

Functional categories for genes and ESTs differentially expressed in the PLN of E-IAA NOD sub phenotype. Each gene is represented once in each functional category. When more than one Affymetrix probe sets, corresponding to the same gene, have been hybridized with the target, all the corresponding probe sets have been grouped. Gene functional category assignment has been realized by manual data mining as described in the text for genes on Table 3. References corresponding to bibliographic search for functions for each gene are shown.

Inflammation & Infection

Putative Function	Gene name	Fold change	GO biological process	GO molecular function	GO cellular component	Affymetrix ID	Public ID	Gene symbol [Reference]
Inflammation, regeneration	Regenerating islet-derived 2	58,44	---	sugar binding	extracellular	95786_at	D14011	Reg2 [1]
Inflammation, regeneration	Regenerating islet-derived 1	57,02	---	sugar binding	extracellular	160213_at; 162312_f_at	D14010	Reg1 [1, 2]
Inflammation, autoimmunity	Trypsin 4	52,9	proteolysis	serine-type	---	101043_f_at	AE000664	Try4 [3]
Inflammation, regeneration	Pancreatitis-associated protein	45,63	acute-phase/ inflammatory response	sugar binding	extracellular	161890_f_at; 96009_s_at	AV371861	Pap [4]; [5]
Infection <i>H. Pylori</i>	Trefoil factor 2 (spasmolytic protein 1)	39,97	---	---	extracellular	93302_at	U78770	Tff2 [6]; [7]; [8]; [9]
Inflammation, autoimmunity	Kallikrein 1	37,92	proteolysis	serine-type/growth factor activity	extracellular	100061_f_at	M13500	Klk1b5 [10]; [11, 12]
Inflammation, autoimmunity	Trypsin 10	28,39	proteolysis	serine-type	---	101338_f_at	AE000664	Try10 [13]
Inflammation, regeneration	Regenerating islet-derived 3 alpha	28,09	acute-phase/ inflammatory response	sugar binding	extracellular	103954_at; 161642_f_at	D63357	Reg3a [14], [2]
Inflammation, autoimmunity	Kallikrein 1-related peptidase b22	21,55	proteolysis	serine-type	extracellular	101289_f_at	M17979	Klk1b22 [10-12]
Inflammation, autoimmunity	Kallikrein 1-related peptidase b9	19,71	proteolysis	serine-type	extracellular	94716_f_at	M17962	Klk1b9 [10-12]
Inflammation, autoimmunity	Kallikrein 1-related peptidase b5	17,34	proteolysis	serine-type	extracellular	104495_f_at	Y00500	Klk1b5 related; [10]; [10-12]
Inflammation, autoimmunity	Similar to Kallikrein 1-related peptidase b9 (KIK1rb9)	14,27	---	---	---	100681_f_at	V00829	mGK2 fragment similar [15]
Inflammation, autoimmunity	Kallikrein 1-related peptidase b1	13,04	proteolysis	serine-type	extracellular	95775_f_at	V00829	Klk1b1 [16]
Inflammation, pancreatitis	CUB and zona pellucida-like domains1	11,73	cell cycle & division	protein binding	extracellular	162196_f_at	AV059956	Cuzd1 [17],
Response to stress	Phospholipase A2, group IB, pancreas	9,69	response to stress/ cell proliferation	phospholipase A2 activity/ calcium ion binding	extracellular	160120_i_at	AI327450	Pla2g1b [18], [19]; [20]
Inflammation	Metallothionein 1	6,81	nitric oxide mediated signal transduction	metal ion binding	lysosome	93573_at	V00835	Mt1 [21]

Inflammation, transcription factor, stress induced	Nuclear protein 1 (p8 family)	6,49	cell growth	---	nucleus	160108_at	A1852641	Nupr1 [22-25],[26]
Inflammation	Metallothionein 2	6,11	nitric oxide mediated signal transduction	metal ion binding	---	101561_at	K02236	Mt2 [27]
Inflammation, cancer autoimmunity, infection	Secreted phosphoprotein 1	5,68	anti-apoptosis /inflammatory response /T-helper 1 type immune response	cytokine activity	extracellular	97519_at	X13986	Spp1, [28]; [29], [30]; [31]; [32]; [33]
Inflammation, autoimmunity	Kallikrein 1-related peptidase b16	3,44	proteolysis	serine-type/growth factor activity	extracellular	100719_f_at	J03877	Klk1b16 [11]
Inflammation, cancer	Keratin 18	3,15	cytoskeleton organization and biogenesis	structural constituent of cytoskeleton	mitochondrion	94270_at	M22832	Krt18 [34]
Inflammation, cancer, infection	Alpha-2-HS-glycoprotein	3	acute-phase response/regulation of inflammatory response	cysteine protease inhibitor activity	extracellular	99862_at	AF025821	Ahsg [35]; [36]; [37]
Inflammation, cancer	Keratin 8	2,15	cellular morphogenesis/cytoskeleton organization and biogenesis/response to other organism	protein kinase activity	intermediate filament	101009_at	X15662	Krt8 [34]; [38]
Inflammation	Vitronectin	2,13	cell adhesion	protein binding	extracellular	98549_at	M77123	Vtn [39]; for opn & vtn see [40]
Inflammation, autoimmunity	Kallikrein 1	2,1	proteolysis positive regulation of phosphoinositide 3-kinase activity	serine-type/growth factor activity	extracellular	100060_i_at	M13500	Klk1 [41], [42]
Inflammation, wound, cancer, hemostasis	Plasminogen	2,08	apoptosis/induction of apoptosis/tissue development /negative regulation of angiogenesis/tissue regeneration	serine-type	extracellular	101985_at	J04766	Plg [43]
Inflammation, autoimmunity	Kallikrein 1-related peptidase b26	1,98	proteolysis	serine-type	extracellular	102693_f_at	J00389	Klk1b26 [41], [42]
Inflammation, cancer, metastasis	S100 calcium binding protein A9 (calgranulin B)	1,81	leukocyte chemotaxis/actin cytoskeleton reorganization	calcium ion binding	---	103887_at	M83219	S100a9 [44]
Inflammation, regeneration	Regenerating islet-derived 3 gamma	1,77	acute-phase response/inflammatory response	sugar binding	extracellular	96064_at	D63362	Reg3g [1], [2]
Inflammation, autoimmunity	Heat shock protein 1A	1,75	telomere maintenance/DNA repair/protein folding/response to heat	nucleotide binding	---	93875_at	M12571	Hspa1a [45]; [46]
Inflammation	Resistin	1,73	---	hormone activity	extracellular	102366_at	AA718169	Retn [47], [48]; [49]; [50]

Inflammation, cancer, metastasis	S100 calcium binding protein A8 (calgranulin A)	1,49	chemotaxis	calcium ion binding	---	103448_at	M83218	S100a8 [44]
Inflammation, cancer, autoim, wound, infect	Solute carrier family 23 (nucleobase transporters), member 3	1,48	transport	transporter activity	membrane	161149_r_at	AV222871	Slc23a3 [51]
Infection, Endocytosis	Growth hormone receptor	1,44	endocytosis	receptor activity	nucleus	99108_s_at	U15012	Ghr [52]

Immune Function

Putative Function	Gene title	Fold change	GO biological process term	GO molecular function term	GO cellular component term	Affymetrix ID	Representative Public ID	Gene symbol [Reference]
Immune function	Ribonuclease, RNase A family, 1 (pancreatic)	93,56	---	nucleic acid binding	extracellular	98041_at	X60103	Rnase1 [53]
Infection	Syncollin	57,36	exocytosis	---	extracellular	95509_at	AA607809	Sycn [54]; [55]
Inflammation, regeneration, malignancy	Deleted in malignant brain tumors 1	41,28	positive regulation of epithelial cell differentiation	scavenger receptor activity	extracellular matrix	99479_at	U37438	Dmbt1 [56]
Expressed in macrophages & Leukocytes	Elastase 1, pancreatic	34,91	proteolysis	serine-type	---	93783_at	M27347	Ela1 [3]; [57], 2005 ; [58]; [59]
Inflammation	Elastase 2A	11,8	proteolysis	serine-type	extracellular	94037_at	X04573	Ela2A [60]
Autoimmunity	Epidermal growth factor binding protein type B	10,26	proteolysis	serine-type	extracellular	161637_f_at	AV053185	Egfbp2 [15]; [12]; [61]; [16]; with opn see [33]; [12]
Vascularization, Viral infection	Angiogenin, ribonuclease, RNase A family, 5	3,42	angiogenesis/response to hypoxia/proliferation/cell differentiation/activation of phospholipase A2 /positive regulation of protein secretion	nucleic acid binding/actin binding	extracellular	94392_f_at	U22516	Ang [62]
Metastasis, hemostasis	Fibrinogen, alpha polypeptide	2,66	signal transduction/platelet activation	receptor binding	extracellular	101553_at	A1876446	Fga [63]; [64]; [43]
Immune function	Cytokine receptor-like factor 1	2,45	---	receptor activity / cytokine binding	extracellular	161046_at	AA270365	Crlf1 [65]
Immune response, innate	Complement component 1, q subcomponent, beta polypeptide	2,23	Innate immune response/complement activation	---	extracellular	162276_i_at	AV367855	C1qb [66]
Immune function, vacsularisation	Ribonuclease, RNase A family 4	2,12	angiogenesis/response to hypoxia /activation of phospholipase A2/ positive regulation of protein secretion	nucleic acid binding	extracellular	96038_at	A1840339	Rnase4 [67]
Innate immune response	Complement factor D (adipsin)	2	proteolysis/complement activation, alternative pathway/innate immune response	complement factor D activity/serine-type	extracellular	99671_at	X04673	Cfd [68], [69, 70], [71]

TGFβ Signaling Pathway	Epidermal growth factor	1,94	activation of MAPKK activity / positive regulation of cell proliferation	calcium ion binding /growth factor activity	extracellular	102774_at	V00741	Egf [72]
Defence response, homeostasis	Neutrophilic granule protein	1,5	defense response	cysteine protease inhibitor activity	extracellular	96153_at	L37297	Ngp [73]
Humoral immune response	Immunoglobulin kappa chain variable 28 (V28)	-0,59	---	---	---	96971_f_at	X00652	Similar to Ig
Humoral immune response, antigen binding	Immunoglobulin kappa chain, constant region	-1,36	humoral immune response	antigen binding	---	93086_at	M18237	Cr1
Immune function protein binding cytokine binding MHC class II protein binding	CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated)	-1,42	immune response /immunoglobulin mediated /antigen processing &presentation /regulation of T cell differentiation	cytokine binding /MHC class II protein binding	lysosome / membrane	101054_at	X00496	Cd74 [74]
Immune function	Myosin Va	-1,49	cytoskeleton organization and biogenesis/insulin secretion /regulation of IP3 receptor activity/ synapse organization and biogenesis	nucleotide binding/actin binding	cytoplasm	98968_at	X57377	Myo5a [75]; [76]; [77], [78]; [79]
Autoimmunity, cancer, infection	CD1d1 antigen	-1,53	antigen processing &presentation/positive thymic T cell selection & NK T cell activation	protein binding/endogenous lipid antigen binding	lysosome	103422_at	M63695	Cd1d1 [80], [81], [81], [82]
Immune system T cells	Cytotoxic T lymphocyte-associated protein 2 beta	-1,56	---	cysteine protease inhibitor activity/protein binding	---	103518_at	X15592	Ctla2b [83]
Immune response	CD55 antigen	-1,65	innate immune response/complement activation, classical pathway	GPI anchor binding	extracellular	103617_at	D63679	Cd55 [84],
Immune function	Cytokine receptor-like factor 3	-1,69	---	---	---	98415_at	AF046060	Crlf3 [85]
Immune related, Signal transduction	Membrane-spanning 4-domains, subfamily A, member 6B	-1,78	signal transduction	receptor activity	membrane	97322_at	A1835093	Ms4a6b [86]
Role in the regulation of integrins	RAS-related protein-1a	-1,81	cell cycle	nucleotide binding	intracellular /// membrane	100048_at	AW049685	Rap1a [87]
Humoral immune response	Expressed sequence A1324046	-1,85	---	---	---	102721_at	D14625	IgG1c [88]
Humoral immune response	Immunoglobulin lambda chain, variable 1	-1,96	humoral immune response	antigen binding	---	93638_s_at	J00579	Igl-V1 [88]
Humoral immune response	Immunoglobulin heavy chain (gamma polypeptide)	-2,17	humoral immune response/immunoglobulin mediated immune response/phagocytosis	antigen binding	membrane	102824_g_at	X67210	Ighg [88]

Cancer

Putative Function	Gene title	Fold change	GO biological process term	GO molecular function term	GO cellular component term	Affymetrix ID	Representative Public ID	Gene symbol [Reference]
Cancer, infection	Mucin 1, trans membrane	5,23	---	actin binding	extracellular	102918_at	M84683	Muc1 [89];[90]
Cancer	Gamma-glutamyl hydrolase	4,76	glutamine metabolic process	catalytic activity	extracellular	93575_at	AF051102	Ggh [91]
Cancer involved but unknown function	Trans membrane protein 97	3,78	---	---	extracellular	95137_at	A1852985	Tmem97 [92]
Cancer	Cytochrome P450, family 3, subfamily a, polypeptide 11	3,42	electron transport	heme binding / metal ion binding	endoplasmic reticulum	101638_s_at	D26137	Cyp3a11 [93]
Cancer, viral infection, ER, ubiquitination	Sel-1 suppressor of lin-12-like (C. elegans)	2,27	Notch signaling pathway	binding	extracellular	92871_at	AW121840	Sel11 [94], [95],[9]
Cancer, metastasis	Hepsin	2,25	proteolysis	serine-type	plasma membrane	160639_at	AF030065	Hpn [96], [97]
Cancer	Actin, beta, cytoplasmic	2,13	---	structural molecule activity	cytoplasm	101578_f_at; 95705_s_at	M12481	Actb[98]
Cell (intercell) communication, cancer in LN	Gap junction membrane channel protein beta 2	1,96	cell-cell signaling & communication	protein binding	membrane	98423_at	M81445	Gjb2 [99]; [100]
Cancer	Asparagine synthetase	1,84	metabolic process	ligase activity	soluble fraction	95133_at; 161221_f_at	AV253908; U38940	Asns [101]
Cancer, wound	Desmoplakin	1,8	---	---	mitochondrion	94247_at	AA600542	Dsp [102]
Cancer involved unknown function	Trans membrane protein 56	1,76	---	---	membrane	103257_at	AA690483	Tmem56 [103]
Cytoskeleton organization and biogenesis actin, nucleotide binding, cancer	Ras homolog gene family, member U	1,74	G1/S transition of mitotic cell cycle	nucleotide binding	intracellular	96747_at	AW121294	Rhou [104]
Cancer, stress response	similar to N-myc downstream regulated 2	1,62	---	---	---	161610_at	AV349686	Ndrg2, EST [105]; [106]
Cancer	Trans membrane protein 30B	1,38	---	---	membrane	96749_f_at	AA619554	Tmem30b [92]
Cancer	Cytochrome P450, family 2, subfamily e, polypeptide 1	1,33	electron transport	monooxygenase activity	extracellular	93996_at	X01026	Cyp2e1 [93]
Cancer, Colorectal	Ribosomal protein S3	-1,44	translation	nucleic acid binding/structural constituent of ribosome	cytoplasm / ribosome	101137_at	X76772	Rps3 [107]
Cancer, leukemia	Topoisomerase (DNA) II beta	-1,81	DNA metabolic process / development	nucleotide binding	nucleus	99462_at	D38046	Top2b [108]

Enzyme

Putative Function	Gene title	Fold change	GO biological process term	GO molecular function term	GO cellular component term	Affymetrix ID	Representative Public ID	Gene symbol [Reference]
TCRβ locus Unknown	Protease, serine, 3	68,26	proteolysis	serine-type	mitochondrion	93208_at	AE000665	Prss3 [13], [109], [110]
TCRβ locus Unknown	Protease, serine, 2	48,73	proteolysis	serine-type	extracellular	92873_f_at	X04574	Prss2 [111]

Proteolysis	Chymotrypsin-like	33,97	proteolysis	serine-type	extracellular	160744_r_at	AA244542	Ctrl [65]; [112]
Proteolysis	Chymotrypsinogen B1	29,23	proteolysis	serine-type	extracellular	160421_r_at	AA590358	Ctrl [112] [3]
Unknown, Highly polymorphic locus	Phenylalanine hydroxylase	9,73	metabolic process	catalytic activity	---	95407_at	X51942	Pah [113]
TCRβ locus, Unknown	Protease, serine, 3	2,43	proteolysis	serine-type	mitochondrion	101339_at	AE000665	Prss3 [114]
Mitochondria, Metabolism	Aldehyde dehydrogenase family 7, member A1	2,42	metabolic process	oxidoreductase activity	mitochondrion	97450_s_at	AA986258	Aldh7a1 [115]
Mitochondria, Metabolism	Glycine C-acetyl transferase (2-amino-3-ketobutyrate-coenzyme A ligase)	2,4	metabolic process	catalytic activity	mitochondrion	160628_at	A1849354	Gcat [116]
Catalytic activity, mitochondria	Malic enzyme, supernatant	2,25	metabolic process/response to hormone stimulus	enzyme activity	cytoplasm	101082_at	J02652	Mod1 [117]
Mitochondrion, catalytic activity, heme binding	Aminolevulinic acid synthase 2, erythroid	2,06	metabolic process	catalytic activity	mitochondrion	92768_s_at	M15268	Alas2 [118]
Lipid metabolic process, Gluconeogenesis	Phosphoenolpyruvate carboxykinase 1, cytosolic	1,93	gluconeogenesis/lipid metabolic process	nucleotide binding	cytoplasm	160481_at	AF009605	Pck1 [119]
Proteolysis, found in T2D	Carboxypeptidase N, polypeptide 1	1,9	proteolysis	carboxypeptidase activity metal ion binding	---	103882_at	A1182588	Cpn1 [115]
Catalytic activity, fatty acid degradation	Lipoprotein lipase	1,87	lipid metabolic process	catalytic activity	extracellular	160083_at; 95611_at	M63335	Lpl [120, 121]; [122]
Catalytic activity, metabolic process, response to toxin	Carboxylesterase 3	1,58	response to toxin	catalytic activity	extracellular	101539_f_at	AW226939	Ces3 [123]
Mitochondrion response to oxidative stress	Aminoacidpate-semialdehyde synthase	1,52	response to oxidative stress	catalytic activity	mitochondrion	103389_at	AJ224761	Aass [124]
Catalytic activity, mitochondrion	Acyl-CoA synthetase long-chain family member 4	-1,59	lipid metabolic process	magnesium ion binding/catalytic activity	mitochondrion	102381_at	AA619207	Acs14 [125]

Diabetes

Putative Function	Gene title	Fold change	GO biological process term	GO molecular function term	GO cellular component term	Affymetrix ID	Representative Public ID	Gene symbol [Reference]
Lipase Diabetes	Pancreatic lipase related protein 1	70,76	lipid metabolic process	catalytic activity	extracellular	92601_at	AA674409	Pnliprp1 [126]
Diabetes related	Amylase 2-1, pancreatic	56,49	metabolic process	catalytic activity	extracellular	97523_i_at; 97524_f_at	X02578	Amy2-1 [127], [128]
Diabetes	Insulin II	45,73	glucose transport	hormone activity	extracellular	100150_f_at	X04724	Ins2

Lipase Diabetes	Carboxyl ester lipase	40,2	lipid catabolic process	carboxylesterase activity	extracellular	99939_at	U37386	Cel [129]; [130]
T2D	Colipase, pancreatic	33,99	digestion/lipid catabolic process	enzyme activator activity	extracellular	160132_at	AA710635	56. Clps [131], [132]
Diabetes	Insulin I	16,28	glucose metabolic process	hormone activity	extracellular	97658_f_at; 97659_r_at	X04725	Ins1
Diabetes related	Amylase 1, salivary	13,63	metabolic process	catalytic activity	extracellular	101058_at	J00356	Amy1
Lipase, Diabetes	Pancreatic lipase-related protein 2	11,15	lipid metabolic process/cellular defense response/digestion	catalytic activity	extracellular	160070_at	M30687	Pnliprp2 [126]; [133, 134]
Apoptosis, vascularization & diabetes	Albumin	7,52	negative regulation of apoptosis	binding/transmembrane transporter activity	extracellular	94777_at	X13060	Alb [113],
Related to T2D, NK cells, protein folding	FK506 binding protein 11	3,11	protein folding	isomerase activity	extracellular	97964_at	AW122851	Fkbp11 [135], [136], [137]
Insulin resistance	Retinol binding protein 4, plasma	2,18	transport	transporter activity	extracellular	96047_at	U63146	Rbp4 [138]

Regeneration & remodeling

Putative Function	Gene title	Fold change	GO biological process term	GO molecular function term	GO cellular component term	Affymetrix ID	Representative Public ID	Gene symbol [Reference]
Remodeling, Regeneration liver	Inter alpha-trypsin inhibitor, heavy chain 4	3,73	hyaluronan metabolic process	serine-type endopeptidase inhibitor activity	cytoplasm	98467_at	AF023919	Itih4 [139]; [13]
Regeneration	Hemoglobin, beta adult minor chain	3,02	transport/oxygen transport	oxygen transporter activity	hemoglobin complex	103534_at; 101869_s_at	V00722	Hbb-b2
Regeneration	Hemoglobin alpha, adult chain 1	2,82	oxygen transport	oxygen transporter activity	mitochondrion	94781_at; 162457_f_at	V00714	70. Hba-a2
Remodeling tissue, tumor invasion	Inter-alpha trypsin inhibitor, heavy chain 2	2,31	hyaluronan metabolic process	serine-type endopeptidase inhibitor activity	extracellular	104519_at	X70392	Itih2 [139], [13],
Wound healing & angiogenesis	Prostaglandin E receptor 3 (subtype EP3)	1,86	signal transduction/G-protein signaling, coupled to IP3 second messenger (phospholipase C activating)/elevation of cytosolic calcium ion concentration	receptor activity	plasma membrane	96588_at	D10204	Ptger3 [140]; [141]
Cell proliferation, myeloid cell differentiation	Zinc finger and BTB domain containing 16	1,42	development/negative regulation of cell proliferation/embryonic pattern specification & morphogenesis/positive regulation of apoptosis/regulation of transcription	nucleic acid binding/specific transcriptional repressor activity	nucleus	92202_g_at	AI553024	Zbtb16 [142]
Cell proliferation & transformation	Ornithine decarboxylase antizyme	-1,32	polyamine metabolic process	enzyme inhibitor activity	---	161360_at	AV212241	Oaz1 [143]
Cell proliferation	Ecotropic viral integration site 2a	-1,79	cell proliferation	transmembrane receptor activity	membrane	98025_at	M34896	Evi2a [144]

Other

Putative Function	Gene title	Fold change	GO biological process term	GO molecular function term	GO cellular component term	Affymetrix ID	Representative Public ID	Gene symbol [Reference]
Cytoskeleton, Actin binding Immune related	Group specific component	3,07	transport/vitamin D metabolic process	actin binding/vitamin D binding	extracellular	99197_at	M55413	Gc [145], [146]
Homeostasis, calcium	Nucleobindin 2	2,48	cellular calcium ion homeostasis	DNA binding/calcium ion binding	extracellular	102197_at	AJ222586	Nucb2 [147]
MHC locus, pherormone for non same MHC selection	Olfactory receptor 93	2,31	signal transduction/sensory perception of smell	signal transducer activity/receptor activity	membrane	102169_at	AL078630	Olf93 [148]
Metabolic process	Carbonic anhydrase 3	2,23	one-carbon compound metabolic process	carbonate dehydratase activity	cytoplasm	160375_at	AJ006474	Car3 [149]
Electron transport/ protein folding Obesity	ERO1-like beta (S. cerevisiae)	2,2	electron transport	oxidoreductase activity	endoplasmic reticulum	103531_f_at	AI049144	Ero1b [150], [151]
Protein binding, vesicle transport	Coatamer protein complex, subunit zeta 2	1,96	protein complex assembly/intracellular protein transport/ER to Golgi vesicle-mediated transport	protein binding	cytoplasm	104143_at	AI843212	Copz2 [152]
Lipoprotein, Receptor activity	Low density lipoprotein receptor-related protein associated protein 1	1,94	---	low-density lipoprotein receptor binding	extracellular	100086_at	D00622	Lrpap1 [153]
Role in Notch/NFkB in neurons	kallikrein 1-related peptidase b4 or alpha-NGF	1,89	proteolysis/small GTPase mediated signal transduction/positive regulation of phosphoinositide 3-kinase activity	serine-type	extracellular	94773_at	X01801	Klk1b4; NGFalpha [41], [10] [42]
Homeostasis	Glutathione transferase zeta 1 (maleylacetate isomerase)	1,87	L-phenylalanine catabolic process	catalytic activity	cytoplasm/mitochondrion	160350_at	AW060750	Gstz1 [154]
Metabolism	Aldehyde dehydrogenase family 1, subfamily A7	1,86	metabolic process	oxidoreductase activity	cytoplasm	94778_at	U96401	Aldh1a7 [115], [155]
Metabolic process	Cysteine dioxygenase 1, cytosolic	1,84	L-cysteine metabolic process	iron ion binding	cytosol	96346_at	AI854020	Cdo1 [156]
Hematopoiesis and Wnt-beta catenin pathway in the brain Ulcerative colitis, cancer	Frizzled homolog 3 (Drosophila)	1,84	signal transduction /multicellular organismal development/Wnt receptor signaling pathway	signal transducer activity/receptor activity	extracellular	98169_s_at	AU020229	Fzd3 [157]
Homeostasis, Gut	Lecithin cholesterol acyltransferase	1,78	lipid metabolic process	catalytic activity	extracellular	103023_at	J05154	Lcat [158]
Cytoskeleton organization and biogenesis nucleotide binding	Actin, alpha 2, smooth muscle, aorta	1,77	cytoskeleton organization and biogenesis	nucleotide binding	cytoplasm	93100_at	X13297	Acta2 [159]
Chromosome	Inactive X specific transcripts	1,6	dosage compensation, by inactivation of X chromosome	---	chromosome	99126_at	L04961	Xist

Apoptosis, translation	Eukaryotic translation elongation factor 1 alpha 1	-1,25	translational elongation	nucleotide binding	cytoplasm	94766_at	M17878	Eef1a1 [160]
DNA synthesis	Proliferating cell nuclear antigen	-1,73	DNA replication/intracellular protein transport	DNA binding	nucleus	101065_at	X57800	Pcna [161]
Development	SLAIN motif family, member 1	-1,76	---	---	---	160236_at	AI835624	Slain1 [162]
Repair of nucleotide-excision establishment and/or maintenance of chromatin architecture	High mobility group nucleosomal binding domain 1	-2	transcription-coupled nucleotide-excision repair/establishment &/or maintenance of chromatin architecture	DNA binding/chromatin binding	nucleus	96699_at	X53476	Hmgn1 [163-165]
Cell Differentiation, vesicle transport, expressed in the brain	Nuclear distribution gene E homolog 1 (Anidulans)	-2,12	cell cycle/mitosis/development/cell differentiation and division	microtubule binding/identical protein binding	cytoplasm	94910_at	AW120739	Nde1 [166]
Meiosis regulated novel Xlr-related (Xmr) family member	Xmr protein	-2,14	---	---	---	102818_at	X72697	Slx, Xmr [167]

Unknown Function

Putative Function	Gene title	Fold change	GO biological process term	GO molecular function term	GO cellular component term	Affymetrix ID	Representative Public ID	Gene symbol [Reference]
Unknown	RIKEN cDNA 1810010M01, Similar to Spink3 gene	42,36	---	sugar binding	---	160145_at	AI593999	1810010M01Rik (EST)
Unknown	RIKEN cDNA 2210010C04 gene, Similar to Trypsinogen 7	20,03	proteolysis	serine-type	extracellular	100103_f_at; 100104_r_at	AE000663	2210010C04Rik (EST)
Unknown, gastrointestinal tract	Cholecystokinin A receptor	11,91	signal transduction /G-protein coupled receptor protein signaling pathway	cholecystokinin receptor activity	membrane	92252_at	D85605	Cckar [168]
Unknown	RIKEN cDNA 1810009J06 gene, TCR V beta locus	3,96	proteolysis	serine-type	extracellular	92712_at; 101336_at	AE000663	TCRVb [110]
Cancer Unknown function in the PaLN	Rho GDP dissociation inhibitor (GDI) gamma	3,85	---	Rho GDP-dissociation inhibitor activity/GTPase activator activity	cytoplasm	102677_at	U73198	Arhgdig [169]
Unknown function in the PaLN	Glycine N-methyl transferase	3,62	---	catalytic activity	cytoplasm	96828_at	D89664	Gnmt [169]
Unknown function in the PaLN, Cofactor for HNF1	Pterin 4 alpha carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) 1	3,37	positive regulation of transcription	transcription coactivator activity	nucleus	99056_at	AW046590	Pcbd1 [170]
Unknown	Murine leukemia retrovirus	2,64	DNA integration/virus assembly	nucleic acid binding/ribonuclease H activity	integral to membrane	103562_f_at	M26005	Gv-1 [171], [172]; [173]

Unknown	cDNA sequence BC003494	2,63	---	---	---	161677_r_at	AV171666	EST
Unknown	Guanidino acetate methyltransferase	2,52	biosynthetic process/organ morphogenesis/regulation of body size	methyltransferase activity	---	101408_at	AF010499	Gamt, [174]; [175]
Unknown function	Glycine amidinotransferase	2,2	transport	receptor activity	mitochondrion	96336_at	AI844626	Gatm, [176]
Unkown, some role in adipocytes	Thyroid hormone responsive SPOT14 homolog (Rattus)	1,88	---	---	---	160306_at	X95279	Thrsp [177]
Unknown	EST	1,87	---	---	---	161131_r_at	AV250694	EST
Unknown	RIKEN cDNA 1810029G24 gene Homologue to Sec11c yeast	1,73	signal peptide processing/proteolysis	serine-type peptidase activity	membrane	160250_at	AW049643	EST
Unknown	cDNA sequence BC008155	1,57	---	---	---	161641_at	AV067171	EST
Unknown	RIKEN cDNA 0610010K14 gene	-0,47	---	DNA binding	nucleus	95634_at	AI848107	0610010K14Rik (EST)
Unknown	RIKEN cDNA 2510049I19 gene	-0,61	---	---	nucleolus	97866_at	AI842858	2510049I19Rik (EST)
Unknown function	RIKEN cDNA C330027C09 gene	-1,44	---	binding	cytoplasm	160973_at	NM_172616 AA590345	RTRtv
Unknown function	PCI domain containing 2	-1,65	---	---	---	96545_s_at	AI447510	Pcid2 [178]
Unknown function	Gene trap ROSA 26, Philippe Soriano	-1,68	---	---	---	160620_at	U83174	Gt(ROSA)26S

Ubiquitination

Putative Function	Gene title	Fold change	GO biological process term	GO molecular function term	GO cellular component term	Affymetrix ID	Representative Public ID	Gene symbol [Reference]
Ubiquitination	Heterogeneous nuclear ribonucleoprotein C	-1,62	mRNA processing and splicing	nucleotide binding	nucleus	160199_at	AF095257	Hnrpc [177]
Related to ubiquitin	Heterogeneous nuclear ribonucleoprotein R	-1,76	---	nucleotide binding	nucleus	97491_at	AW123032	Hnrpr [179]
Ubiquitination, Degradation enzyme	Ubiquitin-conjugating enzyme E2E 1, UBC4/5 homolog (yeast)	-1,74	ubiquitin cycle	ubiquitin-protein ligase activity	---	92660_f_at	X92665	Ube2e1 [180], [181]
Ubiquitination Oncogenesis immune system	Similar to mouse RING finger 1	-1,77	---	protein binding	intracellular	99149_at	AI851230	Trim59 [182]
Ubiquitination, found in diabetcity	Ubiquitin specific peptidase 1	-1,8	ubiquitin-dependent protein catabolic process	ubiquitin thiolesterase activity	---	160234_at	AI848382	Usp1 [115]
Ubiquitin cycle	Zinc and ring finger 2	-2,69	ubiquitin cycle	protein binding	membrane	99574_at	AI850887	Znrf2 [183]

Transcription

Putative Function	Gene title	Fold change	GO biological process term	GO molecular function term	GO cellular component term	Affymetrix ID	Representative Public ID	Gene symbol [Reference]
Transcription, development gut & pancreas	Forkhead box A3	1,76	cell glucose homeostasis/transcription/cellular response to starvation	transcription factor activity	nucleus/transcription factor complex	98324_at	X74938	Foxa3 [184]; [185]
Transcription factor	Trans-acting transcription factor 4	-1,36	regulation of transcription	transcription factor activity	transcription factor complex	92992_i_at	AI324972	Sp4 [186]
Transcription factor in B cells, Ig	Spi-C transcription factor (Spi-1/PU.1 related)	-1,69	transcription	transcription factor activity	nucleus	103454_at	AA182189	Spic [187]

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