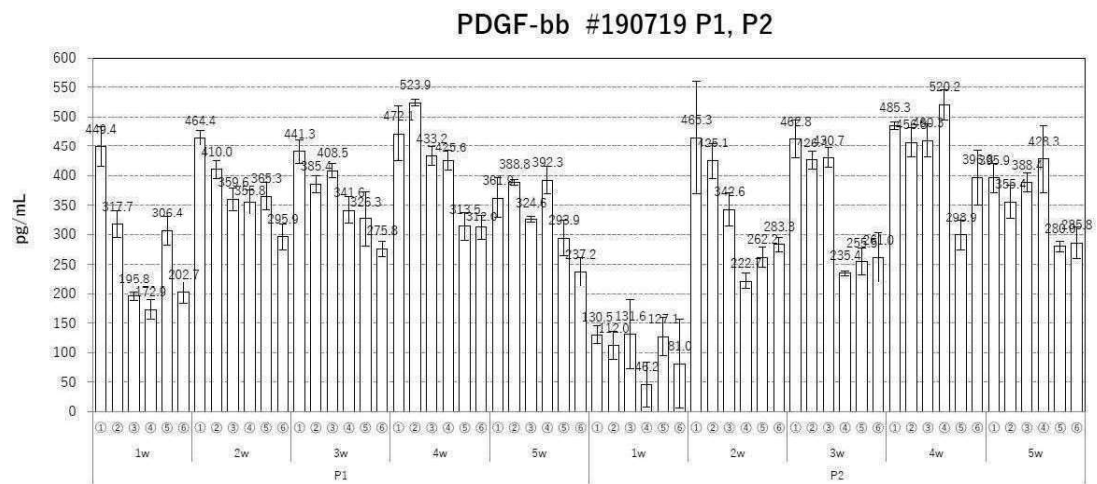


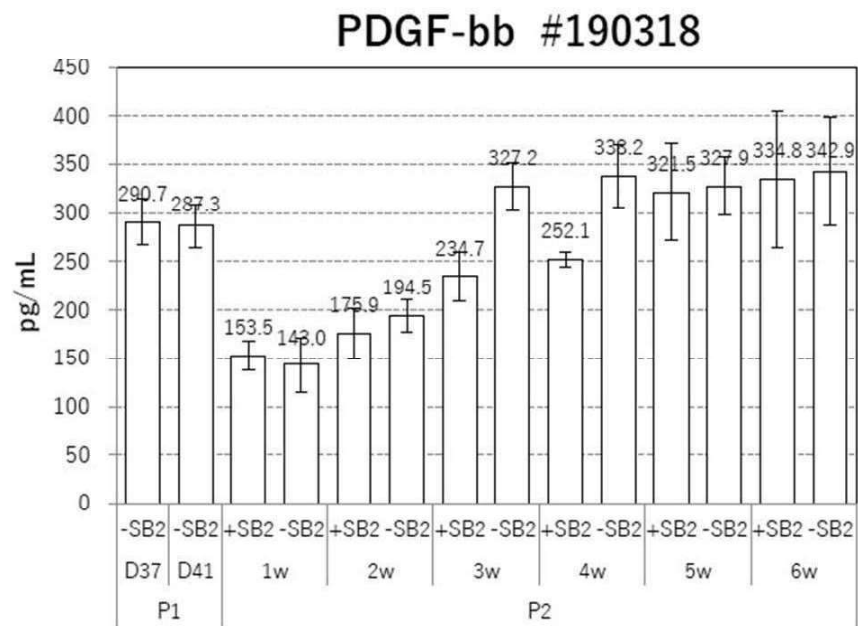
[Fig. 46]





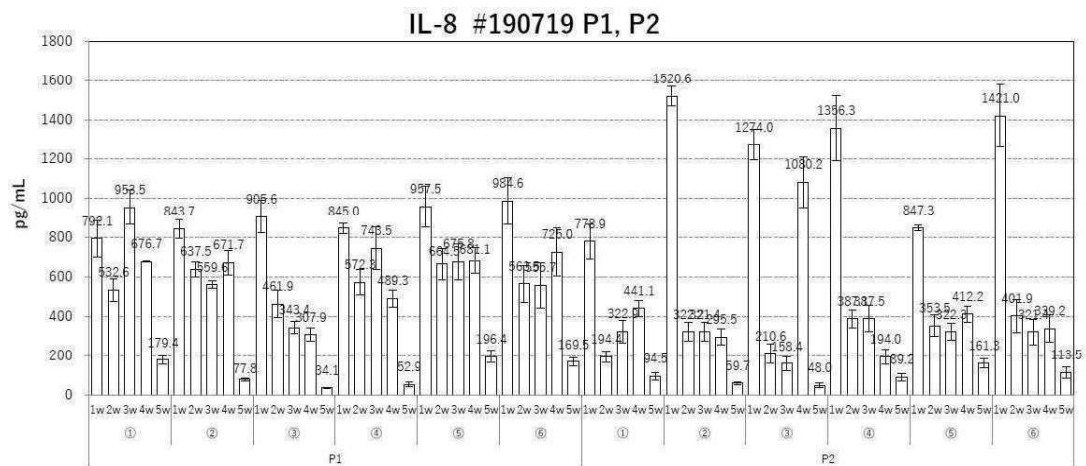
[Fig. 48]

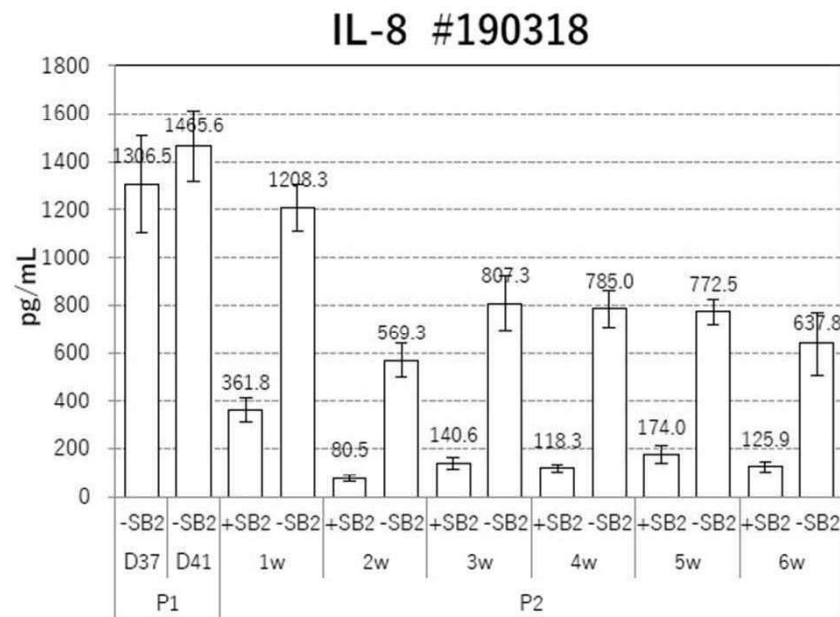




[Fig. 49]

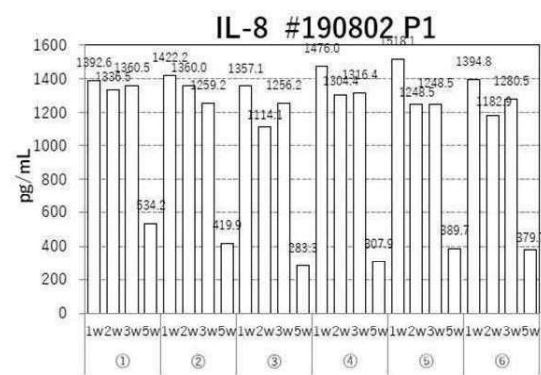
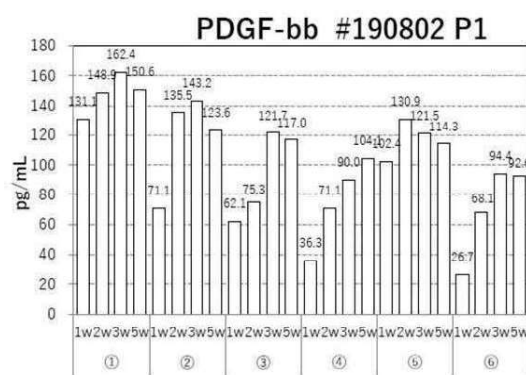
[Fig. 50]

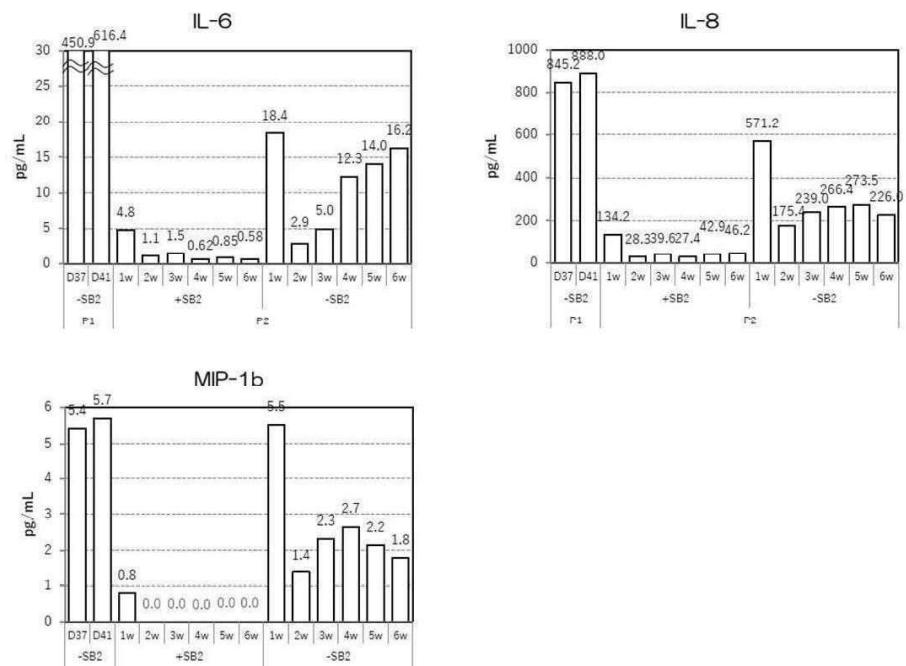




[Fig. 51]

[Fig. 52]



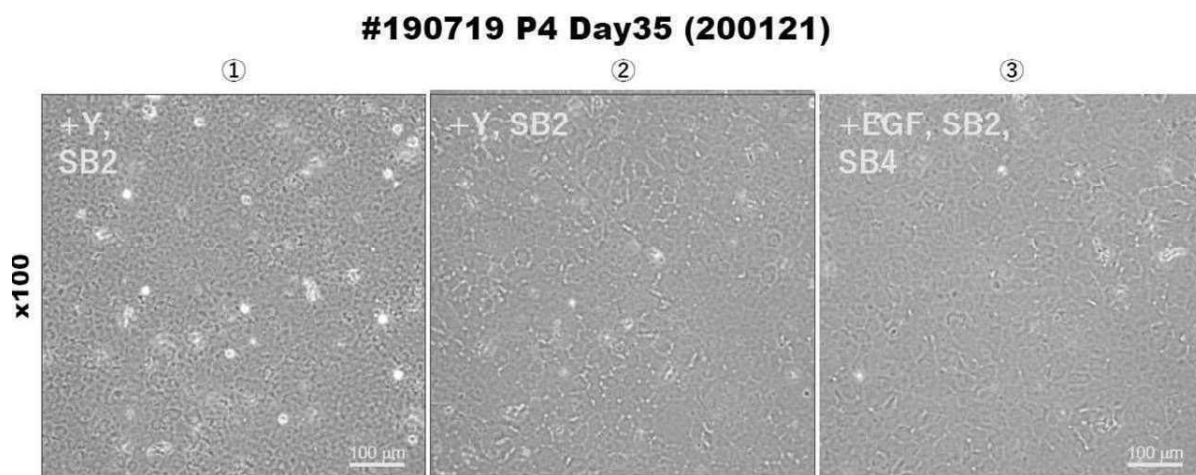


[Fig. 53]

[Fig. 54]

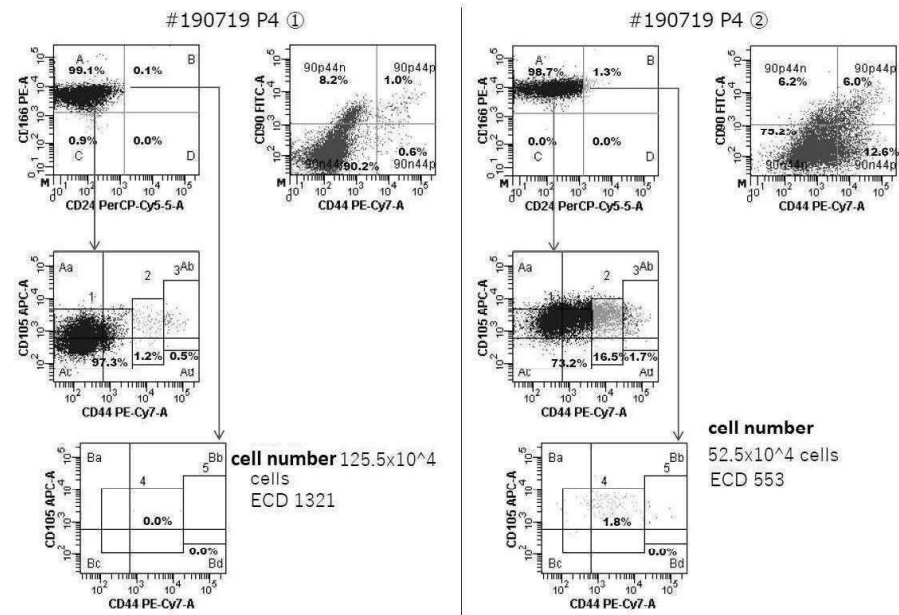
	Day0-3	Day4-	Day10-	Day28-
①	+Y, A			+Y, A, SB2
②	+A		+Y, A	+Y, A, SB2
③	+Y, A	+A, EGF, SB2, SB4		

[Fig. 55]



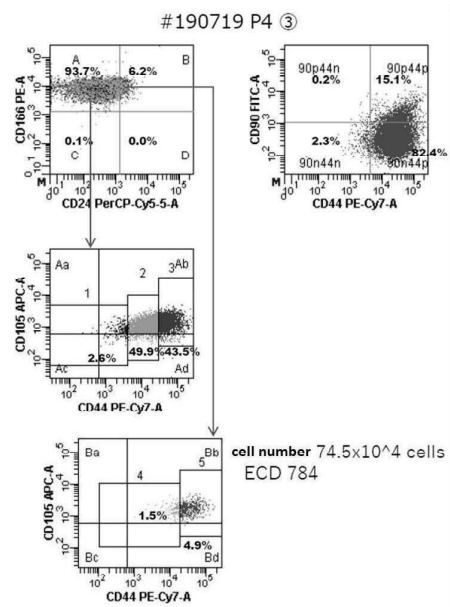
Day35 (200121)

[Fig. 56]

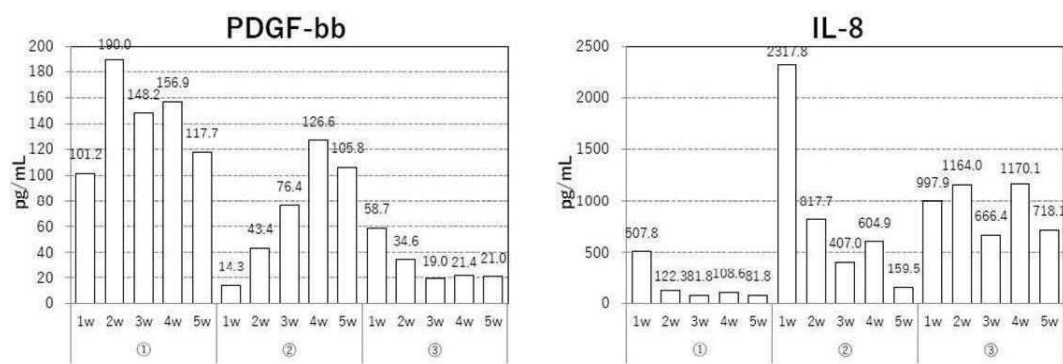


Day35 (200121)

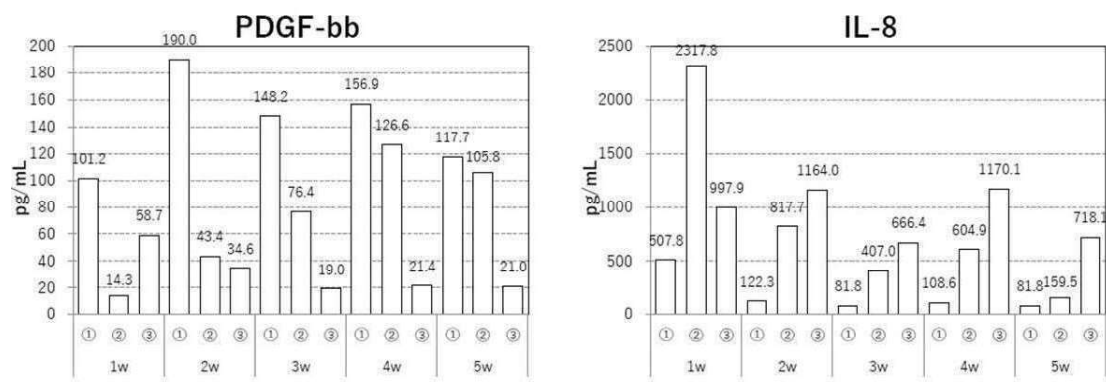
[Fig. 57]



[Fig. 58]



[Fig. 59]



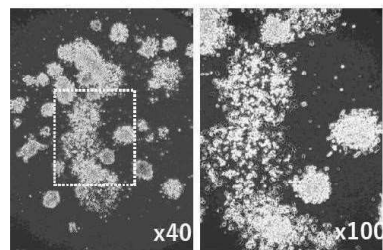
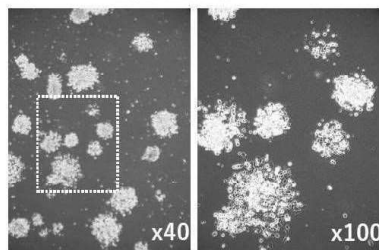
Day 4

[Fig. 60]

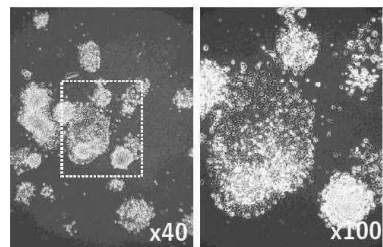
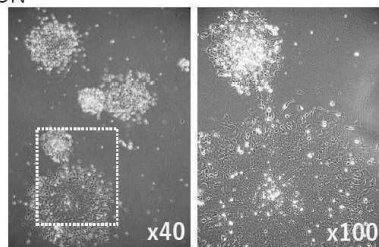
AEM-5100DCN

Visual Field 1

Visual Field 2

Y-, A+

AEM-5100SCN

Y+, A+

Y- : nearly spherical

Y+ : spread out

Day 7

[Fig. 61]

AEM-510DCN

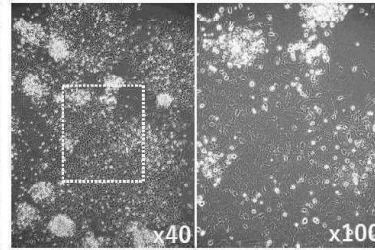
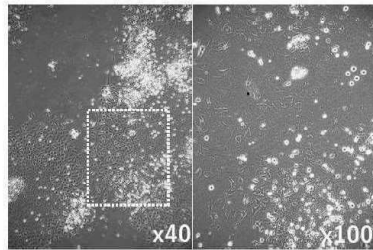
Visual Field 1

Visual Field 2

Y-, A+



Y+, A+

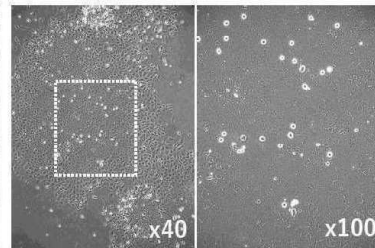
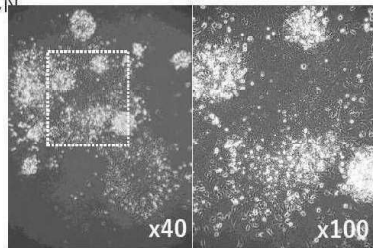


AEM-510SCN

Y+, A+



Y+, A+



Y- : spread out

Y+ : flatter

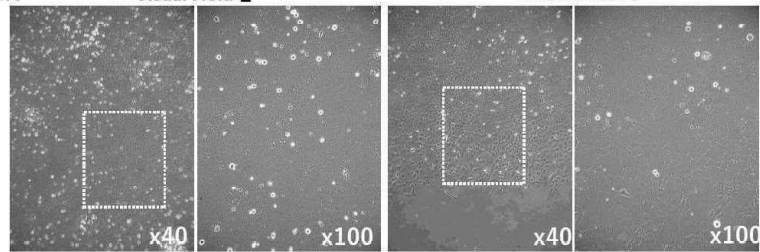
Day 12

[Fig. 62]

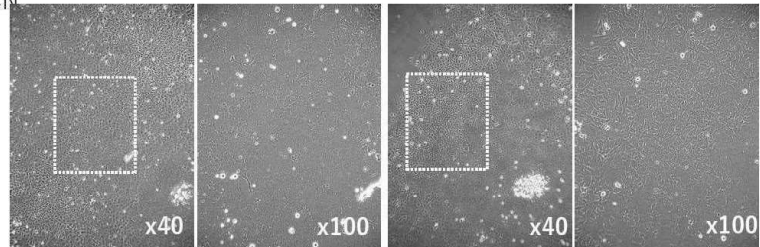
AEM-510DCN

Visual Field 1

Visual Field 2

Y-, A+Y+, A+

AEM-510SCN

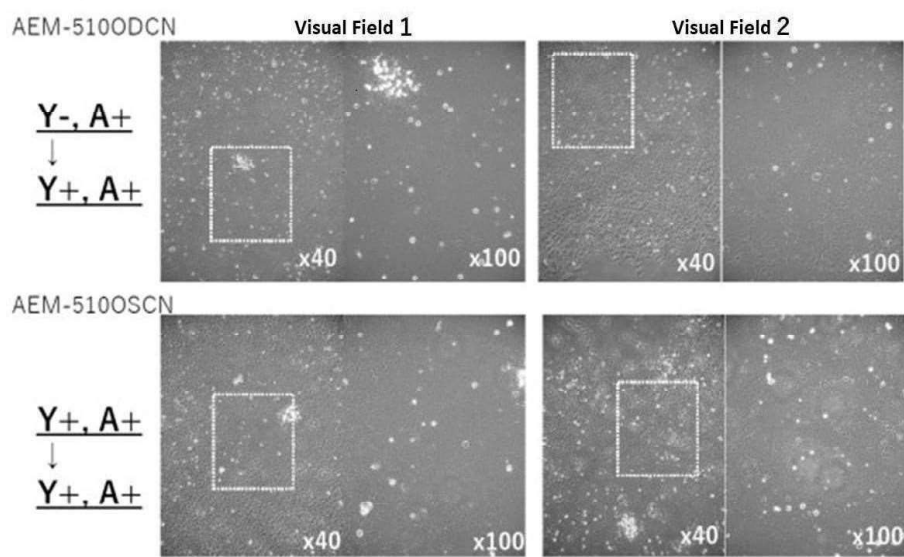
Y+, A+Y+, A+

Y- : flatter

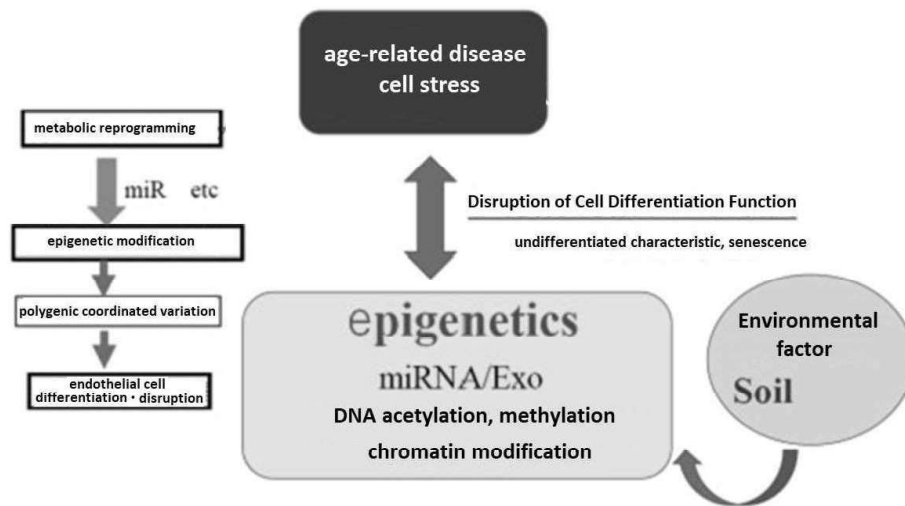
Y+ : flatter

Day 14

[Fig. 63]



Two weeks after the start of culture, no difference was observed.



[Fig. 64]

[Fig. 65]

dedifferentiated progenitor cells	vs	differentiated mature cells	
ACLY		CS	ACLY, ATP-citrate lyase, CS, citrate synthase
ACO1		ACO2	Aconitase 1/2
IDH1		IDH2	Isocitrate dehydrogenase 1/2
MDH1		MDH2	Malate dehydrogenase
ME1		ME3	Malic acid enzyme1/3
ACSS2		ACSS1	
ACAT2		ACAT1	Acetyl-CoA acetyltransferase 1/2
LDH		PDH	Lactate dehydrogenase, Pyruvate dehydrogenase
		BCAT2	
		BCKDH2	Branched-chain ketoacid dehydrogenase 2
cytoplasm + nucleus		mitochondria	

Culture Conditions
Nancy Y(+) A(+)

[Fig. 66]

#184 non-standard cells

P0
SB2(-) 6wp_{x2}
↓
P1 : Day286 (160531)
SB2(-) ECD800
↓
P2 : Day134 (161012)
SB2(-) ECD800
↓
P3 : Day56 (161207)
SB2(+) ECD800
↓
P4 : D135 (170421)
SB2(+) ECD800

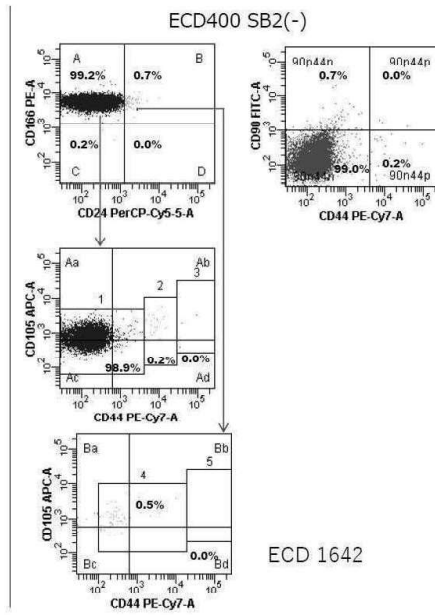
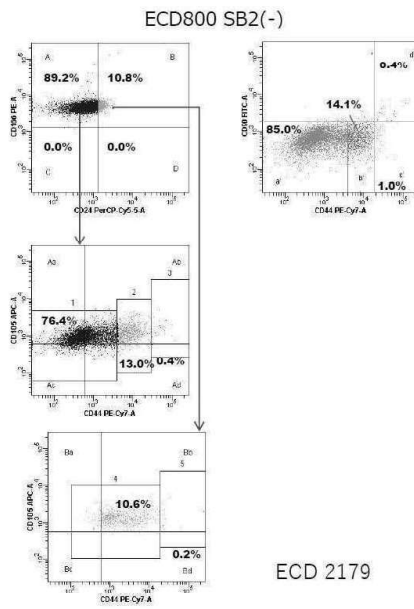
#225 standard cells

P0
SB2(-) 6wp_{x1}
↓
P1 : Day43 (170322)
SB2(-) ECD400
↓
P2 : Day78 (170606)
SB2(-) ECD400
↓
P3 : Day77 (170822)
SB2(-) ECD400
↓
P4 : D45 (171006)
SB2(-) ECD400

#184 P1 Day286 (160531)

#225 P1 Day43 (170322)

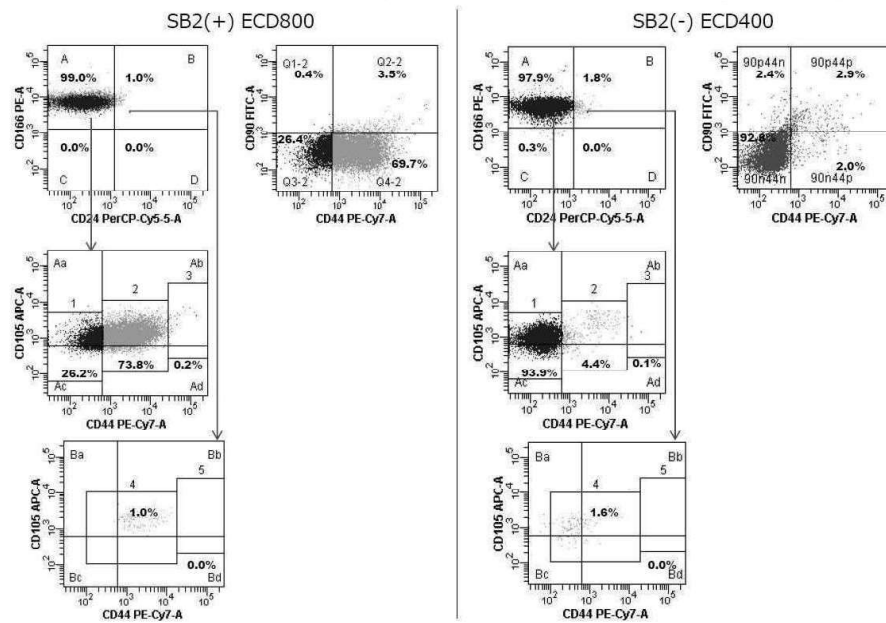
[Fig. 67]



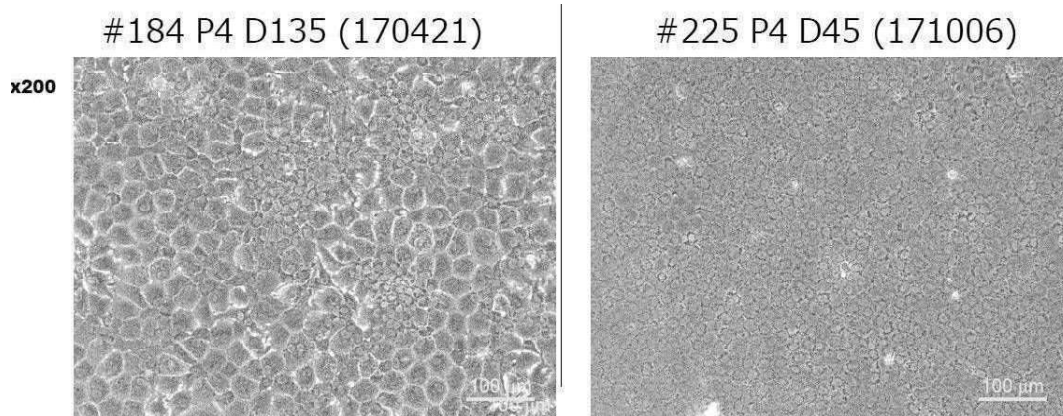
#184 P4 D135 (170421)

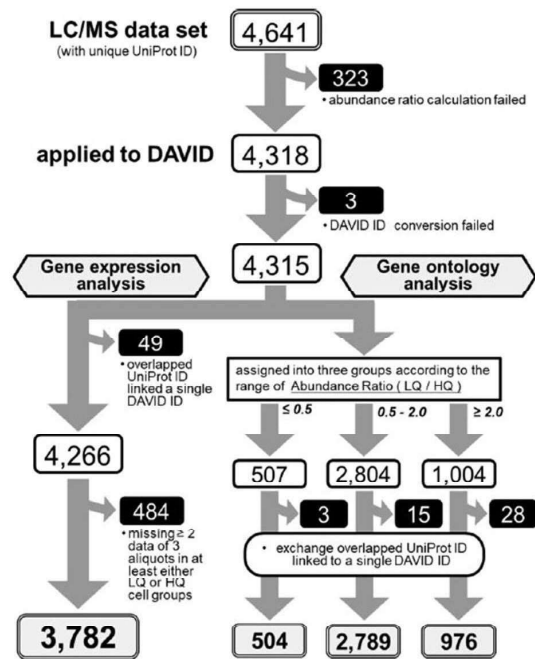
#225 P4 D45 (171006)

[Fig. 68]



[Fig. 69]

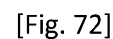




[Fig. 70]

[Fig. 71]

Accession	Description	# Unique Peptides	Score Mascot	Score Sequences HT: Sequences HT	Abundance Ratio: (225) / (184)	Abundances (Normalized): F1: Sample, 184	Abundances (Normalized): F2: Sample, 184	Abundances (Normalized): F3: Sample, 184	Abundances (Normalized): F4: Sample, 225	Abundances (Normalized): F5: Sample, 225	Abundances (Normalized): F6: Sample, 225	Abundance: F1: Sample, 184	Abundance: F2: Sample, 184	Abundance: F3: Sample, 184	Abundance: F4: Sample, 225	Abundance: F5: Sample, 225	Abundance: F6: Sample, 225
P00918	Carbonic anhydrase 2 OS=Homo sapiens GN=CA2 PE=1 SV=2	17	965	174.4	27.691	4531643	3549358	2297898	76395570	1.08E+08	1.22E+08	3021029	2724311	1576987	65576641	94710704	1.22E+08
P07451	Carbonic anhydrase 3 OS=Homo sapiens GN=CA3 PE=1 SV=3	20	2013	374.28	27.667	18194682	10257840	10681652	2.57E+08	4.87E+08	4.76E+08	12129523	7873408	7330538	2.21E+08	4.27E+08	4.76E+08



		Category	Term	Count	%	PValue	Genes
Annotation Cluster 1	Enrichment Score: 72.73354929082193	UP_KEYWORDS	Mitochondrion	154	38.79093	1.66E-90	P24752, P24753, P24754, P24755, P24756, P24757, P24758, P24759, P24760, P24761, P24762, P24763, P24764, P24765, P24766, P24767, P24768, P24769, P24770, P24771, P24772, P24773, P24774, P24775, P24776, P24777, P24778, P24779, P24780, P24781, P24782, P24783, P24784, P24785, P24786, P24787, P24788, P24789, P24790, P24791, P24792, P24793, P24794, P24795, P24796, P24797, P24798, P24799, P24800, P24801, P24802, P24803, P24804, P24805, P24806, P24807, P24808, P24809, P24810, P24811, P24812, P24813, P24814, P24815, P24816, P24817, P24818, P24819, P24820, P24821, P24822, P24823, P24824, P24825, P24826, P24827, P24828, P24829, P24830, P24831, P24832, P24833, P24834, P24835, P24836, P24837, P24838, P24839, P24840, P24841, P24842, P24843, P24844, P24845, P24846, P24847, P24848, P24849, P24850, P24851, P24852, P24853, P24854, P24855, P24856, P24857, P24858, P24859, P24860, P24861, P24862, P24863, P24864, P24865, P24866, P24867, P24868, P24869, P24870, P24871, P24872, P24873, P24874, P24875, P24876, P24877, P24878, P24879, P24880, P24881, P24882, P24883, P24884, P24885, P24886, P24887, P24888, P24889, P24890, P24891, P24892, P24893, P24894, P24895, P24896, P24897, P24898, P24899, P24900, P24901, P24902, P24903, P24904, P24905, P24906, P24907, P24908, P24909, P24910, P24911, P24912, P24913, P24914, P24915, P24916, P24917, P24918, P24919, P24920, P24921, P24922, P24923, P24924, P24925, P24926, P24927, P24928, P24929, P24930, P24931, P24932, P24933, P24934, P24935, P24936, P24937, P24938, P24939, P24940, P24941, P24942, P24943, P24944, P24945, P24946, P24947, P24948, P24949, P24950, P24951, P24952, P24953, P24954, P24955, P24956, P24957, P24958, P24959, P24960, P24961, P24962, P24963, P24964, P24965, P24966, P24967, P24968, P24969, P24970, P24971, P24972, P24973, P24974, P24975, P24976, P24977, P24978, P24979, P24980, P24981, P24982, P24983, P24984, P24985, P24986, P24987, P24988, P24989, P24990, P24991, P24992, P24993, P24994, P24995, P24996, P24997, P24998, P24999, P25000, P25001, P25002, P25003, P25004, P25005, P25006, P25007, P25008, P25009, P25010, P25011, P25012, P25013, P25014, P25015, P25016, P25017, P25018, P25019, P25020, P25021, P25022, P25023, P25024, P25025, P25026, P25027, P25028, P25029, P25030, P25031, P25032, P25033, P25034, P25035, P25036, P25037, P25038, P25039, P25040, P25041, P25042, P25043, P25044, P25045, P25046, P25047, P25048, P25049, P25050, P25051, P25052, P25053, P25054, P25055, P25056, P25057, P25058, P25059, P25060, P25061, P25062, P25063, P25064, P25065, P25066, P25067, P25068, P25069, P25070, P25071, P25072, P25073, P25074, P25075, P25076, P25077, P25078, P25079, P25080, P25081, P25082, P25083, P25084, P25085, P25086, P25087, P25088, P25089, P25090, P25091, P25092, P25093, P25094, P25095, P25096, P25097, P25098, P25099, P25100, P25101, P25102, P25103, P25104, P25105, P25106, P25107, P25108, P25109, P25110, P25111, P25112, P25113, P25114, P25115, P25116, P25117, P25118, P25119, P25120, P25121, P25122, P25123, P25124, P25125, P25126, P25127, P25128, P25129, P25130, P25131, P25132, P25133, P25134, P25135, P25136, P25137, P25138, P25139, P25140, P25141, P25142, P25143, P25144, P25145, P25146, P25147, P25148, P25149, P25150, P25151, P25152, P25153, P25154, P25155, P25156, P25157, P25158, P25159, P25160, P25161, P25162, P25163, P25164, P25165, P25166, P25167, P25168, P25169, P25170, P25171, P25172, P25173, P25174, P25175, P25176, P25177, P25178, P25179, P25180, P25181, P25182, P25183, P25184, P25185, P25186, P25187, P25188, P25189, P25190, P25191, P25192, P25193, P25194, P25195, P25196, P25197, P25198, P25199, P25200, P25201, P25202, P25203, P25204, P25205, P25206, P25207, P25208, P25209, P25210, P25211, P25212, P25213, P25214, P25215, P25216, P25217, P25218, P25219, P25220, P25221, P25222, P25223, P25224, P25225, P25226, P25227, P25228, P25229, P25230, P25231, P25232, P25233, P25234, P25235, P25236, P25237, P25238, P25239, P25240, P25241, P25242, P25243, P25244, P25245, P25246, P25247, P25248, P25249, P25250, P25251, P25252, P25253, P25254, P25255, P25256, P25257, P25258, P25259, P25260, P25261, P25262, P25263, P25264, P25265, P25266, P25267, P25268, P25269, P25270, P25271, P25272, P25273, P25274, P25275, P25276, P25277, P25278, P25279, P25280, P25281, P25282, P25283, P25284, P25285, P25286, P25287, P25288, P25289, P25290, P25291, P25292, P25293, P25294, P25295, P25296, P25297, P25298, P25299, P25300, P25301, P25302, P25303, P25304, P25305, P25306, P25307, P25308, P25309, P25310, P25311, P25312, P25313, P253

Annotation	Cluster	Enrichment Score	GO Term	Count	GO	P-Value	Gene	List Total	Pos Hits	Pos Total	Log Odds Ratio	Benjamini	FDR	
Annotation Cluster 1	Enrichment Score: 9.8920115060488	KEGG_PATHWAY	hsa01300_Carbon metabolism	34	6.464534	8.02E-14	P13388	202	113	6910	7.935599	1.75E-11	8.94E-11	
			GOTERM_BP_DIRECT	GO:0006999_ferri-carboxylic acid cycle	11	2.707781	1.68E-07	P04026	371	29	16792	17.16814	5.61E-07	5.61E-07
			KEGG_PATHWAY	hsa00360_Biosynthesis of antibiotics	28	5.849118	1.67E-09	P24752_Q	202	212	6910	4.193531	3.74E-07	7.48E-08
			KEGG_PATHWAY	hsa00200_Citrate cycle (TCA cycle)	11	2.777781	6.28E-09	P13388	202	30	16792	11.3429	1.14E-08	2.34E-07
			GOTERM_MP_DIRECT	GO:0036074_ferri-carboxylic acid cycle	11	2.707781	1.68E-07	P04026	371	29	16792	17.16814	5.61E-07	5.61E-07
Annotation Cluster 2	Enrichment Score: 8.187965982291915	KEGG_PATHWAY	GO:0033358_Acyl-CoA dehydrogenase activity	9	0.215113	6.11E-08	P49748_P	369	18	15859	12.1622	1.05E-04	1.05E-04	
			GOTERM_MP_DIRECT	GO:0003995_Acyl-CoA dehydrogenase activity	7	1.763234	6.86E-07	P49748_P	369	16	16881	20.01474	4.25E-04	4.49E-05
			GOTERM_MP_DIRECT	GO:0006055_electron carrier activity	12	0.020267	4.06E-06	P49748_P	369	90	16881	6.099729	0.2309	0.40E-04
			INTERPRO	IPRO13796_Acyl-CoA dehydrogenase/oxidase, N-terminal	6	5.511339	4.31E-06	P49748_P	369	13	18559	22.07659	0.00621	8.00E-04
			INTERPRO	IPRO06051_Acyl-CoA dehydrogenase, central domain	6	5.511339	9.71E-06	P49748_P	369	13	18559	19.13299	0.00621	8.00E-04
			INTERPRO	IPRO06075_Acyl-CoA dehydrogenase/oxidase C-terminal	6	5.511339	9.71E-06	P49748_P	369	13	18559	19.13299	0.00621	8.00E-04
			INTERPRO	IPRO09100_Acyl-CoA dehydrogenase/oxidase	6	5.511339	9.71E-06	P49748_P	369	13	18559	19.13299	0.00621	8.00E-04
			GOTERM_MP_DIRECT	GO:0052890_oxidoreductase activity, acting on the CH-group of	6	5.511339	1.20E-05	P49748_P	369	15	16881	18.29919	0.00741	2.98E-04
			GOTERM_BP_DIRECT	GO:0050508_lipid homeostasis	8	0.215113	2.00E-05	P49748_P	369	39	19780	6.294401	0.01355	0.0484E-04
			GOTERM_MP_DIRECT	GO:0006062_fatty-acyl-CoA binding	7	1.763234	3.95E-05	P49748_P	369	10	16881	10.47451	0.0314	0.0024E-04
Annotation Cluster 3	Enrichment Score: 5.03861345705007	KEGG_PATHWAY	GO:0048227_oxidoreductase activity, acting on the CH-group of	14	0.004844	3.34E-04	P49748_P	369	18	15859	12.70773	0.02567	0.788E-04	
			INTERPRO	IPRO06085_Acyl-CoA dehydrogenase, conserved site	4	1.007957	8.85E-04	P49748_P	369	8	18559	21.2588	0.43969	0.00003
			KEGG_PATHWAY	hsa00580_Tryptophan metabolism	10	2.181892	1.65E-06	P24752_Q	202	40	6910	8.51198	3.48E-04	3.37E-05
			KEGG_PATHWAY	hsa00301_Lysine degradation	10	2.181892	1.55E-05	P24752_Q	202	52	6910	6.578446	0.00349	3.18E-04
			KEGG_PATHWAY	hsa00075_Fatty acid degradation	6	2.267003	3.21E-05	P49748_P	369	20	6910	6.997075	0.07168	5.99E-04
Annotation Cluster 4	Enrichment Score: 4.931021570329907	KEGG_PATHWAY	GO:0048227_oxidoreductase activity, acting on the CH-group of	14	0.004844	3.34E-04	P49748_P	369	18	15859	12.70773	0.02567	0.788E-04	
			KEGG_PATHWAY	hsa00075_Fatty acid degradation	6	2.267003	3.21E-05	P49748_P	369	20	6910	6.997075	0.07168	5.99E-04
			KEGG_PATHWAY	hsa01212_Fatty acid metabolism	6	2.267003	6.19E-05	P49748_P	369	22	6910	6.431385	0.01785	0.00106

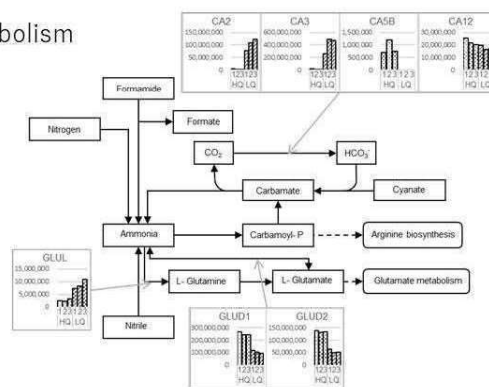
[illegible]

[Fig. 76]

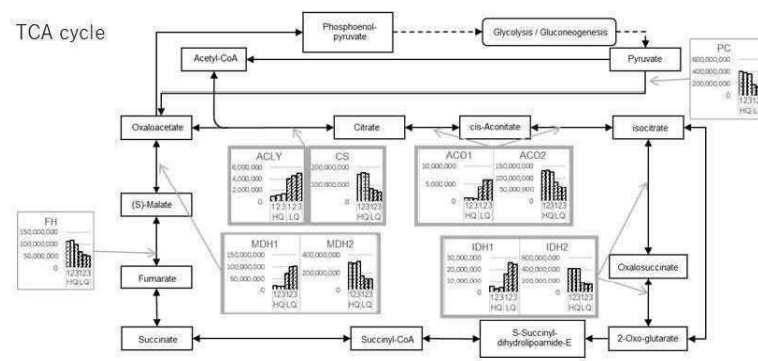
		Nitrogen metabolism Bile secretion Pancreatic secretion Nitrogen metabolism Arginine biosynthesis Alanine, aspartate and glutamate metabolism D-Glutamine and D-glutamate metabolism Metabolic pathways Carbon metabolism Carbon metabolism Oxidative phosphorylation Glycolysis / Gluconeogenesis Valine, leucine and isoleucine degradation (BCAA) Pyruvate metabolism Citrate cycle (TCA cycle) Fatty acid degradation Fatty acid metabolism Cysteine and methionine metabolism beta-Alanine metabolism Alanine, aspartate and glutamate metabolism PPAR signaling pathway Nicotinate and nicotinamide metabolism Glutathione metabolism Fatty acid biosynthesis PPAR signaling pathway Adipocytokine signaling pathway Insulin resistance AMPK signaling pathway
3	Pathway emerging from the analysis of those with a ratio greater than 27	Nitrogen metabolism Carbon metabolism Citrate cycle (TCA cycle) Fatty acid degradation Fatty acid metabolism D-Glutamine and D-glutamate metabolism Arginine biosynthesis Alanine, aspartate and glutamate metabolism ABC transporters Oxidative phosphorylation
5	Pathway emerging from comparison of mitochondria after DAVID analysis	Nitrogen metabolism Carbon metabolism Citrate cycle (TCA cycle) Fatty acid degradation Fatty acid metabolism D-Glutamine and D-glutamate metabolism Arginine biosynthesis Alanine, aspartate and glutamate metabolism ABC transporters Oxidative phosphorylation

[Fig. 77]

Nitrogen metabolism

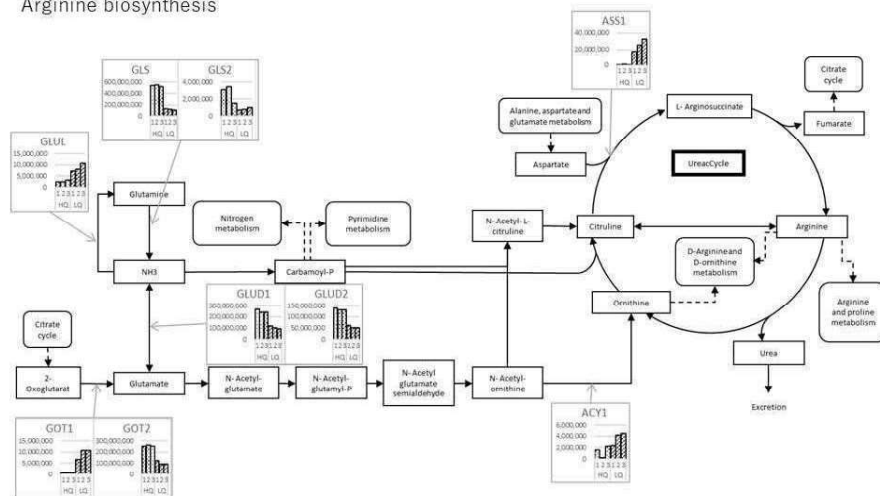


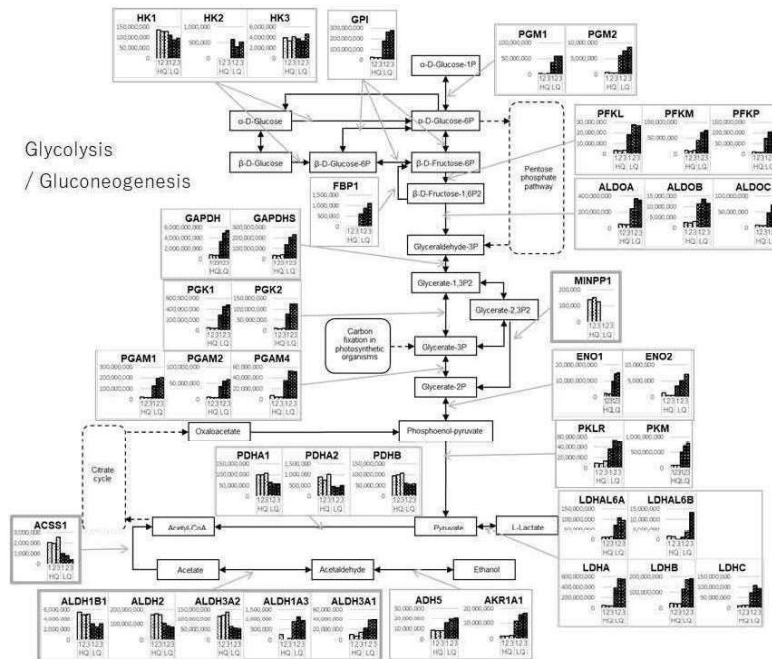
[Fig. 78]



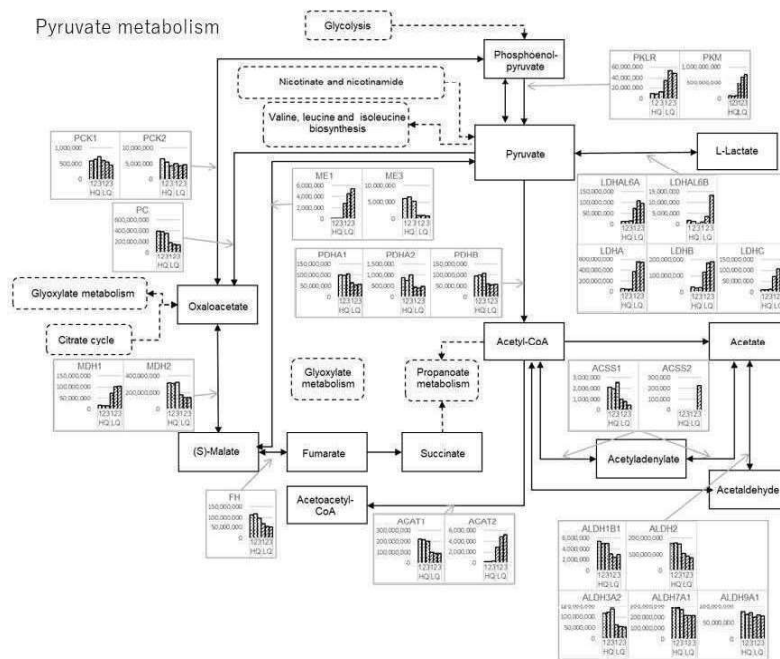
[Fig. 79]

Arginine biosynthesis



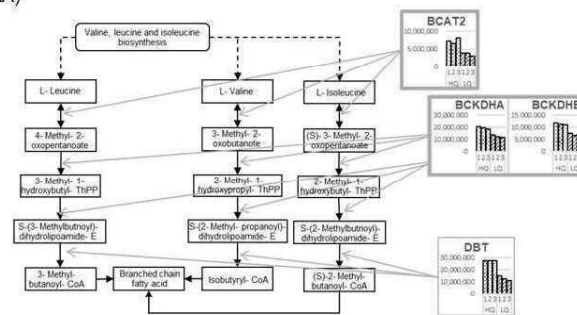


[Fig. 80]



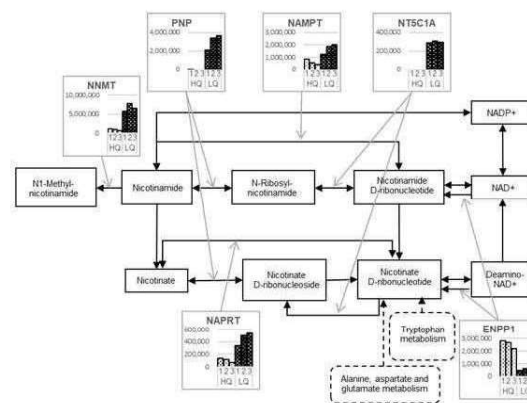
[Fig. 81]

Valine, leucine and isoleucine degradation (BCAA)



[Fig. 83]

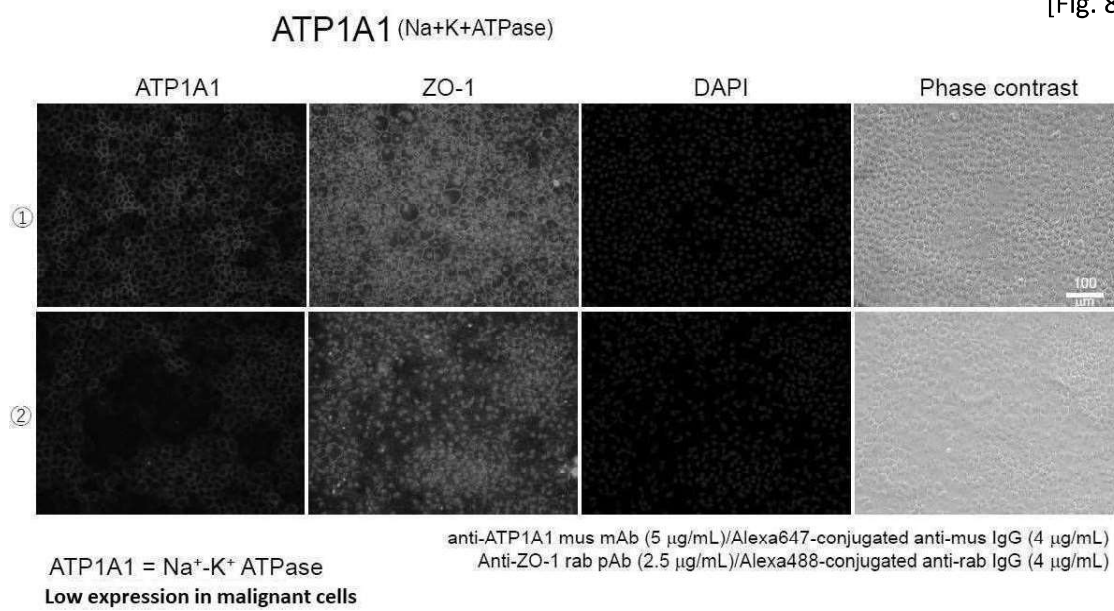
Nicotinate and nicotinamide metabolism

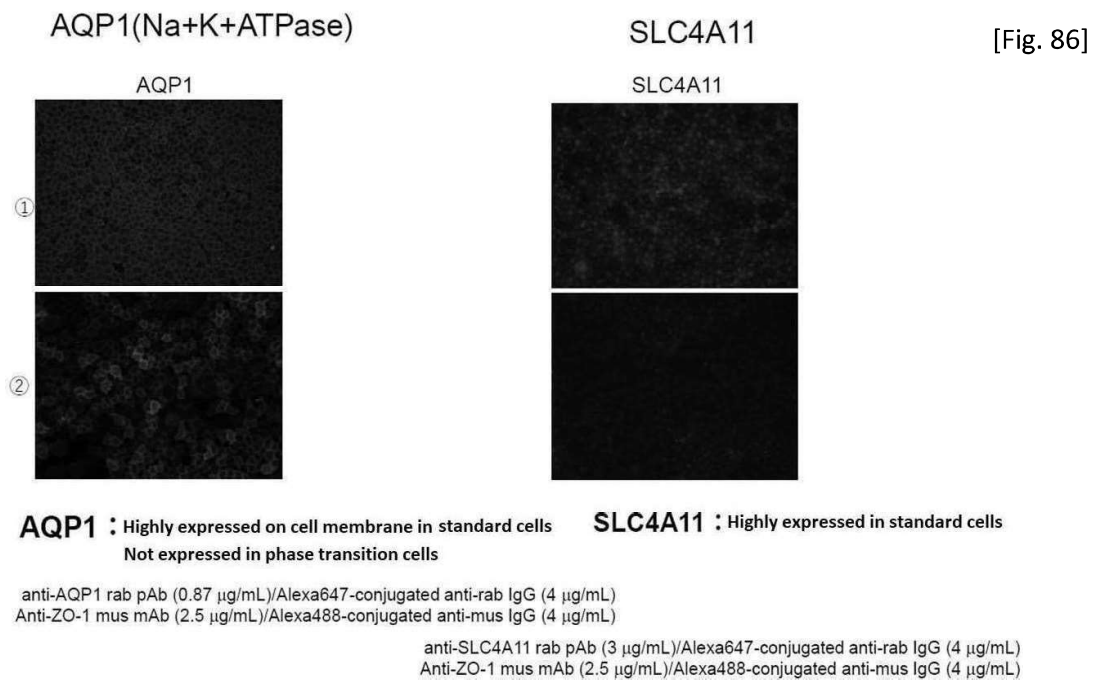


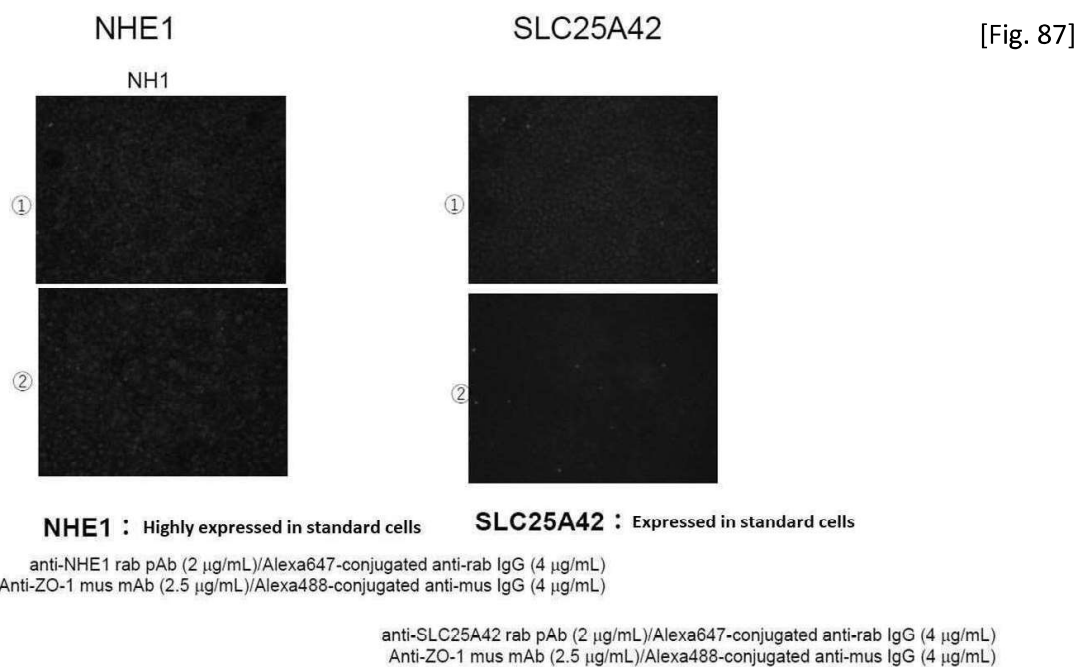
[Fig. 84]

Antigen	Manufacturer	Product Name • Product Number
human ATP1A1 = Na ⁺ /K ⁺ ATPase	millipore	Anti-Na ⁺ /K ⁺ ATPase α -1 Antibody, clone C464.6 05-369
human ATP2B3	abcam	Anti-Calcium Pump PMCA3 ATPase antibody (ab223787)
human AQP1	abcam	Anti-Aquaporin 1 antibody [EPR11588(B)] (ab168387)
human AE1	abcam	Anti-Band 3/AE 1 antibody [EPR1426] (ab108414)
human AE2	invitrogen	SLC4A2 Polyclonal Antibody (Catalog # PA5-82675)
human NBCe1	abcam	Anti-SLC4A4/NBC antibody (ab56215)
human SLC4A11	(sigma)Atlas Antibodies	Anti-SLC4A11 Antibody (HPA018120)
human NHE1	abcam	Anti-Sodium/Hydrogen Exchanger 1/NHE-1 antibody (ab67314)
human MCT1	NOVUS(R&D)	MCT1/SLC16A1 Antibody (NBP1-59656)
human MCT8	(sigma)Atlas Antibodies	Anti-SLC16A2 Antibody (HPA003353)
human MCT4	Abcam	Anti-SLC16A3/MCT 4 antibody (ab234728)
human SLC25A42	invitrogen	SLC25A42 Polyclonal Antibody (Cat #PA5-61975)
human CA2	abcam	Anti-Carbonic anhydrase 2/CA2 antibody (ab191343)
human CA3	abcam	Anti-Carbonic Anhydrase 3/CA3 antibody (ab175309)
human CA5B	abcam	Anti-Carbonic Anhydrase 5B/CA5B antibody (ab196800)
human CA12	abcam	Anti-Carbonic Anhydrase 12/CA12 antibody (ab244309)
human ZO-1	invitrogen	ZO-1 Monoclonal Antibody (ZO1-1A12) (#33-9100)
	invitrogen	ZO-1 Polyclonal Antibody (# 61-7300)
DAPI	Dojindo	D523 Cellstain® DAPI solution (wako code:340-07971)
2nd Abs; anti-rab IgG dye-conjugated	invitrogen	Donkey anti-Rabbit IgG (H+L) Highly Cross-Adsorbed Secondary Antibody, Alexa Fluor Plus 488 (# A32790)
	invitrogen	Donkey anti-Rabbit IgG (H+L) Highly Cross-Adsorbed Secondary Antibody, Alexa Fluor Plus 647 (# A32795)
2nd Abs; anti-mus IgG dye-conjugated	invitrogen	Donkey anti-Mouse IgG (H+L) Highly Cross-Adsorbed Secondary Antibody, Alexa Fluor Plus 488 (# A32766)
	invitrogen	Donkey anti-Mouse IgG (H+L) Highly Cross-Adsorbed Secondary Antibody, Alexa Fluor Plus 647 (# A32787)

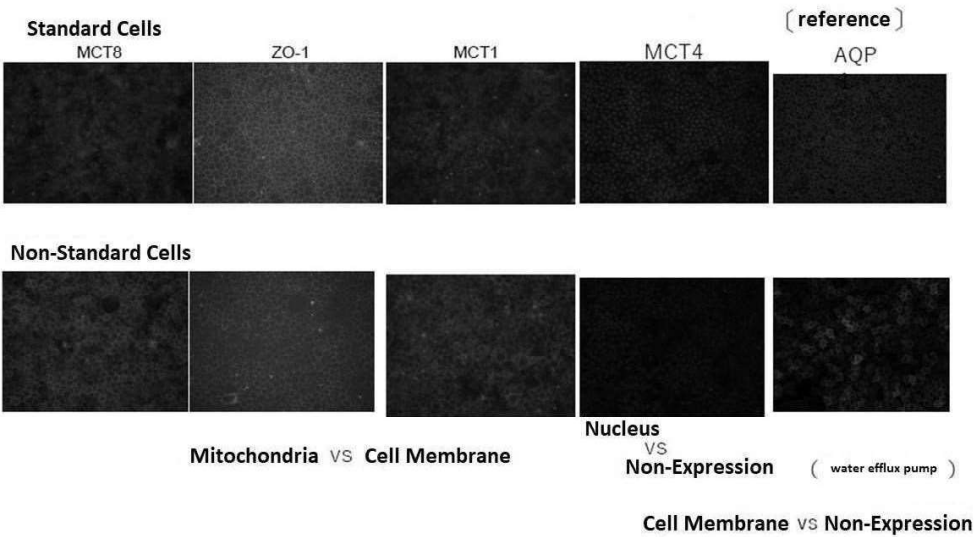
[Fig. 85]





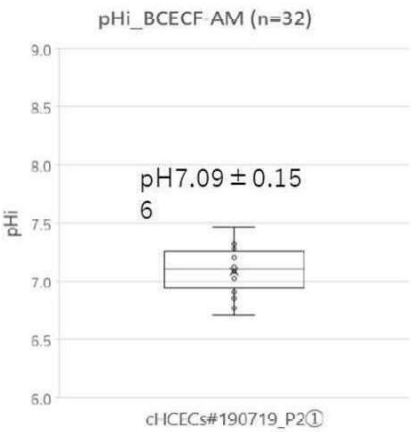
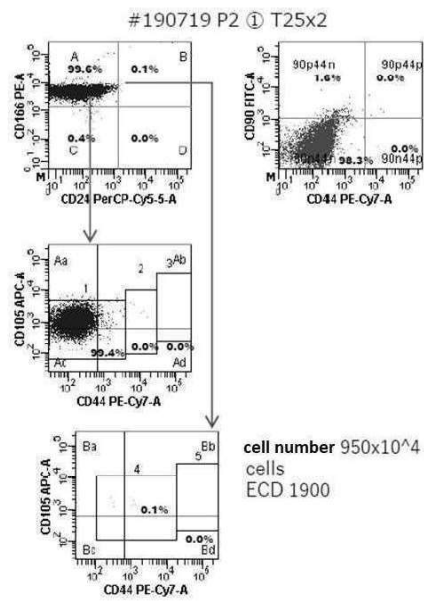


Organelle-Selective Localization of Monocarboxylic Acid Transporter [Fig. 88]



#190719P2 ① Day42 (191108)

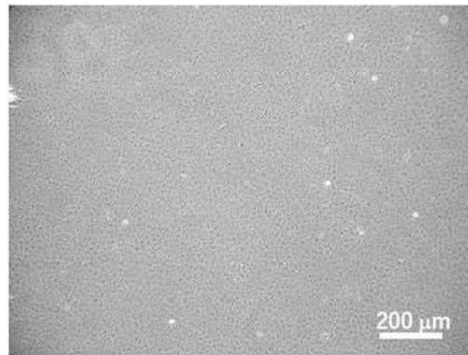
[Fig. 89]



[Fig. 90]

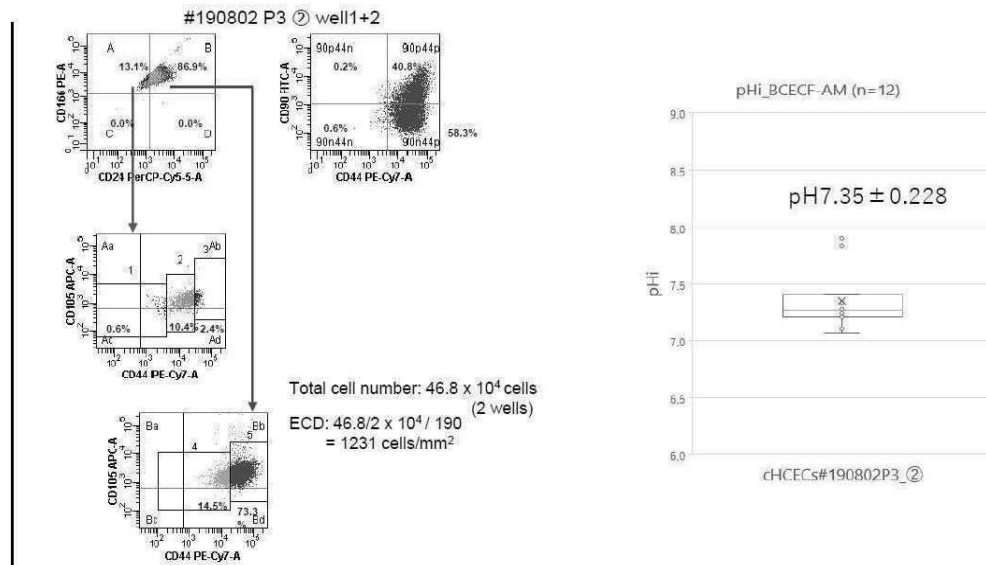
#190719P2 (Day40)_① (Nancy A+Y)well#2

x100



#190802P3 Day40 (200115)

[Fig. 91]

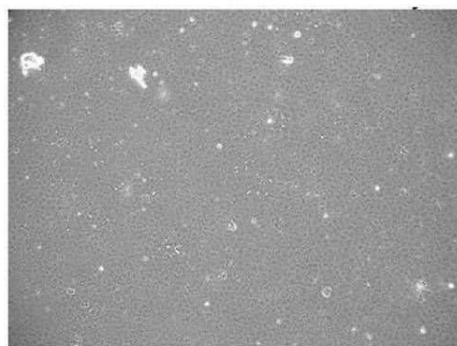


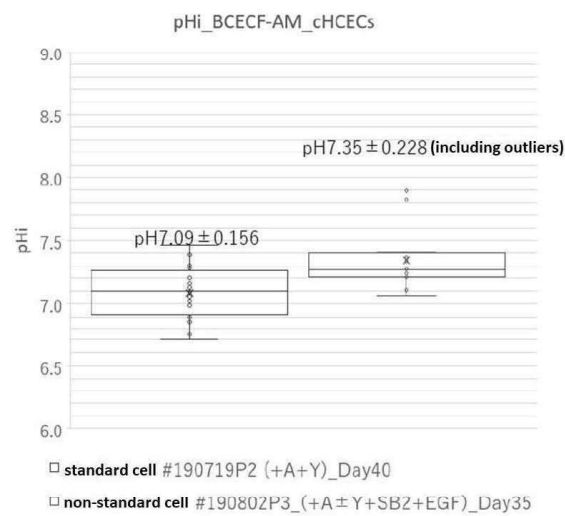
92/114

[Fig. 92]

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

① well#1+2



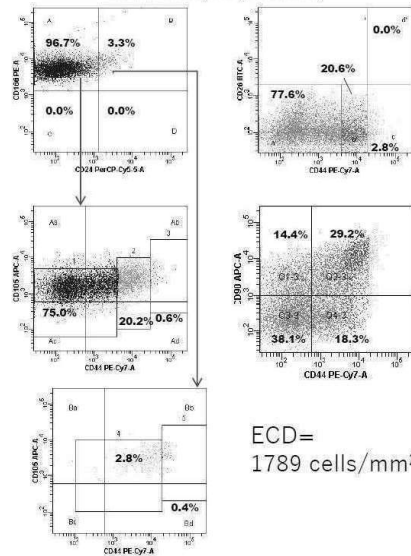


[Fig. 93]

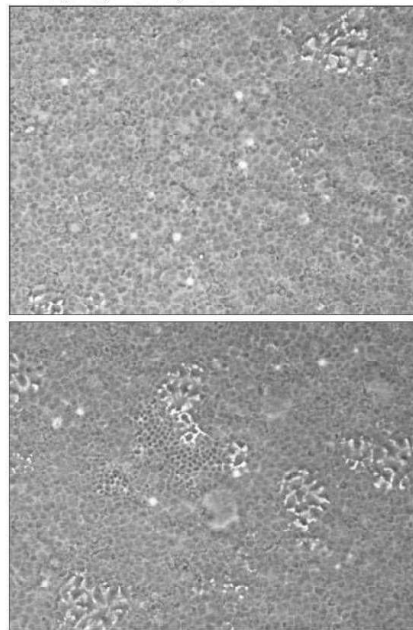
【
【 Statistical Processing_at Median Comparison 】
If outliers are included,
Mann-Whitney U-test: p = 0.003966

The cells below were passaged
to P3 (T-25) → P4 (24wp)
on Day39 and used.

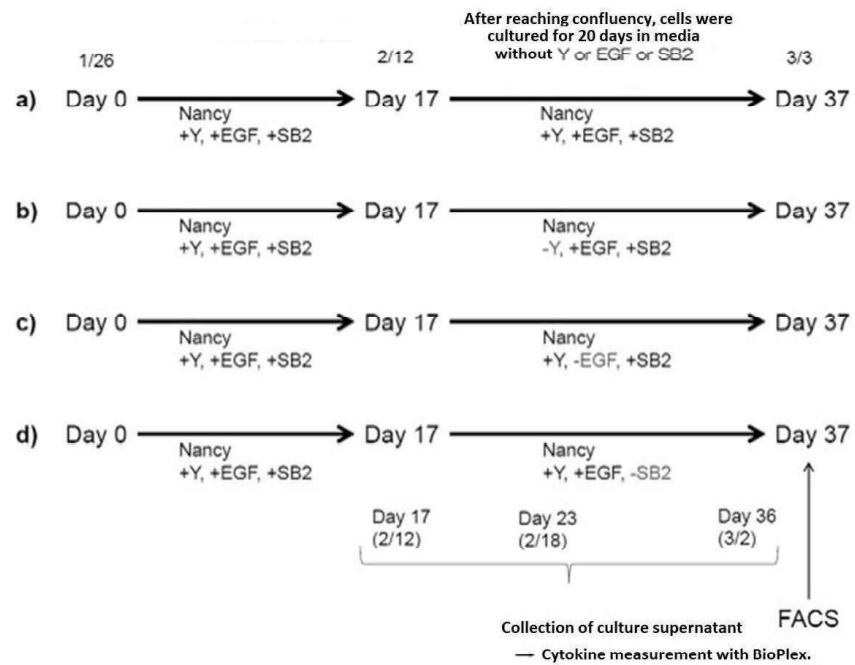
C37 P3 Day39 (160126)



Day38 (160125) CPC photographing x200



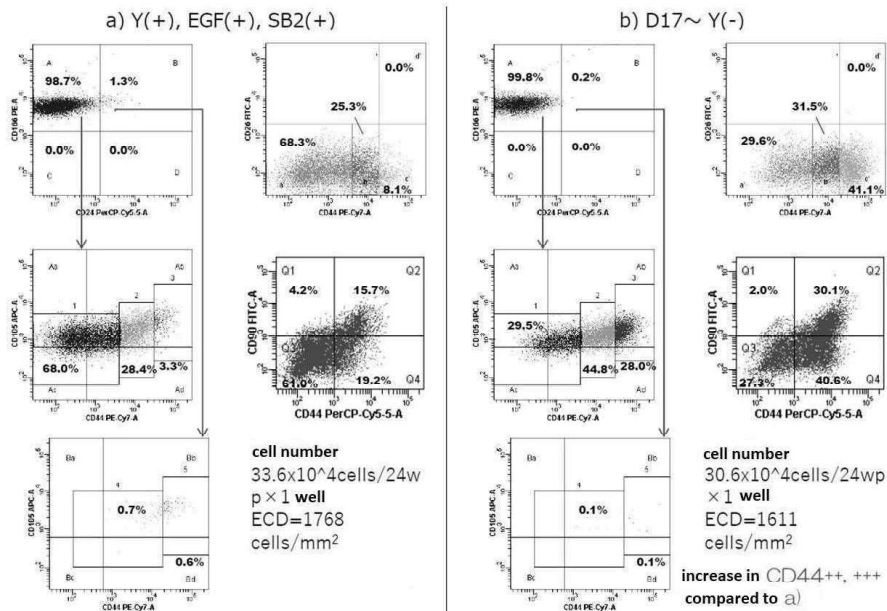
[Fig. 94]



[Fig. 95]

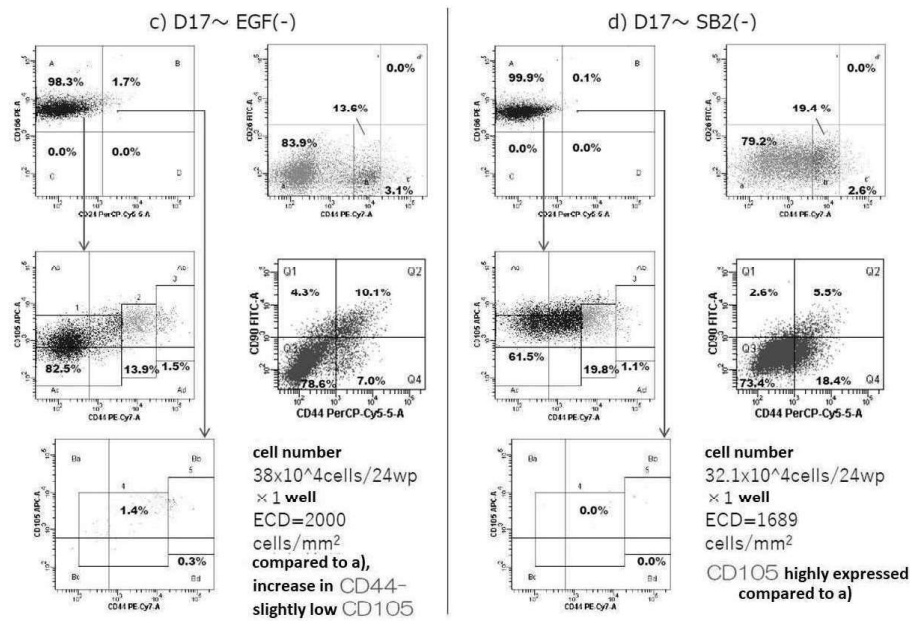
Day37 (20160303)

[Fig. 96]

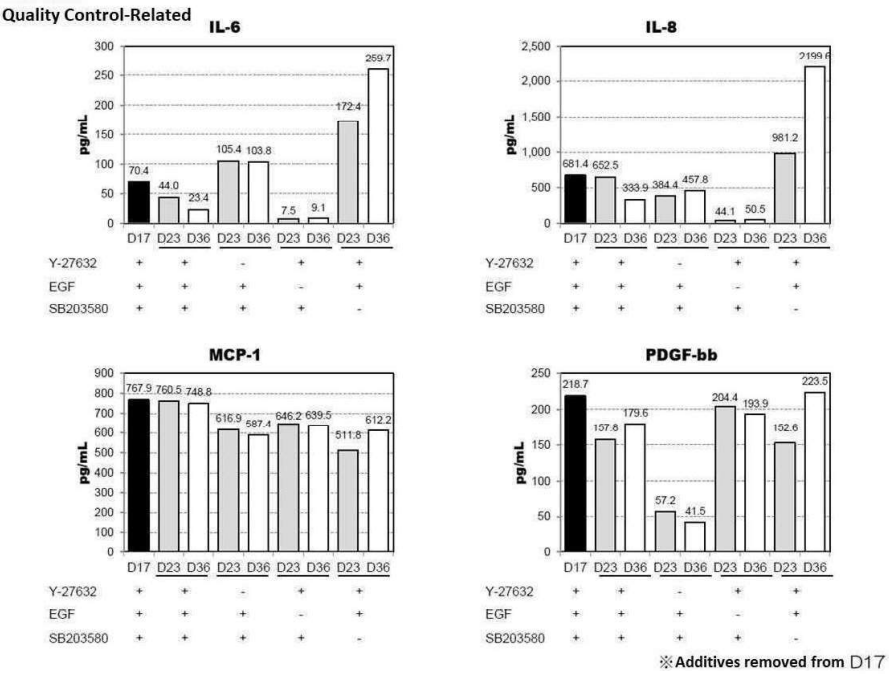


Day 37 (20160303)

[Fig. 97]

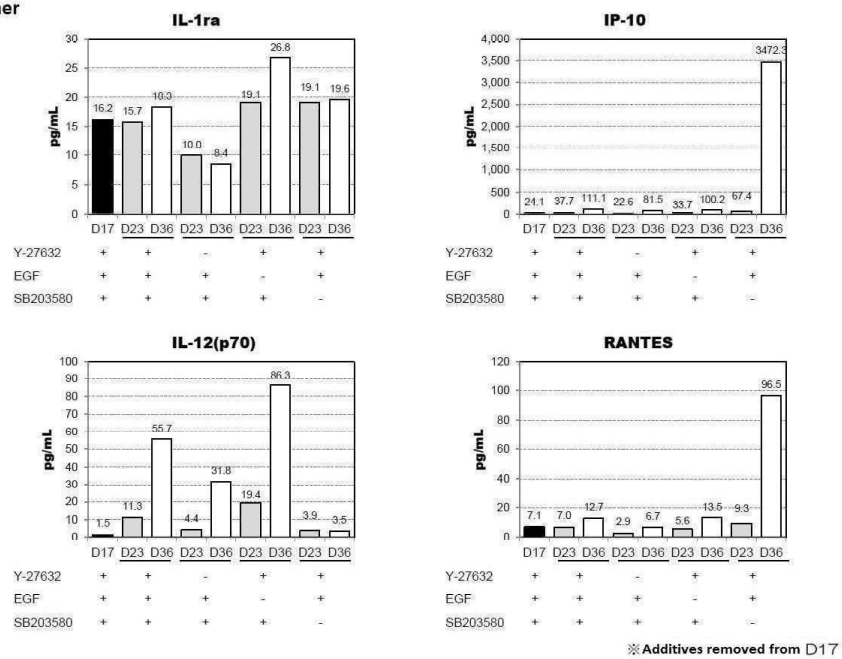


Quality Control-Related

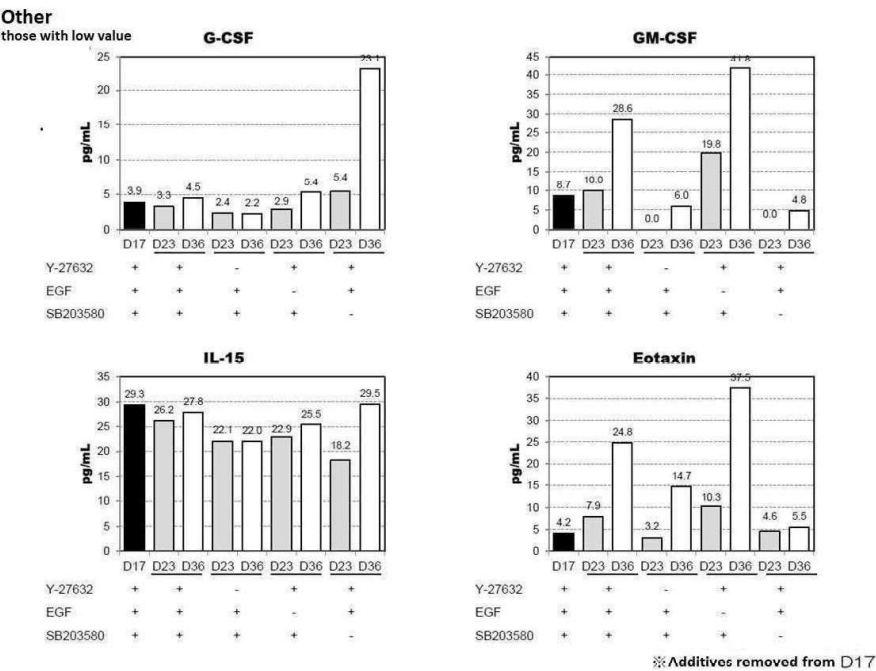


[Fig. 98]

Other



[Fig. 99]



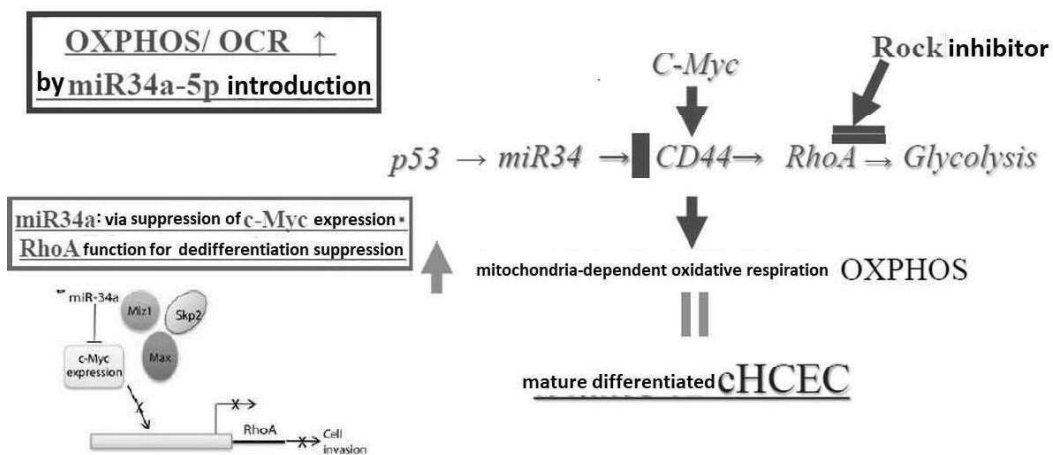
[Fig. 100]

Involvement of MiR34a and CD44 expression and

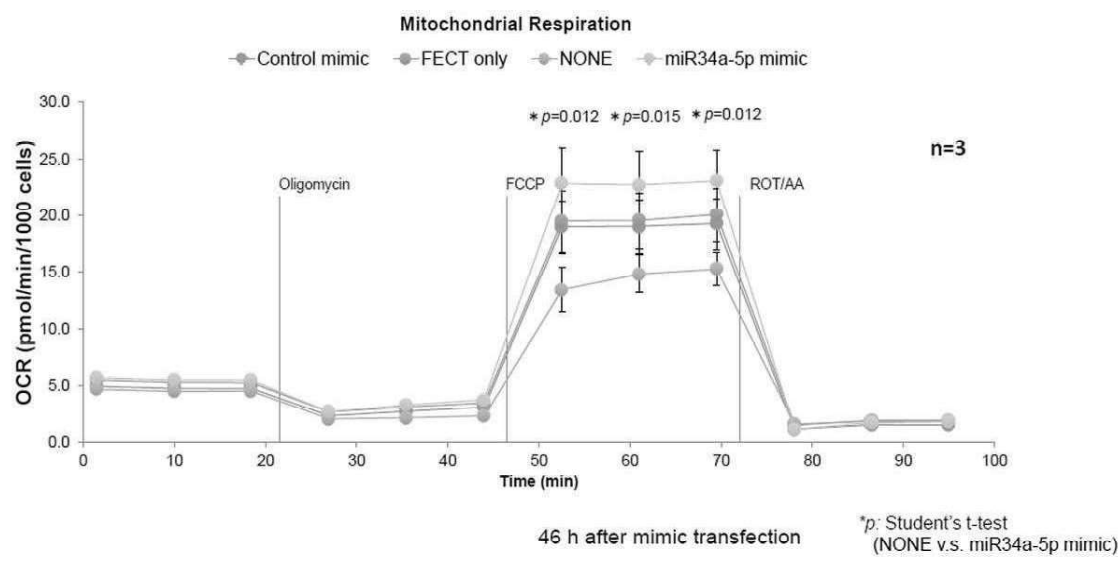
[Fig. 101]

mitochondrial energy metabolism control pathway

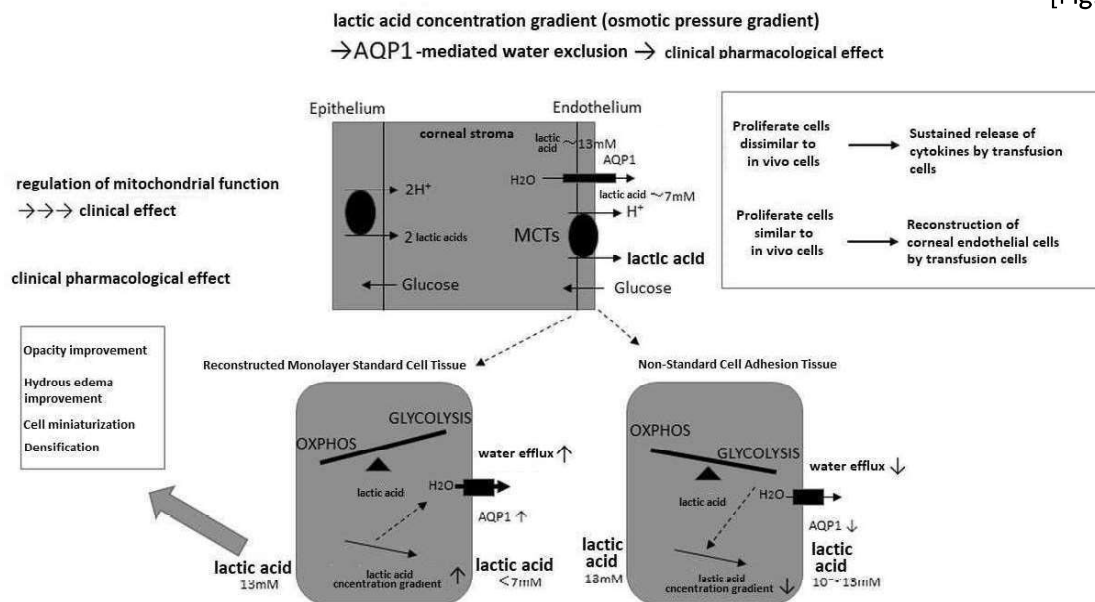
of



[Fig. 102]

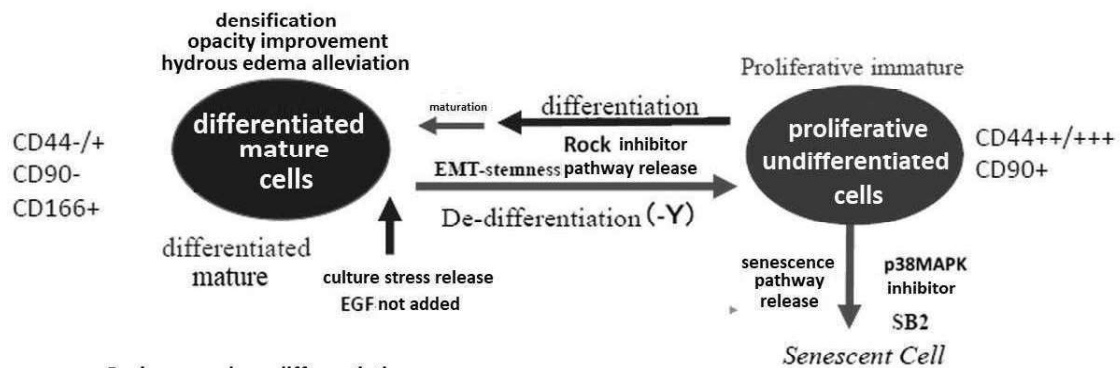


[Fig. 103]

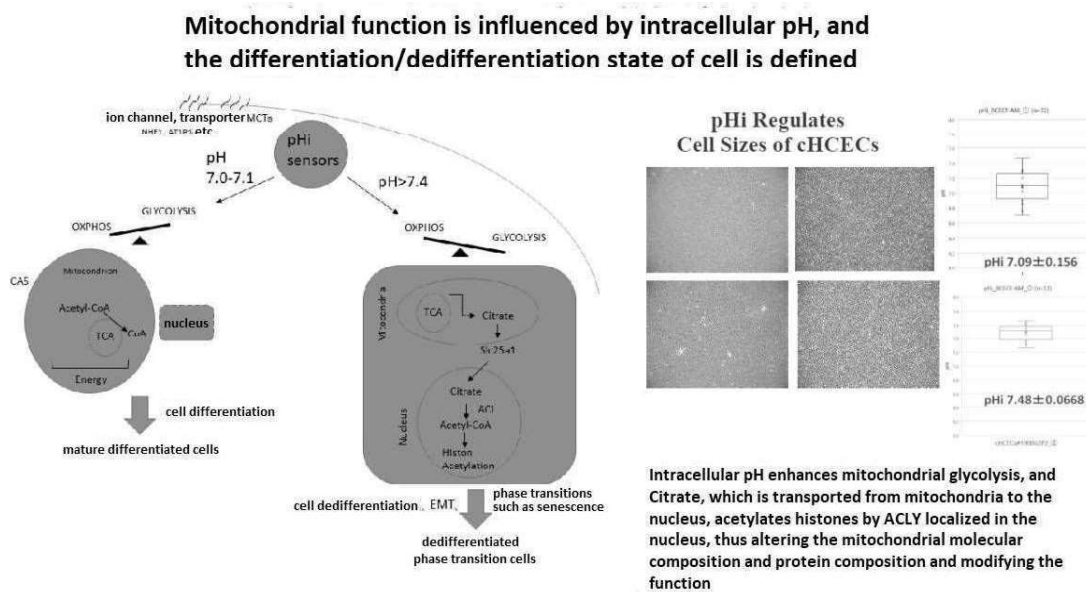


[Fig. 104]

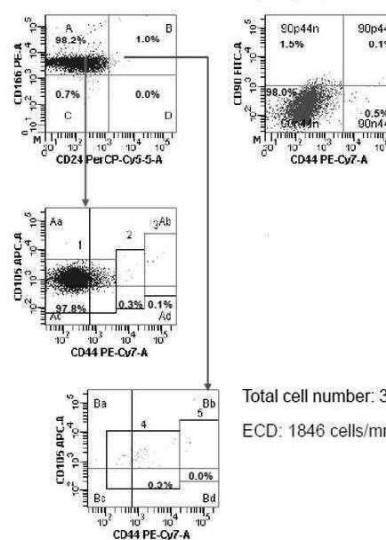
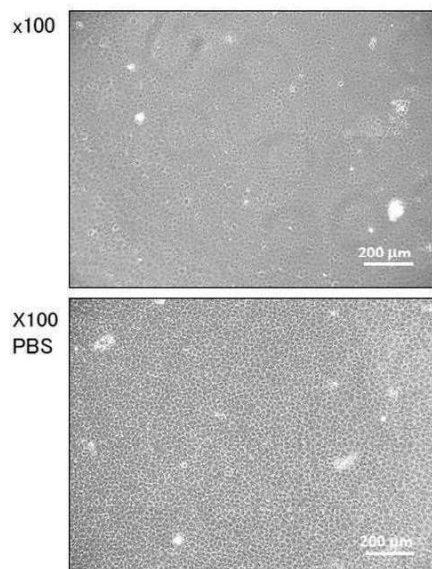
Induction of differentiated or matured, human functional corneal endothelial cells through dedifferentiation pathway from somatic (stem) cells



[Fig. 105]



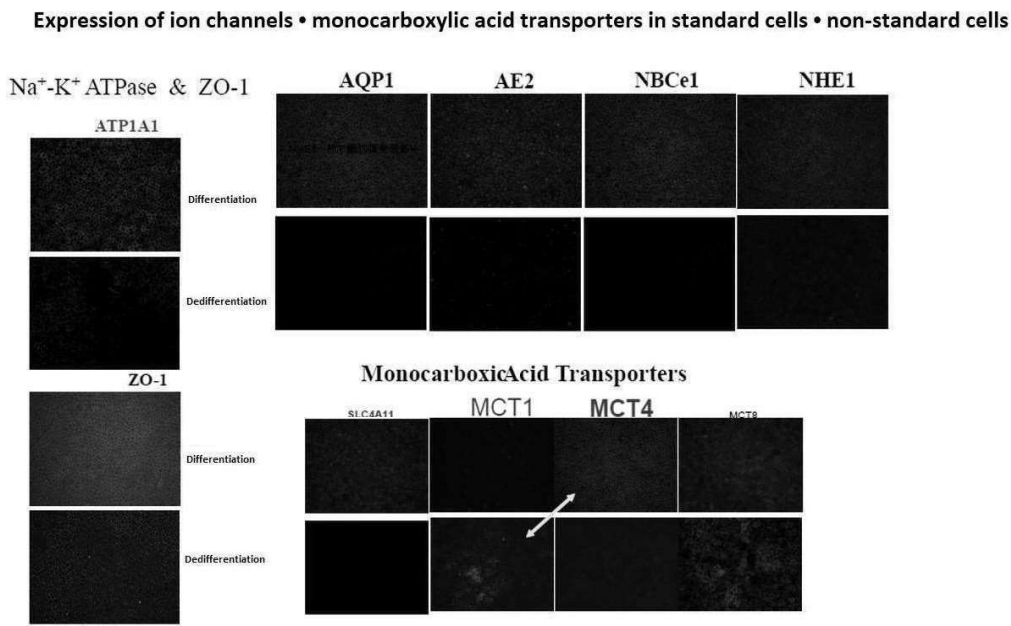
【Cultured for Standard Cell】
#CR04 P3 Day41 (+Y)



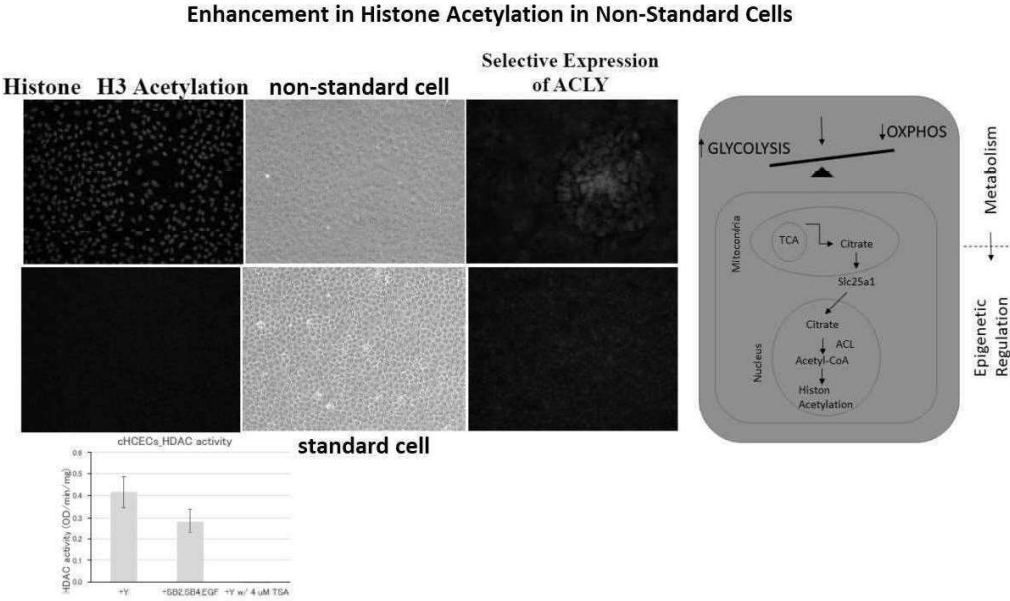
Total cell number: 34.7×10^4 cells

ECD: 1846 cells/mm²

[Fig. 107]

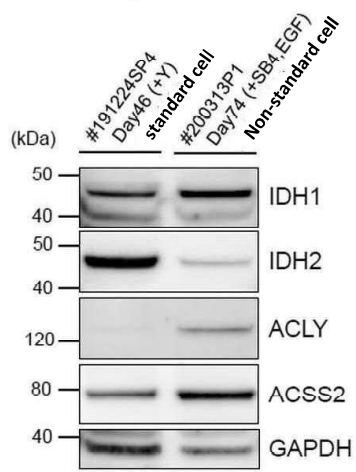


[Fig. 108]



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

[Fig. 109]

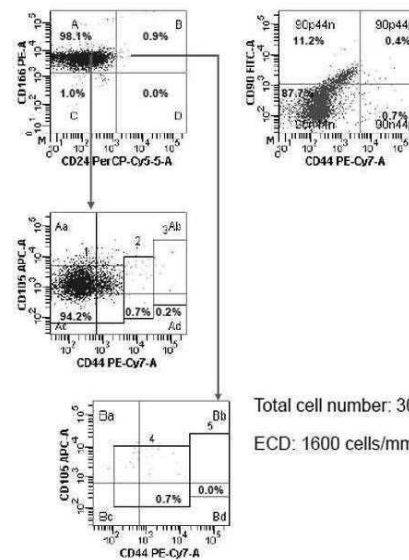
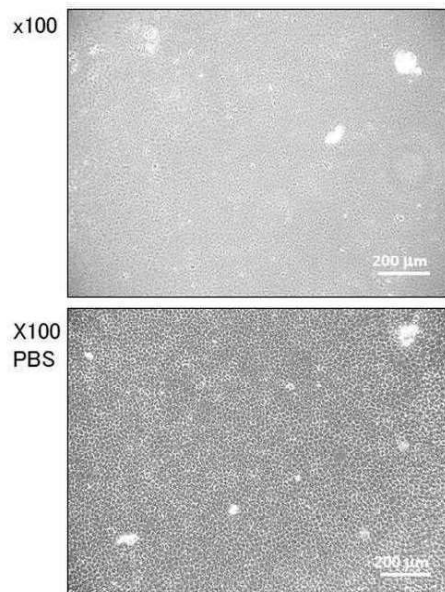


anti-IDH1 rab pAb (1:180 dilution, 5 μ g/mL)
anti-IDH2 rab pAb (1:120 dilution, 5 μ g/mL)
anti-ATP citrate lyase rab pAb (1:2000 dilution, 0.119 μ g/mL)
anti-ACSS2 rab pAb (1:200 dilution, 5 μ g/mL)
anti-GAPDH rab pAb (1:2000 dilution, 15 μ g/mL)

cHCECs_#191224SP4 (Day46)_ ① (Nancy+Y)

[Cultured for Standard Cell]
#191224S P4 Day46 (+Y)

[Fig. 110]



Total cell number: 30.4×10^4 cells
 ECD: 1600 cells/mm²

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

cHCECs_#200313 (Day74)_② (Nancy+SB4+EGF) [Cultured for Non-Standard Cell] #200313 P1 Day74 (+SB4,EGF) [Fig. 111]

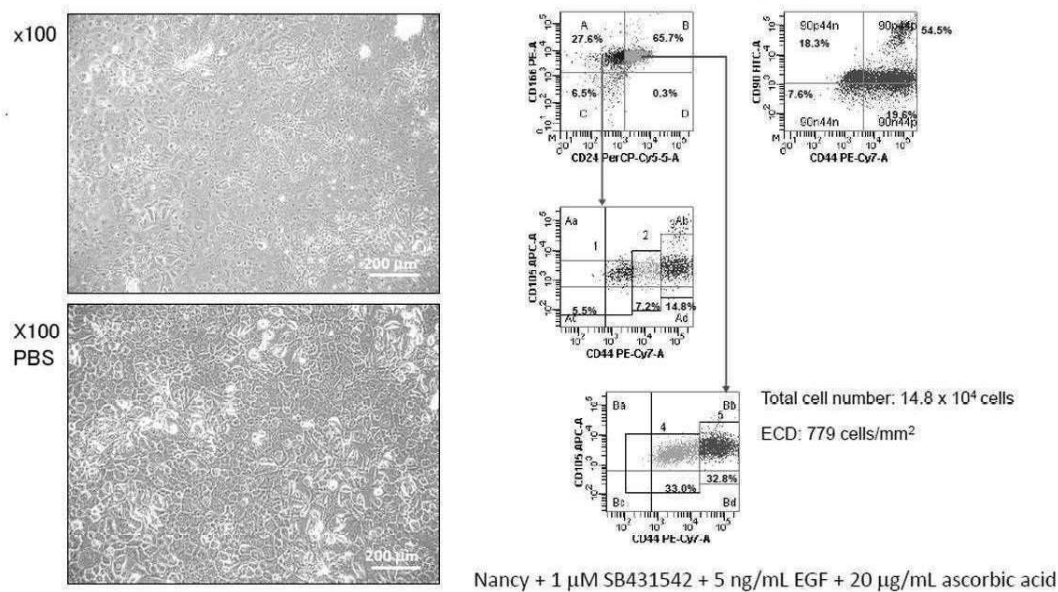
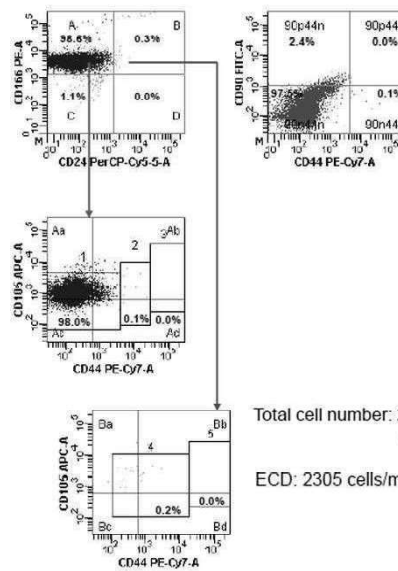


Figure 1 consists of two scanning electron micrographs (SEM) of a polyimide film surface. Image (a) shows the surface after 100x magnification, displaying a relatively smooth texture with some small, bright, irregular features. Image (b) shows the surface after 100x magnification in PBS, revealing a much more granular and textured surface. Both images include a scale bar indicating 200 μm.

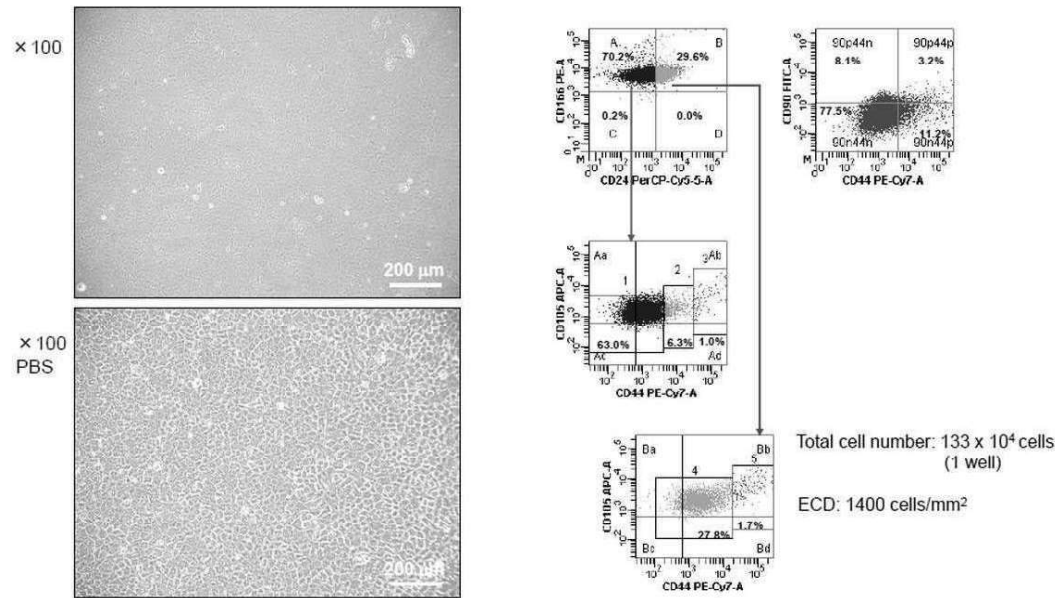


Total cell number: 219×10^4 cells
(1 well)

ECD: 2305 cells/mm²

#191224S P4_Day42_② Nancy+SB4,EGF

[Fig. 113]



HAT/HDAC activity measurement results

[Fig. 114]

