

Category	Symbol	Description	Fold-change	RefSeq	Sequence
1.Energy Metabolism	B4galnt1	beta-1,4-n-acetyl-galactosaminyl transferase 1	6.97	NM_008080	CCATAAAAGC
1.Energy Metabolism	Apod	Apolipoprotein d	3.66	NM_007470	CTATAAAAGG
1.Energy Metabolism	Pfkp	Phosphofructokinase, Platelet	2.1	NM_019703	CCAAATTTAG
1.Energy Metabolism	Acot9	Acyl-CoA Thioesterase 9	2.01	NM_019736	GCTTCTTTGG CCTTCTTTGA
1.Energy Metabolism	Slc27a1	Solute Carrier Family 27 (fatty acid transporter), Member 1	0.49	NM_011977	GCATATATGG
1.Energy Metabolism	Lipc	Lipase, Hepatic	0.45	NM_008280	CCGTCTAAGG GCTTACATGG
1.Energy Metabolism	Fdft1	Farnesyl Diphosphate Farnesyl Transferase 1	0.45	NM_010191	CCATTTCTGG CCAAACTTGG
1.Energy Metabolism	Coasy	Coenzyme A Synthase	0.37	NM_027896	
1.Energy Metabolism	Pafah1b3	Platelet-activating Factor Acetylhydrolase, isoform 1b, alpha1 subunit	0.31	NM_008776	CCATTTAGGG
1.Energy Metabolism	Aadac	Arylacetamide Deacetylase (esterase)	0.22	NM_023383	CCAGTTATGG CTAATTAGG
1.Energy Metabolism	Elovl2	Elongation of Very Long chain fatty acids (fen1/elo2, sur4/elo3, yeast)-like 2	0.2	NM_019423	CCTTATAAGG
1.Energy Metabolism	Akr1c6	Hydroxysteroid (17-beta) Dehydrogenase 5	0.14	NM_030611	CCATAAAAGG
1.Energy Metabolism	Pgk2	Phosphoglycerate Kinase 2	0.1	NM_031190	CCATAGATGG
1.Energy Metabolism	Es1	Esterase 1	0.06	NM_007954	CCATTTATTG CCTTATTAG
1.Energy Metabolism	Apoa1	apolipoprotein a-i	0.02	NM_009692	CCAGAAAAGG
2.Xenobiotic Metabolism	Maoa	Monoamine Oxidase A	2.8	NM_173740	CCATATAAGT
2.Xenobiotic Metabolism	Cyp2b10	Cytochrome p450, family 2, subfamily b, polypeptide 10	2.17	NM_009999	CCTTTTATAG CCAAGAAGG CCAAATTTGG

2.Xenobiotic Metabolism	Sult1a1	Sulfotransferase family 1a, phenol-preferring, member 1	0.45	NM_133670	CCCAATTAGT
2.Xenobiotic Metabolism	Cyp3a16	Cytochrome p450, family 3, subfamily a, polypeptide 16	0.14	NM_007820	CCATTTATGT CCTTGTTTGG CCAAATTTG
2.Xenobiotic Metabolism	Ugt2b5	UDP Glucuronosyltransferase 2 family, polypeptide b5	0.05	NM_009467	CCAAATTTGG CCATAGATGG
2.Xenobiotic Metabolism	Cyp3a11	Cytochrome p450, family 3, subfamily a, polypeptide 11	0.02	NM_007818	CCAGATATGG
2.Xenobiotic Metabolism	Oat	ornithine aminotransferase	0.48	NM_016978	CCTTTTAGGG CCTGATATGG
2.Xenobiotic Metabolism	Bphl	biphenyl hydrolase-like (serine hydrolase, breast epithelial mucin-associated antigen)	0.35	NM_026512	CAATAAATGG CCATGTAAGG
2.Xenobiotic Metabolism	Skb1	protein arginine n-methyltransferase 5	0.31	NM_013768	CCTTATATAG CCTTATATAG
2.Xenobiotic Metabolism	Uox	urate oxidase	0.07	NM_009474	CCAAATATGG
2.Xenobiotic Metabolism	Gnmt	glycine n-methyltransferase	0.06	NM_010321	CCAAAGTAGG CCAAAGTAGG
3.Cytoskeleton	Myl1	Myosin, Light polypeptide 1	4.65	NM_021285	CCCTAAATGG CCATTTATAG
3.Cytoskeleton	Anxa10	annexin a10	31.21	NM_011922	CCATAATTGG
3.Cytoskeleton	Rab8b	Rab8b, member ras oncogene family	4.2	NM_173413	CCTAATTAGG
3.Cytoskeleton	Acta2	Actin, alpha 2, smooth muscle, aorta	3.65	NM_007392	CCCTATATGG CCTTGTTTGG
3.Cytoskeleton	Casq1	Calsequestrin 1	2.81	NM_009813	CCATAGAAGG CTATATAAGG
3.Cytoskeleton	Actn1	Actinin, alpha 1	2.56	NM_134156	CCATAAAATG CCTTTTATGT
3.Cytoskeleton	Myh7	Myosin, Heavy polypeptide 7, cardiac muscle, beta	2.49	NM_080728	CCTTATTTGG CCTTATTTGG
3.Cytoskeleton	Epb4.2	Erythrocyte protein band 4.2	2.49	NM_013513	CCTTTTATGT CCTTATTTGG
3.Cytoskeleton	Dstn	Destrin	2.27	NM_019771	>Dstn_4 () CCTTTTATG

3.Cytoskeleton	Tpm2	Tropomyosin 2, beta	2.08	NM_009416	>Tpm2_5 () CCTAATTAGT >Tpm2_6 () CCAAAAAGG
3.Cytoskeleton	Fmn1	Formin-like 1	0.47	NM_001077698	>Fmn1_1 () CCAGATTGG () CTTTTATGG
3.Cytoskeleton	Vps13c	Vacuolar Protein Sorting 13c (yeast)	0.26	NM_177184	>Vps13c_2 () CCAGAAATGG
3.Cytoskeleton	Syt3	Synaptotagmin iii	0.15	NM_016663	>Syt3_4 () CCAAATAGGG
3.Cytoskeleton	Myh4	Myosin, Heavy polypeptide 4, skeletal muscle	0.05	NM_010855	>Myh4_6 () CCAAAAATGG
3.Cytoskeleton	Tspan8	Tetraspanin 8	0.28	NM_146010	GCATAAAAGG ()
3.Cytoskeleton	Hrc	Hrc histidine rich calcium binding protein	0.36	NM_010473.	
3.Cytoskeleton	Dsc2	Desmocollin 2	0.41	NM_010478	>Dsc2_5 () ACATTTATGG >Dsc2_6 () CCTTTTTTGG
4.Transcription	Fhl1	four and a half lim domains 1	3.03	NM_001077361	() CCAAAGAAGG () CCTAATATGG
4.Transcription	Rps4y2	Ribosomal protein S4, Y-linked 2	2.38	NR_003634	>Rps4y2_3 (-6640) CTAATTTGG (-6758) GCATTTATGG
4.Transcription	Plagl1	pleiomorphic adenoma gene-like 1	6.87	NM_009538	>Plagl1_1 () CCTAATTAGA
4.Transcription	Dlx5	distal-less homeobox 5	4.85	NM_010056	
4.Transcription	Atf3	activating transcription factor 3	4.53	NM_007498	>Atf3_3 () GCAAATTTGG
4.Transcription	Pus1	pseudouridine synthase 1 (tRNA-uridine isomerase I)	4.31	NM_001025561	>Pus1_3 () CCATTTATTG >Pus1_4 () TCATAAAAGG
4.Transcription	Tbp	tata box binding protein	3.85	NM_013684.	>>TBP_3_780_CTTTTTATGG >>TBP_5_948_CTTTTTGG
4.Transcription	Birc1c	baculoviral iap repeat-containing 1c	2.81	U15647	
4.Transcription	Id2	Inhibitor of dna binding 2	2.33	NM_010496	>Id2_4 () CCAAACCTTGG () CCAAATTCGG
4.Transcription	Chx10	ceh-10 homeo domain containing homolog	2.33	NM_007701	>Chx10_2 () CCTAACATGG
4.Transcription	Icsbp1	interferon regulatory factor 8	2.1	NM_008320	>Icsbp1_6 () CCATTTTTGG

4.Transcription	Six3	sine oculis-related homeobox 3 homolog	0.49	NM_011381	>Six3_5 () CCTTTTAGGG
4.Transcription	Eif2s3y	eukaryotic translation initiation factor 2, subunit 3, structural gene y-linked	0.49	NM_012011	>Eif2s3y_1 () CCATAGATGG >Eif2s3y_4 () CTTTTATGG
4.Transcription	Ddx3x	dead/h (asp-glu-ala-asp/his) box polypeptide 3, x-linked	0.47	NM_010028	>Ddx3x_4 () CCAAAGTTGG >Ddx3x_5 () CCATATATGA
4.Transcription	Rps12	ribosomal protein s12	0.47	NM_011295	>Rps12_4 () CCAAAGTAGG >Rps12_6 () CCATATAAGA
4.Transcription	Lhx8	lim homeobox protein 8	0.46	NM_010713	>Lhx8_4 () GCATAAATGG
4.Transcription	Hmx1	h6 homeo box 1	0.44	NM_010445	
4.Transcription	Gtf3c4	general transcription factor iiic, polypeptide 4	0.36	NM_172977	>Gtf3c4_4 () CTTCTTTGG >Gtf3c4_6 () CTATTTATGG
4.Transcription	Sp4	trans-acting transcription factor 4	0.36	NM_009239	>Sp4_1 () CAAAATTTGG >Sp4_3 () CCTTATATAG
4.Transcription	Brca1	breast cancer 1	0.29	NM_009764	>Brca1_4 () CCAAAAATGG () CCAGAAATGG
4.Transcription	Vax2	ventral anterior homeobox containing gene 2	0.27	NM_011912	>Vax2_4 () CCATAAATAG >Vax2_5 () CCAGAAAAGG
4.Transcription	Insm1	Insulinoma-associated 1 (is a Zinc-finger factor)	0.24	NM_016889	>Insm1_2 () CCATTTATAG () TCATAAATGG
4.Transcription	Rps17	ribosomal protein s17	0.22	NM_009092	>Rps17_3 () CCATCAATGG
4.Transcription	Hoxb8	homeo box b8	0.2	NM_010461	>Hoxb8_5 () CCAAATTTGG
4.Transcription	E2f3	E2f transcription factor 3	0.2	NM_010093	>E2f3_6 () CCAGATAAGG () CCATAAATGG
4.Transcription	Ddb1	damage specific dna binding protein 1	0.19	NM_015735	>Ddb1_5 () CCAATCTGG () CTTTCTTTGG
4.Transcription	Rpl34	Ribosomal Protein L34	0.33	NM_026724	N>Rpl34_1 (-8935) CCCTTTTTGG >Rpl34_4 (-4603) CTATAAAAGG
4.Transcription	Tk1	thymidine kinase 1	0.2	NM_009387	>Tk1_3 () TCATAAAAGG
4.Transcription	Rrm1	ribonucleotide reductase m1	0.13	NM_009103	>Rrm1_5 (-2369) CCAAAGATGG (-1643) CCAAGTTTGG

4.Transcription	Nsun2	nol1/nop2/sun domain family 2	0.46	NM_145354	>Nsun2_4 (-3508) CCATTTATG
5.Extracellular Matrix	Postn	Periostin, Osteoblast specific factor	4.36	NM_015784	>>Postn_6_613 N 10 CCATAAATGG 507 R 10 CCAGATAAGG
5.Extracellular Matrix	Ctgf	Connective Tissue Growth Factor	4.34	NM_010217	>Ctgf_4 () CCTTATAGGG
5.Extracellular Matrix	Ptpns1	Protein Tyrosine Phosphatase, Non-receptor type Substrate 1	2.52	NM_007547	>Ptpns1_3 () CCATCAATGG () CCACAGAAGG
5.Extracellular Matrix	Bgn	Biglycan	2.19	NM_007542	>Bgn_2 () CCTGCTTTGG >Bgn_6 () CCATCTAAGG
5.Extracellular Matrix	Fbln1	Fibulin 1	2.18	NM_010180	>Fbln1_1 () CCAGATAAGG () CCAGATAAGG
5.Extracellular Matrix	Col1a1	Procollagen, type i, alpha 1	2.11	NM_007742	>Col1a1_6 () CCAAATTGGG
5.Extracellular Matrix	Cldn11	Claudin 11 (Oligodendrocyte transmembrane protein, Osp, Otm)	0.49	NM_008770	>Cldn11_5 () CCATAAAAAG
5.Extracellular Matrix	Tecta	Tectorin alpha	0.45	NM_009347	>Tecta_1 () CCACAGAAGG >Tecta_6 () CCTTCTTTTG
5.Extracellular Matrix	Cdh15	Cadherin 15	0.22	NM_007662	>Cdh15_4 (-3773) CCCTATATGG
5.Extracellular Matrix	Spock1	Spock1/osteonectin	0.22	NM_009262.	>AV350751_3 () CCTTTTTTGG () CCTTATATAG
5.Extracellular Matrix	Ai447669	ITGA8	0.47	NM_001001309	>Itga8_3 () TCATAAATGG
5.Extracellular Matrix	Plekhh1	Pleckstrin Homology domain containing, family h (with myth4 domain) member 1	0.38	XM_126961	>Plekhh1_1 () GCATAAATGG >Plekhh1_6 () CCAAAGTTGG
6.Stress Response	Hspa1b	heat shock protein 1a/b	4.13	NM_010478	>Hspa1b_4 () CCATTGATGG >Hspa1b_5 () CCAAATATGG
6.Stress Response	Hspa1a	heat shock protein 1a/b	3.66	NM_010479	>Hspa1a_5 () CCTTACATGT
6.Stress Response	Srxn1	sulfiredoxin 1 homolog (S. cerevisiae) [Mus musculus]	3.09	NM_029688.	>Srxn1_6 () CCTACTTTGG
6.Stress Response	Znrf4	zinc and ring finger 4	2.09	NM_011483	>Znrf4_2 (-6728) CCATTTATGT
6.Stress Response	Defcr5	defensin related cryptdin 5	0.49	NM_007851	>Defcr5_6 (-820) CCATATAATG

6.Stress Response	Diablo	diablo homolog (drosophila)	0.32	NM_023232	>Diablo_6 (-1108) CCATTGATGG
6.Stress Response	Dcc	deleted in colorectal carcinoma	0.32	NM_007831	>Dcc_3 (-6314) GCAAATTTGG
6.Stress Response	Tnfaip3	tumor necrosis factor, alpha-induced protein 3	0.27	NM_009397	>Tnfaip3_4 () CCCTGTAAGG
6.Stress Response	Hpx	Hemopexin	0.24	NM_017371	>Hpx_6 () CCTAAGAAGG () CCAGAAAAGG
6.Stress Response	Dclre1a	dna cross-link repair 1a, pso2 homolog	0.49	NM_018831	>Dclre1a_6 (-1433) CCAAAGAAGG
6.Stress Response	Ppil2	peptidylprolyl isomerase (cyclophilin)-like 2	0.28	NM_144954	>Ppil2_6 () CCACAGAAGG
6.Stress Response	Ubd	ubiquitin d	0.27	NM_023137	>Ubd_3 (-5677) CCTGATATGG >Ubd_4 (-3515) CCAAATTTGA
7.Signaling Proteins	Gdf15	Growth Differentiation Factor 15	14	NM_011819	(-4067) CCAGAAAAGG EFN2-like (G4)
7.Signaling Proteins	Avpi1	Arginine Vasopressin-induced 1	6.11	NM_027106	>Avpi1_5 (-2979) CCAAACCTTGG (-2354) CCATTTCTGG
7.Signaling Proteins	Iqgap1	IQ motif containing Gtpase Activating Protein 1	5.1	NM_016721	>Iqgap1_5 () CCATTTATAG
7.Signaling Proteins	Arhgdig	rho gdp dissociation inhibitor (gdi) gamma	4.78	NM_008113	>Arhgdig_6 (-950) CCAGATATGG
7.Signaling Proteins	Gipc1	gipc pdz domain containing family, member 1	4.72	NM_018771	>Gipc1_2 () CCCAATAAGG >Gipc1_6 () TCATAAAAGG
7.Signaling Proteins	Nppa	Natriuretic Peptide Precursor type A	4.48	NM_008725	>Nppa_4 (-3768) CAATAAAAGG >Nppa_6 (-430) CCTTATTGG
7.Signaling Proteins	Emr1	egf-like module containing, mucin-like, hormone receptor-like sequence 1	3.77	NM_010130	>Emr1_3 (-7176) CCTAATTAGG >Emr1_5 (-2968) CCAGATAAGG
7.Signaling Proteins	Bmp10	bone morphogenetic protein 10	3.63	NM_009756	>Bmp10_2 (-7258) CCAGAAATGG
7.Signaling Proteins	Dlg7	discs, large homolog 7	3.2	NM_144553	>Dlg7_4 () CCTTTTATAG >Dlg7_6 () CCATAAAAAG
7.Signaling Proteins	Tgfb3	transforming growth factor, beta 3	3.17	NM_009368	>Tgfb3_5 () CCACATATGG
7.Signaling Proteins	Bdkrb1	bradykinin receptor, beta 1	2.87	NM_007539	>Bdkrb1_3 () CCATAAATCG

7.Signaling Proteins	Il4	Interleukin 4	2.47	NM_021283	>Il4_4 () CCATTTATGG () CCTTAAATGG
7.Signaling Proteins	Rho	Rhodopsin	2.35	NM_145383	>Rho_3 () CTATTTATGG >Rho_4 () CCAAAGTTGG
7.Signaling Proteins	Il3ra	interleukin 3 receptor, alpha chain	2.21	NM_008369	>Il3ra_3 () CCTTTTATTG >Il3ra_5 () CCTGAAATGG
7.Signaling Proteins	Emp1	epithelial membrane protein 1	2.04	AC122820	() CCATTTAAGG >Emp1_3 () CATTTTATGG
7.Signaling Proteins	Inhbc	Inhibin beta-c	0.49	NM_010565	(-7765) CCAGATAAGG (-7743) CCAGATAAGG
7.Signaling Proteins	Apc2	adenomatosis polyposis coli 2	0.47	NM_011789	>Apc2_5 (-1616) CCGAATTTGG
7.Signaling Proteins	Plekha1	pleckstrin homology domain containing, family a (phosphoinositide binding specific) member 1	0.46	NM_133942	
7.Signaling Proteins	Csh1	Chorionic Somatomammotropin Hormone 1	0.42	NM_008864	>Csh1_6 (-1591) CCTTATATTG (-543) CCTTATAAGA
7.Signaling Proteins	Hcrt	Hypocretin	0.38	NM_010410	>Hcrt_1 (-9573) CCATATATGA
7.Signaling Proteins	Il10ra	interleukin 10 receptor, alpha	0.37	NM_008348	>Il10ra_2 () CCAAATTTTG >Il10ra_4 () CCAATGAAGG
7.Signaling Proteins	Arhgap9	rho gtpase activating protein 9	0.35	NM_146011	
7.Signaling Proteins	Efnb3	Ephrin b3	0.31	NM_007911	>Efnb3_5 () CCACATTTGG >Efnb3_6 () CCCAAGAAGG
7.Signaling Proteins	Crk	v-crk sarcoma virus ct10 oncogene homolog (avian)	0.3	NM_133656	>Crk_2 (-8434) CCATAAAAGG >Crk_3 (-6102) CCTTTTAGGG
7.Signaling Proteins	Lifr	leukemia inhibitory factor receptor	0.27	NM_013584	>Lifr_2 (-7679) GCAAATTTGG >Lifr_5 (-3271) CCAGAAATGG
7.Signaling Proteins	Olf18	Olfactory Receptor 18	0.17	NM_146563	>Olf18_4 () CCTTTTATAG >Olf18_6 () CCCTATAAGG
7.Signaling Proteins	Bub1	budding uninhibited by benzimidazoles 1 homolog (s. cerevisiae)	0.17	NM_009772	>Bub1_4 () CAATAAATGG
7.Signaling Proteins	Scg2	secretogranin ii	0.14	NM_009129	(-3361) CCAAGTAAGG >Scg2_5 (-1757) CCATTGATGG

7.Signaling Proteins	Camk2a	Calcium/Calmodulin-dependent protein Kinase ii alpha	0.1	NM_009792	>Camk2a_4 (-4502) CCACAAATGG >Camk2a_5 (-1925) ACTTACATGG
7.Signaling Proteins	Prlpf	Prolactin-like Protein f	0.1	NM_011168	>Prlpf_5 () TCATATATGG >Prlpf_6 () CAATATATGG
7.Signaling Proteins	Homer1	homer homolog 1 (drosophila)	0.09	NM_011982	>Homer1_6 (-1306) CTATTTAAAG (-140) CCCAAAAAGG
7.Signaling Proteins	S100a9	s100 calcium binding protein a9	0.47	NM_009114	>S100a9_1 () CCATAAAAAG >S100a9_4 () CCATGAAAGG
7.Signaling Proteins	Jag2	Jag2 jagged 2	0.45	NM_010588.	
8.Inhibitors	Usp29	UbiquitinSpecific Peptidase 29	3.72	NM_021323	() CCATATATTG () TCTTATATGG
8.Inhibitors	Serpine1	Serine (or cysteine) Peptidase inhibitor, clade e, member 1	2.94	NM_008871	>Serpine1_3 (-5202) CCATTTATGG (-5069) CCATTTATAG
8.Inhibitors	Dpp7	Dipeptidylpeptidase 7	2.8	NM_031843	>Dpp7_4 () CAATTTATGG
8.Inhibitors	Spink3	Serine Peptidase inhibitor, kazal type 3	0.4	NM_009258	(-5153) CCATAAAAAGG >Spink3_4 (-4697) CCTTGTATGG
8.Inhibitors	Pcsk5	Proprotein Convertase Subtilisin / Kexin type 5	0.37	XM_129214	>Pcsk5_4 () CTATAAAAAGG >Pcsk5_5 () CCATAAAAAGG
8.Inhibitors	Capn2	Calpain 2	0.3	NM_009794	>Capn2_6 () ACAAATTTGG
8.Inhibitors	Tesp2	Testicular Serine Protease 2	0.16	NM_009356	>Tesp2_4 (-4474) CCTTTTATAG
8.Inhibitors	Mug1/2	Murinoglobulin 1 & 2	0.14	NM_008645	>Mug1_2 (-8065) CATAAATGG >Mug1_4 (-3915) CCATGTCAGG
8.Inhibitors	Pzp	Pregnancy Zone Protein	0.12	NM_007376	>Pzp_4 () CCAGAAATGG >Pzp_6 () CCAGATAAGG
8.Inhibitors	Cpa3	carboxypeptidase a3, mast cell	0.1	NM_007753	>Cpa3_1 (-9121) CCCAATTTGG
8.Inhibitors	Serpina1a/b/c/d	Serine (or cysteine) Peptidase Inhibitor, clade a, member 1	0.06	NM_009243	>Serpina1a_1 (-9247) CCTTGTITGG >Serpina1a_3 (-5653) CATTATATGG >Serpina1a_5 (-3149) CCAATAAGG (-1730) CATTATATGG
9.Complement	C8g	complement component 8, gamma polypeptide	0.46	NM_027062	() cccaatagg >C8g_6 () CCAGATAAGG
9.Complement	F10	Coagulation Factor X	0.31	NM_007972	>F10_4 (-3411) CCATAAAAAGT

9.Complement	Plg	Plasminogen	0.13	NM_008877	
9.Complement	Cfi	Complement Component Factor i	0.1	NM_007686	>Cfi_1 () TCTAATTAGG
9.Complement	Fgb	Fibrinogen, B beta polypeptide	0.04	NM_181849	>Fgb_6 () CCATATAAAG
9.Complement	Kng1	Kininogen 1	0.03	NM_001102411	>Kng1_3 (-5823) CCTTTTCTGG >Kng1_5 (-2400) TCTTCTTTGG
9.Complement	C8g	C8g complement component 8, gamma subunit	0.46	NM_027062	>C8g_5 () actaatagg () cccaatatgg >C8g_6 () CCAGATAAGG
10.Ion Transport	Slc20a1	Solute Carrier family 20, member 1	2.02	NM_015747	>Slc20a1_2 () CCAGAAAAGG >Slc20a1_5 () CCAAATAAGG
10.Ion Transport	HNEDC2	HNEDC2	2.88	NM_178877	>Nhedc2_1 () CCAAAGAAGG
10.Ion Transport	Aqp4	Aquaporin 4 (Mercurial-insensitive water channel)	0.21	NM_009700	>Aqp4_4 () CCATATTTGG >Aqp4_5 () ACTTATATGG
10.Ion Transport	Slc4a8	Solute Carrier family 4 (anion exchanger), member 8	0.39	NM_021530	>Slc4a8_5 (-1933) CCTTTTATAG (-1803) CCTGTAATGG
10.Ion Transport	Gabra6	Gamma-Aminobutyric Acid (gaba-a) Receptor, subunit alpha 6	0.36	NM_008068	>Gabra6_4 () CCTTTTATGT >Gabra6_6 () TCATTTATGG
10.Ion Transport	Atp1a1	ATPase, Na ⁺ /K ⁺ transporting, alpha 1 polypeptide	0.32	NM_144900	>Atp1a1_4 () CCAGATATGG >Atp1a1_6 () CCATAAAAAG
10.Ion Transport	Trpm7	Transient Receptor Potential cation channel, subfamily m, member 7	0.32	NM_021450	>Trpm7_2 () CCATATAATG >Trpm7_6 () CCAAAGAAGG
10.Ion Transport	Kcnq2	Potassium Voltage-gated Channel, subfamily q, member 2	0.32	NM_001006669	>Kcnq2_5 () CCATATATGT
10.Ion Transport	Gria2	Glutamate Receptor, Ionotropic, Ampa2 (alpha 2)	0.24	NM_001039195	>Gria2_6 () CCTTTTATAG
10.Ion Transport	Gabrb2	Gamma-Aminobutyric Acid (gaba-a) Receptor, subunit beta 2	0.15	NM_008070	>Gabrb2_5 (-2826) CCTATTAGGG (-2713) CCATGAATGG
10.Ion Transport	Slc10a1	Solute Carrier family 10 (sodium/bile acid cotransporter family), member 1	0.12	NM_011387	>Slc10a1_5 () CCATAAAATG
11.Immune Response	Ccl8	chemokine (c-c motif) ligand 8	4.81	NM_021443	>Ccl8_3 () CCTTATATAG >Ccl8_6 () CTATAAAAGG
11.Immune Response	Cxcl12	Chemokine (c-x-c motif) ligand 12	3.7	NM_001012477	>Cxcl12_1 (-9617) CCATAAAAGA >Cxcl12_4 (-4682) CCATATATGT

11.Immune Response	H2-TL-T17-c	histocompatibility 2, t region locus 10	2.84	M35247	
11.Immune Response	H2-DMb1	histocompatibility 2, class ii, locus mb1	2.11	NM_010387	>H2-DMb1_2 (-7982) CCAGATTGG >H2-DMb1_4 (-4267) CCATGTAAG
11.Immune Response	Igh-V	immunoglobulin heavy chain variable region	0.49	L33937	
11.Immune Response	Il1f5	interleukin 1 family, member 5 (delta)	0.41	NM_019451	() CCTAATTAGA >Il1f5_4 () CCATATTAGG
11.Immune Response	Igh-VX24	immunoglobulin heavy chain (x24 family)	0.38	X55984	
11.Immune Response	Orm1	Orosomucoid 1	0.32	NM_008768	>Orm1_4 (-4642) CCATATAATG >Orm1_5 () CCATGAAAGG
11.Immune Response	H2-M10.1	histocompatibility 2, m region locus 10.1	0.28	NM_013544	>H2-M10.1_3 () CAATAAATGG
11.Immune Response	Il15	Interleukin 15,	0.25	NM_008357	>Il15_2 (-7266) CCTTCTTTGT
11.Immune Response	Cr1	ig kappa chain	0.13	U60442	
12.Other Proteins	2610201A13Rik	riken cdna 2610201a13 gene	6.81	AA222883	>2610201A13Rik_4 () CCAAAGATGG
12.Other Proteins	AV169168		5.47	AV169168	
12.Other Proteins	Aqr	Aquarius	4.53	NM_009702	>Aqr_6 (-1547) CCATAAAAGA (-792) CCAAAAAGA
12.Other Proteins	AA408556	expressed sequence aa408556	3.71	NM_199447	>AA408556_Rrp12_1 () CTATAAAAGG >AA408556_Rrp12_4 () ACATATATGG
12.Other Proteins	Dnase1l2	Deoxyribonuclease 1-like 2	3.55	NM_025718	>Dnase1l2_1 () CCTTCTTTTG >Dnase1l2_6 () CCAAATCTGG
12.Other Proteins	Ndr4	n-myc downstream regulated gene 4	3.34	NM_145602	>Ndr4_2 () CCATAAAGGG >Ndr4_5 () CCTTAAATAG
12.Other Proteins	A430107D22Rik	riken cdna a430107d22 gene	3.17	NM_178785	>A430107D22Rik_2 () CCTTTTCTGG >A430107D22Rik_3 () CCTTCTTTTG
12.Other Proteins	BB001228	expressed sequence bb001228	3.15	BB001228	>BB001228_5 () CCATTTTTGG
12.Other Proteins	1700020M16Rik	r3h domain and coiled-coil containing 1	2.77	XM_001479474	() CCATTTTTGG >R3hcc1_2 () CCATATAAGA
12.Other Proteins	Rap2ip	rap2 interacting protein	2.5	NM_016759	>Rap2ip_3 (-6720) GCTTCTTTGG

12.Other Proteins	Wbp5	ww domain binding protein 5	2.37	NM_011712	>Wbp5_2 (-6714) CCAAATTTTG >Wbp5_3 (-6714) CCAAATTTTG
12.Other Proteins	lft81	Intraflagellar transport 81 homolog (chlamydomonas)	0.49	NM_009879	>lft81_5 () CTATATAAGG >lft81_6 () CCAAGTTTGG
12.Other Proteins	Stard10	Start Domain containing 10	0.47	NM_019990	>Stard10_2 () CATTTATGG >Stard10_6 () CCAAATAGGG
12.Other Proteins	Ofa	Oncofetal Antigen	0.46	NM_011627	>Ofa_6 () CCTTTTAAGG
12.Other Proteins	Cdca5	cell division cycle associated 5	0.44	NM_026410	>Cdca5_6 () CCATTTATTG () CCATTTATTG
12.Other Proteins	Gm1419	gene model 1419, (ncbi)	0.44	NG_005612	>Gm1419_1 () CAAAATTTGG
12.Other Proteins	Lgals2	riken cdna 2200008f12 gene	0.44	NM_025622	>Lgals2_5 (-2024) CCATAAAATG
12.Other Proteins	Tyms-ps	thymidylate synthase, pseudogene	0.43	NR_000040	>Tyms-ps_1 () ACAAATTTGG >Tyms-ps_2 () GCTTTTATGG
12.Other Proteins	D8Erttd738e	dna segment, chr 8, erato doi 738, expressed	0.41	NM_001007571	No SRE's
12.Other Proteins	Hba-x	hemoglobin x, alpha-like embryonic chain in hba complex	0.41	NM_010405	>Hba-x_4 (-3571) CCAAGTTTGG >Hba-x_6 (-1168) CCTTTTATAG
12.Other Proteins	Ubtg protein	Loc380988	0.4	XM_001475007.	>AA672647_3 () CCTTTTCTGG
12.Other Proteins	C77681	expressed sequence c77681	0.38	C77681	>C77681_2 () CCTAATATGG
12.Other Proteins	C77691	expressed sequence c77691	0.31	C77691	>C77691_6 () CCATAAATGT
12.Other Proteins	8430410A17Rik	riken cdna 8430410a17 gene	0.3	NM_173737	>8430410A17Rik_3 () CCAATTTTGG
12.Other Proteins	Gm 1418	gene model 1418, (ncbi)	0.29	NG_005612	>Gm1418_3 () CCTTTTATGA
12.Other Proteins	Lanc12	lanc (bacterial lantibiotic synthetase component c)-like 2	0.28	NM_133737	>Lanc12_6 (-977) CCAATGTAGG (-458) CCAATGAAGG
12.Other Proteins	Dmrtb1	dmrt-like family b with proline-rich c-terminal, 1	0.27	XM_205469	>Dmrtb1_6 () ACTTATATGG
12.Other Proteins	Cwf1911	cwf19-like 1, cell cycle control (s. pombe)	0.26	NM_001081077	>Cwf1911_3 () CCATATTTGG
12.Other Proteins	LOC547428	similar to trav19	0.26	X72904.	>LOC547428_4 () CCATGAAAGG () CCATTTAAGG

12.Other Proteins	Gm1060	gene model 1060, (ncbi)	0.18	NM_001033460	
12.Other Proteins	1100001G20Rik	riken cdna 1100001g20 gene	0.12	NM_183249	>1100001G20Rik_4 (-4459) CCATGTAGGG
12.Other Proteins	0610005C13Rik	riken cdna 0610005c13 gene	0.1	AI042964.	>0610005C13Rik_1 () CCAAAGATGG
12.Other Proteins	1500003O03Rik	riken cdna 1500003o03 gene	0.09	NM_019769	
12.Other Proteins	Mup1	major urinary protein 1	0.03	NM_031188	>Mup1_2 (-8164) CCAAATTGG >Mup1_6 (-1109) CCATATAAAG
12.Other Proteins	Mup5	Major Urinary Protein 5	0.03	NM_008649	>Mup5_5 () CCCAATTTGG >Mup5_6 () CCATATAAAG
12.Other Proteins	Mup2	Major Urinary Protein 2	0.02	NM_001045550	>Mup2_3 (-6382) CCATAGATGG >Mup2_6 (-954) CCATATAAAG
12.Other Proteins	Mup3	Major Urinary Protein 3	0.01	NM_001039544	>Mup3_1 (-8543) CCATAGAAGG >Mup3_4 (-4250) CCATAGATGG