

Annotation Cluster 1		Enrichment Score: 1.31			Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_MF_FAT	identical protein binding	RT		7	7.5E-3	8.0E-1
<input type="checkbox"/>	GOTERM_MF_FAT	protein homodimerization activity	RT		4	1.1E-1	9.8E-1
<input type="checkbox"/>	GOTERM_MF_FAT	protein dimerization activity	RT		5	1.4E-1	9.9E-1
Annotation Cluster 2		Enrichment Score: 1.22			Count	P_Value	Benjamini
<input type="checkbox"/>	SP_PIR_KEYWORDS	zinc	RT		21	7.2E-3	7.3E-1
<input type="checkbox"/>	GOTERM_MF_FAT	zinc ion binding	RT		21	2.0E-2	8.8E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	metal-binding	RT		24	4.1E-2	9.2E-1
<input type="checkbox"/>	GOTERM_MF_FAT	transition metal ion binding	RT		23	4.9E-2	9.7E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	zinc-finger	RT		12	1.0E-1	8.6E-1
<input type="checkbox"/>	GOTERM_MF_FAT	ion binding	RT		29	1.5E-1	9.9E-1
<input type="checkbox"/>	GOTERM_MF_FAT	metal ion binding	RT		28	1.8E-1	9.6E-1
<input type="checkbox"/>	GOTERM_MF_FAT	cation binding	RT		28	2.0E-1	9.6E-1
Annotation Cluster 3		Enrichment Score: 1.16			Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	immune effector process	RT		4	4.2E-2	9.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	immune response	RT		7	6.8E-2	9.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	lymphocyte mediated immunity	RT		3	7.9E-2	9.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	leukocyte mediated immunity	RT		3	1.0E-1	1.0E0
Annotation Cluster 4		Enrichment Score: 1.03			Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_FAT	extracellular region	RT		15	5.3E-2	9.4E-1
<input type="checkbox"/>	GOTERM_CC_FAT	extracellular region part	RT		8	1.1E-1	9.9E-1
<input type="checkbox"/>	GOTERM_CC_FAT	extracellular space	RT		6	1.3E-1	9.9E-1
Annotation Cluster 5		Enrichment Score: 1.01			Count	P_Value	Benjamini
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Ig-like 3	RT		3	4.7E-3	8.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Ig-like 2	RT		3	1.1E-2	9.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Ig-like 1	RT		3	1.1E-2	9.2E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	immunoglobulin	RT		3	4.8E-2	8.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	immune response	RT		7	6.8E-2	9.9E-1
<input type="checkbox"/>	INTERPRO	Immunoglobulin C1-set	RT		3	8.8E-2	1.0E0
<input type="checkbox"/>	SMART	IGc1	RT		3	1.1E-1	1.0E0
<input type="checkbox"/>	INTERPRO	Immunoglobulin/major histocompatibility complex, conserved site	RT		3	1.2E-1	1.0E0
<input type="checkbox"/>	SP_PIR_KEYWORDS	duplication	RT		3	1.6E-1	8.8E-1
<input type="checkbox"/>	INTERPRO	Immunoglobulin-like fold	RT		7	1.9E-1	1.0E0
<input type="checkbox"/>	SP_PIR_KEYWORDS	Immunoglobulin domain	RT		5	2.7E-1	9.3E-1
<input type="checkbox"/>	INTERPRO	Immunoglobulin-like	RT		6	2.9E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	sequence variant	RT		4	4.2E-1	1.0E0
<input type="checkbox"/>	INTERPRO	Immunoglobulin subtype	RT		3	5.6E-1	1.0E0
<input type="checkbox"/>	SMART	IG	RT		3	6.2E-1	1.0E0

図9 低分子量ヘパリン投与マウス腎臓で発現低下する遺伝子間に共通する機能的特徴の解析 2回の比較においていずれも発現上昇する155プローブセットを用い、DAVID (<http://david.abcc.ncifcrf.gov>)の遺伝子機能分類を適用した。

症のある病期から認められるかを検証する必要がある。

一方、糖尿病腎症寛解関連因子の探索を目的として糖尿病腎症寛解マウスモデルを用いた解析も試みた。近年、慢性進行性疾患と考えられていた糖尿病腎症が集約的治療にて1型、2型を問わず寛解や退縮することが多く論文で報告されてきたものの、

その作用機序に関しては不明な点が多い。今回同定された発現変動遺伝子群や代謝経路を中心に尿中蛋白質排泄量の低下との関連を検討し、同定した因子の機能を *in vitro*, *in vivo* にて解析することにより、従来よりも効率的な糖尿病腎症の集約的治療の開発や糖尿病腎症のマーカー蛋白の探索・評価が可能になることが期待される。

## F. 文献

- 1) IDF Diabetes Atlas 4th edition, International Diabetes Federation, 2009.
- 2) Gaede P, et al: Multifactorial intervention and cardiovascular disease in patients with type 2 diabetes. N Engl J Med 348: 383-393, 2003.
- 3) Araki S, et al: Factors associated with frequent remission of microalbuminuria in patients with type 2 diabetes. Diabetes 54: 2983-2987, 2005.
- 4) Myint K, et al: RAGE control of diabetic nephropathy in a mouse model. Effects of RAGE gene disruption and administration of low-molecular weight heparin. Diabetes 55: 2510-2522.

## G. 健康危険情報

該当事項なし

## H. 研究発表

該当事項なし

## I. 知的財産権の出願・登録状況（予定を含む）

該当事項なし

表 1 高ブドウ糖負荷により腎糸球体血管内皮細胞において発現上昇した分泌蛋白コード遺伝子

Gene symbol	Gene name	High glucose (HG)	Low glucose (LG)	Ratio (HG/LG)	t-test
	ADAM				
ADAMTS1	metallopeptidase with thrombospondin type 1 motif, 1 arginine-rich,	1721.6	805.3	2.138	0.0042
ARMETL1	mutated in early stage tumors-like 1	11.9	4.4	2.680	0.0294
ARSG	arylsulfatase G	31.19	13.8	2.260	0.0146
CDCP1	CUB domain containing protein 1	24.0	10.2	2.343	0.0199
CST2	cystatin SA ecto-NOX	195.4	53.7	3.636	0.0015
ENOX1	disulfide-thiol exchanger 1	17.7	6.1	2.909	0.0090
FBN2	fibrillin 2 growth	83.2	28.2	2.950	0.0001
GDF15	differentiation factor 15	3621.6	1842.9	1.965	<0.0001
POMZP3	POM (POM121 homolog, rat) and ZP3 fusion protease, serine, 1	60.7	25.9	2.346	0.0101
PRSS1	(trypsin 1)	198.1	84.4	2.348	0.0276
PRSS1	protease, serine, 1 (trypsin 1) / trypsinogen C	290.4	127.6	2.276	0.0032
PRSS3	protease, serine, 3	869.5	400.6	2.171	0.0011
PRSS3	protease, serine, 3 serpin peptidase	1160.5	475.1	2.443	<0.0001
SERPINB2	inhibitor, clade B (ovalbumin), member 2	194.1	102.0	1.904	0.0331
TFPI2	tissue factor pathway inhibitor 2	4446.2	1793.4	2.479	0.0001
TNFRSF11B	tumor necrosis factor receptor superfamily, member 11b	25.8	12.8	2.021	0.0216

表2 低分子量ヘパリン投与により iNOS トランスジェニックマウス腎臓において発現上昇した遺伝子群

AFFYMETRIX_3PRIME _IVT_ID	Gene Name	Fold change* (Exp-1)	Fold change* (Exp-2)
1460437_at	cytohesin 4	1.1	2
1460099_at	ATPase, class II, type 9B	3.8	3
1459831_s_at	transmembrane and coiled-coil domains 5	4	4.6
1459737_s_at	transthyretin	1.4	1.2
1459505_at	-	1.3	2.5
1459406_at	DENN/MADD domain containing 2D transient receptor potential	2.7	1.2
1459367_at	cation channel, subfamily C, member 5	3.4	1.4
1459136_at	BTB and CNC homology 2 glucagon-like peptide 1 receptor;	4.2	4.3
1458719_at	similar to glucagon-like peptide-1 receptor	4.6	3.7
1458714_at	RIKEN cDNA 1700093C20 gene	1	4.6
1458689_at	autophagy-related 10 (yeast)	3.6	1.3
1458076_at	-	1.2	3.8
1457932_at	-	1.6	2.8
1457753_at	toll-like receptor 13	1	1.6
1457337_at	-	1.1	1.1
1457035_at	expressed sequence AI607873	1.4	1.7
1456655_at	exostoses (multiple) 1	1	1.1
1456075_at	protein kinase D2	3.6	2.3
1455790_at	E2F transcription factor 2 eukaryotic translation	1	2.9
1455690_at	elongation factor 1 alpha 2	2.8	1.7
1455342_at	RIKEN cDNA A230083H22 gene	1.5	1.6
1454600_at	RIKEN cDNA 9530086P17 gene	2.5	3.3
1454147_at	RIKEN cDNA 2810429I04 gene	2	3.6
1452408_at	three prime repair exonuclease 1	1.9	2.7

1452117_a_at	FYN binding protein	1.5	1.9
1451951_at	immunoglobulin kappa chain complex	1	1.9
1451804_a_at	leucine rich repeat containing 16A	1.6	1
1451563_at	EGF-like module containing, mucin-like, hormone receptor-like sequence 4	1.7	3
1450826_a_at	serum amyloid A 3	2.4	2.9
1450788_at	serum amyloid A 1	1.4	3.6
1450364_a_at	hepatitis A virus cellular receptor 1	1.2	1.7
1450234_at	membrane-spanning 4-domains, subfamily A, member 6C	1	2.2
1450009_at	lactotransferrin	1.7	1.2
1449863_a_at	distal-less homeobox 5	2.6	1.4
1449175_at	G-protein coupled receptor 65	1.2	2
1448756_at	S100 calcium binding protein A9 (calgranulin B)	4.6	3.2
1448620_at	Fc receptor, IgG, low affinity III	1	2.4
1448520_at	DNA cross-link repair 1B, PS02 homolog (S. cerevisiae)	1.1	1.7
1448025_at	signal-regulatory protein beta 1; similar to SIRP beta 1 cell surface protein	1.1	1.9
1447894_x_at	H2A histone family, member B3	1.9	2.3
1447727_at	aquaporin 3	4.1	4.6
1447673_x_at	RIKEN cDNA 1700015C15 gene	4.6	1.1
1447566_at	histone deacetylase 4	1	3.7
1447520_at	lipopolysaccharide binding protein	2	1.5
1447436_at	expressed sequence AI451250	1.3	2.6
1447145_at	ataxia, cerebellar, Cayman type homolog (human)	4.9	3.1
1446842_at	DNA segment, Chr 4, ERATO Doi 571, expressed	2.7	3.2

1446255_at	KCNQ1 overlapping transcript 1	1.1	2.6
1444987_at	cathepsin B	2.7	1
1444979_at	protein C	1.8	2.1
1444843_at	-	1.4	5.1
1444750_at	insulin degrading enzyme	2.8	1
1444647_at	phospholipase A2, activating protein	2	1
1444610_at	mitochondrial ribosomal protein S30	4.9	2.7
1444393_at	regulating synaptic membrane exocytosis 1	3.3	3.8
1444226_at	forkhead box O3	1	1.7
1443852_at	-	4.2	2.3
1443783_x_at	histocompatibility 2, class II antigen A, alpha; histocompatibility 2, class II antigen E alpha	2.3	2.7
1443732_at	RIKEN cDNA D630045J12 gene	1	2.3
1443531_at	RIKEN cDNA A930005I04 gene	2.1	2.7
1442339_at	stefin A2 like 1	4.4	5
1442074_at	-	1.3	3.9
1441958_s_at	advanced glycosylation end product-specific receptor	4.1	4.8
1441799_at	RIKEN cDNA 6030422H21 gene	1.3	2.2
1441747_at	-	2.3	1.1
1441680_at	RNA binding motif, single stranded interacting protein	1.1	3.9
1441667_s_at	SET and MYND domain containing 1	4	4.2
1441379_at	expressed sequence AU045094	5.3	4.5
1441164_at	RIKEN cDNA 9630014M24 gene; Rho GTPase activating protein 26; predicted gene 5820	2.8	2.8
1440889_at	cDNA sequence BC006965	3.3	1.9
1440865_at	interferon induced transmembrane protein 6	2.2	2.5
1440843_at	RIKEN cDNA A230051N06 gene	3	1.3

1440592_at	CD80 antigen	4.9	1
1440582_at	itchy, E3 ubiquitin protein ligase	5.1	1.2
1440212_at	solute carrier family 12, member 1	4.4	1.8
1440016_at	dihydrolipoamide branched chain transacylase E2	3.2	2.3
1439956_at	membrane-spanning 4-domains, subfamily A, member 6B	1	2
1439431_x_at	bicaudal D homolog 1 (Drosophila)	3.7	5.1
1438998_at	cyclin H	2.6	1.2
1438461_at	KH domain containing, RNA binding, signal transduction associated 1	3.9	4
1437935_at	RIKEN cDNA 4930486G11 gene	2.3	1.3
1437726_x_at	complement component 1, q subcomponent, beta polypeptide	1.1	2.6
1437323_a_at	islet amyloid polypeptide	1.1	1.5
1436975_at	POM121 membrane glycoprotein-like 2 (rat)	2.7	2.7
1436397_at	TRAF-interacting protein with forkhead-associated domain, family member B	3.3	1.8
1436382_at	zinc finger and BTB domain containing 12	1	1.8
1435761_at	cDNA sequence BC100530; stefin A3	4.4	2
1435665_at	expressed sequence AI451617	2.9	5.1
1435628_x_at	cDNA sequence BC005512	1.9	2.2
1434716_at	hepatitis A virus cellular receptor 1	1.2	2.5
1433987_at	hippocalcin-like 4	1.4	1.3
1433837_at	RIKEN cDNA 8430408G22 gene	1.6	1.4
1433836_a_at	RIKEN cDNA 8430408G22 gene	1.4	1.2
1433362_at	RIKEN cDNA 4930527F18 gene	4.7	3.5

	histocompatibility 2, Q region locus 1; histocompatibility 2, Q region locus 9; similar to H-2 class I histocompatibility antigen, L-D alpha chain precursor; histocompatibility 2, Q region locus 8;		
1431008_at	histocompatibility 2, Q region locus 2; similar to MHC class Ib antigen; histocompatibility 2, Q region locus 7;	2	2
	histocompatibility 2, Q region locus 6; hypothetical protein LOC100044307; similar to H-2 class I histocompatibility antigen, Q7 alpha chain precursor (QA-2 antigen); RIKEN cDNA 0610037M15 gene		
1430868_at	RIKEN cDNA 5830403M04 gene	6.6	4.7
1430858_at	RIKEN cDNA 4632433K11 gene	2.5	3.2
1430669_at	keratin associated protein 4-7	4.4	3.1
1430016_at	RIKEN cDNA 4930584F24 gene	2.6	3
1430009_at	heat shock transcription factor, Y linked 2	3.6	1.6
1429954_at	C-type lectin domain family 4, member a3	1.1	3.1
1429524_at	myosin IF	1.2	1.5
1428960_at	enkurin, TRPC channel interacting protein	3.2	3.5
1428352_at	arrestin domain containing 2	1.5	3.6
1427869_at	immunoglobulin heavy chain 6 (heavy chain of IgM)	2.3	3.4
1427851_x_at	similar to RGD1359202 protein	1.5	1.2



	immunoglobulin kappa chain variable 21 (V21)-1; similar to		
1427799_x_at	Chain L, Structural Basis Of Antigen Mimicry In A Clinically Relevant Melanoma Antigen System	1.2	2.2
1427797_s_at	cathepsin E	2	1.4
1427747_a_at	lipocalin 2	1	3.5
1427327_at	paired immunoglobulin-like type 2 receptor alpha	1.6	1.4
1427025_at	myotubularin related protein 7	1.2	1.2
1426936_at	cDNA sequence BC005512	4	2.2
1426112_a_at	CD72 antigen	1.1	1.1
1425645_s_at	cytochrome P450, family 2, subfamily b, polypeptide 10	1	1.3
1425548_a_at	leukocyte specific transcript 1	1	2
1425451_s_at	chitinase 3-like 4	3.2	3.1
1425407_s_at	C-type lectin domain family 4, member a2	1.2	2.5
1425225_at	Fc receptor, IgG, low affinity IV similar to tripartite motif	1.6	2.1
1424857_a_at	protein TRIM34 alpha; tripartite motif-containing 34; similar to Tripartite motif protein 34	1.9	1.2
1424494_s_at	FLYWCH family member 2 similar to Leukocyte	4.5	3.8
1424302_at	immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3	1.1	1.4
1424109_a_at	glyoxalase 1	1.1	1
1422953_at	formyl peptide receptor 2	1.6	1.8
1422708_at	phosphoinositide-3-kinase, catalytic, gamma polypeptide	1.1	3.8
1422347_at	neuropeptide Y receptor Y6	1.4	3.6

1422013_at	C-type lectin domain family 4, member a2	1.5	2.3
1421947_at	guanine nucleotide binding protein (G protein), gamma 12	1.2	1
1421818_at	B-cell leukemia/lymphoma 6	1.2	1.7
1420699_at	C-type lectin domain family 7, member a	1.1	2.3
1420697_at	solute carrier family 15, member 3	1.7	2.2
	hypothetical protein LOC100038909; similar to PIRA2; hypothetical protein LOC100038908; predicted gene 15448; paired-Ig-like receptor A11; paired-Ig-like receptor A5;		
1420464_s_at	paired-Ig-like receptor A6; paired-Ig-like receptor A4; paired-Ig-like receptor A7; predicted gene 15930; paired-Ig-like receptor A1; paired-Ig-like receptor A2; predicted gene 10693 hypothetical protein LOC100044239; killer cell	1.2	2.8
1420421_s_at	lectin-like receptor subfamily B member 1B; hypothetical protein LOC100044240 predicted gene 2135; predicted gene 2104; cytoplasmic	1.1	1.3
1419959_s_at	polyadenylated homeobox similar to Chitinase 3-like protein 3 precursor (Secretory protein Ym1) (Eosinophil chemotactic cytokine) (ECF-L); chitinase 3-like 3; predicted gene 6522	3	1
1419764_at		3.9	3.3

1419691_at	cathelicidin antimicrobial peptide	4.8	4
1419609_at	chemokine (C-C motif) receptor 1	1.2	1.2
1419515_at	FYVE, RhoGEF and PH domain containing 2	1.4	1.4
1419434_at	solute carrier family 2 (facilitated glucose transporter), member 10	2.5	2.2
1419394_s_at	S100 calcium binding protein A8 (calgranulin A)	4.4	3.5
1419201_at	kallikrein related-peptidase 11	2.9	3.9
1418878_at	acrosomal vesicle protein 1	4.9	2
1418867_at	cytochrome P450, family 24, subfamily a, polypeptide 1	2.1	1
1418866_at	cytochrome P450, family 24, subfamily a, polypeptide 1	2.3	1
	hypothetical protein LOC100038909; similar to PIRA2; hypothetical protein LOC100038908; predicted gene 15448; paired-Ig-like receptor A11; paired-Ig-like receptor A5;		
1418809_at	paired-Ig-like receptor A6; paired-Ig-like receptor A4; paired-Ig-like receptor A7; predicted gene 15930; paired-Ig-like receptor A1; paired-Ig-like receptor A2; predicted gene 10693	1	1.7
1418774_a_at	ATPase, Cu <sup>++</sup> transporting, alpha polypeptide	1.7	1.5
1418722_at	neutrophilic granule protein	2.1	2.5
1418655_at	beta-1,4-N-acetyl-galactosaminyl transferase 1	2.8	2.9

1418536_at	<p>histocompatibility 2, Q region locus 1; histocompatibility 2, Q region locus 9; similar to H-2 class I histocompatibility antigen, L-D alpha chain precursor; histocompatibility 2, Q region locus 8;</p> <p>histocompatibility 2, Q region locus 2; similar to MHC class Ib antigen; histocompatibility 2, Q region locus 7;</p> <p>histocompatibility 2, Q region locus 6; hypothetical protein LOC100044307; similar to H-2 class I histocompatibility antigen, Q7 alpha chain precursor (QA-2 antigen); RIKEN cDNA 0610037M15 gene</p>	2.1	2.5
1417822_at	DNA segment, Chr 17, human D6S56E 5	3.1	3
1417821_at	DNA segment, Chr 17, human D6S56E 5	4.1	3.7
1417649_at	cyclin-dependent kinase inhibitor 1C (P57)	1.3	1.3
1417506_at	geminin	1.7	1.1
1416025_at	fibrinogen gamma chain	1.2	2.3

\*Fold change は  $\log_2$  値で表す。

表3 低分子量ヘパリン投与により iNOS トランスジェニックマウス腎臓において発現低下した遺伝子群

AFFYMETRIX_3PRIME _IVT_ID	Gene Name	Fold change* (Exp-1)	Fold change* (Exp-2)
1460606_at	hydroxysteroid (17-beta) dehydrogenase 13	-1.3	-1.3
1460449_at	ankyrin repeat and sterile alpha motif domain containing 1B	-1.3	-3.2
1460365_a_at	dynamamin 1	-3.1	-2.4
1460314_s_at	histone cluster 2, H3b; histone cluster 1, H3f; histone cluster 1, H3e; histone cluster 2, H3c1; histone cluster 1, H3d; histone cluster 1, H3c; histone cluster 1, H3b; histone cluster 2, H3c2; histone cluster 2, H2aa1; histone cluster 2, H2aa2	-2.1	-1.9
1460092_at	limbic system-associated membrane protein	-3.6	-2.6
1460009_at	immediate early response 5 signal transducing adaptor	-2.9	-3
1459427_at	molecule (SH3 domain and ITAM motif) 1	-1.6	-1.4
1458585_at	-	-1.9	-1.4
1458355_x_at	WD repeat domain 92 similar to Dual-specificity	-2.8	-2.5
1457667_x_at	tyrosine-(Y)-phosphorylation regulated kinase 2	-3.3	-3.5
1457588_at	expressed sequence C76213	-3.6	-5.1
1457545_at	RIKEN cDNA 9530036011Rik	-3.7	-2.6
1457306_at	aminolevulinate, delta-, dehydratase	-1.1	-1.1
1457102_at	RIKEN cDNA A030001D16 gene	-4.1	-3
1456839_at	GRAM domain containing 1B	-2	-3.2

1456787_at	RIKEN cDNA 2810055G20 gene	-3.9	-2.5
1456493_at	similar to Sp110 nuclear body protein	-2.9	-3.6
1455530_at	immunoglobulin heavy variable V14-2	-5.4	-1.2
1455471_at	canopy 1 homolog (zebrafish)	-1.1	-3.5
1454536_at	transmembrane protein 30C	-2.8	-4.5
1454297_at	RIKEN cDNA 4631402F24 gene	-2.6	-3.7
1454065_at	RIKEN cDNA 4930562D21 gene	-4	-3.6
1454015_a_at	cadherin 13	-3.7	-2.8
1453823_a_at	coiled-coil domain containing 76 predicted gene,	-1.6	-1.1
1453780_at	ENSMUSG00000043151	-4.5	-3.1
1453770_at	carboxypeptidase A4	-3.1	-3.3
1453472_a_at	SLAM family member 7	-1.3	-1.2
1453233_s_at	calreticulin 3	-2.9	-1.8
1453132_a_at	gastrokine 2	-2.6	-1
1452677_at	similar to polynucleotide phosphorylase-like protein; polyribonucleotide nucleotidyltransferase 1 histocompatibility 2, D region;	-1.5	-1.7
1452544_x_at	histocompatibility 2, D region locus 1	-4.6	-3.8
1452277_at	arylsulfatase G	-1	-2.3
1452014_a_at	insulin-like growth factor 1	-1.9	-1
1451901_at	helicase-like transcription factor	-3.7	-2.1
1451886_at	SPEG complex locus	-3.1	-2.7

	predicted gene 5353; immunoglobulin heavy chain (J558 family); similar to Ig heavy chain V region 108A precursor; similar to Ig heavy chain V-I region V35 precursor; predicted gene 900;		
1451632_a_at	immunoglobulin heavy chain complex; similar to Ig H-chain V-JH1-region; immunoglobulin heavy variable V1-31; immunoglobulin heavy chain 2 (serum IgA)	-8.2	-6.4
1451594_s_at	serine (or cysteine) peptidase inhibitor, clade B, member 6c	-4.3	-1.7
1451228_a_at	syncollin	-2.2	-5.1
1451060_at	G protein-coupled receptor 146	-1.4	-2.3
1450979_at	carcinoembryonic antigen-related cell adhesion molecule 14	-5.2	-5.6
1450336_at	SET domain containing 1A	-2.1	-1.8
1450238_at	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme	-3.4	-4.6
1450130_at	xenotropic and polytropic retrovirus receptor 1	-1.1	-1.1
1449486_at	carboxylesterase 1	-1.7	-3.8
1449280_at	endothelial cell-specific molecule 1	-1	-1.4
1449030_at	synapsin II	-4	-1.2
1448735_at	ceruloplasmin	-2.1	-1.7
1448239_at	heme oxygenase (decycling) 1	-1.4	-1.5
1447792_x_at	G protein-coupled receptor 174 resistance to inhibitors of	-5.7	-1.7
1447553_x_at	cholinesterase 3 homolog (C. elegans)	-4.8	-1
1447044_at	-	-1	-3.6
1447020_at	zinc finger protein, multitype 2	-2	-1.2

1446944_at	DNA segment, Chr 1, ERATO Doi 84, expressed	-2.7	-4.1
1446781_at	DNA segment, Chr 8, ERATO Doi 54, expressed	-3.2	-5.1
1445944_at	RIKEN cDNA 4930522L14 gene	-2.4	-2.1
1445354_at	family with sequence similarity 55, member C	-1	-1.4
1444995_at	chromodomain protein, Y chromosome-like 2	-2.3	-2.1
1444980_at	one cut domain, family member 2	-2.7	-3.4
1444589_at	predicted gene 4944	-2.1	-2
1444493_at	TBC1 domain family, member 2B	-2.8	-2.2
1443546_at	high density lipoprotein (HDL) binding protein	-1.3	-1.7
1443322_at	-	-1.7	-3.5
1443296_at	PCTAIRE-motif protein kinase 1	-3.1	-1.9
1442911_at	RIO kinase 2 (yeast)	-1.9	-2.4
1442558_at	predicted gene 10421	-1.4	-2.9
1442494_at	expressed sequence C79242	-1.9	-1.2
1442400_at	-	-3.1	-2.1
1442340_x_at	cysteine rich protein 61	-1.3	-2.6
1442167_at	cytoplasmic FMR1 interacting protein 2	-2.7	-3.7
1441784_at	collagen and calcium binding EGF domains 1	-3.4	-3.9
1441732_at	teashirt zinc finger family member 1	-2.9	-2.9
1441697_at	mastermind like 1 (Drosophila)	-2.5	-2.9
1441618_at	Rho GTPase activating protein 29	-3.7	-3.3
1441560_at	catenin (cadherin associated protein), alpha 3	-3.2	-1.9
1441471_at	RIKEN cDNA 2810002D19 gene	-2.5	-2.1
1441273_at	leucine-rich repeats and calponin homology (CH) domain containing 2	-3.2	-2.4
1441190_at	actin related protein 2/3 complex, subunit 5-like	-1.9	-3.2



1441112_at	similar to Zinc finger BED domain containing protein 4	-1.1	-1.1
1440887_at	RIKEN cDNA C330005M16 gene	-1.5	-3
1440638_at	RIKEN cDNA A230107N01 gene	-5.4	-4
1440511_at	proteasome (prosome, macropain) activator subunit 4	-1.5	-1.2
1439944_at	-	-3.7	-1.1
1439886_at	-	-2.2	-2.3
1439812_at	RIKEN cDNA 4930402H24 gene	-3.1	-3.1
1439780_at	ribosomal protein L7-like 1; predicted gene 11222	-2.5	-2.7
1439651_at	LIM domain only 4	-3.9	-3.4
1439289_s_at	PNMA-like 1	-3.6	-3.5
1438751_at	solute carrier family 30, member 10	-2	-3.4
1437784_at	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	-1.6	-1.9
1437311_at	small nucleolar RNA host gene 11 (non-protein coding)	-2.3	-2.3
1437128_a_at	RIKEN cDNA A630033E08 gene	-2.6	-2.4
1436957_at	gamma-aminobutyric acid (GABA) A receptor, subunit alpha 3	-1.1	-3.3
1436569_at	phosphatidylinositol-3,4,5-tris phosphate-dependent Rac exchange factor 2	-1.1	-1
1436362_x_at	predicted gene 4638	-1.1	-1.1
1436250_at	RIKEN cDNA 5430405G05 gene	-3.3	-3.9
1435751_at	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	-3.6	-1.9
1434295_at	RAS guanyl releasing protein 1	-1.1	-2.1
1434292_at	small nucleolar RNA host gene 11 (non-protein coding)	-7.1	-6.2
1434280_at	widely-interspaced zinc finger motifs	-1.2	-1
1433944_at	HECT domain containing 2	-2.6	-3.3

1433311_at	RIKEN cDNA D530031A16 gene	-3.7	-3.6
1432598_at	germ cell-less homolog 1 (Drosophila)	-1.5	-2.8
1432327_at	RIKEN cDNA 9530067L11 gene	-1.8	-1.8
1432278_at	RIKEN cDNA 4930471M09 gene	-3.5	-2.5
1432255_at	microtubule associated serine/threonine kinase 1	-3	-3.4
1432141_x_at	gasdermin A2	-2.2	-3.7
1431314_a_at	RIKEN cDNA 5830417I10 gene; similar to GON-4-like protein (GON-4 homolog); similar to Dingo protein isoform 2	-3.4	-3.5
1431216_s_at	DnaJ (Hsp40) homolog, subfamily C, member 6	-5	-3.6
1431210_at	ATP/GTP binding protein-like 3	-3.4	-3
1430988_at	RIKEN cDNA 2810407C02 gene	-2.7	-3
1430971_a_at	aquarius	-3.4	-1.6
1430903_at	RIKEN cDNA 4933416017 gene	-2.5	-2
1430446_at	RIKEN cDNA 2310057B04 gene	-4.2	-2.9
1429922_at	predicted gene 13629	-1.1	-3.8
1428799_at	Leber congenital amaurosis 5 (human)	-3.5	-2.2
1428033_at	predicted gene 4979; predicted gene 14139	-2.1	-2.6
1428010_at	translocase of inner mitochondrial membrane 9 homolog (yeast)	-2.5	-2.7
1427651_x_at	histocompatibility 2, D region; locus 1	-3.4	-2.8
1427451_a_at	cDNA sequence BC018473	-5.8	-6.3
1427351_s_at	immunoglobulin heavy chain 6 (heavy chain of IgM)	-5.3	-1.6
1427329_a_at	immunoglobulin heavy chain 6 (heavy chain of IgM)	-5.1	-1.4

1426340_at	solute carrier family 1 (glial high affinity glutamate transporter), member 3 similar to tripartite motif	-2.8	-1.1
1426093_at	protein TRIM34 alpha; tripartite motif-containing 34; similar to Tripartite motif protein 34	-1.7	-1.6
1425917_at	histocompatibility 28	-4.7	-5.1
1425722_at	interferon inducible GTPase 1; interferon-inducible GTPase-like	-1.1	-1.8
1425614_x_at	histocompatibility 2, D region; histocompatibility 2, D region locus 1	-5.5	-4.8
1425500_x_at	-	-4	-3.7
1425469_a_at	-	-1	-1
1425261_at	CCAAT/enhancer binding protein (C/EBP), gamma	-1	-1.8
1425166_at	retinoblastoma-like 1 (p107)	-2.4	-1.8
1425165_at	granzyme N similar to DNA cytosine-5 methyltransferase 3-like	-2.4	-1.6
1425035_s_at	protein; DNA (cytosine-5-)-methyltransferase 3-like	-4.4	-1
1424233_at	mesenchyme homeobox 2	-2.9	-2
1424007_at	growth differentiation factor 10	-1.8	-1.2
1423412_at	RNA binding motif protein 47 vesicle-associated membrane	-4	-3.4
1423152_at	protein, associated protein B and C	-1	-1.1
1422812_at	chemokine (C-X-C motif) receptor 6	-2	-1.6
1422758_at	carbohydrate sulfotransferase 2 similar to X-linked	-2.2	-2.1
1422011_s_at	lymphocyte-regulated protein pM1; X-linked	-1.2	-1.4

	lymphocyte-regulated complex; predicted gene 14599		
1421596_s_at	histocompatibility 28	-2.6	-2.1
1421434_at	dynein, axonemal, heavy chain 5 similar to guanylate nucleotide	-2.8	-2.6
1420549_at	binding protein 1; guanylate binding protein 1	-4.2	-3.5
1420352_at	protease, serine, 22	-3.1	-2.7
1420009_at	WW, C2 and coiled-coil domain containing 1	-2.6	-2.6
1419771_at	voltage-dependent anion channel 1	-1.3	-2.8
1419686_at	testis specific gene A14	-4.6	-4.1
1419670_at	formiminotransferase cyclodeaminase	-2.1	-1.4
1418697_at	indolethylamine N-methyltransferase	-1.1	-1.3
1418535_at	ral guanine nucleotide dissociation stimulator,-like 1	-1	-1.3
1418441_at	collagen, type VIII, alpha 1	-1.8	-1.5
1418276_at	E74-like factor 2	-3.2	-2.7
1417889_at	apolipoprotein B mRNA editing enzyme, catalytic polypeptide 2; similar to APOBEC-2 protein	-2.3	-2.5
1417356_at	paternally expressed 3; antisense transcript gene of Peg3	-3.4	-1.5
1417079_s_at	lectin, galactose-binding, soluble 2	-3.1	-3.9
1416487_a_at	yes-associated protein 1	-1.3	-1.6

\*Fold change は  $\log_2$  値で表す。