表１０　各処理時点ですべての処理に対して共通して変動した遺伝子のリスト

	Common Name	GeneBank ID	Description
4 hr	-		
24 hr	**Down-Regulate Gene (6 genes)**		
	BTF2, TFIIH, BTF2P44, T-BTF2P44	AF078847	General transcription factor IIH, polypeptide 2 (44kD subunit)
	MRCKB, KIAA1124	NM_006035	CDC42-binding protein kinase beta (DMPK-like)
	KYNU	D55639	Kynureninase (L-kynurenine hydrolase)
	BTN3A3	NM_006994	Butyrophilin, subfamily 3, member A3
	S100P	NM_005980	S100 calcium-binding protein P
	KIAA0878	N21138	yx52h03.s1 Soares melanocyte 2NbHM
	Up-Regulate Gene (3 genes)		
	NRP	BC002387	Nucleosome assembly protein 1-like 1
	C1, C-1, PFD4	NM_002623	Prefoldin 4
	ACADSB	NM_001609	Acyl-Coenzyme A dehydrogenase, short/branched chain
48 hr	**Down-Regulate Gene (9 genes)**		
	HLA-F	BE138825	xw96a07.x1 NCI_CGAP_Pan1
	ANGPTL4	NM_016109	Angiopoietin-like 4
	FLJ20674	NM_019086	Hypothetical protein FLJ20674
	IGFALS	AW338791	he66a11.x1 NCI_CGAP_Pan1 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN
	HOMG2, ATP1G1	NM_021603	FXYD domain-containing ion transport regulator 2
	CDHN, NCAD	M34064	Cadherin 2, type 1, N-cadherin (neuronal)
	HRY	BE973687	601680868F1 NIH_MGC_83
	TRAMP	BC000687	Translocating chain-associating membrane protein
	PTPRF	AI762627	wl55g01.x1 NCI_CGAP_Co16
	Up-Regulate Gene (54 genes)		
	DKFZP566E104	AL110238	DKFZP566E104 protein
	MAN1A1	BG287153	602381868F1 NIH_MGC_93
	DONSON	AF232674	Downstream neighbor of SON
	MGC1223	NM_030969	Hypothetical protein MGC1223
	DC37, RPMS15, MPR-S15, FLJ11564	NM_031280	Mitochondrial ribosomal protein S15
	MGC4276	NM_030940	Hypothetical protein MGC4276 similar to CG8198
	FLJ11068	NM_018314	Hypothetical protein FLJ11068
	FLJ11269	NM_018372	Hypothetical protein FLJ11269
	FLJ10996	NM_019044	Hypothetical protein
	HSPC125	NM_014165	HSPC125 protein
	133K02	NM_018691	Chromosome 5 open reading frame 3
	HPT, MRS2	NM_020662	MRS2 (S. cerevisiae)-like, magnesium homeostasis factor
	PELI1	NM_020651	Pellino (Drosophila) homolog 1
	TMPT27	NM_018475	TPA regulated locus
	BM-002	NM_016617	Hypothetical protein
	AF1P, AF-1P, MLLT5	NM_001981	Epidermal growth factor receptor pathway substrate 15
	ALEX3	NM_016607	ALEX3 protein
	EEF1A1	AL035687	Eukaryotic translation elongation factor 1 alpha 1
	TXN delta 3	AF065241	SEE ALSO
	ATP2B1	L14561	PMCA1; alternatively spliced; plasma membrane calcium ATPase isoform 1 (ATP2B1) gene
	TNRC9	U80736	Trinucleotide repeat containing 9
	PAC 106H8	AL035295	SEE ALSO
	TPT1	AI888178	wm40b09.x1 NCI_CGAP_Ut4 TRANSLATIONALLY CONTROLLED TUMOR PROTEIN (HUMAN)
	DKFZP586C1620	AA524525	ng44h03.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE937685 3', mRNA sequence.
	RIKEN cDNA 1700029F09 gene	BE748563	601571521T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE3838541 3', mRNA sequence.
	DKFZP564F1123	AI346504	qp51b12.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE1926527 3', mRNA sequence.
	PRO2751	BF791738	602251923F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE4344389 5', mRNA sequence.
	FLJ21927 fis, HEP04178	AK025580	SEE ALSO
	HHD, BCPM, PMR1, ATP2C1A, KIAA1347	AB037768	ATPase, Ca++ transporting, type 2C, member 1
	XPOT	AI984005	wt52c06.x1 NCI_CGAP_Pan1
	GNAI1	AL049933	Guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1
	RABGGTB	U49245	Rab geranylgeranyltransferase, beta subunit
	CD164	AF299343	CD164 antigen, sialomucin
	CLGN	NM_004362	Calmegin
	MAFG	NM_002359	V-maf musculoaponeurotic fibrosarcoma (avian) oncogene family, protein G
	EBAG9	AA812215	ob84g01.s1 NCI_CGAP_GCB1
	NUCB2	NM_005013	Nucleobindin 2
	KIAA0305	NM_014733	Endosome-associated FYVE-domain protein
	GOLTC1	AU152134	AU152134 NT2RP3
	CIS2, SSI2, SSI-2, SOCS-2	NM_003877	STAT induced STAT inhibitor-2
	ATV, NBS, AT-V1, AT-V2	NM_002485	Nijmegen breakage syndrome 1 (nibrin)
	DCHT, SPAK	NM_013233	Ste-20 related kinase
	KIAA0259	NM_007027	Topoisomerase (DNA) II binding protein
	CNOT8	NM_004779	CCR4-NOT transcription complex, subunit 8
	HUMAUANTIG	NM_013285	Nucleolar GTPase
	NIPSNAP2	NM_001483	Glioblastoma amplified sequence
	NU, HC2, PROS30	NM_002786	Proteasome (prosome, macropain) subunit, alpha type, 1
	DJ971N18.2	AL544094	AL544094 LTI_NFL006_PL2
	RCN2	NM_002902	Reticulocalbin 2, EF-hand calcium binding domain
	EIF4E	NM_001968	Eukaryotic translation initiation factor 4E
	NDUFA5	NM_005000	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5 (13kD, B13)
	RAMP4	AL136807	Stress-associated endoplasmic reticulum protein 1; ribosome associated membrane protein 4
	HH72, PRL1, PRL-1, PTP4A2, PTPCAAX1, PTP(CAAX1)	U48296	Protein tyrosine phosphatase type IVA, member 1
	KIAA0244	NM_015153	KIAA0244 protein
72 hr	**Down-Regulate Gene (2 genes)**		
	APOC3	NM_000040	Apolipoprotein C-III
	CYB5-M	NM_030579	Cytochrome b5 outer mitochondrial membrane precursor
	Up-Regulate Gene (7 genes)		
	MEKK2	AF239798	
	R32184_3	AI805266	ta32c02.x1 Soares_NFL_T_GBC_S1
	SQV7L	AJ005866	Nucleotide-sugar transporter similar to C. elegans sqv-7
	TIP120A	AB020636	TBP-interacting protein
	CP34, NF-25, P450C3, P450PCN1	AF182273	Cytochrome P450, subfamily IIIA (niphedipine oxidase), polypeptide 4
	Rab11-FIP2	BG249608	602319671F1 NIH_MGC_89
	DKFZP564A122	NM_015626	DKFZP564A122 protein

表１１ Troglitazone (30μM, 3μM), Rosiglitazone (30μM, 3μM), YH-1 (10μM, 1μM), YH-16 (10μM, 1μM)処理によって発現変動した遺伝子数の経時変化

		Troglitazone 30 μM	共通	Troglitazone 3 μM	Rosiglitazone 30 μM	共通	Rosiglitazone 3 μM	YH-1 10 μM	共通	YH-1 1 μM	YH-16 10 μM	共通	YH-16 1 μM
1 hr	解析遺伝子数	6628		8004	7473		8003	7205		7228	8168		8204
	Down-Regulate	570	18	75	140	9	50	157	20	80	101	10	61
	Up-Regulate	98	14	32	64	9	33	41	11	63	34	11	42
4 hr	解析遺伝子数	7060		6638	6736		7318	7435		7586	7510		7690
	Down-Regulate	52	5	38	62	4	30	37	7	62	62	0	69
	Up-Regulate	106	17	61	70	18	77	97	23	84	104	33	134
24 hr	解析遺伝子数	9305		8533	8801		8411	9961		8359	10025		9292
	Down-Regulate	103	14	132	87	23	134	58	4	208	89	10	49
	Up-Regulate	87	20	69	84	18	96	34	12	82	67	17	59
72 hr	解析遺伝子数	7376		8731	8403		8555	8561		9020	9245		9221
	Down-Regulate	519	8	52	139	11	83	67	6	79	115	23	102
	Up-Regulate	105	12	46	65	11	51	56	15	86	141	51	114

表１２　YH-1 と YH-16 の両濃度で共通に変動する遺伝子数と Troglitazone と Rosiglitazone の両濃度で共通に変動する遺伝子数

		Troglitazone	共通	Rosiglitazone	YH-1	共通	YH-16
1 hr	Down-Regulate	18	3	9	20	4	10
	Up-Regulate	14	3	9	11	3	11
4 hr	Down-Regulate	5	0	4	7	0	0
	Up-Regulate	17	7	18	23	7	33
24 hr	Down-Regulate	14	5	23	4	0	10
	Up-Regulate	20	6	18	12	1	17
72 hr	Down-Regulate	8	3	11	6	3	23
	Up-Regulate	12	2	11	15	5	51

表１３　YH-1 および YH-16 によって発現変動する遺伝子の Troglitazone と Rosiglitazone 処理時に変動する遺伝子との共通性

		YH-1			YH-16		
		Troglitazone	共通	Rosiglitazone	Troglitazone	共通	Rosiglitazone
1 hr	Down-Regulate	4	2	2	4	2	2
	Up-Regulate	5	1	1	3	1	2
4 hr	Down-Regulate	1	0	0	0	0	0
	Up-Regulate	5	3	6	2	2	2
24 hr	Down-Regulate	0	0	0	3	2	3
	Up-Regulate	3	0	0	4	2	4
72 hr	Down-Regulate	1	0	0	1	0	1
	Up-Regulate	1	1	1	1	1	1
Total		20	7	10	18	10	15

表１４　TSA (0.01μM, 0.1μM), SAHA (1μM, 10μM), P-Me (10μM, 100μM), P-Urea (10μM, 100μM)処理によって発現変動した遺伝子数の経時変化

		TSA 0.01 μM	共通	TSA 0.1 μM	SAHA 1 μM	共通	SAHA 10 μM	P-Me 10 μM	共通	P-Me 100 μM	P-Urea 10 μM	共通	P-Urea 100 μM
1 hr	解析遺伝子数	8585		8003	8994		7911	8407		8439	9184		8379
	Down-Regulate	39	2	52	29	2	54	68	5	33	29	2	55
	Up-Regulate	61	20	92	69	9	55	53	16	61	67	14	43
4 hr	解析遺伝子数	6324		4361	6342		2776	5606		6498	7449		7843
	Down-Regulate	631	277	898	1209	327	1380	1849	537	795	298	60	254
	Up-Regulate	128	51	335	150	79	403	185	46	144	103	16	64

表１５　TSA と SAHA の両濃度で共通に変動する遺伝子数と P-Me と P-Urea の両濃度で共通に変動する遺伝子数

		TSA	共通	SAHA	P-Me	共通	P-Urea
1 hr	Down-Regulate	2	0	2	5	0	2
	Up-Regulate	20	3	9	16	6	14
4 hr	Down-Regulate	277	100	327	537	26	60
	Up-Regulate	51	22	79	46	5	16

表１６　P-Me および P-Urea によって発現変動する遺伝子の TSA と SAHA 処理時に変動する遺伝子との共通性

		P-Me			P-Urea		
		TSA	共通	SAHA	TSA	共通	SAHA
1 hr	Down-Regulate	0	0	0	0	0	0
	Up-Regulate	4	2	2	7	3	3
4 hr	Down-Regulate	95	34	81	8	1	3
	Up-Regulate	15	9	18	6	3	4
Total		114	45	101	21	7	10

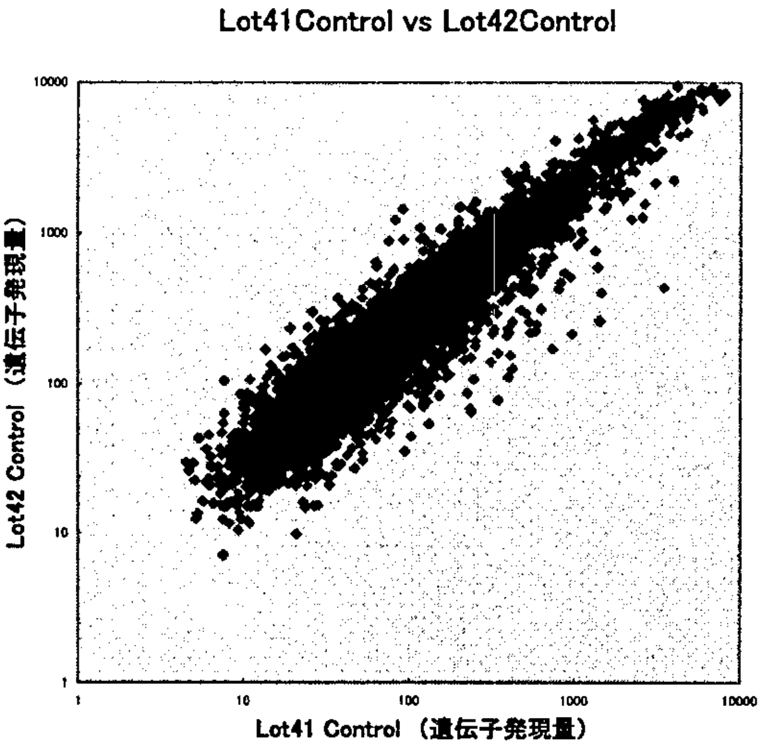


図１　非凍結型 Lot41 と非凍結型 Lot42 の無処理時における遺伝子発現強度の比較

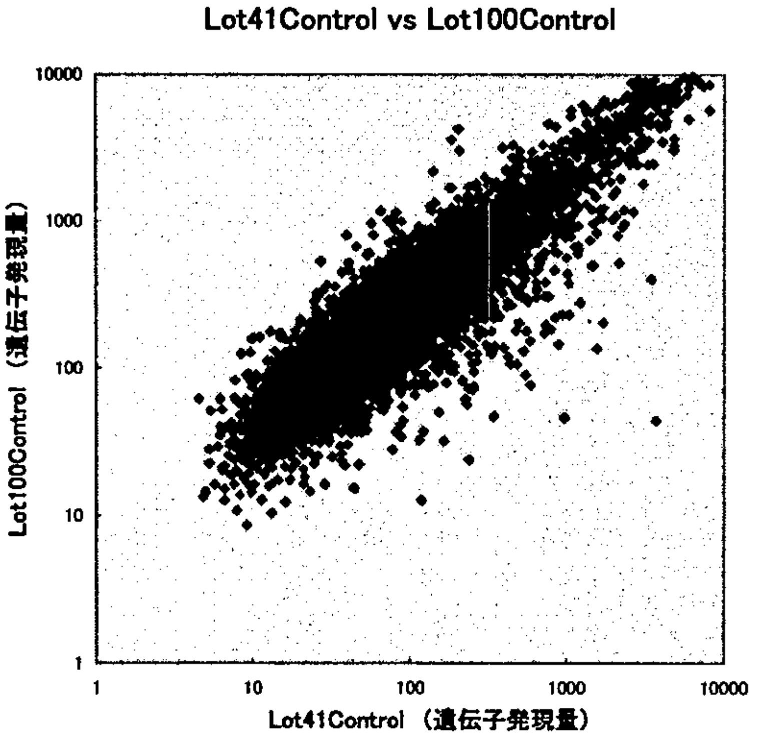


図２　非凍結型 Lot41 と接着型凍結 Lot100 の無処理時における遺伝子発現強度の比較

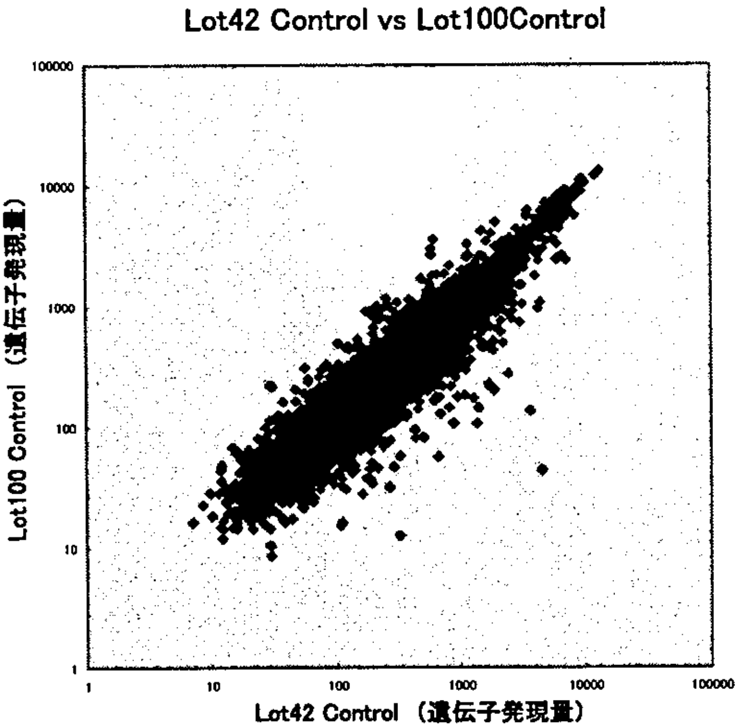


図３　非凍結型Lot42と接着型凍結Lot100の無処理時における遺伝子発現強度の比較

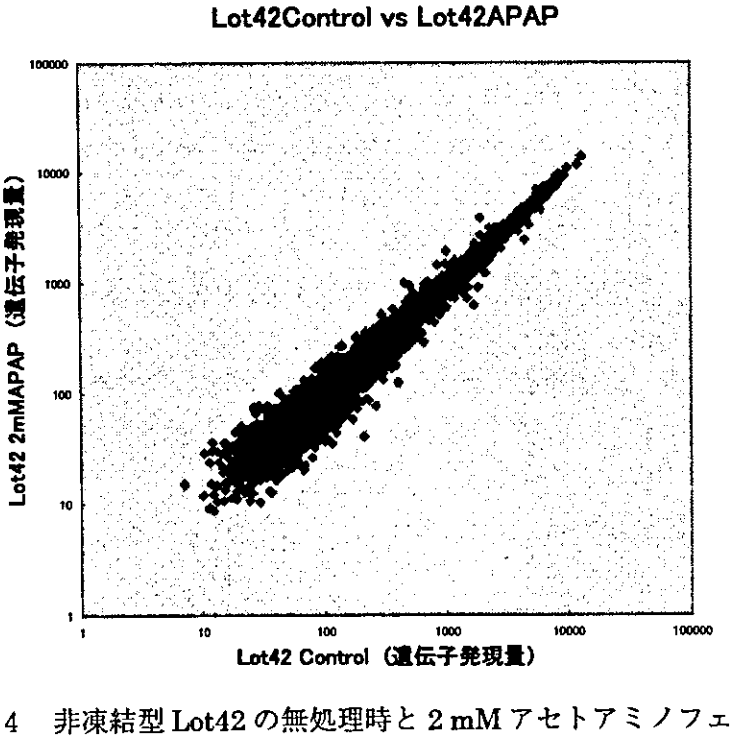


図４　非凍結型Lot42の無処理時と２mMアセトアミノフェン処理時における遺伝子発現強度の比較

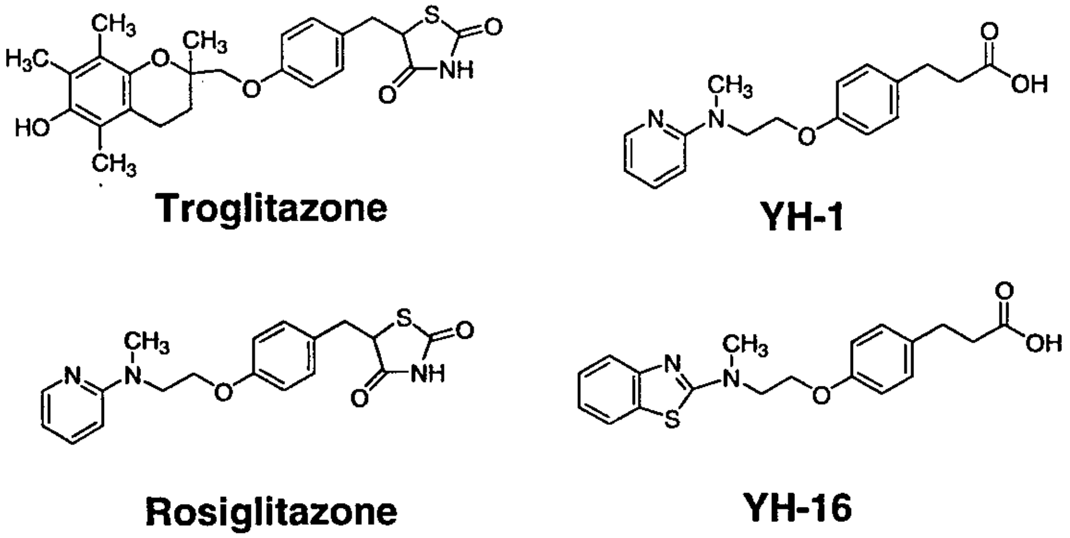


図5　研究に用いたPPARγ作用薬

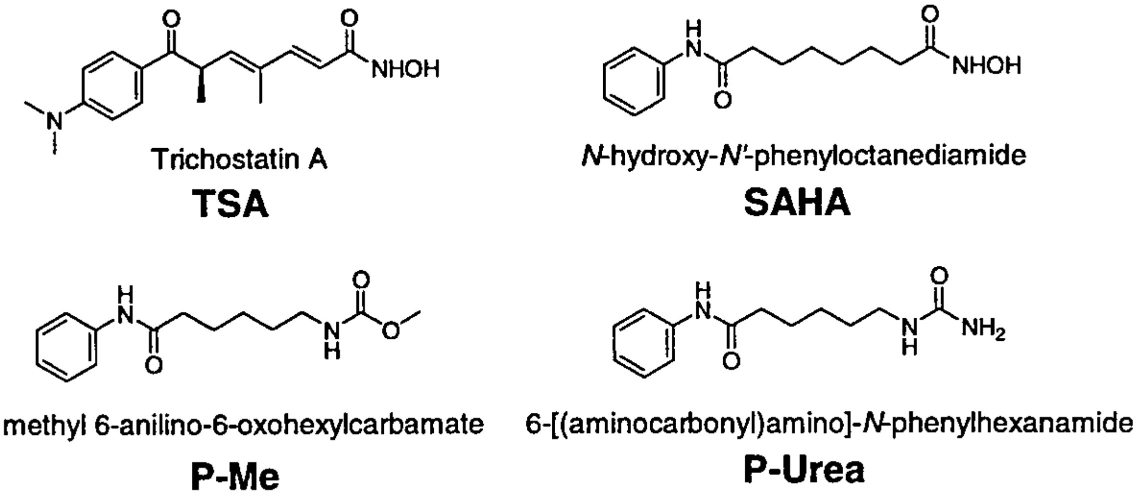


図6　研究に用いたヒストン脱アセチル酵素阻害剤

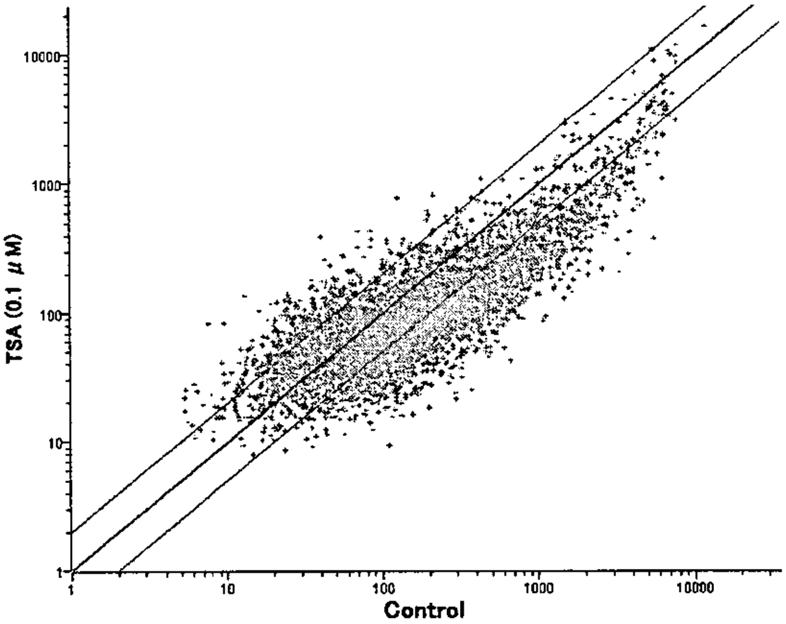


図7　凍結型Lot100に対してTSA (0.1 μM)4時間処理を行った時のコントロールに対する遺伝子発現強度の比較

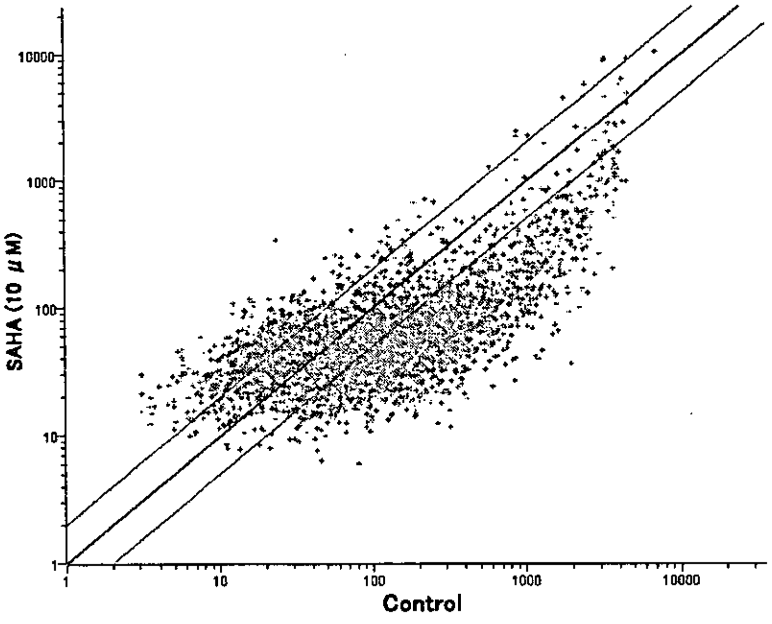


図8　凍結型Lot100に対してSAHA(10 μM)4時間処理を行った時のコントロールに対する遺伝子発現強度の比較

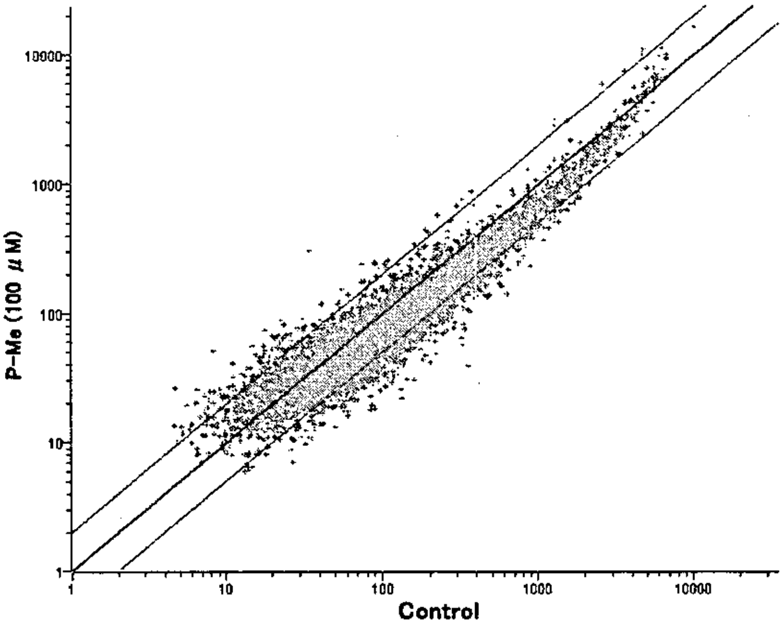


図９　凍結型Lot100に対してP-Me (100μM)処理を行った時のコントロールに対する遺伝子発現強度の比較

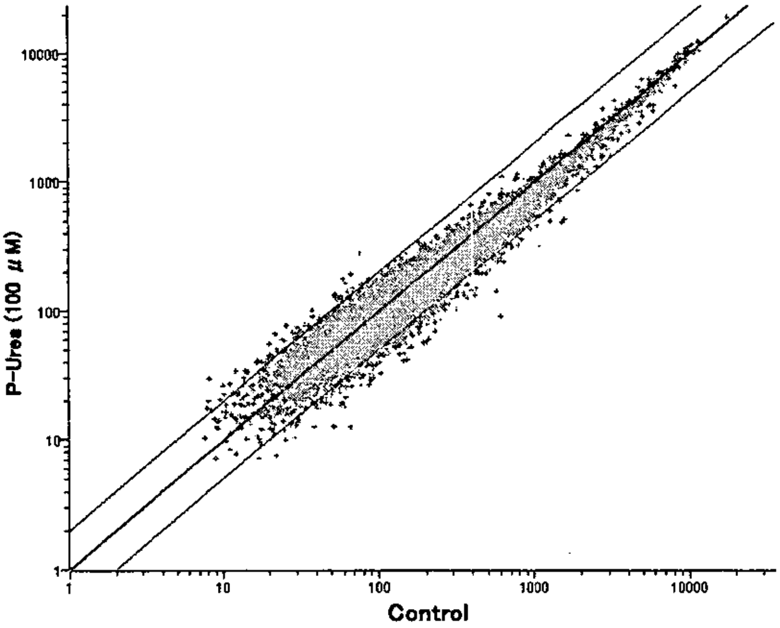


図１０　凍結型Lot100に対してP-Urea (100μM)処理を行った時のコントロールに対する遺伝子発現強度の比較

表１　肝毒性薬剤暴露時の発現変動遺伝子数

	>2	<-2	>3	<-3	>4	<-4	>5	<-5	>10	<-10
Acetaminophen	311	530	33	56	7	10	2	3	0	0
CCl4	877	465	155	61	44	13	14	7	2	0
Carbamazepine	1450	1233	364	443	147	233	73	154	10	33
Isoniazid	1001	250	148	19	41	1	11	0	1	0

表２　各処理時点での遺伝子発現パターンの相関係数（すべてのデータを使用）

遺伝子発現変動データ全てを使用

	Acetaminopl	Acetaminopl	Acetaminopl	CCl4 4hr	CCl4 24hr	CCl4 72hr	Isoniazid 4hr	Isoniazid 24	Isoniazid 72h
Acetaminophen 4h	1	0.017	0.103	0.351	−0.067	0.042	0.347	−0.061	0.042
Acetaminophen 24	0.017	1	0.039	−0.129	0.644	−0.162	−0.088	0.619	−0.186
Acetaminophen 72	0.103	0.039	1	0.079	−0.102	0.452	0.079	−0.070	0.467
CCl4 4hr	0.351	−0.129	0.079	1	−0.163	0.110	0.793	−0.140	0.131
CCl4 24hr	−0.067	0.644	−0.102	−0.163	1	−0.281	−0.138	0.744	−0.175
CCl4 72hr	0.042	−0.162	0.452	0.110	−0.281	1	0.063	−0.263	0.434
Isoniazid 4hr	0.347	−0.088	0.079	0.793	−0.138	0.063	1	−0.108	0.121
Isoniazid 24hr	−0.061	0.619	−0.070	−0.140	0.744	−0.263	−0.108	1	−0.092
Isoniazid 72hr	0.042	−0.186	0.467	0.131	−0.175	0.434	0.121	−0.092	1

表３　各処理時点での遺伝子発現パターンの相関係数（Threshold 2.0 以上）

Threshold 2.0 以上のデータを使用

	Acetaminopl	Acetaminopl	Acetaminop	CCl4 4hr	CCl4 24hr	CCl4 72hr	Isoniazid 4hr	Isoniazid 24	Isoniazid 72h
Acetaminophen 4hr	1	0.028	0.084	0.411	−0.092	0.046	0.413	−0.094	0.033
Acetaminophen 24hr	0.028	1	0.054	−0.031	0.651	−0.186	0.006	0.640	−0.151
Acetaminophen 72hr	0.084	0.054	1	0.060	−0.148	0.502	0.069	−0.108	0.506
CCl4 4hr	0.411	−0.031	0.060	1	−0.139	0.121	0.815	−0.113	0.085
CCl4 24hr	−0.092	0.651	−0.148	−0.139	1	−0.351	−0.117	0.781	−0.181
CCl4 72hr	0.046	−0.186	0.502	0.121	−0.351	1	0.069	−0.332	0.474
Isoniazid 4hr	0.413	0.006	0.069	0.815	−0.117	0.069	1	−0.086	0.062
Isoniazid 24hr	−0.094	0.640	−0.108	−0.113	0.781	−0.332	−0.086	1	−0.105
Isoniazid 72hr	0.033	−0.151	0.506	0.085	−0.181	0.474	0.062	−0.105	1

表４　各処理時点での遺伝子発現パターンの相関係数（Threshold 3.0 以上）

Threshold 3.0 以上のデータを使用

	Acetaminopl	Acetaminopl	Acetaminop	CCl4 4hr	CCl4 24hr	CCl4 72hr	Isoniazid 4hr	Isoniazid 24	Isoniazid 72h
Acetaminophen 4hr	1	0.038	0.059	0.450	−0.154	0.053	0.439	−0.125	0.061
Acetaminophen 24hr	0.038	1	0.100	−0.055	0.850	−0.211	−0.013	0.636	−0.136
Acetaminophen 72hr	0.059	0.100	1	0.088	−0.194	0.506	0.088	−0.135	0.470
CCl4 4hr	0.450	−0.055	0.088	1	−0.233	0.163	0.855	−0.181	0.103
CCl4 24hr	−0.154	0.650	−0.194	−0.233	1	−0.444	−0.194	0.839	−0.209
CCl4 72hr	0.053	−0.211	0.506	0.163	−0.444	1	0.113	−0.403	0.492
Isoniazid 4hr	0.439	−0.013	0.088	0.855	−0.194	0.113	1	−0.157	0.050
Isoniazid 24hr	−0.125	0.636	−0.135	−0.181	0.839	−0.403	−0.157	1	−0.123
Isoniazid 72hr	0.061	−0.136	0.470	0.103	−0.209	0.492	0.050	−0.123	1

表 5　PPARγ 作用薬暴露時の発現変動遺伝子数（マウス）

Threshold 2.0

	1hr Up	4hrs Up	24hrs Up	72hrs Up	1hr Down	4hrs Down	24hrs Down	72hrs down
Pioglitazone 200mg/kg	489	39	64	50	-69	-307	-39	-174
Rosiglitazone 200mg/kg	411	63	86	54	-89	-38	-585	-61
Troglitazone 200mg/kg	238	29	34	46	-162	-22	-89	-178

Threshold 3.0

	1hr Up	4hrs Up	24hrs Up	72hrs Up	1hr Down	4hrs Down	24hrs Down	72hrs down
Pioglitazone 200mg/kg	108	4	8	5	-7	-62	-4	-21
Rosiglitazone 200mg/kg	89	8	18	8	-10	-5	-135	-8
Troglitazone 200mg/kg	60	4	5	4	-11	0	-11	-10

表 6　PPARγ 作用薬暴露時の発現変動遺伝子数（プライマリーヒト肝細胞）

		Troglitazone 30 μM	Troglitazone 3 μM	Rosiglitazone 30 μM	Rosiglitazone 3 μM
	解析遺伝子数	6628	8004	7473	8003
1hr	**発現増加**	570	75	140	50
	発現減少	98	32	64	33
	解析遺伝子数	7060	6638	6736	7318
4hr	**発現増加**	52	38	62	30
	発現減少	106	61	70	77
	解析遺伝子数	9305	8533	8801	8411
24hr	**発現増加**	103	132	87	134
	発現減少	87	69	84	96
	解析遺伝子数	7376	8731	8403	8555
72hr	**発現増加**	519	52	139	83
	発現減少	105	46	65	51

表 7　FXR 欠損型マウス 1%LCA 投与実験における発現変動遺伝子数（Threshold 2.0）

	野性型1%LCA投与／野性型陰性対照群	欠損型1%LCA投与／欠損型陰性対照群	欠損型陰性対照群／野性型陰性対照群	欠損型1%LCA投与／野性型1%LCA投与
発現増加	1444	293	423	991
発現減少	944	110	1812	2080

表8　FXR 欠損型マウスの実験において興味がもたれた遺伝子群

Energy and cell component transport:

Abca1 (Cholesterol efflux to HDL), Abca3 (Peptide transport), Abca11 (Bsep), Slc16a1 (Lactic acid uptake), Slc35a5 (UDP-GlucNAc), Atp7a (Mit. Cu++ transporting ATPase), Atp6vs

Sinusoid:

Nidogen 1 (TGFb-activated), Occludin (Bile duct tight junction)

Dyling or regenerating:

Calpain, Glucosaminyl transferase, Adam 9, 10, 17, Tcf4, Metaloproteinase, Ubiquitin associated 26S proteins (Proteasome)

Hypoxia:

Von Hippel-Lindau protein, HIF1a, Hypoxia-induced gene 1

Growth factor & Cytokine:

Epidermal growth factor receptor interacting protein, FGFR inducible 14, NS-1 associated, IGF binding protein 7, Platelet-derived growth factor receptor, TGFbR, Activin A, TGFb-induced, TNFa-induced protein 1& 2, RIP, Cofilin

Threshold 3.0

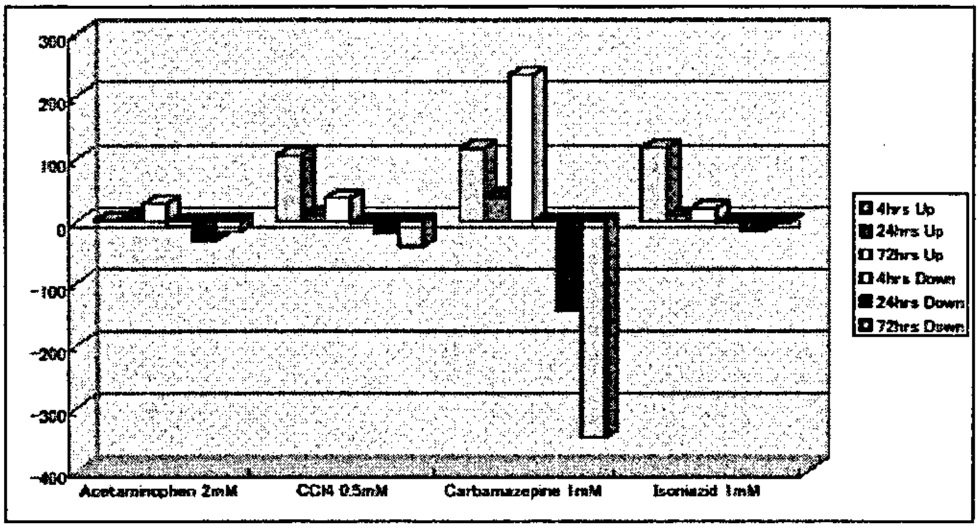


図１　肝毒性薬剤暴露時の経時的発現変動遺伝子数（Threshold 3.0）

Threshold 4.0

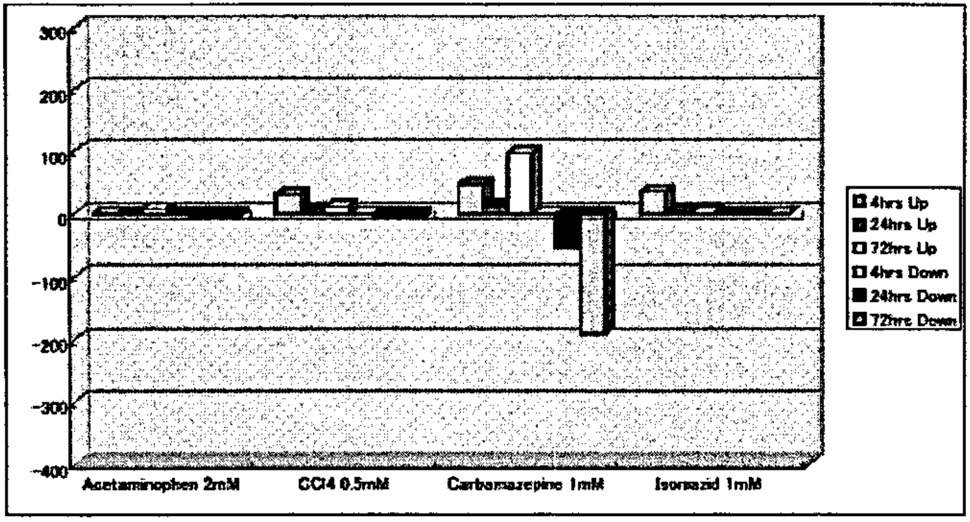


図２　肝毒性薬剤暴露時の経時的発現変動遺伝子数（Threshold 4.0）

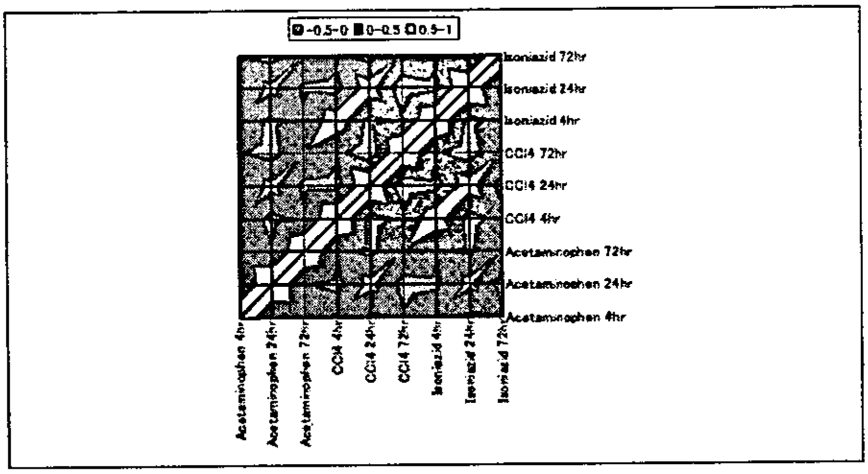


図３　遺伝子発現パターンの行列相関図（すべてのデータを使用）

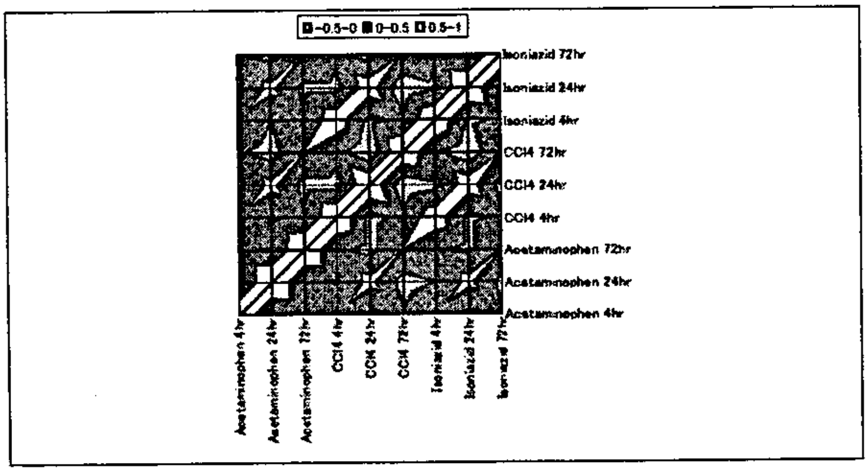


図４　遺伝子発現パターンの行列相関図（Threshold 2.0 以上）

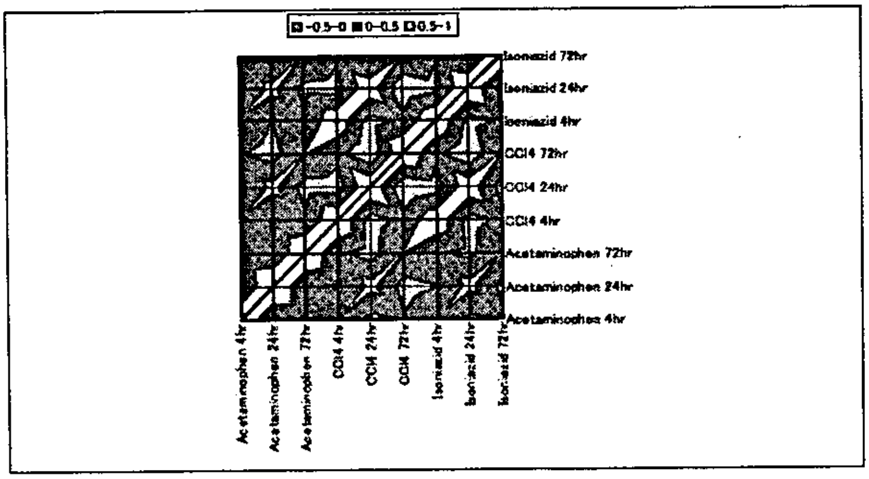


図５　遺伝子発現パターンの行列相関図（Threshold 3.0 以上）

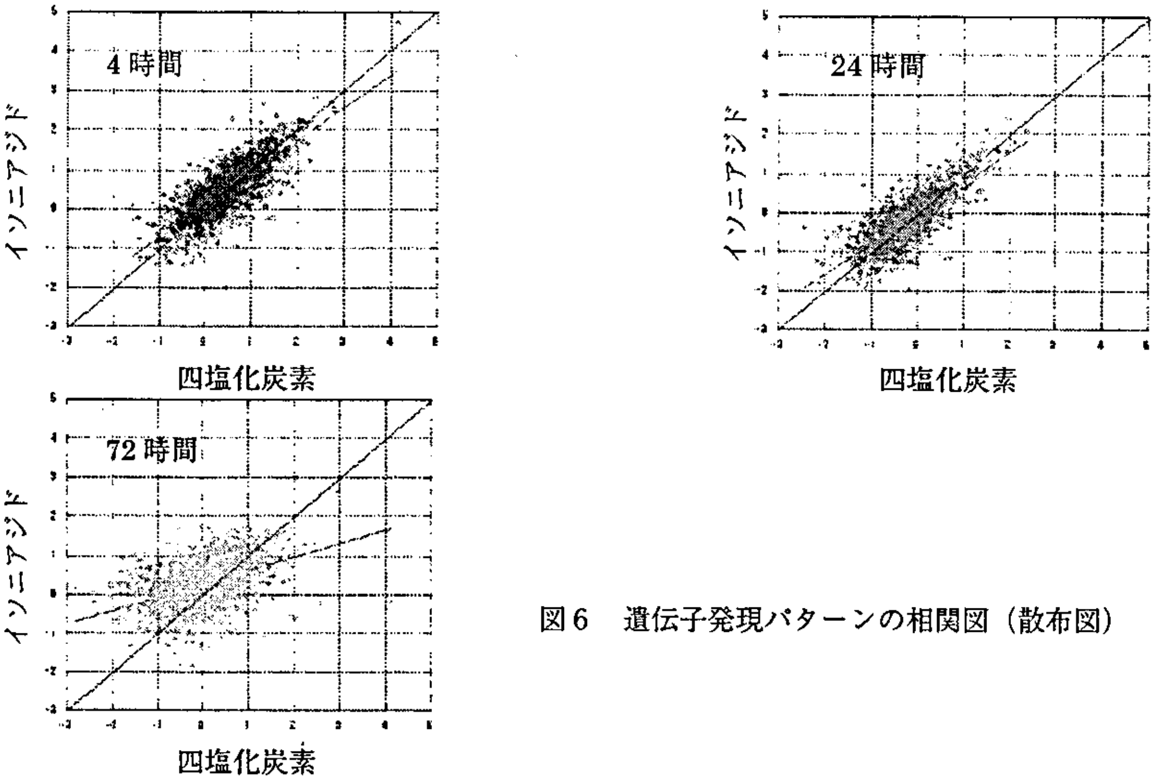
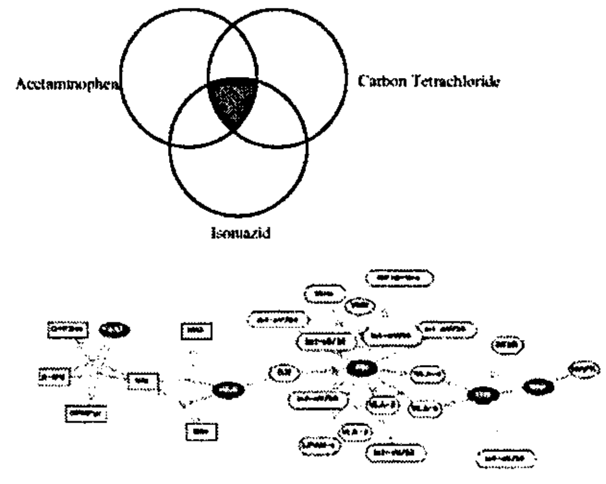
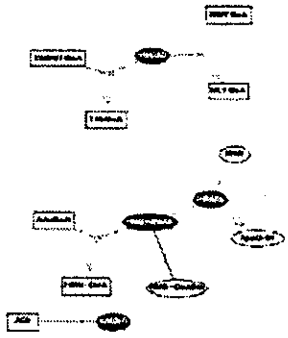


図6　遺伝子発現パターンの相関図（散布図）

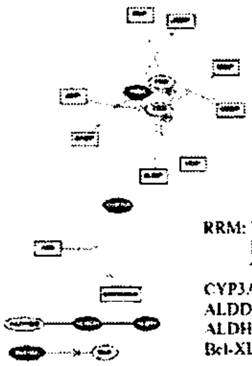
Threshold 2.0 Up-regulation



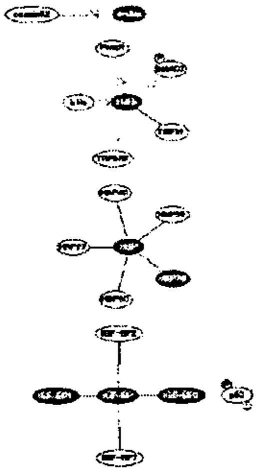


SBCAD: Acyl-CoA dehydrogenase short/branched chain specific、イソロイシン異化経路、バリン異化経路
PPARa: Peroxisome proliferator activated receptor alpha
HMG-CoAS: Hydroxylmethylglutaryl-CoA synthase ステロール同化経路
nAChr: nicotinic acetylcholine receptor

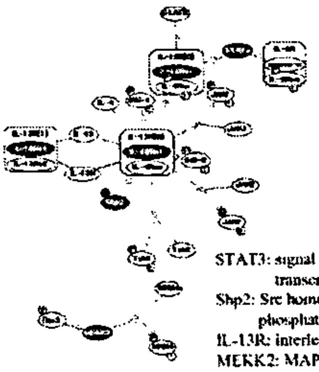
FN: Fibronectin
tTG: tissue transglutaminase
RAR: retinoic acid receptor
GLS: Glutaminase アミノ基代謝、4-アミノ酪酸代謝
PSAT: Phosphoserine aminotransferase、グリシン代謝、セリン代謝、トレオニン代謝



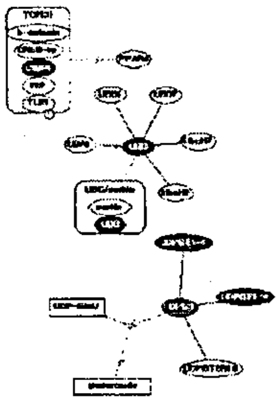
RRM: Ribonucleoside-diphosphate reductase
ピリミジン代謝、ピリミジン同化経路
プリン代謝
CYP3A: Cytochrome P450 3A
ALDDH: Aldehyde dehydrogenase
ALDH: Aldehyde dehydrogenase (NAD+)
Bcl-XL



c-Jun
TGFb: transforming growth factor beta
HSP: heat shock protein
HSP70: heat shock protein 70
IGF-BP: insulin-like growth factor binding protein
IGF-BP1,IGF-BP3



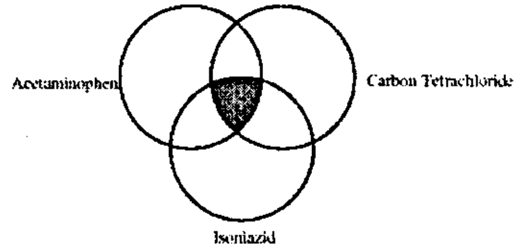
STAT3: signal transducer and activator of transcription 3
Shp2: Src homology 2 containing protein tyrosine phosphatase 2
IL-13R: interleukin-13 receptor
MEKK2: MAPK/ERK kinase kinase 2

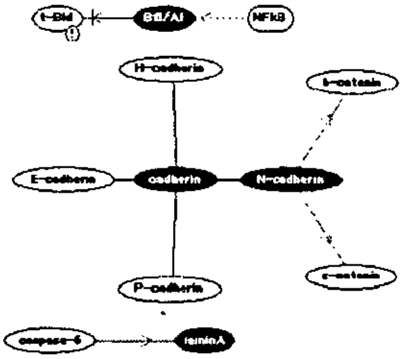


CtBP1: C-terminal binding protein 1
UBC: ubiquitin carrier protein
UDPGT: UDP-glucuronosyl transferase
UDPGT1-4, UDPGT1-1

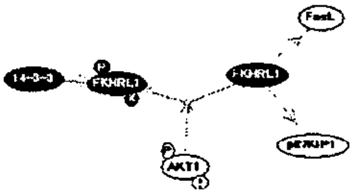
図７　アセトアミノフェン，四塩化炭素，イソニアジドで共通に発現増加した分子ネットワーク

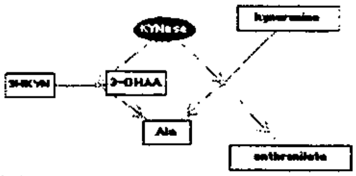
Threshold 2.0 Down-regulation



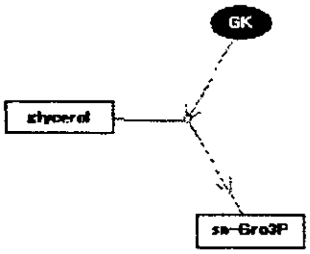


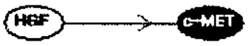
Bfl/A1: Bcl-2 related protein A1
Cadherin:
N-cadherin:
lamin A:

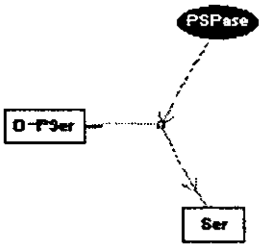




FKHRL1: forkhead protein O3A
14-3-3: 14-3-3 protein
KYNase: Kyrureninase キヌレニン経路、トリプトファン代謝
グルクロン酸抱合



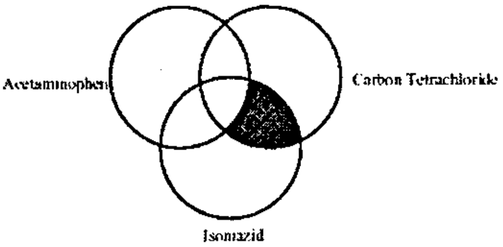


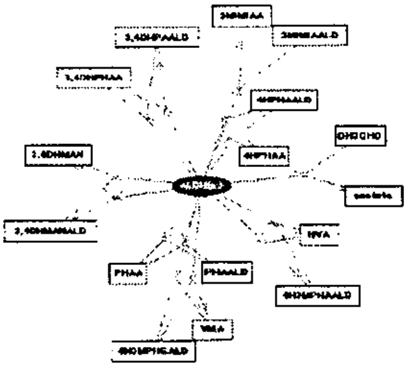


GK: Glycerolkinase グリセリン脂質同化経路、フルクトース代謝
c-MET: met proto-oncogene tyrosine kinase
PSPase: Phosphoserine phosphatase グリシン代謝、セリン代謝
トレオニン代謝

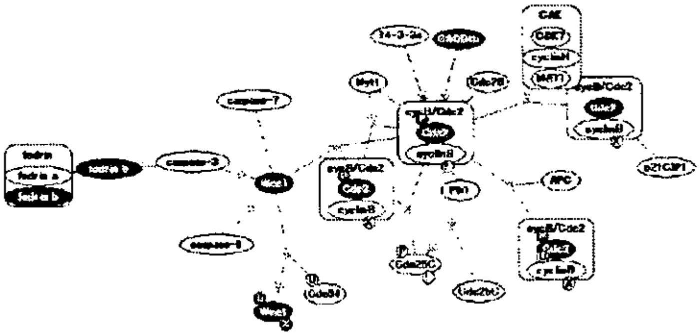
図８　アセトアミノフェン，四塩化炭素，イソニアジドで共通に発現減少した分子ネットワーク

Threshold 2.0 Up-regulation

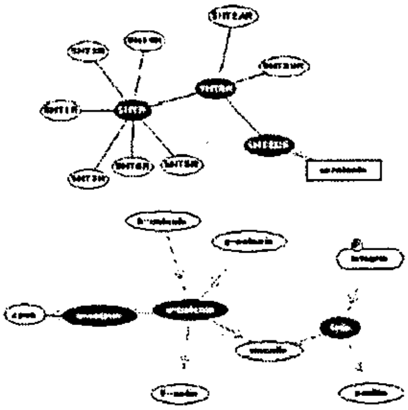


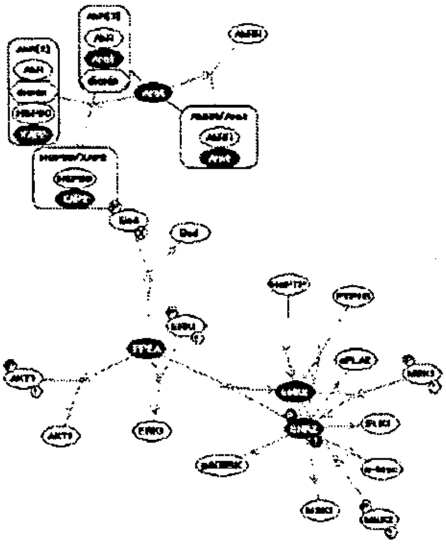


ALDH(p): Aldehyde dehydrogenase (NAD(p)+)
カテコールアミン代謝、グリシン代謝
セリン代謝、チロシン代謝、
トレオニン代謝、ヒスタミン代謝、
ヒスチジン代謝、フェニルアラニン代謝



cdc2: cell division cycle 2
GADD: growth arrest and DNA damage inducible protein
Wee1: Wee1-like protein kinase
Fodrinb: fodrin beta chain



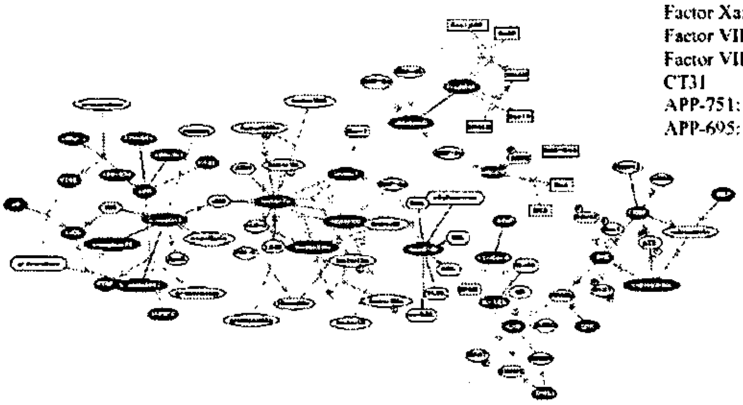


5HTR: 5-hydroxytryptamine receptor
5HT2R: 5-hydroxytryptamine 2 receptor
5HT2CR: 5-hydroxytryptamine 2C receptor

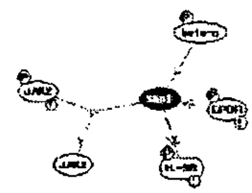
a-catenin: alpha-catenin
a-actinin: alpha-actinin

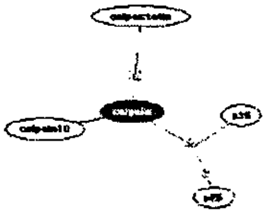
Arnt: AhR nuclear translocator
XAP2: X associated protein 2
ERk2: extracellular signal regulated kinase 2
PP2A: serine/threonine protein phosphatase 2A

CHP: calcium-binding protein CHP
FKBP: FK-506 binding protein
Cyclophilin
JNK: c-Jun N-terminal kinase
ERK: extracellular signal regulated kinase
IL-8: interleukin-8
IL-12B: interkeukin-12 beta chain
A1-AdoR: A1 adenosine receptor
AdoR: Adenosine receptor
HMGCR: hydroxymethylglutaryl-CoA reductase(NADPH)
ApoC-III: apolipoprotein C-III
FruBPAL: Fructose-bisphosphate aldolase
Aldolase B: Fructose-bisphosphate aldolase B
Factor X: blood coagulation factor X
Factor Xa: blood coagulation factor x activated
Factor VII: blood coagulation factor VII
Factor VIIa: blood coagulotion factor VII activated
CT31
APP-751: Amyloid beta A4 protein-751
APP-695: Amyloid beta A4 protein-695

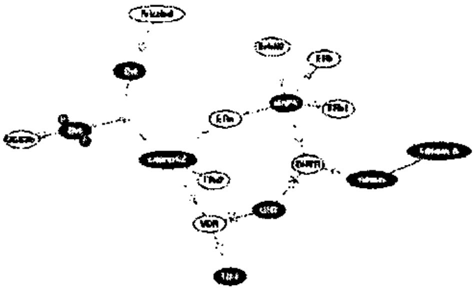


APP: Amyloid beta A4 protein
APP-770:
b-amyloid42: amyloid beta protein 42
APPs-b: Soluble APP-beta
b-amyloid40: amyloid beta protein 40
CT99
AICD: APP intracellular domain
APPs-a: Soluble APP-alpha
CT-83
p3

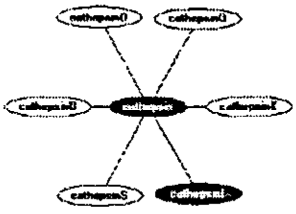




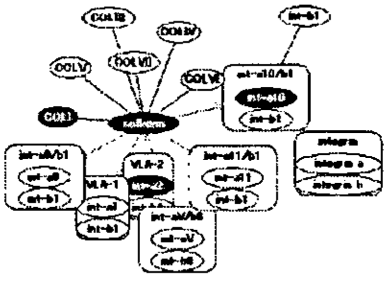
Shp1:
TC10:
Calpain:

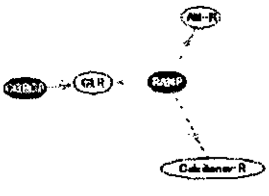


Dvl: segment polarity protein dishevelled homology
caseinK2: casein kinase 2
MAPK: MAP kinase
CRT: calreticulin
TIF1: transcription intermediary factor 1
Filamin
Filamin A



Cathepsin:
Cathepsin L





CGRCP: Calcitonin gene-related peptide-receptor component protein
RAMP: Receptor activity-modifying protein

Collagen
COLI: collagen type I
Int-a2: integrin alpha-2
Int-a10/b1: integrin alpha-10/beta-1