TABLE S1. Yeast two-hybrid screen results.

ERRα-interacting Clones	**Number**
ERRα	12
AKAP1	10
Zinedin	10
SRC1	5
IκBα	4
CBF1 interacting corepressor (CIR)	1
Clones without ORF	4

Numbers represent redundancies.

TABLE S2. Metabolic gene expression array results for Bcl3-regulated genes in cardiac myoyctes

Glycolysis	Fold Induction
Ketohexokinase (Khk)	2.5
6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2 (Pfkfb2)	2.4
6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 (Pfkfb3)	2.0
6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4 (Pfkfb4)	2.2
Phosphofructokinase, muscle (Pfkm)	2.5
Enolase 3, Beta (Eno3)	5.6
Phosphoglycerate mutase 2 (Pgam2)	3.7
Phoshpoglycerate mutase 5 (Pgam5)	2.1
Glyceraldehyde-3-phosphate dehydrogenase (Gapd)	2.0
Lactate dehydrogenase D (Ldhd)	2.0
Other glucose metabolism	
Pyruvate dehydrogenase kinase 4 (Pdk4)	4.1
Pyruvate dehydrogenase kinase 3 (Pdk3)	2.2
Solute carrier family 2 (facilitated glucose transporter), member 4 (Slc2a4)	2.2
Solute carrier family 2 (facilitated glucose transporter), member 3 (Slc2a3)	2.6
Fatty acid binding proteins	
Fatty acid binding protein 3 (Fabp3)*	2.4
Mitochondrial fatty acid oxidation (β-oxidation)	
Acyl-CoA synthetase long-chain family member 1 (Acsl1)	2.0
Acyl-CoA synthetase long-chain family member 3 (Acsl3)	2.1
Acyl-CoA Oxidase 2, branch-chain (Acox2)	6.0
Carnitine O-octanoyltransferase (Crot)	2.0
Carnitine palmitoyltransferase 1b, muscle (Cpt1b)	3.0
Carnitine palmitoyltransferase 1a, liver (Cpt1a)	2.2
Acyl-Coenzyme A dehydrogenase, very long chain (Acadvl)*	2.0

Acyl-Coenzyme A dehydrogenase family, member 11, predicted (Aad11 predicted)	**2.0**
Acyl-Coenzyme A dehydrogenase, medium chain (Acadm)*	**2.3**
Hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase, trifunctional protein, alpha Subunit (Hadha)*	**2.0**
Hydroxyacyl-Coenzyme A dehydrogenase type II (Hadh2)	**2.0**
2,4-dienoyl CoA reductase 1, mitochondrial (Decr1)	**2.2**
Peroxisomal fatty acid oxidation (α-oxidation)	
Phytanoyl-CoA hydroxylase (Phyh)	**2.3**
Fatty acid and triacylglycerol synthesis	
Acyl-CoA Synthetase short-chain member 1, predicted (Acss1 predicted)	**6.0**
Fatty acid synthase (Fasn)	**2.4**
Elongation of long chain fatty acids, ELOVL family member 6 (Elovl6)	**2.0**
Fatty acid desaturase 3 (Fads3)	**2.1**
Stearoyl-Coenzyme A desaturase 1 (Scd1)	**2.2**
Stearoyl-Coenzyme A desaturase 2 (Scd2)*	**2.0**
Glycerol-3-phosphate dehydrogenase 1 (Gpd1)	**2.1**
Diacylglycerol O-acyltransferase homolog 2 mouse (Dgat2)	**2.1**
Glycerol-3-phosphate acyltransfersae, mitochondrial (Gpam)	**2.6**
Diacylglycerol kinase, gamma (Dgkg)	**2.0**
1-acylglycerol-3-phosphate O-acyltransferase 6, lysophosphatidic acid acyltransferase, zeta (Agpat6)	**2.3**
1-acylglycerol-3-phosphate O-acyltransferase 4, lysophosphatidic acid acyltransferase, delta (Agpat4)	**2.0**
Acyl-CoA metabolism	
Diazepam binding inhibitor (Dbi)	**2.8**
Cytosolic Acyl-CoA thioesterase 1 (Cte1)	**2.9**

Mitochondrial Acyl-CoA thioesterase 1 (Mte1)	**2.5**
Acyl-CoA thioesterase 7 (Acot7)	**2.0**
Acyl-CoA thioesterase 8 (Acot8)	**2.1**
Malonyl-CoA decarboxylase (Mlycd)	**2.7**
Sterol metabolism	
Sterol-C5-desaturase , fungal ERG3, delta-5-desaturase, homolog ,S. cerevisae (Sc5d)	**2.0**
Oxysterol binding protein, predicted (Osbp predicted)	**2.8**
Oxysterol binding protein-like 1A (Osbpl1a)	**2.4**
Oxysterol binding protein-like 6, predicted (Osbpl6)	**3.1**
Cholesterol 25-hydroxylase (Ch25h)	**2.0**
Sterol O-acyltransferase 1 (Soat1)	**2.0**
O-acyltransferase ,membrane bound, domain containing 2 (Oact2)	**3.0**
Oxidized low density lipoprotein , lectin-like, receptor 1 (Oldlr1)	**2.0**
Low density lipoprotein receptor-related protein associated protein 1 (Lrpap1)	**2.0**
Lipolysis stimulated lipoprotein receptor (Lsr)	**2.9**
Very low density lipoprotein receptor (Vldlr)*	**3.1**
Lipid metabolism (miscellaneous)	
Serine palmitoyltransferase, long chain base subunit 1, predicted (Sptlc1 predicted)	**2.0**
Hormone sensitive lipase (Lipe)	**7.9**
Angiopoietin-like 4 (Angptl4)	**4.2**
Fibroblast growth factor 21 (Fgf21)	**2.3**
Peroxisomal biogenesis factor 12 (Pex12)	**2.0**
Peroxisomal biogenesis factor 6 (Pex6)	**2.1**
Peroxisomal biogenesis factor 11c, predicted (Pex11c)	**2.1**
Adipose differentiation related protein (Adfp)	**2.0**
Glycogen metabolism	

Phosphoglucomutase 1, predicted (Pgm1 predicted)	**2.0**
Solute carrier family 37 (glycerol-6-phosphate transporter), member 4 (Slc37a4)	**2.6**
Respiratory chain/Oxidative Phosphorylation (Ox-Phos)	
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit e (Atp5i)	**2.0**
Mitochondrial ATP synthase regulatory component factor B (Atp5s)	**2.1**
NADH dehydrogenase, ubiquinone, 1 alpha subcomplex, 2, predicted (Ndufa2 predicted)	**2.1**
NADH dehydrogenase, ubiquinone, Fe-S protein 6 (Ndufs6)	**2.3**
NADH dehydrogenase, ubiquinone, 1 beta subcomplex, 5, predicted (Ndufb5 predicted)*	**2.5**
Similar to NADH-ubiquinone oxidoreductase B9 subunit, Complex I-B9, CI-B9 (LOC691001)	**2.0**
NADH dehydrogenase, ubiquinone, flavoprotein 2 (Ndufv2)	**2.1**
NADH dehydrogenase, ubiquinone, flavoprotein 3-like (Ndufv3l)	**2.1**
Ubiquinol cytochrome c reductase core protein 2 (Uqcrc2)	**2.0**
Creatine kinase, mitochondrial 1, ubiquitous (Ckmt1)	**3.9**
Creatine kinase, brain (Ckb)*	**2.6**
Uncoupling protein 2 (Ucp2)	**2.0**
Uncoupling protein 3 (Ucp3)	**2.2**
Antioxdidant activity	
Thioredoxin-like 4B (Txnl4b)	**2.3**
Thioredoxin domain containing 11, predicted (Txndc11)	**3.3**
Thioredoxin domain containing 12, endoplasmic reticulum (Txndc12)	**2.0**
Glutaredoxin 1, thioltransferase (Glrx1)	**2.0**
Glutaredoxin 2, thioltransferase (Glrx2)	**2.5**
Glutathione peroxidase 2 (Gpx2)	**2.1**
Glutathione peroxidase 7, predicted (Gpx7 predicted)	**2.0**
Peroxiredoxin 3 (Prdx3)	**2.0**

Superoxide dismutase 2, mitochondrial (Sod2)	**2.0**

TABLE S2. Metabolic gene expression array results after Spotfire analysis and organization into classic metabolic pathways. Upregulated genes are fold change (AdBcl3/AdGFP) ≥ 2.0; downregulated genes are fold change ≤ 0.5; $P \leq 0.05$ (n=4. * represents genes that were also identified as ERRα targets previously via gene expression array or ChIP-on-Chip studies (13, 29).

TABLE S3. The complete gene expression array results for Bcl3-regulated genes in cardiac myocytes.

Fold change	Accession Number	Unigene Gene Name	Unigene Gene Symbol
49.702	BF284307	Vestigial like 2 homolog (Drosophila) (predicted)	Vgll2_predicted
38.844	AI764437		
18.684	AW529938	B-box and SPRY domain containing	Bspry
17.049	AI028874		
16.920	AF068268	2-5 oligoadenylate synthetase 1B	Oas1b
16.661	AA963273	Transcribed locus	
15.789	BF405569	Transcribed locus	
15.148	AB026903	Decay accelarating factor 1	Daf1
12.236	NM_012817	Insulin-like growth factor binding protein 5	Igfbp5
11.989	BF386180	Transcribed locus, strongly similar to XP_346992.2 PREDICTED: similar to epididymal protein [Rattus norvegicus]	
11.545	BE106145	Transcribed locus	
10.865	AI059468	Hypothetical protein LOC308990	LOC308990
10.680	NM_012582	Haptoglobin	Hp
9.391	AW532890	Similar to OEF2 (predicted)	RGD1563091_predicted
9.235	BE099840	Similar to Expressed sequence AW547186 (predicted)	RGD1563286_predicted
7.941	NM_012859	Lipase, hormone sensitive	Lipe
7.702	NM_031031	Glycine amidinotransferase (L-arginine:glycine amidinotransferase)	Gatm
7.524	AI576297	Programmed cell death 4	Pdcd4
7.459	AI171480	Transcribed locus	
7.331	BE106796	Transcribed locus, weakly similar to NP_778159.1 hypothetical protein LOC211039 [Mus musculus]	
7.111	BI296482	Transcribed locus	
7.087	AI045150	Transcribed locus, strongly similar to XP_573755.1 PREDICTED: similar to	

		hypothetical gene supported by AK044523 [Rattus norvegicus]	
7.047	BI283883	Crumbs homolog 3 (Drosophila)	Crb3
7.008	BF557891	Interferon regulatory factor 6 (predicted)	Irf6_predicted
7.004	BF392357		
6.826	AF134409	RASD family, member 2	Rasd2
6.753	AA998516	Cyclin A2	Ccna2
6.570	BF410603	Interferon regulatory factor 6 (predicted)	Irf6_predicted
6.560	AW253690	DEP domain containing 1a (predicted)	Depdc1a_predicted
6.556	NM_134350	Myxovirus (influenza virus) resistance 2	Mx2
6.424	AI175045	Transcribed locus, weakly similar to XP_575132.1 PREDICTED: similar to LRRGT00012 [Rattus norvegicus]	
6.404	BI302778	Transcribed locus, strongly similar to XP_344880.2 PREDICTED: similar to Uroplakin Ia (UPIa) (UPKa) [Rattus norvegicus]	
6.396	NM_012604	Myosin, heavy polypeptide 3, skeletal muscle, embryonic	Myh3
6.072	AW920026	Similar to RIKEN cDNA 4933417L10	LOC364393
6.069	BI303853	Transcribed locus, moderately similar to XP_234745.3 PREDICTED: similar to Ig heavy chain V-I region HG3 precursor [Rattus norvegicus]	
6.022	BG379319	Transforming growth factor, beta induced	Tgfbi
6.017	AI176565	Acyl-CoA synthetase short-chain family member 1 (predicted)	Acss1_predicted
5.907	AI764144	RT1 class Ib, locus Aw2	RT1-Aw2
5.779	BF282370	Thymidylate kinase family LPS-inducible member (predicted)	Tyki_predicted
5.608	AI714002	Antigen identified by monoclonal antibody Ki-67 (predicted)	Mki67_predicted

5.587	NM_012949	Enolase 3, beta	Eno3
5.539	BM383329	Cyclin E2 (predicted)	Ccne2_predicted
5.443	AW520508	Transcribed locus, moderately similar to XP_578837.1 PREDICTED: similar to Ac1147 [Rattus norvegicus]	
5.397	NM_023094	ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyltransferase)	Abo
5.396	NM_013174	Transforming growth factor, beta 3	Tgfb3
5.343	NM_017097	Cathepsin C	Ctsc
5.329	AI407953	Transcribed locus	
5.324	AA818849	Similar to hypothetical protein FLJ11354 (predicted)	RGD1310093_predicted
5.303	BF550033		
5.270	AI044253	Transcribed locus, strongly similar to XP_232620.3 PREDICTED: similar to transcriptional regulatory protein [Rattus norvegicus]	
5.197	BI275929	Coilin	Coil
5.193	AW921174	Pregnancy-specific beta 1-glycoprotein	Psgb1
5.161	AI137518	Coxsackie virus and adenovirus receptor	Cxadr
5.067	AI410749	Transcribed locus	
5.002	NM_133523	Matrix metallopeptidase 3	Mmp3
4.969	AA901350	Transcribed locus, strongly similar to XP_227762.3 PREDICTED: similar to Guanylate nucleotide binding protein 4 [Rattus norvegicus]	
4.921	AW534332	Transcribed locus	
4.888	AI010322	Muscleblind-like 3 (Drosophila) (predicted)	Mbnl3_predicted
4.862	BI284344	Keratin complex 2, basic, gene 7	Krt2-7
4.832	BI289329	Similar to RIKEN cDNA 2310042D19	RGD1304931
4.794	BE109109	Similar to RIKEN cDNA 6530401L14 gene	RGD1309107
4.784	AA799557		

4.779	**NM_019174**	**Carbonic anhydrase 4**	**Ca4**
4.745	**AA996882**	**Serine/threonine kinase 6**	**Stk6**
4.654	**AA851385**		
4.608	**BE118697**	**Interferon-induced protein with tetratricopeptide repeats 2**	**Ifit2**
4.570	**BF282318**	**Similar to Serum amyloid A-3 protein precursor**	**LOC691143**
4.545	**AA956417**	**Transcribed locus**	
4.512	**BF282712**	**Similar to Hypothetical protein MGC37938 (predicted)**	**RGD1566169_predicted**
4.511	**NM_019205**	**Chemokine (C-C motif) ligand 11**	**Ccl11**
4.498	**NM_019335**	**Protein kinase, interferon-inducible double stranded RNA dependent**	**Prkr**
4.482	**U05341**	**Cell division cycle 20 homolog (S. cerevisiae)**	**Cdc20**
4.423	**BE110723**	**M-phase phosphoprotein 1 (predicted)**	**Mphosph1_predicted**
4.403	**BF567808**		
4.352	**AA818377**	**Zinc finger protein 533 (predicted)**	**Zfp533_predicted**
4.341	**AI408440**	**Similar to interferon-inducible GTPase**	**MGC108823**
4.301	**BE104060**	**Transcribed locus**	
4.268	**AW531714**	**Ubiquitin-conjugating enzyme E2T (putative) (predicted)**	**Ube2t_predicted**
4.242	**AA818262**	**Angiopoietin-like 4**	**Angptl4**
4.233	**BI286411**	**Keratin complex 2, basic, gene 5**	**Krt2-5**
4.216	**AI578135**	**Ect2 oncogene (predicted)**	**Ect2_predicted**
4.197	**BE108276**		
4.170	**BI295150**	**Cytoskeleton associated protein 2 (predicted)**	**Ckap2_predicted**
4.149	**AI501320**	**Transcribed locus**	
4.125	**AI411541**	**Prostaglandin E receptor 3 (subtype EP3)**	**Ptger3**
4.118	**AA819227**	**Tumor necrosis factor (TNF superfamily, member 2)**	**Tnf**
4.117	**NM_053551**	**Pyruvate dehydrogenase kinase, isoenzyme 4**	**Pdk4**
4.115	**BG666306**	**Thrombomodulin**	**Thbd**
4.073	**AI010157**	**Similar to hypothetical protein MGC33926**	**MGC94782**

4.054	**BF398114**	**Transcribed locus, strongly similar to XP_862455.1 PREDICTED: similar to Axin 2 (Axis inhibition protein 2) (Conductin) (Axin-like protein) (Axil) isoform 2 [Canis familiaris]**	
4.039	**BF281994**	**Transducin (beta)-like 1X-linked receptor 1 (predicted)**	**Tbl1xr1_predicted**
4.021	**BF283320**	**Transcribed locus**	
4.020	**BE102202**	**Transcribed locus**	
4.020	**BF393567**	**Similar to vacuolar protein sorting 13C protein (predicted)**	**RGD1560364_predicted**
4.003	**BI289546**	**Brain expressed X-linked 4**	**Bex4**
4.001	**NM_019348**	**Somatostatin receptor 2**	**Sstr2**
3.996	**AI169749**	**Transcribed locus, strongly similar to XP_580054.1 PREDICTED: hypothetical protein XP_580054 [Rattus norvegicus]**	
3.980	**AI555284**	**Transcribed locus**	
3.948	**NM_031766**	**Carboxypeptidase Z**	**Cpz**
3.925	**BI301453**	**Creatine kinase, mitochondrial 1, ubiquitous**	**Ckmt1**
3.918	**AW524109**	**Transcribed locus**	
3.912	**AA957260**	**Ribonucleotide reductase M2 (mapped)**	**Rrm2_mapped**
3.911	**BI284296**	**G protein-coupled receptor 126 (predicted)**	**Gpr126_predicted**
3.857	**NM_053749**	**Aurora kinase B**	**Aurkb**
3.846	**BF411794**	**Abhydrolase domain containing 6**	**Abhd6**
3.805	**BF410644**	**Transcribed locus**	
3.736	**Z18877**	**2',5'-oligoadenylate synthetase 1, 40/46kDa**	**Oas1**
3.732	**BF552738**	**Similar to DnaJ (Hsp40) homolog, subfamily B, member 10 isoform 2**	**LOC689593**
3.723	**NM_053318**	**Hemopexin**	**Hpx**
3.710	**NM_021696**	**Serine (or cysteine) proteinase inhibitor, clade B, member 2**	**Serpinb2**
3.707	**BG662490**	**Abhydrolase domain containing 3 (predicted)**	**Abhd3_predicted**
3.695	**BF396237**	**Nuclear receptor subfamily 4,**	**Nr4a3**

		group A, member 3	
3.694	AI500951	Serine (or cysteine) peptidase inhibitor, clade E, member 1	Serpine1
3.693	NM_017328	Phosphoglycerate mutase 2	Pgam2
3.690	AI408713	Imprinted and ancient	Impact
3.658	AF253065	Chemokine-like factor	Cklf
3.651	BI303598	Spindle pole body component 24 homolog (S. cerevisiae) (predicted)	Spbc24_predicted
3.648	BI289692	Transcribed locus	
3.646	AI235499	Transcribed locus	
3.612	AA799328	Similar to expressed sequence AW413625 (predicted)	RGD1560913_predicted
3.586	AI137995	Sodium channel, voltage-gated, type IV, beta	Scn4b
3.585	BF415216	Transcribed locus	
3.546	BI290662	Similar to CG3880-PA	LOC680531
3.542	BI296084	Ubiquitin-conjugating enzyme E2C (predicted)	Ube2c_predicted
3.533	X52711	Myxovirus (influenza virus) resistance 1	Mx1
3.531	BM385105	Phospholipase C, delta 3 (predicted)	Plcd3_predicted
3.512	AA800004	Septin 4	4-Sep
3.506	BM386609	Syndecan binding protein (syntenin) 2	Sdcbp2
3.492	BM384841	RAB15, member RAS onocogene family	Rab15
3.468	AW531805	Interferon-induced protein with tetratricopeptide repeats 3	Ifit3
3.440	BF399394		
3.434	BE109322	Polo-like kinase 4 (Drosophila) (predicted)	Plk4_predicted
3.393	AA963004	Transforming growth factor, beta 2	Tgfb2
3.382	BM387419	Transcribed locus, strongly similar to XP_216941.3 PREDICTED: similar to Matrilin 2 [Rattus norvegicus]	
3.378	NM_012532	Ceruloplasmin	Cp
3.364	BE113148	Transcribed locus, strongly similar to XP_223397.3 PREDICTED: similar to hypothetical protein [Rattus	

		norvegicus]	
3.358	AI045201	Tumor necrosis factor receptor superfamily, member 21 (predicted)	Tnfrsf21_predicted
3.327	AI232819	Thioredoxin domain containing 11 (predicted)	Txndc11_predicted
3.327	BF288208	Transcribed locus	
3.315	BE121050	CDNA clone IMAGE:7318427	
3.302	AA964152	Transcribed locus	
3.300	BF386852	ATP-binding cassette, sub-family A (ABC1), member 8b (predicted)	Abca8b_predicted
3.292	AI502790	Similar to mitochondrial carrier family protein	RGD1308774
3.277	BE096287	Transcribed locus, strongly similar to XP_345994.2 PREDICTED: similar to cysteine sulfinic acid decarboxylase [Rattus norvegicus]	
3.276	BF284903	Transcribed locus	
3.271	BF411331	Serine (or cysteine) proteinase inhibitor, clade B, member 1a	Serpinb1a
3.264	BG371744	Similar to zinc finger protein 458	LOC685865
3.251	AA997596	Similar to CG4502-PA, isoform A	LOC679949
3.243	AW534209	Transcribed locus	
3.233	AI712694	Similar to hypothetical protein FLJ10156 (predicted)	RGD1308747_predicted
3.220	AA819788	Receptor transporter protein 4 (predicted)	Rtp4_predicted
3.209	BI285978	Poly (ADP-ribose) polymerase family, member 12 (predicted)	Parp12_predicted
3.198	BF388785	Budding uninhibited by benzimidazoles 1 homolog (S. cerevisiae) (predicted)	Bub1_predicted
3.197	AI227963	Similar to protein phosphatase 1, regulatory (inhibitory) subunit 1C; thymocyte ARPP; DNA segment, Chr 9, Brigham & Womens Genetics 1012	RGD1307215

		expressed	
3.184	**D14839**	**Fibroblast growth factor 9**	**Fgf9**
3.165	**AI716194**	**Fibrinogen-like 2***	**Fgl2***
3.163	**BE104344**	**Similar to RIKEN cDNA G630055P03 gene**	**RGD1309383**
3.161	**BF417541**	**Similar to hypothetical protein FLJ11354 (predicted)**	**RGD1310093_predicted**
3.151	**NM_017187**		
3.151	**AA891826**	**Tumor-associated calcium signal transducer 2**	**Tacstd2**
3.127	**AA819629**	**Similar to histocompatibility 28**	**LOC310968**
3.118	**AA901035**	**Oxysterol binding protein-like 6 (predicted)**	**Osbpl6_predicted**
3.118	**BF403249**	**Similar to RIKEN cDNA 4931400A14 (predicted)**	**RGD1307234_predicted**
3.111	**BG671371**	**Similar to ankyrin repeat domain 13c**	**LOC685374**
3.108	**BM385936**	**Transcribed locus**	
3.106	**NM_133615**	**TAF9-like RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kDa**	**Taf9l**
3.106	**AA998104**	**Transcribed locus**	
3.102	**L15011**	**Cortexin**	**Ctxn**
3.094	**AI227677**	**Neural precursor cell expressed, developmentally down-regulated gene 4A**	**Nedd4a**
3.075	**BF561454**	**Fibrinogen-like 2***	**Fgl2***
3.070	**NM_013155**	**Very low density lipoprotein receptor***	**Vldlr***
3.053	**AA963085**	**Transcribed locus**	
3.038	**BF413643**	**Von Willebrand factor A domain containing 1**	**Vwa1**
3.038	**BF564273**	**Kinetochore associated 1 (predicted)**	**Kntc1_predicted**
3.037	**AF159103**	**Tumor necrosis factor alpha induced protein 6**	**Tnfaip6**
3.026	**AI502703**	**Keratin complex 1, acidic, gene 23**	**Krt1-23**
3.015	**BI284262**	**Protein regulator of cytokinesis 1 (predicted)**	**Prc1_predicted**
3.014	**NM_013104**	**Insulin-like growth factor binding protein 6**	**Igfbp6**

3.012	**AF361355**	**Transmembrane protein 37**	**Tmem37**
3.007	**NM_013200**	**Carnitine palmitoyltransferase 1b, muscle**	**Cpt1b**
3.002	**AA874827**	**Discs, large homolog 7 (Drosophila) (predicted)**	**Dlg7_predicted**
2.981	**BG665934**	**O-acyltransferase (membrane bound) domain containing 2**	**Oact2**
2.967	**AA996870**	**Chemokine-like receptor 1**	**Cmklr1**
2.953	**AB032828**	**Erythrocyte protein band 4.1-like 3**	**Epb4.1l3**
2.941	**NM_017029**	**Neurofilament 3, medium**	**Nef3**
2.937	**NM_032616**	**Lipolysis stimulated lipoprotein receptor**	**Lsr**
2.929	**BM388891**	**Interferon-induced protein 35**	**Ifi35**
2.923	**BG666368**	**Signal transducer and activator of transcription 2**	**Stat2**
2.920	**AW914913**	**Similar to CG4502-PA, isoform A**	**LOC679949**
2.919	**BG672426**	**Transcribed locus**	
2.918	**NM_031315**	**Cytosolic acyl-CoA thioesterase 1**	**Cte1**
2.915	**AA945915**	**Transcribed locus, strongly similar to XP_573295.1 PREDICTED: similar to deltex 3-like [Rattus norvegicus]**	
2.915	**BF394545**	**Transcribed locus**	
2.914	**NM_053779**	**Serine (or cysteine) peptidase inhibitor, clade I, member 1**	**Serpini1**
2.912	**NM_053819**	**Tissue inhibitor of metallopeptidase 1**	**Timp1**
2.900	**BM387260**	**Transcribed locus**	
2.898	**NM_022008**	**FXYD domain-containing ion transport regulator 7**	**Fxyd7**
2.883	**AA946413**	**Transcribed locus**	
2.883	**AW916067**	**Transcribed locus**	
2.876	**BF397823**	**Transcribed locus**	
2.873	**BF546570**	**Similar to cDNA sequence BC003331 (predicted)**	**RGD1307830_predicted**
2.871	**AW526714**	**Transcribed locus**	
2.841	**BG378463**	**RGD1563547 (predicted)**	**RGD1563547_predicted**
2.838	**AW525366**	**Interferon gamma induced GTPase**	**Igtp**
2.836	**NM_134472**		

2.832	NM_024388	Nuclear receptor subfamily 4, group A, member 1	Nr4a1
2.825	BM388478	TRAF4 associated factor 1	Traf4af1
2.825	BI296734	Transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	Tap1
2.821	BE120572	Zinc finger protein 612 (predicted)	Zfp612_predicted
2.812	AW533234	Similar to cardiomyopathy associated 5	LOC688915
2.803	AA997590	Osteoglycin (predicted)	Ogn_predicted
2.801	M60616	Matrix metallopeptidase 13	Mmp13
2.797	NM_012488	Alpha-2-macroglobulin	A2m
2.792	BI275815	Transcribed locus, strongly similar to XP_580230.1 PREDICTED: hypothetical protein XP_580230 [Rattus norvegicus]	
2.791	AA926180	Similar to angiopoietin-like 1	LOC679942
2.790	BI296089	Similar to very large G-protein coupled receptor 1 (predicted)	RGD1562101_predicted
2.770	AW532159	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase-like 1	B3gntl1
2.770	AI175488	Oxysterol binding protein (predicted)	Osbp_predicted
2.767	NM_021596	Diazepam binding inhibitor-like 5	Dbil5
2.759	AI409634	Best5 protein	Best5
2.737	NM_053477	Malonyl-CoA decarboxylase	Mlycd
2.730	BF552877	Solute carrier family 24, member 5 (predicted)	Slc24a5_predicted
2.729	BG671264	ATP-binding cassette, sub-family A (ABC1), member 8a (predicted)	Abca8a_predicted
2.724	BI295947	Similar to leiomodin 3 (fetal) (predicted)	RGD1564924_predicted
2.721	BF404433	Ankyrin repeat domain 52 (predicted)	Ankrd52_predicted
2.713	BI292425	Complement component 1, r subcomponent	C1r
2.705	BF284360	Transcribed locus	
2.702	AI639237	THO complex 2 (predicted)	Thoc2_predicted

2.701	**AI502837**	**Integrin beta 8 (predicted)**	**Itgb8_predicted**
2.691	**AA799431**	**Similar to leucine rich repeat containing 39 isoform 2**	**LOC691307**
2.690	**AF322216**	**Immunoglobulin superfamily, member 1**	**Igsf1**
2.679	**BE111697**	**Kinesin family member 20A (predicted)**	**Kif20a_predicted**
2.666	**BE095824**	**Chemokine (C-C motif) ligand 6**	**Ccl6**
2.662	**BE108569**	**Guanylate nucleotide binding protein 4 (predicted)**	**Gbp4_predicted**
2.661	**BF417638**	**Cell division cycle associated 3**	**Cdca3**
2.658	**AI764605**	**Transcribed locus**	
2.655	**AI599350**	**Proteosome (prosome, macropain) subunit, beta type 9**	**Psmb9**
2.644	**AA943147**	**Potential ubiquitin ligase**	**Herc6**
2.643	**NM_031589**	**Solute carrier family 37 (glycerol-6-phosphate transporter), member 4**	**Slc37a4**
2.639	**NM_133624**	**Guanylate nucleotide binding protein 2**	**Gbp2**
2.635	**NM_012976**	**Lectin, galactose binding, soluble 5**	**Lgals5**
2.633	**U36771**	**Glycerol-3-phosphate acyltransferase, mitochondrial**	**Gpam**
2.632	**AI409259**	**Rac GTPase-activating protein 1 (predicted)**	**Racgap1_predicted**
2.628	**BI279216**	**Ubiquitin-conjugating enzyme E2L 6**	**Ube2l6**
2.627	**BM385445**	**Topoisomerase (DNA) 2 alpha**	**Top2a**
2.626	**BF556985**	**Wingless-related MMTV integration site 2**	**Wnt2**
2.626	**NM_022391**	**Pituitary tumor-transforming 1**	**Pttg1**
2.621	**AI717736**	**Hypothetical protein LOC503164**	**LOC503164**
2.619	**L27487**	**Calcitonin receptor-like**	**Calcrl**
2.606	**AI145035**	**Transcribed locus**	
2.601	**NM_017102**	**Solute carrier family 2 (facilitated glucose transporter), member 3**	**Slc2a3**
2.600	**AA964219**	**Transcribed locus, strongly similar to XP_225720.3 PREDICTED: similar to Lipase, endothelial [Rattus norvegicus]**	
2.597	**NM_012548**	**Endothelin 1**	**Edn1**

2.590	**BM389254**	**Annexin A8**	**Anxa8**
2.590	**BF281980**	**Transcribed locus**	
2.587	**M14400**	**Creatine kinase, brain***	**Ckb***
2.586	**BM385476**	**Bone marrow stromal cell antigen 2**	**Bst2**
2.586	**AI172141**	**Ankyrin 1, erythroid**	**Ank1**
2.583	**AA945178**	**Transferrin**	**Tf**
2.578	**AI102560**	**Rap guanine nucleotide exchange factor (GEF) 5**	**Rapgef5**
2.576	**AI555044**	**Hypothetical RNA binding protein RGD1359713**	**RGD1359713**
2.550	**NM_024483**	**Adrenergic receptor, alpha 1d**	**Adra1d**
2.545	**AI234119**	**Transcribed locus**	
2.531	**BF555448**	**Mitochondrial acyl-CoA thioesterase 1**	**Mte1**
2.520	**BF558518**	**Glutaredoxin 2 (thioltransferase)**	**Glrx2**
2.514	**L09752**	**Cyclin D2**	**Ccnd2**
2.504	**BG381524**	**Cell division cycle associated 2**	**Cdca2**
2.502	**BF414118**	**Transcribed locus**	
2.501	**NM_013151**	**Plasminogen activator, tissue**	**Plat**
2.500	**NM_019211**	**RAS guanyl releasing protein 1**	**Rasgrp1**
2.488	**BE120953**	**Ligand of numb-protein X 1 (predicted)**	**Lnx1_predicted**
2.486	**BG663483**	**Protocadherin alpha 4**	**Pcdha4**
2.484	**BE098538**	**Transcribed locus**	
2.481	**AI639142**	**Similar to RAD51 associated protein 1**	**LOC689055**
2.478	**M25804**	**Nuclear receptor subfamily 1, group D, member 1**	**Nr1d1**
2.475	**BF406973**	**Similar to DKFZP434P1750 protein (predicted)**	**RGD1311490_predicted**
2.467	**BI291434**	**Phosphofructokinase, muscle**	**Pfkm**
2.467	**X57764**	**Endothelin receptor type B**	**Ednrb**
2.466	**BE108648**	**Transcribed locus**	
2.466	**BG663837**	**PDZ binding kinase (predicted)**	**Pbk_predicted**
2.463	**BE117126**	**Similar to RIKEN cDNA 2310005N03 gene**	**RGD1309105_predicted**
2.456	**BF561546**	**Transcribed locus**	
2.455	**AA944898**	**Aminoadipate-semialdehyde synthase (predicted)**	**Aass_predicted**
2.452	**NM_031855**	**Ketohexokinase**	**Khk**

2.451	**AA901341**	**Transcribed locus**	
2.445	**BG379338**	**Transcribed locus, strongly similar to NP_033130.1 ribonucleotide reductase M2 [Mus musculus]**	
2.444	**AI502114**	**ATP-binding cassette, sub-family A (ABC1), member 1**	**Abca1**
2.444	**AW534220**	**Oxysterol binding protein-like 1A**	**Osbpl1a**
2.444	**NM_017020**	**Interleukin 6 receptor, alpha**	**Il6ra**
2.443	**AI145247**	**Transcribed locus**	
2.442	**NM_017332**	**Fatty acid synthase**	**Fasn**
2.441	**BM986214**	**6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2**	**Pfkfb2**
2.441	**BI280278**	**Similar to hypothetical protein DKFZp434A1319 (predicted)**	**RGD1307357_predicted**
2.437	**AI711233**	**Transcribed locus**	
2.434	**AI556917**	**Transforming, acidic coiled-coil containing protein 3**	**Tacc3**
2.433	**NM_017256**	**Transforming growth factor, beta receptor III**	**Tgfbr3**
2.424	**AW524858**	**Transcribed locus**	
2.418	**AI385371**	**Extra spindle poles like 1 (S. cerevisiae) (predicted)**	**Espl1_predicted**
2.410	**D83598**	**ATP-binding cassette, sub-family C (CFTR/MRP), member 9**	**Abcc9**
2.409	**BF559673**	**Tumor necrosis factor receptor superfamily, member 17 (predicted)**	**Tnfrsf17_predicted**
2.407	**BM386847**	**N-myc (and STAT) interactor**	**Nmi**
2.398	**NM_031633**	**Forkhead box M1**	**Foxm1**
2.398	**NM_053552**	**Tumor necrosis factor (ligand) superfamily, member 4**	**Tnfsf4**
2.395	**NM_016986**	**Acetyl-Coenzyme A dehydrogenase, medium chain***	**Acadm***
2.395	**AI716196**	**Transcribed locus, strongly similar to XP_577026.1 PREDICTED: similar to transcription elongation factor A (SII)-like 3 [Rattus norvegicus]**	
2.395	**BF283340**	**Transcribed locus**	

2.390	**BE102400**	**Similar to talin 2 (predicted)**	**RGD1565416_predicted**
2.376	**NM_024162**	**Fatty acid binding protein 3***	**Fabp3***
2.374	**L11995**	**Cyclin B1**	**Ccnb1**
2.372	**BI295179**	**Transcribed locus, strongly similar to NP_036039.1 ubiquitin specific protease 18 [Mus musculus]**	
2.366	**NM_017066**	**Pleiotrophin**	**Ptn**
2.360	**AW524463**	**Similar to RIKEN cDNA 5730410E15 gene (predicted)**	**RGD1564335_predicted**
2.359	**AW142969**	**Transcribed locus**	
2.353	**AI716512**	**Solute carrier family 4, sodium bicarbonate transporter-like, member 10**	**Slc4a10**
2.345	**NM_012608**	**Membrane metallo endopeptidase**	**Mme**
2.344	**AA851904**	**1-acylglycerol-3-phosphate O-acyltransferase 6 (lysophosphatidic acid acyltransferase, zeta)**	**Agpat6**
2.342	**BF414751**	**Similar to Hypothetical protein LOC270802 (predicted)**	**RGD1565498_predicted**
2.341	**BI291396**	**Similar to Traf2 and NCK interacting kinase, splice variant 4 (predicted)**	**RGD1561817_predicted**
2.338	**NM_019223**	**NADH dehydrogenase (ubiquinone) Fe-S protein 6**	**Ndufs6**
2.336	**BI279044**	**Myosin, light polypeptide 9, regulatory (predicted)**	**Myl9_predicted**
2.328	**AI102021**	**Similar to THO complex subunit 4 (Tho4) (RNA and export factor binding protein 1) (REF1-I) (Ally of AML-1 and LEF-1) (Aly/REF)**	**LOC690585**
2.327	**BI289045**	**Guanine nucleotide binding protein, alpha 14**	**Gna14**
2.324	**BE112921**	**Similar to chromosome 14 open reading frame 145**	**LOC500700**
2.323	**NM_130752**	**Fibroblast growth factor 21**	**Fgf21**
2.319	**AW522872**	**Transcribed locus, weakly similar to NP_766020.1 RIKEN cDNA C030002O17 [Mus musculus]**	
2.319	**BI281307**	**NADH dehydrogenase (ubiquinone) 1 beta subcomplex,**	**Ndufb5_predicted***

		5 (predicted)*	
2.318	AA800742	Similar to Protein C20orf129 homolog (predicted)	RGD1565583_predicted
2.317	BF285089	Thioredoxin-like 4B	Txnl4b
2.311	AI713319	E2F transcription factor 1	E2f1
2.305	X55812	Cannabinoid receptor 1 (brain)	Cnr1
2.300	NM_053442	Solute carrier family 7 (cationic amino acid transporter, y+ system), member 8	Slc7a8
2.297	AI029057	Phytanoyl-CoA hydroxylase	Phyh
2.293	AA875348	Similar to RIKEN cDNA 1110001A07 gene	RGD1307084
2.292	BE109095	Similar to Serine/threonine-protein kinase WNK3 (Protein kinase, lysine-deficient 3) (predicted)	RGD1563131_predicted
2.284	AJ010392	Vacuolar protein sorting 54 (yeast)	Vps54
2.282	AA955871	Insulin-like growth factor 1	Igf1
2.261	NM_017139	Preproenkephalin, related sequence	Penk-rs
2.259	BM388202		
2.258	AI145457	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B)	Elavl2
2.257	NM_052809	Cysteine dioxygenase 1, cytosolic	Cdo1
2.256	BE108158	Transcribed locus	
2.248	BG371889		
2.247	BE111727	Longevity assurance homolog 4 (S. cerevisiae) (predicted)	Lass4_predicted
2.242	AI179119	Pyruvate dehydrogenase kinase, isoenzyme 3 (mapped)	Pdk3
2.236	AI102401	Transcribed locus	
2.235	NM_019157	Aquaporin 7	Aqp7
2.230	BI277879	Solute carrier family 30 (zinc transporter), member 2	Slc30a2
2.220	U88294	Carnitine palmitoyltransferase 1a, liver	Cpt1a
2.220	AW527492	Metal response element binding transcription factor 2	Mtf2
2.219	AI169829	Mannan-binding lectin serine peptidase 1	Masp1
2.215	AW253821	Cyclin B2	Ccnb2

2.215	**BF398599**	**Transcribed locus, strongly similar to XP_577455.1 PREDICTED: similar to Diap3 protein [Rattus norvegicus]**	
2.214	**BE096453**	**Ubiquitin-activating enzyme E1-like (predicted)**	**Ube1l_predicted**
2.210	**AI575264**	**DEAD (Asp-Glu-Ala-Asp) box polypeptide 58 (predicted)**	**Ddx58_predicted**
2.206	**BI296885**	**PHD finger protein 17 (predicted)**	**Phf17_predicted**
2.205	**U22520**	**Chemokine (C-X-C motif) ligand 10**	**Cxcl10**
2.203	**AI717543**	**Similar to leucine rich repeat containing 39 isoform 2**	**LOC691307**
2.203	**BF283256**	**Sodium channel associated protein 1**	**Sap1**
2.202	**NM_053908**	**Protein tyrosine phosphatase, non-receptor type 6**	**Ptpn6**
2.201	**NM_057103**	**A kinase (PRKA) anchor protein (gravin) 12**	**Akap12**
2.201	**AI230669**	**Guanine nucleotide binding protein, beta 1**	**Gnb1**
2.200	**BF419319**	**2'-5' oligoadenylate synthetase-like 1**	**Oasl1**
2.200	**NM_057197**	**2,4-dienoyl CoA reductase 1, mitochondrial**	**Decr1**
2.199	**AA850751**		
2.198	**AW920352**	**Transcribed locus**	
2.197	**NM_031530**	**Chemokine (C-C motif) ligand 2**	**Ccl2**
2.195	**NM_024355**	**Axin2**	**Axin2**
2.191	**BI290037**	**Junction adhesion molecule 2**	**Jam2**
2.188	**AI059150**	**Integrin alpha 8**	**Itga8**
2.186	**NM_013026**	**Syndecan 1**	**Sdc1**
2.185	**H33148**	**Similar to mKIAA0256 protein (predicted)**	**RGD1559930_predicted**
2.176	**BE118450**	**Retinoid X receptor gamma**	**Rxrg**
2.173	**AI411941**	**Fibronectin type III domain containing 1**	**Fndc1**
2.173	**BF411036**	**Interferon regulatory factor 7**	**Irf7**
2.171	**U92069**	**Uncoupling protein 3 (mitochondrial, proton carrier)**	**Ucp3**
2.169	**NM_019333**	**6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4**	**Pfkfb4**

2.168	**J02585**	**Stearoyl-Coenzyme A desaturase 1**	**Scd1**
2.167	**BI395810**	**Neuropeptide Y receptor Y1**	**Npy1r**
2.166	**AI600031**	**Transcribed locus, strongly similar to NP_573483.1 serum/glucocorticoid regulated kinase 3 [Mus musculus]**	
2.164	**AI175539**	**Parvalbumin**	**Pvalb**
2.164	**AI598581**	**Neurturin**	**Nrtn**
2.160	**BI290077**	**Transcribed locus**	
2.157	**BI292045**	**Similar to SH3 binding domain protein 5 like**	**LOC690898**
2.157	**AI317842**	**Kinesin family member 22**	**Kif22**
2.155	**BG673439**	**Claudin 11**	**Cldn11**
2.151	**AI179403**	**Activating signal cointegrator 1 complex subunit 3 (predicted)**	**Ascc3_predicted**
2.148	**BF290862**	**Transcribed locus, strongly similar to NP_666196.1 expressed sequence AW060714 [Mus musculus]**	
2.146	**NM_080767**	**RT1 class II, locus Bb**	**RT1-Bb**
2.144	**AW434380**	**Similar to leucine rich repeat containing 27 (predicted)**	**RGD1559981_predicted**
2.141	**NM_057125**	**Peroxisomal biogenesis factor 6**	**Pex6**
2.141	**AI230014**	**Phosphoglycerate mutase family member 5**	**Pgam5**
2.139	**AA945761**	**Similar to 9230105E10Rik protein**	**RGD1304579**
2.138	**BI277463**	**Diacylglycerol O-acyltransferase homolog 2 (mouse)**	**Dgat2**
2.137	**BI274399**	**Lysyl oxidase-like 3 (predicted)**	**Loxl3_predicted**
2.133	**BG672767**	**TBC1 domain family, member 19 (predicted)**	**Tbc1d19_predicted**
2.133	**BF408421**	**Peroxisomal biogenesis factor 11c (predicted)**	**Pex11c_predicted**
2.133	**BI290897**	**Similar to chromosome 2 open reading frame 3; transcription factor 9 (binds GC-rich sequences) (predicted)**	**RGD1304792_predicted**
2.133	**BI288855**	**Transcribed locus**	
2.132	**AI045970**	**Transcribed locus, strongly similar to XP_341931.1 PREDICTED: similar to hypothetical protein**	

		B130036O03 [Rattus norvegicus]	
2.120	**AW142608**	**Transcribed locus**	
2.120	**BI296531**	**Mitochondrial ATP synthase regulatory component factor B**	**Atp5s**
2.118	**AF303035**	**Antisense RNA overlapping MCH protein**	
2.115	**BI277042**	**Glycerol-3-phosphate dehydrogenase 1 (soluble)**	**Gpd1**
2.113	**NM_022607**	**NADH dehydrogenase (ubiquinone) flavoprotein 3-like**	**Ndufv3l**
2.112	**BF282933**	**Acyl-CoA thioesterase 8**	**Acot8**
2.111	**BI279838**	**NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2 (predicted)**	**Ndufa2_predicted**
2.107	**AI575616**	**Transcribed locus**	
2.105	**AF104399**	**Cbp/p300-interacting transactivator with Glu/Asp-rich carboxy-terminal domain 1**	**Cited1**
2.094	**NM_057107**	**Acyl-CoA synthetase long-chain family member 3**	**Acsl3**
2.089	**BF549923**	**Proprotein convertase subtilisin/kexin type 5**	**Pcsk5**
2.081	**NM_053681**	**S100 calcium binding protein A3**	**S100a3**
2.079	**AW533321**	**Fatty acid desaturase 3**	**Fads3**
2.068	**D88891**	**Acyl-CoA thioesterase 7**	**Acot7**
2.058	**M22756**	**NADH dehydrogenase (ubiquinone) flavoprotein 2**	**Ndufv2**
2.058	**AI029749**	**Short coiled-coil protein**	**Scoc**
2.057	**AI177761**	**CD68 antigen**	**Cd68**
2.054	**AW532165**	**Sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3D**	**Sema3d**
2.050	**BE120904**	**Transcribed locus**	
2.049	**AA964902**	**Similar to CG1998-PA**	**LOC691221**
2.046	**BF284106**	**Similar to hypothetical protein MGC29390 (predicted)**	**RGD1310490_predicted**
2.043	**BG377082**	**TRAF-interacting protein (predicted)**	**Traip_predicted**
2.041	**NM_133406**	**1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid**	**Agpat4**

		acyltransferase, delta)	
2.039	**NM_131902**	**Cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)**	**Cdkn2c**
2.039	**AW252811**	**Similar to Moloney leukemia virus 10**	**LOC310756**
2.037	**BF546148**	**LOC363015 (predicted)**	**RGD1310444_predicted**
2.036	**BI301008**	**CDNA clone IMAGE:7317308**	
2.036	**AA925583**	**B-cell linker**	**Blnk**
2.036	**NM_031564**	**Eph receptor A3**	**Epha3**
2.034	**NM_022278**	**Glutaredoxin 1 (thioltransferase)**	**Glrx1**
2.033	**BF416400**	**Similar to glycosyltransferase 8 domain containing 2 (predicted)**	**RGD1560432_predicted**
2.031	**BF282631**	**Complement component 7**	**C7**
2.031	**BG381587**	**Beta-site APP-cleaving enzyme 2**	**Bace2**
2.028	**AI113308**	**Transcribed locus**	
2.027	**BE100009**	**Transcribed locus, strongly similar to XP_232942.3 PREDICTED: similar to hypothetical protein [Rattus norvegicus]**	
2.027	**AA875647**	**Transcribed locus**	
2.027	**AI236188**	**Transcribed locus**	
2.026	**BG668816**	**Ethanolamine kinase 1 (predicted)**	**Etnk1_predicted**
2.025	**AI013730**	**Similar to hypothetical protein (predicted)**	**RGD1305269_predicted**
2.025	**NM_012955**	**FSH primary response 1**	**Fshprh1**
2.024	**BM384521**	**Similar to putative N-acetyltransferase Camello 2 (predicted)**	**RGD1305719_predicted**
2.024	**BM392002**	**Coenzyme A synthase**	**Coasy**
2.023	**BF387780**		
2.021	**BE107760**	**Stearoyl-Coenzyme A desaturase 2***	**Scd2***
2.021	**AA859496**	**GTP cyclohydrolase 1**	**Gch**
2.017	**BM389001**	**Procollagen, type IX, alpha 3 (predicted)**	**Col9a3_predicted**
2.017	**AA875107**	**Similar to NADH-ubiquinone oxidoreductase B9 subunit (Complex I-B9) (CI-B9)**	**LOC691001**

2.017	**AI012418**	**Sterol O-acyltransferase 1**	**Soat1**
2.017	**BF393945**	**Transcribed locus**	
2.017	**AI011772**	**Peroxiredoxin 3**	**Prdx3**
2.017	**BI303342**	**Adipocyte-specific adhesion molecule**	**Asam**
2.016	**NM_019296**	**Cell division cycle 2 homolog A (S. pombe)**	**Cdc2a**
2.015	**AI071166**	**Similar to 1110007F12Rik protein**	**MGC109491**
2.015	**BM389302**	**Nidogen 2**	**Nid2**
2.012	**NM_012589**	**Interleukin 6**	**Il6**
2.011	**NM_053921**	**Peroxisomal biogenesis factor 12**	**Pex12**
2.011	**BG671549**	**Superoxide dismutase 2, mitochondrial**	**Sod2**
2.011	**AF399874**	**Troponin T1, skeletal, slow**	**Tnnt1**
2.010	**AA957288**	**Acyl-CoA synthetase long-chain family member 1**	**Acsl1**
2.009	**NM_053482**	**Sperm autoantigenic protein 17**	**Spa17**
2.008	**BG377729**	**Similar to thrombospondin, type I, domain containing 2 (predicted)**	**RGD1563246_predicted**
2.008	**AI170333**	**Low density lipoprotein receptor-related protein associated protein 1**	**Lrpap1**
2.007	**BI284800**	**Guanine nucleotide binding protein beta 4 subunit**	**Gnb4**
2.007	**NM_133514**	**Matrix metallopeptidase 10**	**Mmp10**
2.005	**AI177957**	**SP110 nuclear body protein**	**Sp110**
2.002	**BF543355**	**Immunoglobulin superfamily, member 10**	**Igsf10**
2.001	**AF058787**	**Similar to Heme oxygenase 3 (HO-3)**	**LOC365909**
2.001	**AI102641**	**Ubiquitin carboxyl-terminal hydrolase L5**	**Uchl5**
1.999	**AI706508**	**Peroxisome proliferative activated receptor, gamma, coactivator-related 1 (predicted)**	**Pprc1_predicted**
1.997	**AI101330**	**Neurocalcin delta**	**Ncald**
1.997	**BI303342**	**Adipocyte-specific adhesion molecule**	**Asam**
1.993	**AI169398**	**Cholesterol 25-hydroxylase**	**Ch25h**
1.990	**BE098463**	**Ubiquitin specific protease 43 (predicted)**	**Usp43_predicted**

1.984	**BE116152**	**ELOVL family member 6, elongation of long chain fatty acids (yeast)**	**Elovl6**
1.980	**NM_013126**	**Diacylglycerol kinase, gamma**	**Dgkg**
1.977	**NM_133306**	**Oxidized low density lipoprotein (lectin-like) receptor 1**	**Oldlr1**
1.976	**AW916358**	**Serine palmitoyltransferase, long chain base subunit 1 (predicted)**	**Sptlc1_predicted**
1.975	**BF406975**	**Thioredoxin domain containing 12 (endoplasmic reticulum)**	**Txndc12**
1.972	**AI104303**	**Hypothetical LOC314467 (predicted)**	**RGD1305627_predicted**
1.969	**NM_080481**	**ATP synthase, H+ transporting, mitochondrial F0 complex, subunit e**	**Atp5i**
1.969	**BF408445**	**Glutathione peroxidase 7 (predicted)**	**Gpx7_predicted**
1.968	**BF290998**	**Ubiquinol cytochrome c reductase core protein 2**	**Uqcrc2**
1.967	**NM_031347**	**Peroxisome proliferative activated receptor, gamma, coactivator 1 alpha**	**Ppargc1a**
1.967	**AI176913**	**Phosphoglucomutase 1 (predicted)**	**Pgm1_predicted**
1.964	**NM_031987**	**Carnitine O-octanoyltransferase**	**Crot**
1.963	**BI296347**	**Acyl-Coenzyme A dehydrogenase family, member 11 (predicted)**	**Acad11_predicted**
1.958	**NM_019354**	**Uncoupling protein 2 (mitochondrial, proton carrier)**	**Ucp2**
1.958	**AI535136**	**Hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit***	**Hadha***
1.957	**AI145761**	**Lactate dehydrogenase D**	**Ldhd**
1.957	**BF394106**	**Tumor necrosis factor (ligand) superfamily, member 9**	**Tnfsf9**
1.956	**NM_012891**	**Acyl-Coenzyme A dehydrogenase, very long chain***	**Acadvl***
1.955	**AI137547**	**Transcribed locus, weakly similar to XP_125510.6 PREDICTED: hypothetical**	

		protein LOC73112 [Mus musculus]	
1.954	L09653	Transforming growth factor, beta receptor II	Tgfbr2
1.952	AW522833	Transcribed locus	
1.951	BI298434	Transcribed locus, strongly similar to XP_236967.3 PREDICTED: similar to OTTHUMP00000039916 [Rattus norvegicus]	
1.946	NM_031682	Hydroxyacyl-Coenzyme A dehydrogenase type II	Hadh2
0.542	BF413560	Transcribed locus	
0.511	AI011920	RCSD domain containing 1 (predicted)	Rcsd1_predicted
0.484	BF392830	Contactin associated protein 1	Cntnap1
0.478	NM_053669	Adaptor protein with pleckstrin homology and src homology 2 domains	Aps
0.476	NM_133570	Gastrin releasing peptide	Grp
0.461	BI296374	Transcribed locus	
0.432	BM388888	Similar to SUN2 (predicted)	RGD1563141_predicted
0.348	BE349836	Transcribed locus	
0.345	NM_031557	Prostaglandin I2 (prostacyclin) synthase	Ptgis
0.308	AA996557	Similar to immunoglobulin heavy chain 6 (Igh-6)	RGD1359202
0.257	AI230591	Similar to ctla-2-beta protein (141 AA) (predicted)	RGD1565540_predicted
0.242	BI288825	Ankyrin repeat domain 1 (cardiac muscle)	Ankrd1
0.134	NM_017341	Lipase, gastric	Lipf
0.081	AF290212	Calcium channel, voltage-dependent, T type, alpha 1G subunit	Cacna1g
0.077	AI535458	Rcd1 (required for cell differentiation) homolog 1 (S. pombe)	Rqcd1
0.073	AW521327	Transcribed locus	
0.072	AA957487	Similar to novel protein (predicted)	RGD1561932_predicted

*** represents genes that were also identified as ERRα targets by others through expression array or ChIP-on-Chip (13, 29).**