

<別紙2>

298	mitochondrial acyl-CoA thioesterase 1	0.0494
299	mitochondrial ribosomal protein L11	0.0051
300	mitochondrial ribosomal protein L30 (predicted)	0.0066
301	mitochondrial ribosomal protein L46 (predicted)	0.0427
302	mitochondrial ribosomal protein S15	0.0141
303	mitochondrial ribosome recycling factor (predicted)	0.0061
304	mitochondrial translation optimization 1 homolog (<i>S. cerevisiae</i>) (predicted)	0.0059
305	mitochondrial tumor suppressor 1	0.0245
306	mitochondrial tumor suppressor 1	0.0031
307	Mitogen-activated protein kinase 9	0.0133
308	molybdenum cofactor sulfurase (predicted)	0.0054
309	monoamine oxidase A	0.0019
310	Monoglyceride lipase	0.0375
311	motile sperm domain containing 3 (predicted)	0.0021
312	Murinoglobulin 1 homolog (mouse)	0.0188
313	Murinoglobulin 1 homolog (mouse) /// alpha-1-inhibitor III	0.0060
314	N-acetyltransferase 1 (arylamine N-acetyltransferase)	0.0434
315	N-acetyltransferase 8 (camello like)	0.0001
316	NAD synthetase 1	0.0173
317	NAD(P) dependent steroid dehydrogenase-like	0.0117
318	NAD(P)H dehydrogenase, quinone 2	0.0016
319	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 3 (predicted)	0.0100
320	NADH dehydrogenase (ubiquinone) Fe-S protein 7 (predicted)	0.0031
321	NADH dehydrogenase (ubiquinone) Fe-S protein 8 (predicted)	0.0097
322	nebulin-related anchoring protein (predicted)	0.0242
323	nesprin-1	0.0235
324	neuralized-like 2 (<i>Drosophila</i>) (predicted)	0.0191
325	nicotinamide N-methyltransferase (predicted)	0.0036
326	nicotinate phosphoribosyltransferase-like protein	0.0143
327	nicotinate phosphoribosyltransferase-like protein	0.0111
328	nuclear factor I/A	0.0044
329	nuclear factor I/A	0.0022
330	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4 (predicted)	0.0106
331	nuclear factor, erythroid derived 2 (predicted)	0.0197
332	Nuclear receptor coactivator 2	0.0036
333	nuclear receptor subfamily 0, group B, member 2	0.0036
334	nuclear receptor subfamily 1, group I, member 3	0.0001
335	nuclear receptor subfamily 3, group C, member 1	0.0036

336	nuclear receptor subfamily 3, group C, member 1	0.0050
337	nucleoside phosphorylase	0.0117
338	nucleosome binding protein 1 (predicted)	0.0064
339	olfactory receptor 59	0.0007
340	opioid receptor, sigma 1	0.0049
341	optineurin	0.0032
342	ornithine aminotransferase	0.0016
343	OTU domain, ubiquitin aldehyde binding 2 (predicted)	0.0027
344	paraoxonase 1	0.0059
345	paraoxonase 3	0.0025
346	PDZ domain containing 1	0.0042
347	peroxiredoxin 5	0.0084
348	peroxisomal acyl-CoA thioesterase 1	0.0010
349	peroxisomal biogenesis factor 13 (predicted)	0.0044
350	peroxisomal biogenesis factor 14	0.0161
351	peroxisomal biogenesis factor 3	0.0154
352	peroxisomal membrane protein 2	0.0031
353	peroxisomal membrane protein 4	0.0158
354	peroxisome biogenesis factor 16 (predicted)	0.0047
355	phosphate cytidyltransferase 2, ethanolamine	0.0024
356	phosphatidylcholine transfer protein	0.0124
357	phosphodiesterase 2A, cGMP-stimulated	0.0263
358	phosphodiesterase 3B	0.0315
359	phosphoenolpyruvate carboxykinase 1	0.0004
360	phospholipase C, beta 1	0.0014
361	plakophilin 4 (predicted)	0.0055
362	plasma glutamate carboxypeptidase	0.0086
363	pleckstrin homology domain containing, family E (with leucine rich repeats) member 1	0.0244
364	plexin A2 (predicted)	0.0059
365	polymerase (DNA directed), gamma	0.0268
366	polymerase (DNA directed), gamma	0.0307
367	polymerase (DNA-directed), delta 4 (predicted)	0.0045
368	polymerase (DNA-directed), delta interacting protein 2 (predicted)	0.0246
369	polymerase (DNA-directed), delta interacting protein 2 (predicted)	0.0021
370	polymerase (RNA) mitochondrial (DNA directed) (predicted)	0.0059
371	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 2	0.0058
372	probasin	0.0022
373	progesterone receptor membrane component 2 (predicted)	0.0431

<別紙2>

374	progesterone receptor membrane component 2 (predicted)	0.0113
375	programmed cell death 8	0.0028
376	Progressive ankylosis homolog (mouse)	0.0154
377	propionyl-coenzyme A carboxylase, alpha polypeptide	0.0028
378	Proprotein convertase subtilisin/kexin type 5	0.0009
379	prostaglandin D2 synthase 2	0.0318
380	Prostaglandin E receptor 3 (subtype EP3)	0.0028
381	Prostaglandin E receptor 3 (subtype EP3)	0.0030
382	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9	0.0139
383	protein C	0.0003
384	protein distantly related to to the gamma subunit family	0.0108
385	protein disulfide isomerase-associated 5	0.0043
386	Protein kinase C, epsilon	0.0288
387	Protein kinase C, mu	0.0036
388	protein phosphatase 1, regulatory (inhibitor) subunit 3B	0.0018
389	Protein phosphatase 1, regulatory (inhibitor) subunit 3B	0.0078
390	protein phosphatase 1, regulatory (inhibitor) subunit 3C (predicted)	0.0008
391	Protein phosphatase V	0.0136
392	protein S (alpha)	0.0074
393	Protein tyrosine phosphatase, receptor type, U	0.0262
394	proteosome (prosome, macropain) subunit, beta type 8	0.0028
395	proteosome (prosome, macropain) subunit, beta type 9	0.0349
396	protoporphyrinogen oxidase (predicted)	0.0083
397	PTEN induced putative kinase 1 (predicted)	0.0033
398	PTEN induced putative kinase 1 (predicted)	0.0024
399	purinergic receptor P2Y, G-protein coupled 2	0.0014
400	Putative chloride channel (similar to Mm Clcn4-2)	0.0000
401	Pyruvate carboxylase	0.0010
402	pyruvate dehydrogenase kinase 1	0.0109
403	pyruvate dehydrogenase kinase, isoenzyme 2	0.0034
404	pyruvate dehydrogenase kinase, isoenzyme 4	0.0260
405	pyruvate kinase, liver and RBC	0.0029
406	quinoid dihydropteridine reductase	0.0026
407	quinolinate phosphoribosyltransferase (predicted)	0.0026
408	Rab38, member of RAS oncogene family	0.0297
409	Rab40b, member RAS oncogene family (predicted)	0.0056
410	Radixin	0.0056
411	ras homolog gene family, member N (predicted)	0.0276
412	RAS-related C3 botulinum substrate 2 (predicted)	0.0178

413	Ras-related GTP-binding protein Rab29	0.0068
414	Reticulon 4 receptor-like 1	0.0168
415	Reticulon 4 receptor-like 2	0.0005
416	Retinoic acid receptor, beta	0.0478
417	retinol dehydrogenase 11 (predicted)	0.0075
418	retinol dehydrogenase 5 (predicted)	0.0010
419	ribonuclease P 21kDa subunit (human)	0.0026
420	Ribosomal protein L31	0.0287
421	ring finger protein 141	0.0119
422	Ring finger protein 141	0.0101
423	ring finger protein 8 (predicted)	0.0022
424	RT1 class Ib, locus Aw2	0.0036
425	RT1 class Ib, locus Aw2 /// histocompatibility 2, T region locus 24 /// RT1 class I, CE14 /// RT1 class I, CE2 /// RT1 class I, CE15 /// RT1 class I, CE10	0.0362
426	RT1 class Ib, locus S3	0.0003
427	RT1 class Ib, locus S3	0.0009
428	RT1 class II, locus Bb	0.0020
429	RT1 class II, locus Db1	0.0275
430	RWD domain containing 3	0.0133
431	S-adenosylhomocysteine hydrolase	0.0034
432	scavenger receptor class B, member 1	0.0041
433	scavenger receptor class B, member 1	0.0164
434	SEC14-like 2 (<i>S. cerevisiae</i>)	0.0034
435	secernin 2 (predicted)	0.0084
436	secreted and transmembrane 1	0.0002
437	selenocysteine lyase	0.0004
438	selenophosphate synthetase 1 (predicted)	0.0170
439	selenophosphate synthetase 2 (predicted)	0.0004
440	selenoprotein P, plasma, 1	0.0369
441	sepiapterin reductase	0.0282
442	serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antipeptidase, antitrypsin), member 7	0.0004
443	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 6	0.0033
444	Serine (or cysteine) proteinase inhibitor, clade F), member 1	0.0017
445	serine (or cysteine) proteinase inhibitor, clade F, member 2 (predicted)	0.0059
446	serine hydroxymethyl transferase 1 (soluble) (predicted)	0.0132
447	serine hydroxymethyl transferase 2 (mitochondrial) (predicted)	0.0085
448	Serine protease inhibitor	0.0002

<別紙2>

449	Serine protease inhibitor	0.0216
450	Sertolin	0.0266
451	serum amyloid A 4 (predicted)	0.0076
452	serum amyloid P-component	0.0023
453	serum deprivation response protein	0.0066
454	SH3 domain protein 2 C1	0.0013
455	SH3 domain protein 4	0.0240
456	Sh3 domain YSC-like 1 (predicted)	0.0174
457	sialyltransferase 10 (alpha-2,3-sialyltransferase VI)	0.0017
458	signal transducer and activator of transcription 1	0.0246
459	Signal transducer and activator of transcription 1	0.0025
460	signal transducer and activator of transcription 5A	0.0108
461	Sil1 protein	0.0025
462	similar to 9230105E10Rik protein (predicted)	0.0083
463	similar to Aa2-174 (predicted)	0.0172
464	similar to Ab2-225 (predicted)	0.0025
465	similar to abhydrolase domain containing 1; alpha/beta hydrolase-1; lung alpha/beta hydrolase 1 (predicted)	0.0050
466	similar to aldehyde oxidase structural homolog 2 (predicted)	0.0168
467	similar to Antxr2 protein	0.0017
468	similar to Apolipoprotein C2	0.0377
469	similar to armadillo repeat-containing protein	0.0054
470	similar to ATP-binding cassette transporter ABCG3	0.0038
471	similar to binding protein	0.0007
472	similar to binding protein	0.0034
473	similar to C530044N13Rik protein (predicted)	0.0054
474	similar to cDNA sequence BC006662 (predicted)	0.0002
475	similar to cDNA sequence BC021608	0.0003
476	similar to choline phosphotransferase 1; cholinephosphotransferase 1 alpha; cholinephosphotransferase 1	0.0205
477	similar to chromosome 16 open reading frame 5 (predicted)	0.0087
478	similar to chromosome 20 open reading frame 116 (predicted)	0.0179
479	similar to chromosome 20 open reading frame 155 (predicted)	0.0232
480	similar to DNA segment, Chr 16, ERATO Doi 472, expressed	0.0276
481	similar to Dorz1 (predicted)	0.0028
482	similar to ezrin-binding partner PACE-1 (predicted)	0.0445
483	similar to genethonin 1 (predicted)	0.0146
484	similar to glioma-amplified sequence-41 (predicted)	0.0071
485	similar to HSPC288 (predicted)	0.0052
486	similar to hypothetical p38 protein (predicted)	0.0145

<別紙2>

487	similar to hypothetical protein D4ErtD765e (predicted)	0.0009
488	similar to hypothetical protein DKFZp313N0621	0.0070
489	similar to hypothetical protein FLJ11354 (predicted)	0.0087
490	similar to hypothetical protein FLJ12660 (predicted)	0.0041
491	similar to hypothetical protein FLJ14146 (predicted)	0.0208
492	similar to hypothetical protein FLJ33868 (predicted)	0.0213
493	similar to hypothetical protein FLJ37953 (predicted)	0.0374
494	Similar to Hypothetical protein KIAA0141	0.0276
495	similar to Hypothetical protein MGC19163 (predicted)	0.0061
496	similar to Hypothetical protein MGC19163 (predicted)	0.0024
497	similar to hypothetical protein MGC37914 (predicted)	0.0000
498	similar to hypothetical protein MGC39389; MAQ1 paralog (predicted)	0.0089
499	similar to Hypothetical protein MGC59076 (predicted)	0.0041
500	similar to hypothetical protein supported by AL449243 (predicted)	0.0019
501	similar to igf2 mRNA-binding protein 3 (predicted)	0.0019
502	similar to IQ motif and WD repeats 1	0.0348
503	similar to KIAA1730 protein (predicted)	0.0344
504	similar to leucine zipper domain protein	0.0043
505	similar to maestro	0.0001
506	similar to MGC4645 protein	0.0055
507	similar to mKIAA1002 protein (predicted)	0.0267
508	similar to N-acetylglucosaminyltransferase IVb	0.0137
509	Similar to Nur77 downstream protein 2	0.0121
510	similar to Peci protein /// similar to RIKEN cDNA 1810022C23 (predicted)	0.0036
511	similar to protein phosphatase type 1B (formely 2C), Mg-dependent, beta isoform (predicted)	0.0171
512	similar to Pseudoautosomal GTP-binding protein-like protein (predicted)	0.0186
513	similar to RIKEN cDNA 0610012D14 (predicted)	0.0002
514	similar to RIKEN cDNA 0610038L10 gene	0.0250
515	Similar to RIKEN cDNA 0610042E07 (predicted)	0.0061
516	similar to RIKEN cDNA 0610042E07 (predicted)	0.0411
517	similar to RIKEN cDNA 1100001H23 (predicted)	0.0028
518	similar to RIKEN cDNA 1110013G13 (predicted)	0.0034
519	similar to RIKEN cDNA 1110025H10 (predicted)	0.0008
520	similar to RIKEN cDNA 1110038M16 (predicted)	0.0009
521	similar to RIKEN cDNA 1110055L24 (predicted)	0.0028
522	similar to RIKEN cDNA 1200006F02 (predicted)	0.0056
523	similar to RIKEN cDNA 1300002A08 (predicted)	0.0033
524	similar to RIKEN cDNA 1300006L01 (predicted)	0.0056

<別紙2>

525	similar to RIKEN cDNA 1700108L22 (predicted)	0.0061
526	similar to RIKEN cDNA 1700108L22 (predicted)	0.0095
527	similar to RIKEN cDNA 1700108L22 (predicted)	0.0200
528	similar to RIKEN cDNA 1810021J13 (predicted)	0.0124
529	similar to RIKEN cDNA 1810074P20 (predicted)	0.0387
530	similar to RIKEN cDNA 2010012O05 (predicted)	0.0189
531	similar to RIKEN cDNA 2010305A19 (predicted)	0.0124
532	similar to RIKEN cDNA 2310001A20 (predicted)	0.0012
533	Similar to RIKEN cDNA 2310036D22	0.0040
534	similar to RIKEN cDNA 2310036D22	0.0094
535	similar to RIKEN cDNA 2310067G05	0.0023
536	similar to RIKEN cDNA 2310067G05	0.0054
537	similar to RIKEN cDNA 2310079N02 (predicted)	0.0137
538	similar to RIKEN cDNA 2610318G18	0.0339
539	similar to RIKEN cDNA 2610528J11 (predicted)	0.0226
540	similar to RIKEN cDNA 2810405K02 (predicted)	0.0294
541	similar to RIKEN cDNA 2810408E11 (predicted)	0.0083
542	similar to RIKEN cDNA 2810428I15	0.0138
543	similar to RIKEN cDNA 2810451A06 (predicted)	0.0019
544	similar to RIKEN cDNA 4632417N05 (predicted)	0.0013
545	similar to RIKEN cDNA 4833422P03 (predicted)	0.0075
546	similar to RIKEN cDNA 4931406C07 (predicted)	0.0049
547	similar to RIKEN cDNA 5730469M10 (predicted)	0.0117
548	similar to RIKEN cDNA 5830404H04	0.0002
549	similar to RIKEN cDNA 5830404H04	0.0032
550	similar to RIKEN cDNA 5830468K18 (predicted)	0.0112
551	similar to RIKEN cDNA 6330416G13 gene (predicted)	0.0189
552	similar to RIKEN cDNA 9230117N10 (predicted)	0.0206
553	similar to RIKEN cDNA 9930118K05	0.0095
554	similar to RIKEN cDNA A530088I07 gene	0.0094
555	similar to RIKEN cDNA B430104H02	0.0013
556	similar to RIKEN cDNA C030006K11	0.0282
557	similar to RIKEN cDNA C330023F11 (predicted)	0.0023
558	similar to RIKEN cDNA D130038B21 (predicted)	0.0019
559	similar to RIKEN cDNA D130059P03 gene (predicted)	0.0044
560	similar to serine proteinase inhibitor A11 gene (SERPINA11)	0.0003
561	similar to Succinate semialdehyde dehydrogenase (NAD(+)-dependent succinic semialdehyde dehydrogenase)	0.0068
562	similar to This ORF is capable of encoding 404aa which is homologous to two human interferon-inducible proteins, 54 kDa and 56 kDa proteins;	0.0130

<別紙2>

	ORF	
563	similar to tumor-related protein (predicted)	0.0014
564	similar to U2 small nuclear ribonucleoprotein auxiliary factor 35 kDa subunit related-protein 1 (U2(RNU2) small nuclear RNA auxillary factor 1-like 1) (SP2)	0.0220
565	similar to Ubr2 protein	0.0011
566	similar to Veph-A (predicted)	0.0225
567	similar to zinc finger protein 650	0.0118
568	similar to zinc-finger homeodomain protein 4	0.0092
569	sirtuin 3 (silent mating type information regulation 2, homolog) 3 (S. cerevisiae) (predicted)	0.0012
570	SNF related kinase	0.0059
571	solute carrier family 16 (monocarboxylic acid transporters), member 10	0.0003
572	solute carrier family 16 (monocarboxylic acid transporters), member 7	0.0078
573	solute carrier family 20, member 2	0.0023
574	solute carrier family 21, member 10	0.0000
575	solute carrier family 25 (mitochondrial oxodicarboxylate carrier), member 21	0.0082
576	solute carrier family 28 (sodium-coupled nucleoside transporter), member 2	0.0141
577	solute carrier family 31 (copper transporters), member 1	0.0152
578	solute carrier family 37 (glycerol-6-phosphate transporter), member 4	0.0014
579	solute carrier organic anion transporter family, member 1a4	0.0001
580	Solute carrier organic anion transporter family, member 2a1	0.0220
581	solute carrier organic anion transporter family, member 2b1	0.0002
582	solute carrier organic anion transporter family, member 2b1	0.0003
583	sorbitol dehydrogenase	0.0029
584	sorting nexin 24 (predicted)	0.0041
585	spermidine/spermine N1-acetyl transferase 2 (predicted)	0.0060
586	spermine binding protein	0.0480
587	Sphingosine phosphate lyase 1	0.0061
588	Sphingosine-1-phosphate phosphatase 1	0.0232
589	stabilin 1 (predicted)	0.0176
590	stearoyl-Coenzyme A desaturase 1	0.0118
591	steroid 5 alpha-reductase 1	0.0013
592	sterol regulatory element binding factor 1	0.0207
593	stromal cell derived factor receptor 2 (predicted)	0.0141
594	succinate dehydrogenase complex, subunit D, integral membrane protein	0.0282
595	succinate dehydrogenase complex, subunit D, integral membrane protein	0.0094
596	sulfite oxidase	0.0117

<別紙2>

597	sulfotransferase family 1B, member 1	0.0145
598	sulfotransferase, estrogen preferring	0.0001
599	suppressor of cytokine signaling 2	0.0181
600	Suppressor of cytokine signaling 2	0.0285
601	Surfeit 1	0.0168
602	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	0.0040
603	Synaptobrevin-like 1	0.0297
604	synaptojanin 2 binding protein	0.0389
605	Synaptonemal complex protein 3	0.0060
606	synovial sarcoma, X breakpoint 2 interacting protein	0.0258
607	target of myb1 homolog (chicken) (predicted)	0.0137
608	T-box 3 (ulnar mammary syndrome)	0.0379
609	tec protein tyrosine kinase	0.0136
610	TERF1 (TRF1)-interacting nuclear factor 2	0.0056
611	thioredoxin 2	0.0081
612	thioredoxin reductase 2	0.0036
613	thyroid hormone receptor beta	0.0013
614	transcription factor 1	0.0098
615	transcription factor Pur-beta	0.0330
616	transferrin receptor 2 (predicted)	0.0007
617	translocase of inner mitochondrial membrane 8 homolog a (yeast)	0.0473
618	transmembrane 4 superfamily member 2	0.0489
619	transmembrane 9 superfamily protein member 4 (predicted)	0.0328
620	transmembrane protein 24 (predicted)	0.0234
621	Transporter	0.0399
622	trimethyllysine hydroxylase, epsilon	0.0050
623	tumor necrosis factor (ligand) superfamily, member 13 (predicted)	0.0032
624	tumor necrosis factor type 1 receptor associated protein	0.0031
625	tumor suppressing subtransferable candidate 5	0.0119
626	tumor suppressor pHyde	0.0119
627	Ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, C. elegans)	0.0028
628	UBX domain containing 2 (predicted)	0.0128
629	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 11 (GalNAc-T11)	0.0213
630	UDP-N-acetylglucosamine-2-epimerase/N-acetylmannosamine kinase	0.0020
631	Unknown (protein for MGC:72591)	0.0108
632	Unknown (protein for MGC:72981)	0.0190
633	Unknown (protein for MGC:72996)	0.0052
634	upstream transcription factor 2	0.0203

<別紙2>

635	urate oxidase	0.0271
636	vacuolar protein sorting 33A (yeast)	0.0019
637	vascular cell adhesion molecule 1	0.0178
638	V-maf musculoaponeurotic fibrosarcoma oncogene family, protein B (avian)	0.0003
639	Vps54-like	0.0120
640	Williams-Beuren syndrome chromosome region 14 homolog (human)	0.0060
641	Williams-Beuren syndrome chromosome region 14 homolog (human)	0.0027
642	xylosyltransferase II	0.0285
643	xylosyltransferase II	0.0121
644	Yamaguchi sarcoma viral (v-yes-1) oncogene homolog	0.0054
645	YY1 transcription factor	0.0221
646	zinc binding alcohol dehydrogenase, domain containing 2 (predicted)	0.0095
647	zinc finger protein 110 (predicted)	0.0159
648	zinc finger protein 213 (predicted)	0.0051
649	zinc finger protein 307 (predicted)	0.0328
650	zinc finger protein 324 (predicted)	0.0498
651	zinc finger protein 37	0.0469
652	zinc finger protein 455	0.0064
653	zinc finger protein 592 (predicted)	0.0380
654	zinc finger protein 67 (predicted)	0.0075
655	zinc finger, FYVE domain containing 21 (predicted)	0.0064

<別紙2>

ラット小型肝細胞において、成熟肝細胞と
比較して発現が誘導されている
遺伝子のリスト

No.	Gene Title	P value
1	1-acylglycerol-3-phosphate O-acyltransferase 1	0.0028
2	1-acylglycerol-3-phosphate O-acyltransferase 1	0.0073
3	2-4-dienoyl-Coenzyme A reductase 2, peroxisomal	0.0271
4	3-phosphoglycerate dehydrogenase	0.0023
5	a disintegrin and metalloproteinase domain 15 (metargidin)	0.0405
6	a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 1	0.0394
7	a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (predicted)	0.0355
8	A kinase (PRKA) anchor protein 13	0.0307
9	A kinase (PRKA) anchor protein 8	0.0068
10	Ac1158	0.0019
11	acidic nuclear phosphoprotein 32 family, member B	0.0055
12	acidic ribosomal phosphoprotein P0	0.0016
13	actin related protein 2/3 complex, subunit 1B	0.0027
14	actin related protein 2/3 complex, subunit 3 (predicted)	0.0004
15	actinin, alpha 1	0.0065
16	actinin, alpha 1	0.0059
17	activated leukocyte cell adhesion molecule	0.0016
18	activating transcription factor 4	0.0166
19	active BCR-related gene (predicted)	0.0353
20	acylphosphatase 1, erythrocyte (common) type (predicted)	0.0036
21	adaptor protein complex AP-1, gamma 2 subunit (predicted)	0.0110
22	adaptor protein complex AP-1, sigma 1 (predicted)	0.0101
23	adaptor-related protein complex 3, delta subunit (predicted)	0.0171
24	adducin 1 (alpha)	0.0122
25	ADP-ribosylarginine hydrolase	0.0232
26	ADP-ribosylation factor interacting protein 2 (arfaptin 2)	0.0115
27	ADP-ribosylation factor-like 3	0.0118
28	ADP-ribosyltransferase (NAD ⁺ ; poly (ADP-ribose) polymerase)-like 1 (predicted)	0.0247
29	adrenomedullin	0.0052
30	agrin	0.0020
31	ajuba homolog (Xenopus laevis)	0.0036
32	aldehyde dehydrogenase family 1, member A1	0.0036
33	aldolase A	0.0023
34	Alpha thalassemia/mental retardation syndrome X-linked homolog (human)	0.0101

<別紙2>

35	alpha-2,3-sialyltransferase ST3Gal IV	0.0206
36	alpha-2-macroglobulin	0.0135
37	anaphase promoting complex subunit 2 (predicted)	0.0073
38	ankyrin repeat domain 1 (cardiac muscle)	0.0002
39	ankyrin repeat domain 1 (cardiac muscle)	0.0008
40	Ankyrin repeat domain 1 (cardiac muscle)	0.0002
41	annexin A2	0.0021
42	annexin A4	0.0017
43	annexin A7	0.0031
44	apoptosis antagonizing transcription factor	0.0341
45	apurinic/aprimidinic endonuclease 1	0.0012
46	Arfaptin 1	0.0034
47	arginase 2	0.0044
48	arginyl-tRNA synthetase (predicted)	0.0001
49	armadillo repeat gene deleted in velo-cardio-facial syndrome (predicted)	0.0214
50	ARP2 actin-related protein 2 homolog (yeast) (predicted)	0.0023
51	ARF6 actin-related protein 6 homolog (yeast) (predicted)	0.0059
52	arrestin domain containing 1 (predicted)	0.0118
53	Arylsulfatase B	0.0079
54	arylsulfatase E (chondrodysplasia punctata 1) (predicted)	0.0188
55	ATP/GTP binding protein 1 (predicted)	0.0499
56	ATPase, Cu ⁺⁺ transporting, alpha polypeptide	0.0132
57	ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump), subunit 1	0.0028
58	ATPase, H ⁺ transporting, V0 subunit	0.0070
59	ATPase, Na ⁺ /K ⁺ transporting, beta 1 polypeptide	0.0199
60	ATP-binding cassette, sub-family A (ABC1), member 5	0.0192
61	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	0.0012
62	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	0.0042
63	ATP-binding cassette, sub-family G (WHITE), member 1	0.0039
64	B/K protein	0.0066
65	basic leucine zipper and W2 domains 2	0.0337
66	BCL2/adenovirus E1B 19 kDa-interacting protein 3-like	0.0151
67	bcl2-associated death promoter	0.0001
68	Bcl2-associated X protein	0.0024
69	Bcl2-like 1 /// similar to bcl-x short	0.0104
70	Bcl-2-related ovarian killer protein	0.0045
71	Bcl-2-related ovarian killer protein	0.0052
72	benzodiazepin receptor	0.0034
73	betacellulin	0.0013

<別紙2>

74	bicaudal D homolog 2 (<i>Drosophila</i>)	0.0056
75	bleomycin hydrolase (predicted)	0.0045
76	blocked early in transport 1 homolog (<i>S. cerevisiae</i>) like	0.0277
77	BMP and activin membrane-bound inhibitor, homolog (<i>Xenopus laevis</i>)	0.0036
78	bone morphogenic protein receptor, type II (serine/threonine kinase)	0.0237
79	brain abundant, membrane attached signal protein 1	0.0003
80	brain abundant, membrane attached signal protein 1	0.0012
81	brain glycogen phosphorylase	0.0085
82	brain protein 16	0.0305
83	brain-specific angiogenesis inhibitor 1-associated protein 2	0.0187
84	brain-specific angiogenesis inhibitor 1-associated protein 2	0.0464
85	branched chain aminotransferase 1, cytosolic	0.0174
86	breast cancer metastasis-suppressor 1 (predicted)	0.0266
87	budding uninhibited by benzimidazoles 1 homolog (<i>S. cerevisiae</i>) (predicted)	0.0165
88	C1q and tumor necrosis factor related protein 1	0.0290
89	cadherin 1	0.0028
90	cadherin 13	0.0301
91	cadherin 17	0.0231
92	cadherin 3, type 1, P-cadherin (placental)	0.0075
93	cadherin 6	0.0039
94	calbindin 3, (vitamin D-dependent calcium binding protein)	0.0308
95	calcineurin binding protein 1	0.0052
96	calcitonin-related polypeptide, beta	0.0004
97	calcium binding protein 39 (predicted)	0.0086
98	calcium binding protein 39 (predicted)	0.0031
99	calcium channel, voltage-dependent, beta 3 subunit	0.0036
100	calcium homeostasis endoplasmic reticulum protein (predicted)	0.0150
101	Calmodulin 1	0.0105
102	calmodulin 1	0.0100
103	calpain 1	0.0159
104	calpain 10	0.0110
105	calponin 3, acidic	0.0157
106	CaM-kinase II inhibitor alpha	0.0080
107	cAMP responsive element binding protein 3 (predicted)	0.0006
108	capicua homolog (<i>Drosophila</i>) (predicted)	0.0169
109	carbohydrate sulfotransferase 12 (predicted)	0.0403
110	carbonyl reductase 1	0.0013
111	carboxypeptidase E	0.0023
112	Casein kinase 1, delta	0.0293

<別紙2>

113	casein kinase 1, epsilon	0.0074
114	Casein kinase 1, gamma 3	0.0106
115	caspase 2	0.0047
116	catenin (cadherin-associated protein), alpha 1, 102kDa	0.0025
117	cathepsin E	0.0004
118	CCR4-NOT transcription complex, subunit 8 (predicted)	0.0026
119	CD151 antigen	0.0001
120	CD44 antigen	0.0001
121	CD63 antigen	0.0049
122	CDK2 (cyclin-dependent kinase 2)-associated protein 1 (predicted)	0.0076
123	CDK5 activator-binding protein	0.0223
124	cell division cycle 2 homolog A (<i>S. pombe</i>)	0.0362
125	cell division cycle 37 homolog (<i>S. cerevisiae</i>)	0.0027
126	cell division cycle associated 7 (predicted)	0.0023
127	centromere autoantigen B (predicted)	0.0030
128	ceruloplasmin	0.0263
129	CG6210-like	0.0027
130	chaperonin containing TCP1, subunit 2 (beta)	0.0036
131	chaperonin subunit 4 (delta)	0.0087
132	chaperonin subunit 7 (eta) (predicted)	0.0013
133	chemokine (C-C motif) ligand 7	0.0448
134	chemokine (C-X-C motif) ligand 2	0.0002
135	chemokine-like factor 1	0.0324
136	chloride intracellular channel 1	0.0012
137	choline transporter	0.0168
138	choline transporter	0.0042
139	chondroitin polymerizing factor	0.0013
140	chromobox homolog 6 (predicted)	0.0002
141	chromobox homolog 7	0.0027
142	Citrate synthase	0.0056
143	claudin 4 (predicted)	0.0015
144	clusterin	0.0049
145	coagulation factor 3	0.0041
146	coagulation factor II (thrombin) receptor	0.0105
147	cofactor required for Sp1 transcriptional activation, subunit 3 (predicted)	0.0074
148	cofilin 1	0.0003
149	collagen, type 1, alpha 1	0.0147
150	Collagen, type XXVII, alpha 1	0.0071
151	COMM domain containing 4 (predicted)	0.0020

<別紙2>

152	connective tissue growth factor	0.0025
153	copine II (predicted)	0.0050
154	core promoter element binding protein	0.0180
155	Core promoter element binding protein	0.0115
156	coronin, actin binding protein 1C (predicted)	0.0307
157	cortactin isoform B	0.0165
158	creatine kinase, brain	0.0097
159	crystallin, zeta (quinone reductase)-like 1 (predicted)	0.0064
160	CSX-associated LIM	0.0010
161	C-terminal binding protein 1	0.0021
162	CUG triplet repeat, RNA-binding protein 2	0.0362
163	Cyclic AMP phosphoprotein, 19 kDa	0.0260
164	cyclin D1	0.0095
165	cyclin D1	0.0249
166	cyclin D1	0.0145
167	cyclin dependent kinase inhibitor 2A	0.0025
168	cyclin-dependent kinase 5	0.0033
169	cyclin-dependent kinase 9	0.0083
170	cyclin-dependent kinase inhibitor 1A	0.0310
171	cystatin E/M	0.0112
172	cytochrome c oxidase subunit VIIa polypeptide 2 like (predicted)	0.0104
173	cytochrome P450, family 20, subfamily A, polypeptide 1	0.0087
174	cytoplasmic linker associated protein 1 (predicted)	0.0279
175	cytoskeleton associated protein 2 (predicted)	0.0099
176	cytoskeleton-associated protein 4 (predicted)	0.0043
177	Damage-specific DNA binding protein 1	0.0078
178	DEAD (Asp-Glu-Ala-Asp) box polypeptide 24	0.0155
179	DEAD (Asp-Glu-Ala-Asp) box polypeptide 24	0.0091
180	DEAD (Asp-Glu-Ala-Asp) box polypeptide 27 (predicted)	0.0226
181	DEAD (Asp-Glu-Ala-Asp) box polypeptide 41 (predicted)	0.0116
182	DEAD (Asp-Glu-Ala-Asp) box polypeptide 42 (predicted)	0.0320
183	DEAH (Asp-Glu-Ala-His) box polypeptide 40	0.0136
184	DEAH (Asp-Glu-Ala-His) box polypeptide 9 (predicted)	0.0245
185	death-associated protein	0.0246
186	degenerative spermatocyte homolog (Drosophila)	0.0091
187	DEK oncogene (DNA binding)	0.0064
188	deleted in malignant brain tumors 1	0.0033
189	deoxyribonuclease II	0.0333
190	diablo homolog (Drosophila) (predicted)	0.0056

<別紙2>

191	diacylglycerol kinase, alpha (80 kDa)	0.0119
192	dickkopf homolog 3 (<i>Xenopus laevis</i>)	0.0363
193	DiGeorge syndrome critical region gene 8 (predicted)	0.0297
194	Dihydropyrimidinase-like 2	0.0021
195	dimethylarginine dimethylaminohydrolase 1	0.0119
196	dimethylarginine dimethylaminohydrolase 2	0.0034
197	dipeptidylpeptidase 7	0.0106
198	discs, large homolog 7 (<i>Drosophila</i>) (predicted)	0.0089
199	dispatched homolog 1 (<i>Drosophila</i>) (predicted)	0.0095
200	DMT1-associated protein	0.0288
201	DNA (cytosine-5-)-methyltransferase 1	0.0033
202	docking protein 1 (predicted)	0.0004
203	Dopamine responsive protein	0.0153
204	down-regulator of transcription 1 (predicted)	0.0066
205	downstream of Stk11 (predicted)	0.0232
206	dual specificity phosphatase 18 (predicted)	0.0213
207	Dual specificity phosphatase 5	0.0242
208	dusty protein kinase	0.0301
209	dynactin 1	0.0179
210	dynactin 3 (predicted)	0.0046
211	Dynactin 4	0.0022
212	dynein, axonemal, light chain 4 (predicted)	0.0081
213	E74-like factor 1	0.0078
214	EBNA1 binding protein 2 (predicted)	0.0030
215	EGF-containing fibulin-like extracellular matrix protein 2	0.0097
216	EH-domain containing 4	0.0165
217	ELK3, member of ETS oncogene family (predicted)	0.0132
218	embigin	0.0076
219	embryonic ectoderm development (predicted)	0.0048
220	Ena-vasodilator stimulated phosphoprotein	0.0114
221	endosulfine alpha	0.0379
222	ependymin related protein 2	0.0002
223	epithelial membrane protein 1	0.0022
224	Epsin 2	0.0327
225	erythrocyte protein band 4.1-like 4a (predicted)	0.0016
226	ets variant gene 1 (predicted)	0.0287
227	ets variant gene 5 (ets-related molecule) (predicted)	0.0020
228	eukaryotic translation elongation factor 1 beta 2 (predicted)	0.0173
229	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	0.0025

<別紙2>

230	eukaryotic translation elongation factor 1 epsilon 1 (predicted)	0.0142
231	eukaryotic translation initiation factor 2 alpha kinase 3	0.0266
232	eukaryotic translation initiation factor 2, subunit 1 alpha	0.0119
233	eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa	0.0029
234	eukaryotic translation initiation factor 2B, subunit 2 beta	0.0033
235	eukaryotic translation initiation factor 3 subunit k (predicted)	0.0173
236	eukaryotic translation initiation factor 3, subunit 5 (epsilon) (predicted)	0.0068
237	eukaryotic translation initiation factor 4A, isoform 1	0.0200
238	eukaryotic translation initiation factor 4A2 (predicted)	0.0017
239	extra spindle poles like 1 (S. cerevisiae) (predicted)	0.0365
240	FAM3C-like protein	0.0026
241	family with sequence similarity 38, member A (predicted)	0.0025
242	farnesyltransferase, CAAX box, alpha	0.0047
243	Fas apoptotic inhibitory molecule	0.0191
244	fat tumor suppressor homolog (Drosophila)	0.0018
245	fatty acid desaturase 3	0.0012
246	F-box and leucine-rich repeat protein 6	0.0172
247	F-box only protein 30	0.0189
248	fertility related protein WMP1	0.0028
249	fetal Alzheimer antigen (predicted)	0.0426
250	Fibroblast growth factor receptor 1	0.0007
251	FIP1 like 1 (S. cerevisiae) (predicted)	0.0008
252	FK506 binding protein 14 (predicted)	0.0352
253	FK506 binding protein 9	0.0007
254	FK506-binding protein 1a	0.0201
255	flightless I homolog (Drosophila) (predicted)	0.0104
256	FLN29 gene product	0.0025
257	flotillin 2	0.0195
258	Follistatin	0.0008
259	follistatin-like 3	0.0013
260	follistatin-like 3	0.0353
261	forkhead box M1	0.0357
262	fos-like antigen 1	0.0115
263	FtsJ homolog 3 (E. coli) (predicted)	0.0078
264	fused toes (predicted)	0.0141
265	fyn proto-oncogene	0.0117
266	G protein-coupled receptor associated sorting protein 1	0.0182
267	galactosidase, beta 1-like (predicted)	0.0177
268	gamma-aminobutyric acid (GABA) B receptor 1	0.0042

<別紙2>

269	Gamma-aminobutyric acid (GABA) B receptor 1	0.0237
270	gap junction membrane channel protein alpha 1	0.0019
271	GATA binding protein 6	0.0023
272	gene model 1960, (NCBI)	0.0184
273	gene rich cluster, C2f gene (predicted)	0.0045
274	general transcription factor IIF, polypeptide 1, 74kDa	0.0117
275	general transcription factor IIF, polypeptide 1, 74kDa	0.0146
276	glucosamine-6-phosphate deaminase 2 (predicted)	0.0159
277	glucose-6-phosphate dehydrogenase	0.0485
278	glutaminase	0.0003
279	glutaminase	0.0076
280	glutamine synthetase 1	0.0048
281	glutaminyl-tRNA synthetase	0.0023
282	Glutaredoxin 2 (thioltransferase) (predicted)	0.0013
283	glutathione peroxidase 2	0.0023
284	glutathione peroxidase 7 (predicted)	0.0343
285	glycoprotein m6a	0.0056
286	Glycosylphosphatidylinositol specific phospholipase D1	0.0093
287	glypican 3	0.0067
288	Golgi reassembly stacking protein 1	0.0013
289	GPI-anchored metastasis-associated protein homolog	0.0095
290	G-protein signalling modulator 1 (AGS3-like, C. elegans)	0.0228
291	granulin	0.0067
292	growth arrest and DNA-damage-inducible 45 beta (predicted)	0.0405
293	growth arrest specific 5	0.0199
294	growth arrest specific 6	0.0041
295	GTP binding protein 2 (predicted)	0.0243
296	Guanine deaminase	0.0469
297	guanine nucleotide binding protein, alpha inhibiting 2	0.0198
298	Guanine nucleotide binding protein, beta 1	0.0100
299	guanine nucleotide binding protein, beta 1	0.0031
300	Guanine nucleotide binding protein, beta 1	0.0167
301	Guanosine monophosphate reductase 2	0.0178
302	HCR (alpha-helix coiled-coil rod homolog)	0.0087
303	heat shock 27kDa protein 1	0.0024
304	heat shock 70kD protein 1A /// heat shock 70kD protein 1B	0.0147
305	heat shock 90kDa protein 1, beta	0.0068
306	heat shock protein 1, alpha	0.0071
307	Heat shock transcription factor 1	0.0057

<別紙2>

308	helicase with zinc finger domain (predicted)	0.0088
309	hepatoma-derived growth factor, related protein 2	0.0047
310	Hepatoma-derived growth factor, related protein 3	0.0007
311	hepatoma-derived growth factor, related protein 3	0.0006
312	Hermansky-Pudlak syndrome 1 homolog (human)	0.0153
313	heterogeneous nuclear ribonucleoprotein A/B	0.0026
314	Heterogeneous nuclear ribonucleoprotein A1	0.0159
315	heterogeneous nuclear ribonucleoprotein D-like (predicted)	0.0068
316	heterogeneous nuclear ribonucleoprotein U	0.0026
317	hexokinase 1	0.0013
318	hexosaminidase B (predicted)	0.0152
319	high mobility group box 2	0.0036
320	high mobility group box 2-like 1 (predicted)	0.0249
321	high mobility group nucleosomal binding domain 3	0.0055
322	HIV-1 tat interactive protein, homolog (human)	0.0094
323	HLA-B associated transcript 5	0.0396
324	HLA-B-associated transcript 3	0.0123
325	Hspb associated protein 1	0.0300
326	hyaluronan mediated motility receptor	0.0158
327	hyaluronidase 2	0.0038
328	hypothetical LOC287199 (predicted)	0.0374
329	hypothetical LOC287534	0.0004
330	hypothetical LOC299075 (predicted)	0.0065
331	hypothetical LOC303211 (predicted)	0.0267
332	hypothetical LOC361797	0.0069
333	Hypoxanthine guanine phosphoribosyl transferase	0.0060
334	hypoxanthine guanine phosphoribosyl transferase	0.0425
335	immunoglobulin superfamily, member 4A (predicted)	0.0113
336	Incisor protein	0.0022
337	Inhibitor of DNA binding 1, helix-loop-helix protein (splice variation)	0.0078
338	inhibitor of growth family, member 3 (predicted)	0.0100
339	inositol polyphosphate phosphatase-like 1	0.0084
340	Insulin-like growth factor 2 receptor	0.0491
341	insulin-like growth factor 2 receptor	0.0054
342	insulin-like growth factor binding protein 6	0.0288
343	integrin beta 1	0.0059
344	integrin beta 3 binding protein (beta3-endonexin) (predicted)	0.0203
345	integrin beta 4 binding protein (predicted)	0.0151
346	integrin linked kinase	0.0024